



# GEOMED 2017

INTERNATIONAL CONFERENCE ON SPATIAL  
STATISTICS, SPATIAL EPIDEMIOLOGY  
& SPATIAL ASPECTS OF PUBLIC HEALTH

DEEPER INSIGHT FROM BIG DATA AND SMALL AREAS

PORTO | PORTUGAL | 07 - 09 SEPTEMBER 2017

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# Welcome

GEOMED 2017 is the **X international, interdisciplinary conference on spatial statistics, geographical epidemiology and geographical aspects of public health.**

The conference aims to bring together statisticians, geographers, epidemiologists, computer scientists, and public health professionals to discuss methods of spatial analysis, as well as present and debate the results of such analyses.

The first GEOMED conference was held in Rostock (Germany) in 1997 and since then it has been held in Paris (France) in 1999 and 2001, Baltimore (USA) in 2003, Cambridge (UK) in 2005, Charleston (USA) in 2009, Victoria (Canada) in 2011, Sheffield (UK) in 2013 and Florence (Italy) in 2015.

**In 2017, the Geomed meeting will be held in Porto, Portugal!**

*The organizing committee*



## Organisation

### Chair

Maria de Fátima de Pina

### Organizing Committee

Alexandre Magalhães

Carla Maria Oliveira

Hugo Teixeira

Marcos Gomes

Mónica Avelar Magalhães

Renata Gracie

Sandra Maria Alves

### Scientific Committee

Ana Diez Roux

Andrew Lawson

Annibale Biggeri

David Martin

Denisa Mendonça

Duncan Lee

Emanuela Dreassi

Jamie Pearce

Maria de Fátima de Pina

Marilia Sá Carvalho

Peter Diggle

Renato Assunção

Robert Haining

Trevor Bailey



## Venue

The conference will take place at  
**i3S - Instituto de Investigação e Inovação  
da Universidade do Porto**

### Address

Rua Alfredo Allen, 208  
4200-135 Porto, Portugal

### Telephone

+351 220 408 800

### Google map link

<https://goo.gl/maps/yvstCwa8Wmp>

### Website

[www.i3s.up.pt](http://www.i3s.up.pt)

### E-mail

[events@i3s.up.pt](mailto:events@i3s.up.pt)



# Social Programme

## 07 September 2017

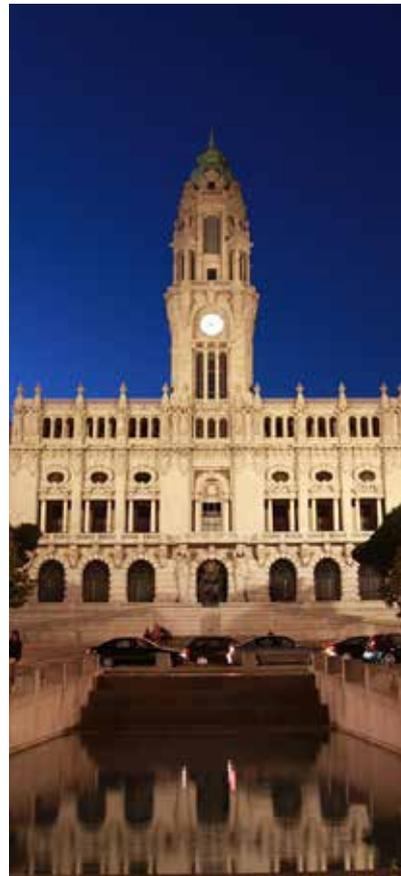
18.30 | Porto drink at i3S

## 08 September 2017

19.00 | Bus from i3S to Quinta da Boeira Restaurant at Vila Nova de Gaia (Rua Teixeira Lopes, 170, Vila Nova de Gaia)

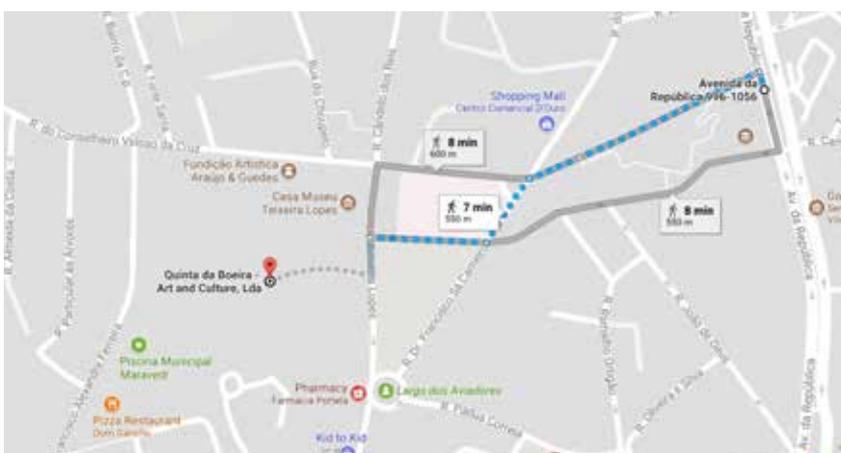
20.00 | Dinner at Quinta da Boeira Restaurant





Before dinner you will have the opportunity to visit an exhibition of typical boats (caravels) placed at the wine store and taste a Port Wine.

**23.00** | Bus from Quinta da Boeira Restaurant to i3S, with a brief stop at Avenida dos Aliados.



As an alternative, participants can walk 7 minutes' foot and pick up the Metro at Câmara de Gaia station, line D – yellow (destination Hospital de S. João), single travel ticket price: 1,20 €.

## Extra Social Programme

The organization prepared an optional social programme on September 9th, afternoon. It will include a walking tour around historical center of Porto with duration of approximately 2,5 hours and a visit to the Calem Port Wine Cellars. This extra social programme has an extra cost of 22€.

Participants will visit some of the most historic buildings and places of Porto, starting at the Cathedral, São Bento railway station, passing by Clérigos tower, Lello's Library, Vitoria gazebo with a panoramic view of the Porto city, Bolsa Palace, Infante square, San Francisco Church and Ribeira.

Placed near the Douro river at Vila Nova de Gaia, Calem Port Wine Cellars is recognized not only for the exceptional quality of its wines, but also for its secular history. The visit has a duration of 40 minutes and at the end you will have the opportunity of tasting two kinds of Calem Port Wine.





## Programme

**14:30** | Meeting point in Aliados, in front of Intercontinental Hotel, and Walking Visit Tour

**17:15** | Visit to Port Wine Cellars

**22.00** | Music concert at Aliados (free of charge)

Participants can enjoy a music concert of the Orquestra Sinfónica do Porto Casa da Música at Av. Aliados



## From i3S

The easiest way to reach Aliados is by metro. At Pólo Universitário station, take Line D - yellow (destination Santo Ovídio) and leave at station: Aliados (no connections - direct line) | Average time: 15 minutes | Single travel ticket price: 1,20 €.

# Informations

## Registration Desk

Registrations will take place at i3S main entrance. On 6th September, the registration desk will open at 13:20 and on 7th September will open at 08:20.

## Name badges

For identification and security purposes, participants must wear their name badges when in the venue. The use of the badge is mandatory for the access to the conferences, coffee breaks, lunches and dinner.

## Presentation instructions

The plenary sessions should last up to 30 minutes followed by a 10-minute discussion. The invited lectures should last up to 15 minutes followed by 5-minute discussion. Oral communications should last up to 15 minutes followed by 5 minute-discussion. The chairs are requested to lead the discussion and to ensure that the times are strictly followed.

Plenary sessions will take place in Auditorium Mariano Gago, while live streaming will be available at Auditorium Corino de Andrade. In the latter Auditorium, participants will also have the opportunity to interact with the speaker, asking questions and receiving the answers. Seat occupancy will be made on a first-come-first-serve basis.

Speakers presenting in the morning should hand in their presentations in the auditorium until 8:45 of the present day. Those having their presentations in the afternoon sessions, should hand in their presentations during lunch break.

A data show and personal computer will be at the presenters' disposal. Technicians will be available to make sure that you have successfully uploaded your presentation. You will be requested to provide your presentation in a USB key. If strictly necessary, you may use your own computer, which should be installed and properly tested prior to your presentation at the indicated times.

## Poster presentations

Posters should have 1.20m high and 0.90m wide, and will be presented on the designated poster area at i3S main entrance. Authors are requested to put up their posters before poster session 1 and remove it in the end of the poster session 3. Conference staff will be present to provide assistance. Authors should remain next to their poster during the poster session.

Chairs will discuss the posters with the authors. Each poster will have 2 minutes of presentation followed by 1 minute of discussion.

### Poster Session 1

**Poster 1 to 31** (Thursday, September 07th, 16:10-16:50)

### Poster Session 2

**Poster 32 to 60** (Friday, September 08th, 16:10-16:50)

### Poster Session 3

**Poster 61 to 92** (Saturday, September 09th, 10:40-11:20)

## Internet access

Wireless Internet is available for free in the venue.

## Meals and coffee breaks

Coffee breaks will be served at i3S main entrance in the foyer. Lunch will be served at the foyer of Auditorium Corino de Andrade.

Participants with food restrictions should ask for their special meals

## Pre- Conference Workshops

**6th September | 14:00 - 18:20**

### **Modelling spatial and spatio-temporal areal unit data in R with CARBayes**

Auditorium Corino de Andrade

*Duncan Lee*

Spatial and spatio-temporal areal unit data are prevalent in the fields of epidemiology, geography and statistics, and the spatial autocorrelation in these data is typically modelled by a conditional autoregressive (CAR) model as part of a Bayesian hierarchical framework. These models can be implemented in the R packages CARBayes (spatial data) and CARBayesST (spatio-temporal data), and this workshop will describe the models that can be fitted and illustrate the process on real data examples. These examples will be a full spatio-temporal data analysis, including reading in and formatting data, producing exploratory maps and measures of spatial autocorrelation, model fitting and checking, and visualising the results. Univariate and multivariate spatial data models will be discussed, as will spatio-temporal data modelling.

## **Health Applications of Google Earth Engine**

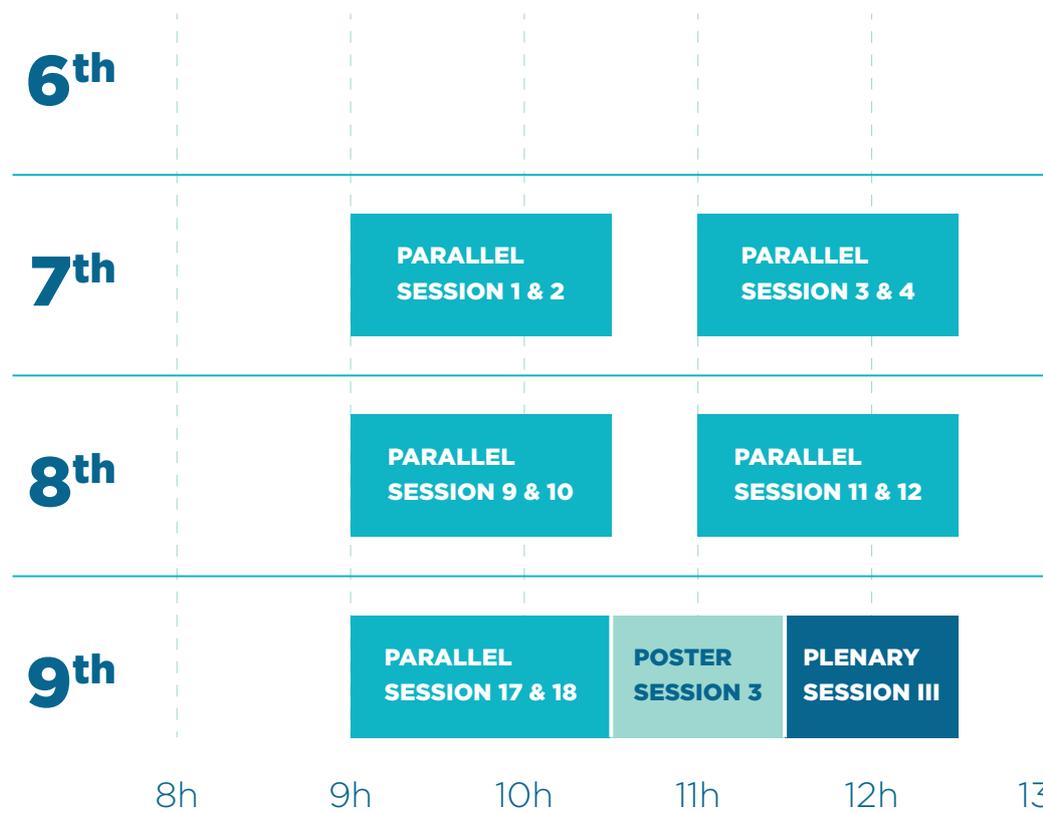
Meeting Room A

*Allison Lieber*

Google Earth Engine is a planetary-scale platform for Earth science data & analysis, powered by Google's cloud infrastructure. Google Earth Engine combines a multi-petabyte catalog of satellite imagery and geospatial datasets with planetary-scale analysis capabilities and makes it available for scientists, researchers, and developers to detect changes, map trends, and quantify differences on the Earth's surface.

This workshop will discuss many of the health applications of Google Earth Engine. We will walk through a short lab that will introduce you to health-specific and other relevant in the data catalog and to Earth Engine scripts to get you started.

## Scientific Programme





## 6th September

### Pre-Conference Workshops

13.20	<b>Opening registration</b>	
14.00 – 16.00	<b>WORKSHOP 1</b> <i>Duncan Lee, University of Glasgow, UK</i> <b>Modelling spatial and spatio-temporal areal unit data in R with CARBayes</b> Auditorium Mariano Gago	<b>WORKSHOP 2</b> <i>Allison Lieber, Google, USA</i> <b>Health Applications of Google Earth Engine</b> Meeting Room A
16.00 – 16.20	<b>Coffee Break</b>	
16.20 – 18.20	<b>WORKSHOP 1</b> <i>Duncan Lee, University of Glasgow, UK</i> <b>Modelling spatial and spatio-temporal areal unit data in R with CARBayes</b> Auditorium Mariano Gago	<b>WORKSHOP 2</b> <i>Allison Lieber, Google, USA</i> <b>Health Applications of Google Earth Engine</b> Meeting Room A

## 7th September

08.20	<b>Opening registration</b>	
08.45 – 09.00	<b>Opening Session: Welcome to Geomed 2017 – Auditorium Mariano Gago</b>	
09.00 – 10.40	<b>PARALLEL SESSION 1</b> <b>GIS in Public Health I</b> Auditorium Corino de Andrade  <b>CHAIR:</b> <i>Robert Haining, University of Cambridge, UK</i>  <b>(INVITED) Mapping urban scale air quality using Big Data: accounting for uncertainty</b> <i>Eun-Hye Enki Yoo, State University of New York, USA</i>  <b>(INVITED) A geospatial analysis of factors influencing maternal hospital delivery in rural China: a case study from Sichuan Province</b> <i>Wang Yu, School of Public Health, Peking University, China</i>	<b>PARALLEL SESSION 2</b> <b>Spatial Health Surveillance I</b> Auditorium Mariano Gago  <b>CHAIR:</b> <i>Andrew Lawson, Medical University of South Carolina, USA</i>  <b>(INVITED) Spatio-temporal modelling and probabilistic forecasting of infectious disease counts</b> <i>Sebastian Meyer, University of Zurich, Switzerland</i>  <b>(INVITED) Multivariate Bayesian hierarchical models for the analysis of zoonoses</b> <i>Ana Corberan-Vallet, University of Valencia, Spain</i>





09.00 – 10.40

**(ORAL) Urban green spaces in the proximity of residences may reduce the effect of socioeconomic inequalities in the practice of sports among teenage girls**

*Alexandre Magalhães, I3S/ INEB, Universidade do Porto, Portugal*

**(ORAL) Spatial hotspots of dementia risks: an approach to inform policy**

*Nasser Bagheri, Research School of Population Health, ANU College of Medicine, Biology and Environment, The Australian National University, Canberra, Australia*

**(ORAL) Evaluating the impact of residential mobility on health care accessibility for children with birth defects.**

*Eric Delmelle, University of North Carolina at Charlotte and Center for Applied Geographic Information Science (CaGIS), 9201 University City Boulevard, Charlotte, NC USA*

**(INVITED) Bayesian surveillance reproduction number for infectious diseases**

*Chawarat Rotejanaprasert, Faculty of Tropical Medicine, Mahidol University, Thailand*

**(ORAL) Identification of hotspots of rat abundance in a Brazilian slum community using indirect abundance metrics**

*Poppy Miller, CHICAS, Faculty of Health and Medicine, Lancaster University, UK*

**(ORAL) Spatio-temporal modelling of the number of calls to Saúde24 line to assess hospital savings**

*Paula Simões, CMA - FCT, UNL and ADM- ISEL, IPL, Portugal*

10.40 – 11.00

**Coffee Break**

11.00 – 12.40

**PARALLEL SESSION 3**

**Spatial Health Surveillance II**  
*Auditorium Corino de Andrade*

**CHAIR:** *Victor Javier Del Rio Vilas, School of Veterinary Medicine, University of Surrey, UK*

**(ORAL) Crime victimization and the implications for individual health and wellbeing**

*Su-Yin Tan, University of Waterloo, Canada*

**(ORAL) Spatio-temporal variation of county-level rates of very low birth weight in the United States, 1989–2010**

*Monica P. Shah, Emory University, Atlanta, Georgia, USA*

**(INVITED) Statistical inference from infectious disease modelling: guiding rabies control and elimination programmes**

*Katie Hampson, University of Glasgow, UK*

**PARALLEL SESSION 4**

**Spatial survival and registry data analysis I**  
*Auditorium Mariano Gago*

**CHAIR:** *Andrew Lawson, Medical University of South Carolina, USA*

**(INVITED) Spatially-explicit Survival Modeling with Discrete Spatial Grouping of Cancer Predictors**

*Andrew Lawson, Medical University of South Carolina, USA*

**(INVITED) Joint spatial frailty model for modeling multiple time to events data**

*Cindy Feng, University of Saskatchewan, Canada*

**(INVITED) A transformation class for spatio-temporal survival data with a cure fraction**

*Sandra M Hurtado Rua, Cleveland State University, USA*





<p>11.00 – 12.40</p>	<p><b>(INVITED) An Information-theoretic Portfolio Model for Disease Surveillance Evaluation</b> <i>Matteo Convertino, University of Minnesota, USA</i></p> <p><b>(INVITED) Efforts to integrate evidence: a multi-dimensional challenge</b> <i>Victor Javier Del Rio Vilas, School of Veterinary Medicine, University of Surrey, UK</i></p>	<p><b>(ORAL) In My Time of Dying: A Spatial Epidemiological Re-analysis of John Graunt's Observations Made Upon the Bills of Mortality</b> <i>Olaf Berke, University of Guelph, Canada</i></p> <p><b>(INVITED) Bayesian cure-rate survival model with spatially structured censoring</b> <i>Georgiana Onicescu, Western Michigan University, USA</i></p>
<p>12.40 – 13.40</p>	<p><b>Lunch</b></p>	
<p>13.45 – 14.25</p>	<p><b>PLENARY SESSION I</b> <i>CHAIR: Maria de Fátima de Pina, I3S, Fiocruz, Brazil &amp; Porto University, Portugal</i></p> <p><b>Cholera in London, 1854. Zika in Brazil, 2015</b> <i>Marília Carvalho, Oswaldo Cruz Foundation, Brazil</i></p> <p>Auditorium Mariano Gago</p>	
<p>14.30 – 16.10</p>	<p><b>PARALLEL SESSION 5</b> <b>Spatial survival and registry data analysis II</b> Auditorium Corino de Andrade</p> <p><b>CHAIR: Annette Erbsböll, University of Southern Denmark, Denmark</b></p> <p><b>(INVITED) A new approach to small area cancer survival estimation</b> <i>Susanna Cramb, Cancer Council Queensland, Australia</i></p> <p><b>(ORAL) Spatial patterns in multiple sclerosis: A case-control study using Danish register data 1971-2013</b> <i>Kristine Bihrmann, University of Southern Denmark, Denmark</i></p> <p><b>(ORAL) Acute Myocardial Infarction Via Verde (AMI-VV): A geographical approach to assess its impact on in-hospital mortality</b> <i>Francesca Fiorentino, CEMBE-Faculdade de Medicina da Universidade de Lisboa, Portugal</i></p>	<p><b>PARALLEL SESSION 6</b> <b>Clustering of temporal trends in space-time disease mapping</b> Auditorium Mariano Gago</p> <p><b>CHAIR: Duncan Lee, University of Glasgow, UK</b></p> <p><b>(INVITED) A multivariate model for estimating the changes in health inequalities across Scotland over time</b> <i>Eilidh Jack, University of Glasgow, UK</i></p> <p><b>(INVITED) Spatio-temporal log-Gaussian Cox processes for public health data</b> <i>Theresa Smith, University of Bath, UK</i></p> <p><b>(INVITED) Understanding the mortality burden of air pollution in Michigan accounting for preferential sampling</b> <i>Veronica Berrocal, University of Michigan, USA</i></p> <p><b>(ORAL) Using Hierarchical clustering of timeseries for variable selection in Dengue forecasting</b> <i>Flávio Codeço Coelho, Getulio Vargas Foundation</i></p>





<p>14.30 – 16.10</p>	<p><b>(INVITED) From politics to mathematics: Exploring optimal air ambulance base locations in Norway using advanced mathematical modeling</b>  <i>Jo Røislien, Department of Medical Statistics, University of Stavanger, Norway</i></p> <p><b>(INVITED) Geographical clustering of service goal fulfillment for emergency ambulances in the capital region of Denmark</b>  <i>Annette Kjær Ersbøll, University of Southern Denmark, Denmark</i></p>	<p><b>(ORAL) A Bayesian Space-Time Model for Clustering Areal Units based on their Disease Trends</b>  <i>Gary Napier, University of Glasgow</i></p>
<p>16.10 – 16.50</p>	<p><b>Coffee Break &amp; Poster Session 1</b></p>	
<p>16.50 – 18.30</p>	<p><b>PARALLEL SESSION 7</b>  <b>Data Science applied to Health: Strategies and tools for big data, machine learning and data mining</b>  <i>Auditorium Corino de Andrade</i></p> <p><b>CHAIR:</b> <i>Jorge Magalhães, Oswaldo Cruz Foundation, Fiocruz, Brazil</i></p> <p><b>(ORAL) Mining big data for environmental epidemiological analyses</b>  <i>Anna Freni-Sterrantino, Imperial College London, UK</i></p> <p><b>(ORAL) Relative risk estimates from spatial and space-time scan statistics: Are they biased?</b>  <i>Marcos Prates, Universidade Federal de Minas Gerais, Brazil</i></p> <p><b>(INVITED) Big Data and Healthcare</b>  <i>João Gama, INESC TEC, University of Porto, Portugal</i></p> <p><b>(INVITED) Spatial Aspects of Collaborative Demography via Genealogical Data</b>  <i>Ewen Gallic, Université de Rennes, France</i></p> <p><b>(INVITED) Anomaly detection in the Brazilian Health Care Payment System</b>  <i>Renato Assunção, Federal University of Minas Gerais, Brazil</i></p>	<p><b>PARALLEL SESSION 8</b>  <b>Modifiable areal unit issues and methods</b>  <i>Auditorium Mariano Gago</i></p> <p><b>CHAIR:</b> <i>David Martin, University of Southampton, UK</i></p> <p><b>(INVITED) Multiscale spatiotemporal models for aggregated small area health outcomes</b>  <i>Andrew Lawson, Medical University of South Carolina, Charleston, USA</i></p> <p><b>(ORAL) Promoting understanding of the modifiable areal unit problem in public health and epidemiology with dynamic geovisualization</b>  <i>Brittany Krzyzanowski, University of Minnesota</i></p> <p><b>(ORAL) The effects of spatial resolution in disease mapping: A simulation study</b>  <i>Garyfallos Konstantinoudis, University of Bern, Switzerland</i></p> <p><b>(INVITED) Using Change of Support (COSP) approach in disease mapping: an application to mapping malaria in low transmission settings</b>  <i>Victor Alegana, Worldpop group, University of Southampton</i></p> <p><b>(INVITED) Investigating aggregation effects in small area health data using synthetic microdata and automated zone design</b>  <i>David Martin, University of Southampton, UK</i></p>
<p>18.30 – 20.30</p>	<p><b>Group photo &amp; Porto drink</b></p>	

## 8th September

### PARALLEL SESSION 9

**Social networks and spatial epidemiology: tools, opportunities and challenges**

Auditorium Corino de Andrade

**CHAIR:** Renato Assunção, Federal University of Minas Gerais, Brazil

**(INVITED) On the promises, challenges and risks of Pokémon Go and similar geosocial (location-based) exergames**

Maged Nabih Kamel Boulos, International Journal of Health Geographics, UK

**(INVITED) Support Vector Subset Scan for Spatial Pattern Detection**

Dylan Fitzpatrick, Carnegie Mellon University, USA

**(ORAL) Going beyond with social network data: from disease accounting to identification of risk zones**

Renato Assunção, Universidade Federal de Minas Gerais

**(ORAL) Developing a web-based survey application to collect contextually-relevant geographic data with exposure times**

Abby E. Rudolph, Boston University School of Public Health, USA

**(ORAL) Georeferenced Twitter data to estimate the temporal variation of the density of people in each sample area in Madrid using GIS technology.**

Francisco Javier Escobar Martínez, Universidad de Alcalá, Spain

### PARALLEL SESSION 10

**Modelling climate-sensitive disease I**

Auditorium Mariano Gago

**CHAIR:** Rachel Lowe, London School of Hygiene & Tropical Medicine, UK

**(INVITED) The climatic constraints on the present and future global spread of dengue and Zika**

Oliver Brady, London School of Hygiene & Tropical Medicine, UK

**(INVITED) Dengue spatial diffusion in Brazil. How far will this go? Will Zika follow the same steps?**

Christovam Barcellos, Fiocruz, Brazil

**(INVITED) Google Earth Engine: Health Applications of Google's Cloud Platform for Big Earth Data**

Allison Lieber, Google, USA

**(INVITED) Use of GEE for climate, environmental and disease modelling**

Pietro Ceccato, International Research Institute for Climate and Society, USA

**(INVITED) Spatial-temporal analysis of climate factors effects on hospitalization due to falls**

Carla Oliveira, I3S, Porto University, Portugal

09.00 – 10.40

10.40 – 11.00

**Coffee Break**





### PARALLEL SESSION 11

#### Modelling climate-sensitive disease II

Auditorium Corino de Andrade

**CHAIR:** *Pietro Ceccato, International Research Institute for Climate and Society, USA*

#### (INVITED) Probabilistic dengue predictions based on ensemble seasonal climate forecasts

*Rachel Lowe, London School of Hygiene & Tropical Medicine, UK and Barcelona Institute for Global Health (ISGLOBAL), Spain*

#### (INVITED) Climate and malaria analysis for national decision-making. Data, methodologies and tools.

*Madeleine Thomson, International Research Institute for Climate and Society and Department of Environmental Health Sciences, Mailman, Columbia University, USA*

#### (ORAL) The influence of air temperature on hospital admissions due to mental disorders in Lisbon

*Ricardo Almendra, Centre of Studies on Geography and Spatial Planning (CEGOT), University of Coimbra, Portugal*

#### (ORAL) Modelling climate and non-climate impacts on malaria in Malawi for effective control interventions

*James Chirombo, CHICAS, Lancaster Medical School, Lancaster University, UK and Malawi Liverpool Wellcome Trust Clinical Research Programme, Blantyre, Malawi*

#### (INVITED) Space-time modelling of mosquito densities: application to *Aedes albopictus*, vector of viruses, in Reunion Island

*Emmanuel Roux, French National Research Institute for Sustainable Development*

### PARALLEL SESSION 12

#### Agent-based modelling

Auditorium Mariano Gago

**CHAIR:** *Marília Carvalho, Oswaldo Cruz Foundation, Brazil*

#### (INVITED) Using agent-based models to investigate the impact of firearms disqualification criteria on firearm-related homicide and suicide.

*Magdalena Cerdá, University of California, USA*

#### (INVITED) Why Integrating Environmental Modelling and Spatially-explicit ABM? Revisiting Max Sorre's Ideas can be the Answers of Why and How.

*Miguel Monteiro, Brazilian National Institute for Space Research (INPE), Brazil*

#### (ORAL) A comercial airline network model for chikungunya spread in the Caribbean

*Carlos Dommar, Barcelona Institute for Global Health (ISGLOBAL), Spain*

11.00 – 12.40

12.40 – 13.40

**Lunch**





13.45 – 14.25

## PLENARY SESSION II

**CHAIR:** *Sandra Alves, ESTSP/IPP, I3S/INEB, Portugal*

### Space-Time Modeling of Small Area Data in a Developing World Setting

*Jon Wakefield, University of Washington, USA*

Auditorium Mariano Gago

14.30 – 16.10

## PARALLEL SESSION 13

### GIS in Public Health II

Auditorium Corino de Andrade

**CHAIR:** *Robert Haining, University of Cambridge, UK*

#### (INVITED) An interactive Spatial Decision Support System to manage Public Health in Gulbarga taluk, Karnataka, India.

*Sulochana Shekhar, Kuvempu University, India, & Syed Ashfaq Ahmed, Central University of Karnataka, India*

#### (INVITED) Is more always better? Exploring indicators of quality of green space in relation to self-reported general health

*Paul Brindley, The University of Sheffield, UK*

#### (ORAL) An activity space approach to assessing food-related spatial behavior of urban African-American women in Atlanta, GA, USA

*Ilana G. Raskind, Emory University, USA*

#### (ORAL) Spatial and Temporal Analysis of Malaria and Risk Factors in the Brazilian Amazon, 2010-2015

*Tiago Canelas, University of São Paulo, Brazil, and Global Public Health Observatory, USA*

#### (ORAL) Fine-scale visualization of pollen concentrations across the Eastern United States: A space-time parallel approach

*Michael Desjardins, Department of Geography & Earth Sciences and Center for Applied Geographic Information Science (CAGIS), University of North Carolina at Charlotte, Charlotte*

## PARALLEL SESSION 14

### Modelling and inference in infectious disease epidemiology

Auditorium Mariano Gago

**CHAIR:** *Duncan Lee, University of Glasgow, UK*

#### (ORAL) Spatiotemporal heterogeneity in leptospirosis transmission in northeastern Thailand

*Katharine A. Owers, Yale University School of Public Health, USA*

#### (INVITED) Modelling human mobility for respiratory pathogen transmission

*Jonathan Read, Lancaster University, UK*

#### (INVITED) Individual level infectious disease models incorporating aggregate level spatial structure

*Robert Deardon, Faculty of Veterinary Medicine, University of Calgary, Canada*

#### (ORAL) Using Genotyping and Geospatial Analyses to Study Multi-drug Resistant Tuberculosis Transmission and Migrants

*Erjia Ge, Dalla Lana School of Public Health, University of Toronto*

#### (ORAL) Delay in diagnosis of Pulmonary Tuberculosis: space matters!

*C. Nunes, Centro de Investigação em Saúde Pública, Escola Nacional de Saúde Pública, Universidade Nova de Lisboa, Portugal*





16.10 – 16.50

**Coffee Break & Poster Session 2**

16.50 – 18.30

**PARALLEL SESSION 15****The use of linked data in spatial epidemiology**

Auditorium Corino de Andrade

**CHAIR:** *Tom Clemens, University of Edinburgh, UK***(INVITED) Using people's spatial movement as 'natural experiments' for environment-health effects – possibilities and problems using large scale administrative data studies.***Chris Dibben, University of Edinburgh, UK***(INVITED) The Exposome: Use of linked data to build a whole life course approach to environmental and social exposures***Clive Sabel, University of Aarhus, Aarhus, Denmark***(INVITED) Using linked individual health data to study air pollution and pregnancy outcomes: a bayesian spatial modelling approach***Tom Clemens, University of Edinburgh, UK***(ORAL) Can the geographical patterns in acute myocardial infarction in Denmark be explained by the sociodemographic structure of the population?***Thora Majlund Kjærulff, University of Southern Denmark, Denmark***(ORAL) State-level Minimum Wage and Heart Disease Death Rates in the United States, 1980-2015***Miriam Van Dyke, Emory University, USA***PARALLEL SESSION 16****Joint Modelling with Spatial Variation**

Auditorium Mariano Gago

**CHAIR:** *Denisa Mendonça, University of Porto, Portugal***(INVITED) Bayesian joint modeling of longitudinal and spatial survival AIDS data***Giovani L. Silva, University of Lisbon, Portugal***(INVITED) Joint modeling of longitudinal biomarkers and recurrence in breast cancer with spatial effects***Inês Sousa, University of Minho, Portugal***(INVITED) Joint Modeling of Spatial Outcomes: Benefits to Understanding the Underlying Process and Power Gains***Charmaine Dean, University of Western Ontario, Canada***(ORAL) Bayesian Inference for High Dimensional Dynamic Spatio-Temporal Models***Sofia Maria Karadimitriou, University of Sheffield, UK***(ORAL) An evaluation of multi pollutant profiles and respiratory mortality in London and Oxford.***Anna Freni-Sterrantino, UK Small Area Health Statistic Unit (SAHSU), MRC-PHE Centre for Environment and Health, School of Public Health, Imperial College London, UK*

19.00 – 23.00

**Congress Dinner**

## 9th September

	<p><b>PARALLEL SESSION 17</b></p> <p><b>Remote sensing applications in health</b> Auditorium Corino de Andrade</p> <p><b>CHAIR:</b> <i>Emmanuel Roux, French National Research Institute for Sustainable Development (IRD), France</i></p> <p><b>(INVITED) Remote sensing for studying and modelling infectious diseases: advances and challenges</b> <i>Emmanuel Roux, French National Research Institute for Sustainable Development (IRD), France</i></p> <p><b>(INVITED) CNES activities in tele-epidemiology</b> <b>Cécile Vignolles, Centre National d'Études Spatiales (CNES), France</b></p> <p><b>(INVITED) How the Earth Observation (EO) Community can help Bridging the Gap between Research and Services in Public Health Operational Programs? The Joint INPE and FIOCRUZ Experience</b> <i>Miguel Monteiro, Brazilian National Institute for Space Research, Brazil</i></p> <p><b>(INVITED) Integrating Remotely-Sensed Climate and Environmental Information into Public Health</b> <i>Pietro Ceccato, The International Research Institute for Climate and Society, NYC, USA</i></p> <p><b>(ORAL) Environmental changes and the incidence of visceral leishmaniasis in Teresina, Brazil through 1996 to 2007.</b> <i>Guilherme L. Werneck, State University of Rio de Janeiro and IESC, Federal University of Rio de Janeiro, Brazil</i></p>	<p><b>PARALLEL SESSION 18</b></p> <p><b>Challenges and Advances in Spatio-Temporal Disease Modelling</b> Auditorium Mariano Gago</p> <p><b>CHAIR:</b> <i>Trevor Bailey, University of Exeter, UK &amp; Theodoros Economou, University of Exeter, UK</i></p> <p><b>(INVITED) Global Estimation of Air Quality and the Burden of Disease associated with Ambient Air Pollution</b> <i>Gavin Shaddick, University of Bath, Bath, UK</i></p> <p><b>(ORAL) A spatio-temporal process-convolution model for quantifying health inequalities in respiratory prescription rates in Scotland</b> <i>Duncan Lee, University of Glasgow, UK</i></p> <p><b>(INVITED) TB or not TB?</b> <i>Trevelyan J. McKinley, Exeter University, UK</i></p> <p><b>(ORAL) Spatial tracking of a Measles outbreak in England and Wales using data assimilation</b> <i>Ashok Krishnamurthy, Mount Royal University, Canada</i></p> <p><b>(INVITED) Modelling reporting delays of surveillance data</b> <i>Leonardo Bastos, Fiocruz, Brazil</i></p>
<p>09.00 – 10.40</p>	<p><b>Coffee Break &amp; Poster Session 3</b></p>	





**PLENARY SESSION III**

**CHAIR:** *Maria de Fátima de Pina, I3S, Fiocruz, Brazil & Porto University, Portugal*

11.25 – 12.05

**An Integrated Vector Management (IVM) Surveillance System for Malaria Using Remote Sensing Based on Satellite and Unmanned Aerial Vehicle (UAV) Technologies**

*Daniel Griffith, University of Texas, USA*

Auditorium Mariano Gago

12.10 – 12.30

**Prizes | Closing Geomed 2017 & Presenting Geomed 2019**

12.30 – 13.30

**Lunch**

14.30 – 18.00

**Social Programme**

## Invited Speakers



**Allison Lieber.**

Google, USA

Allison Lieber is a Program Manager on the Google Earth Outreach team, where she leads Google's efforts to support nonprofits, scientists and other public benefit groups using Google's mapping tools and technology for infectious disease mapping and risk assessment. Allison has a degree in Economics from Washington University in St. Louis, and has been at Google for more than five years, managing the Nonprofits Geo Grants Program and other initiatives.



**Ana Corberan-Vallet,**

University of Valencia, Spain

Dr. Ana Corberán-Vallet received a PhD in Statistics from the University of Valencia, Spain. Her PhD research involved development of multivariate time-series modeling and forecasting techniques.

She held a postdoctoral position at the Medical University of South Carolina, where she built on her previous background in statistical modeling expanding upon space-time disease surveillance models. Currently, she is a professor in the Department of Statistics and Operations Research at the University of Valencia.



**Andrew Lawson.**

Medical University of South Carolina, USA

Andrew Lawson is a Distinguished Professor and Vice Chair for Research at the Department of Public Health, University of South Carolina.

He has a background in Geography (1973), Quantitative Methods (1975) and Environmental Science (1986) and a PhD in Statistics (1990). His research interests are mainly in the area of spatial and environmental statistics particularly spatio-environmental epidemiology, which include disease mapping. He has published several papers in leading journals and books on spatial statistics. He is a WHO advisor in Disease Mapping and Risk Assessment and an editor-in-chief of Spatial and Spatio-temporal Epidemiology journal.



**Annette Kjær Ersbøll.**

University of Southern Denmark, Denmark

Annette Kjær Ersbøll is professor at The National Institute of Public Health, University of Southern Denmark.

She is an engineer and has a PhD in statistics. Her primary areas of research are spatial epidemiology and spatial statistics within public health using individual-level register-based health data.



**Carla Oliveira,**

i3S, Porto University, Portugal

Carla Oliveira is a mathematics graduate (2002) from the University of Beira Interior (UBI), has a postgraduation in Applied Mathematics for Life Sciences (2004) from the Agronomy Institute of the Lisbon University (ISA), a MSc in Biomedical Engineering (2009) from the Faculty of Engineering of the University of Porto (FEUP) and a PhD in Public Health (2016) from the Faculty of Medicine of the University of Porto (FMUP).

Carla began her professional career in 2002 as professor of mathematics and conducted research in the Institute of Biomedical Engineering (INEB) of the University of Porto in the research group of GeoEpidemiology since 2007, first as a trainee research, then as a MSc student and later as a PhD student and as research assistant. Her doctoral thesis was also developed as a researcher at the Public Health Institute (ISPUP) and the Institute of Health Research (i3s) of the University of Porto. During her PhD Carla was a visiting researcher at the Faculty of Engineering, Mathematics and Physical Sciences of the Exeter University (UK).

Carla is currently a researcher i3S/INEB and a lecturer in statistics at the Health School of the Polytechnic Institute of Porto (ESS-IPP), and biostatistician in Blueclinical - Research and Development in Health, Ltd since 2014. Her research interests include statistical modeling and spatio-temporal analysis of health events and statistical techniques applied to clinical trials.

**Cécile Vignolles,**

Centre National d'Études Spatiales (CNES),  
France

Engineer in Agriculture and holder of a doctorate degree in Remote Sensing and Agriculture, Cécile Vignolles served from 1998 to 2001 as research assistant at the Space Applications Institute of the EU Joint Research Centre, where she contributed to the development of the agrometeorological bulletin within the "Monitoring Agriculture with Remote Sensing" project. From 2002 to 2005, she worked at SCOT, a subsidiary of Cnes (The French Space Agency) as a research engineer on R & D in Agriculture and Remote Sensing projects. Research engineer at the GIP Medias-France from 2005 to 2008, she was in charge of R & D projects in tele-epidemiology. She has joined the Cnes in 2009, where she is affiliated to the Direction of Innovation, Applications and Science in the 'Earth-environment-climate' team in charge of the "Earth Observation programmes ". Within this team, she is responsible of the "Tele-epidemiology" and "Forests" programmes.



**Charmaine Dean,**

University of Western Ontario, Canada

Charmaine Dean is Professor and Vice-President, University Research at the University of Waterloo in Canada. Dr. Dean was 2007 President of the Statistical Society of Canada, and 2002 President of WNAR.

She has served on several grant review panels including for the US National Institutes of Health, the Natural Sciences and Engineering Research Council of Canada and the UK Engineering and Physical Sciences Research Council. She has served on many editorial boards including currently for Biometrics, Environmetrics, Statistics in Biosciences and Spatial and Spatio-temporal Epidemiology. In 2003, Dr. Dean was awarded the CRM-SSC prize; in 2007 she was named Fellow of the American Statistical Association; and in 2007 awarded the University of Waterloo Alumni Achievement Medal; in 2010 she was named Fellow of the American Association for the Advancement of Science and in 2012 received a Trinidad and Tobago High Commission Award. Dr. Dean's leadership has a focus on accelerating research within the faculty, enhancing and fortifying collaborations with other faculties, with industry, government agencies and the broader community, as well as supporting a superb training environment for students. Her research interest lies in the development of methodology for disease mapping, longitudinal studies, the design of clinical trials, and spatio-temporal analyses. Much of this work has been motivated by direct applications to important practical problems in biostatistics and ecology. Her current main research applications are in survival after coronary artery bypass surgery, mapping disease and mortality rates, forest ecology, fire management, smoke exposure estimation from satellite imagery, and modeling of temporary and intermittent stream flow for flood analysis and predictions.

**Chawarat Rotejanprasert,**

Faculty of Tropical Medicine, Mahidol  
University, Thailand

Chawarat received his Ph.D. in Biostatistics at Medical University of South Carolina in 2015 with a focus on spatial epidemiology, his M.S. in Statistics and Stochastic Modeling from the University of California, Santa Cruz and his B.S. in Mathematics from Chiang Mai University, Thailand. Before joining the faculty at Mahidol University, he was a statistical researcher at the Thai National Center for Genetic Engineering and Biotechnology with a research focus on tropical diseases. His research interests include spatial epidemiology and surveillance.



**Chris Dibben,**

University of Edinburgh, UK

Chris Dibben is a Professor of health geography at the University of Edinburgh, is the Director of the Economic and Social Research Council's Longitudinal Studies Centre Scotland and the Administrative Data Research Centre - Scotland.

He has worked on, amongst other subjects, epidemiological studies into recovery after heart attacks, the causes of Low Birth Weight, the survival of drug misusers and the health impact of air pollution. He has also contributed to work on the UK NHS health funding formula and on measuring health inequalities, for example developing the Health Poverty Index for the Department of Health. Other work includes the development of national deprivation indices across the UK and in South Africa and evaluations of government area based initiatives. He also has an interest in the methodological issues that arise from the use of routine or administrative data in research.



**Christovam Barcellos,**

Fiocruz, Brazil

Christovam Barcellos is an Health Geographer, specialized in Public Health (1985), PhD in Geosciences (1995). He is a senior researcher at Oswaldo Cruz Foundation, Rio de Janeiro, Brazil. Professor, acting in the Public Health postgraduate program (ENSP-Fiocruz) and health information and communication postgraduate program (PPGICS-Fiocruz). In the past, he worked in the State Secretary of Health of Rio de Janeiro. His main research interests are spatial epidemiology, GIS and health surveillance.



**Cindy Feng**

University of Saskatchewan, Canada

Cindy Feng is an assistant professor in Biostatistics at the School of Public Health at the University of Saskatchewan and has a PhD in statistics (2011) from Simon Fraser University.

Her primary research interest focuses on the development of statistical methods to analyse spatial and space-time data to understand spatial and temporal patterns applied to epidemiology and public health problems.



**Clive Sabel.**

University of Aarhus, Aarhus, Denmark

Clive Sabel got his BSc (Hons) in Geography from Lancaster in 1990 and an MSc in GIS from Edinburgh University in 1991

In 1999 he completed his PhD 1999 under Profs Tony Gatrell and Robin Flowerdew at Lancaster University, using an Exploratory Spatial Data Analysis approach to investigate Spatial and Temporal relationships between environmental exposure and health.

Clive has academic interests in spatial epidemiology, spatial statistics, spatial and environmental sensors, the 'exposome', Big Data, and working with point-pattern data (often residential location) to reveal epidemiological relationships to environmental exposures.



**David Martin.**

University of Southampton, UK

Dave Martin is currently Professor of Geography. He has been a member of staff in Geography and Environment at the University of Southampton since 1992.

He is the leader of the Population, Health and Wellbeing research group and served as Head of Department from 2000 - 03. He was Coordinator of ESRC's Census Programme from 2002 - 12 and is currently involved in the leadership of three major ESRC initiatives: the UK Data Service, the Administrative Data Research Centre for England and the National Centre for Research Methods. He is also a member of ESRC Council.



**Denisa Mendonça,**

University of Porto, Portugal

Denisa Mendonça was graduated in Applied Mathematics, Faculty of Sciences, University of Porto (1976). She joined the Institute of Biomedical Sciences Abel Salazar, University of Porto (1977).

Completed her PhD in Biostatistics, Faculty of Sciences University of Exeter, UK (1987). In 1991 she became Associate Professor and in 2006 a member of the Board of Directors of the Institute of Public Health, University of Porto-ISPUP. She was a member of the Scientific Committee of the Master in Public Health, UP and has taught a wide variety of general and specialised topics in Biostatistics at Under Graduate and Post Graduate level. Currently, she conducts research at the Institute of Public Health (Department of Biostatistics/ Biostatistics and Health Metrics Group, EPIUnit) and at the Institute of Biomedical Sciences Abel Salazar involved in PhD project supervision (Applied Math, Biomedical Sciences, Medical Sciences and Nursing Sciences). Her research interests are in applied statistical modelling (particularly: spatial statistics).



**Duncan Lee,**

University of Glasgow, UK

Duncan Lee is a reader in statistics at the University of Glasgow, and has a PhD in statistical epidemiology (2007) from the University of Bath.

His research develops novel Bayesian spatio-temporal statistical methodology for environmental epidemiology, particularly focusing on quantifying the effects of air pollution on human health and investigating spatio-temporal trends in disease risk. He has led numerous grants and has over 35 papers in these areas, as well as being the author of freely available R software for spatial (CARBayes) and spatio-temporal (CARBayesST) areal unit modelling. Using conditional autoregressive (CAR) priors. He is an associate editor of a Royal Statistical Society (RSS) journal and the Biometrical journal, a member of the ESRC peer review college, a research assessor for the Carnegie Trust, and secretary of the environmental Section of the RSS.



**Dylan Fitzpatrick.**

Carnegie Mellon University, USA

Dylan Fitzpatrick is a joint PhD student in Machine Learning and Public Policy at Carnegie Mellon University. His research focuses on development of scalable statistical machine learning algorithms for pattern detection, motivated by applications in public health and criminology. Dylan earned a BA in Economics from Middlebury College and an MS in Computer Science from Carnegie Mellon University.



**Eilidh Jack,**

University of Glasgow, UK

Eilidh Jack is currently completing a PhD in statistics at the University of Glasgow.

Her research interests lie in disease mapping with particular focus on estimating health inequalities across Scotland. Her aim is to develop novel Bayesian multivariate spatio-temporal models and associated freely available software.

**Emmanuel Roux.**

French National Research Institute for Sustainable Development (IRD), France

Emmanuel Roux is a researcher at the French National Research Institute for Sustainable Development (IRD), in the ESPACE-DEV research unit which develops methods to characterize, model and monitor socio-ecological systems by exploiting remotely sensed data and multidisciplinary knowledge integration.

He received his Ph.D. degree in Industrial and Human Automation control and Computer Science from the University of Valenciennes, France, in 2002. His skills concern the data science and his research interests are the spatial modelling of entomological and/or epidemiological data, the objective characterization of the environment and of the landscape from satellite data, the data- or knowledge-driven modelling of the environment-health relationships. He co-supervises or participates to several partnership and research projects that contribute to the construction of cross-border observatories of the vector-borne diseases, between French Guiana and Brazil and within other cross-border contexts.



**Eun-Hye Enki Yoo,**

State University of New York, USA

Enki Yoo is an Associate Professor of Geography at The State University of New York (SUNY) at Buffalo and is a member of the National Center for Geographic Information and Analysis (NCGIA).

She trained as a quantitative geographer specializing in Geographic Information Science (GIS), receiving her PhD from the University of California at Santa Barbara in 2006.

Her primary research interests are in utilizing geostatistics to address issues associated with spatial and temporal scale discrepancies (so called 'change of support problems') in spatial data transformation/fusion.



**Ewen Gallic,**

Université de Rennes, France

Ewen Gallic is a Ph. D. student in economics at the University of Rennes 1. His research interests focus on environmental economics and applied statistical modeling.

In recent years, he has worked on point processes and genealogical data with Arthur Charpentier who will be his postdoctoral supervisor next September.



**Gavin Shaddick,**

University of Bath, Bath, UK

Prof. Shaddick's research interests include the theory and application of Bayesian hierarchical models and spatio-temporal modelling in a number of fields including epidemiology, environmental modelling and disease progression in rheumatology.

He is a co-author of *Spatio-Temporal Methods in Environmental Epidemiology* and the *Oxford Handbook of Epidemiology for Clinicians*. Of particular interest are computational techniques that allow the implementation of complex statistical models to real-life applications where the scope over both space and time may be very large. Publications have included methods for estimating personal exposures to environmental hazards, detecting increased risk around putative point sources of pollution, incorporating spatial modelling into studies of the effects of pollution on health and the global estimation of air quality and the associated burden on health. He is also actively engaged in research with the power industry, using big data and data reduction techniques to model demand profiles, forecasting demands and identifying customer profiles.



**Georgiana Onicescu,**

Western Michigan University, USA

Dr. Onicescu is Assistant Professor at Western Michigan University. She received a PhD in Biostatistics from the Medical University of South Carolina in 2015 and a Master of Science in Biostatistics from Johns Hopkins Bloomberg School of Public Health.

Her research interest are in applying and developing statistical methods in spatial statistics for public health and medical research. She has published more than 20 peer-reviewed articles in various journals and presented her research at many national and international conferences.



**Giovani L. Silva,**

University of Lisbon, Portugal

Giovani (Loiola da) Silva is Professor of Statistics (Department of Mathematics - Instituto Superior Tecnico) at the University of Lisbon (Portugal), where he is also member of the Centre of Statistics and Applications CEAUL, dealing with different research problems/projects in Statistics. His main research interests are in survival analysis, spatio-temporal models and joint generalized linear and additive modelling, in particular under a Bayesian approach. He has also been involved in the development of survival analysis with research groups of the Oncology Portuguese Institute of Lisbon, as well as of spatial statistics with research groups of some Canadian, Brazilian and Portuguese universities. He is associated editor of the Brazilian Journal of Probability and Statistics and guest editor of RevStat - Statistical Journal.



**Inês Sousa,**

University of Minho, Portugal

Inês Sousa is currently Assistant Professor at the Department of Mathematics and Applications of Minho University. She has a PhD in Medical Statistics at Lancaster University and her main research interests are in longitudinal and survival data analysis, mainly motivated by data from biomedical or environmental sciences.



**Jo Røislien,**

Department of Medical Statistics, University of Stavanger, Norway

Jo Røislien is a Professor of medical statistics at the University of Stavanger, Norway.

Røislien holds an MSc in industrial mathematics (1998) and a PhD in geostatistics (2004), before turning to biostatistics and medical research where he did his postdoc, and has since co-authored almost 100 peer reviewed research papers within the health sciences. His focus has been on the introduction and application of non-traditional mathematical and statistical methods into various medical research fields, ranging from gait analysis and addiction, to obesity and pre-hospital critical care.

Røislien is one of Scandinavia's most renowned science communicators, and has hosted several science TV-series for a general audience in Norway and Scandinavia, on mathematics, statistics, engineering and life sciences.

**João Gama.**

INESC TEC, University of Porto, Portugal

João Gama received his Ph.D. in Computer Science in 2000. He is a senior researcher at INESC TEC. He has worked in several National and European projects on Incremental and Adaptive learning systems, Ubiquitous Knowledge Discovery, Learning from Massive, and Structured Data, etc. He served as Program chair at several Machine Learning and Data Mining conferences. He is author of a monography on Knowledge Discovery from Data Streams and more than 200 peer-reviewed papers in areas related to machine learning, data mining, and data streams.



**Jonathan Read.**

Lancaster University, UK

Following a PhD in ecology and postdoctoral work modelling vegetation and insect population dynamics, Jon moved into infectious disease modelling at the Universities of Cambridge and Warwick as a postdoc with Prof Matt Keeling.

He is currently a Senior Lecturer at Lancaster Medical School, Lancaster University, and holds an honorary Senior Lectureship at the University of Liverpool. His research interests lie at the interface of field work and modelling of infectious diseases, in particular the quantification of human behaviours relevant to the transmission of pathogens. Related interests include understanding the structure of contact networks, pathogen ecology and evolution, and improving human mobility modelling. He has designed and conducted epidemiological field studies on influenza in China, USA and Vietnam, and has past or ongoing projects on pneumococcal infection, rotavirus, norovirus, Ebola, and seasonal and pandemic influenza.

**Jorge Magalhães,**

Oswaldo Cruz Foundation, Fiocruz, Brazil

Jorge Magalhães is Researcher in Public Health at FIOCRUZ and Coordinator of the Master's Program in Management, Research, Development and Innovation in Pharmaceutical Industry at FIOCRUZ/Farmanguinhos.

He has several publications (papers, books, chapters) in the areas of management and technological innovation with emphasis in technological forecasting, collaborative intelligence and Big Data in Health. His research interests include high research and development on Cancer, HIV/Aids, Diabetes and Neglected Diseases to support Public Health and Pharmaceutical sector's using Big Data in Health, Web 2.0 and Science Information tools.

He has a post-doctorate from the Université de Provence Aix-Marseille (France) in Competitive Intelligence Survey for public health. PhD Jorge was in management strategic for neglected diseases in Brazil at Federal University of Rio de Janeiro - UFRJ, Brazil. He is leader of the Research Group Knowledge Management and Prospecting in Health at CNPq in FIOCRUZ, RJ, Brazil.



**Katie Hampson,**

University of Glasgow, UK

Katie Hampson is a Reader at the University of Glasgow, UK, where she works on the epidemiological dynamics and control of rabies. Katie completed her PhD at Princeton University in the US in 2007 before returning to the UK on a Wellcome Trust fellowship.

Her work involves close collaborations with public health and veterinary practitioners, governments, NGOs and international agencies involved in rabies control in Latin America, Southeast Asia and Africa, and includes long-term field research in Tanzania. Together with collaborators she is collecting and analysing data on rabies transmission and the impacts of mass vaccination programmes and uses a variety of statistical inference techniques to analyse surveillance data of differing quality and spatial scale.



**Leonardo Bastos,**

Fiocruz, Brazil

Leonardo Bastos is a Brazilian researcher working at Oswaldo Cruz Foundation. He graduated in Statistics at the Federal University of Minas Gerais, Brazil (2002), has a MSc in Statistics from the Federal University of Rio de Janeiro, Brazil (2003), and PhD in Statistics from the University of Sheffield, UK (2010). He is an applied Bayesian statistician working on several epidemiology and biomedical research problems. His main research focus is developing Bayesian hierarchical models applied on epidemiological surveillance systems, hard-to-reach population datasets, and molecular dynamics.



**Madeleine Thomson,**

International Research Institute for Climate and Society and Department of Environmental Health Sciences, Mailman, Columbia University, USA

Madeleine Thomson is a Senior Research Scientist at the International Research Institute for Climate and Society (IRI) and Senior Scholar at the Mailman School of Public Health, Department of Environmental Health Sciences – at Columbia University, New York where she directs the IRI/PAHO-WHO Collaborating Centre (US 430) for Early Warning Systems for Malaria and Other Climate Sensitive Diseases. She is also a visiting Professor at Lancaster University in the UK.

Her research focuses on the development of new data, methodologies and tools for improving climate-sensitive health interventions Her focus has been on vector-borne diseases (e.g. malaria, onchocerciasis, visceral leishmaniasis etc.) but in recent years has expanded to include air and water-borne infections as well as broader health challenges associated with food security/nutrition and disasters. She is developing a “health and climate” disciplinary interface and a “climate smart” public health community through the ‘Climate Information for Public Health Action (CIPHA)’ initiative.

She trained originally as a field entomologist and has spent much of her career engaged in operational research in support of large-scale health interventions, mostly in Africa. She has a BSc. in Animal and Plant Biology (Sheffield 1982) an MSc. in applied pest management from Imperial College London (1985) and a Ph.D. from the University of Liverpool based on her field work on the ecology and identification of the *Simulium damnosum* vectors of *Onchocerciasis volvulus* in Sierra Leone (1989). She joined the IRI in May 2002.



**Magdalena Cerdá,**

University of California, USA

Magdalena Cerdá is the Vice Chancellor's Chair in Violence Prevention, and an Associate Professor in the Department of Emergency Medicine, at the University of California, Davis. In her research, Dr. Cerdá integrates approaches from social and psychiatric epidemiology to examine how social contexts shape violent behavior, substance use and common forms of mental illness. Her research focuses primarily on two areas: (1) the causes, consequences, and prevention of violence; and (2) the social and policy determinants of substance use from childhood to adulthood. Dr. Cerdá has more than 100 publications in peer-reviewed journals, in addition to five chapters in major textbooks. Current studies include a simulation of the impact that different types of firearms disqualification criteria could have on population-level rates of firearm-related homicide and suicide, a national study on the impact that prescription drug monitoring program characteristics have on prescription opioid and heroin overdose, and a multi-country study on the health and social consequences of marijuana legalization.



**Maged Nabih Kamel Boulos,**

International Journal of Health Geographics,  
UK

Professor Maged N. Kamel Boulos is a British scientist and Chair of Digital Health at the University of the Highlands and Islands, Scotland, UK.

He worked before that at Plymouth University, of Bath and City University London. He has more than 26 years of combined clinical and informatics experience, spanning the clinical, industry and academic/research worlds (1990-2016).

As well as his medical degree and Master's in Clinical Dermatology, he holds a Master's in Medical Informatics from King's College, University of London, and a PhD in Measurement and Information in Medicine (GIS) from City University London. Maged teaches and has >150 publications (h-index: 33) on a specialist range of medical/public health informatics and geoinformatics topics. He is Senior Member of IEEE, Fellow of the UK Higher Education Academy, and was Co-Chair of WG IV/4 within ISPRS Commission IV, 2008-2012. He served as Expert Adviser/External Expert for the WHO (European Office) and the ECDC. He is the founding editor (2001) and Editor-in-Chief of the MEDLINE-indexed Int J Health Geogr. His research received wide media coverage, and is/has been funded by national and international bodies, including World Health Organization EMRO and EURO; European Commission; UK TSB KTP Programme; UK AHRC; and Public Health Agency of Canada (funding one of his former PhD students).



**Maria de Fátima de Pina**

Maria de Fátima de Pina graduated in Cartographic Engineering, in 1985, in the State University of Rio de Janeiro.

She concluded the Master's in Systems and Computers (1994) in the Militar Institute of Engineering, in Rio de Janeiro, and the PhD in Biomedical Engineering (2001), in the Federal University of Rio de Janeiro. Since 1994 she is researcher of the Oswaldo Cruz Foundation, a teaching and research institute of the Health Ministry of Brazil. In 2004 she became researcher at the Biomedical Engineering Institute - INEB, of Porto University, where coordinates the research group of GeoEpidemiology. Since 2006 she is Associate Professor of the Medical School of Porto University, in the discipline of Epidemiology. Since 2015 she is Adjunct Professor in the Faculty of Engineering in the State University of Rio de Janeiro. Her main research interests are health inequalities and ageing of population.



**Matteo Convertino.**

University of Minnesota, USA

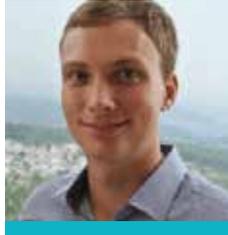
Dr. Convertino is a MnDRIVE Assistant Professor in the School of Public Health, Division of Environmental Health Sciences and Public Health Informatics Program, at the University of Minnesota. At the same institution he is also Faculty Fellow at the Institute on the Environment, Institute for Engineering in Medicine, and at the Bioinformatics and Computational Biology Program. He is actively involved in the Risk Unit of the Center for Animal Health and Food Safety, and in the Ecosystem Health Division both of the College of Veterinary Medicine at the University of Minnesota. Internationally he is a Foreign Fellow of the International Institute for Applied Systems Analysis (IIASA) in Vienna, Austria.

**Miguel Monteiro,**

Brazilian National Institute for Space  
Research (INPE), Brazil

Antonio Miguel V. Monteiro is a senior researcher at INPE (Brazilian National Institute for Space Research) where he leads the Urban Systems, Health and Environment Group and acts as the Head of the Space and Society Institutional Program.

He has a degree in Electrical Engineering from the Federal University of Espirito Santo (UFES) and holds a DPhil in Electronic Engineering and Control/Computer Science (1993) from the University of Sussex at Brighton, UK. His research work involves the development of geographically-aware methods oriented to bridging the gap between research and services in public health programs and urban planning. He has been acting as the coordinator of national-scale projects organised as multi-institutional networks of cooperation centred on the use of spatial information tools for shaping informed urban/health public policies. His recent work is focused on using computer models and simulation as mediator objects for bringing up the discussion of the socio-territorial inequalities derived from the Brazilian urbanisation. He was head of the Image Processing Division (DPI, 1999-2006) and Chief Executive and Head of the Earth System Science Center (CCST, 2008-2010) at INPE.



**Oliver Brady,**

London School of Hygiene & Tropical  
Medicine, UK

Oliver Brady is an epidemiological modeler with a research focus on vector borne diseases. He has a PhD from the University of Oxford and now works at the London School of Hygiene and Tropical Medicine as a research fellow.

His research aims to improve how diseases are controlled by identifying and estimating gaps in disease surveillance. Past projects have included estimating the global distribution and burden of different arboviruses (dengue, Zika, chikungunya) as well as understanding the role of their principle mosquito vectors (*Ae. aegypti* and *Ae. albopictus*). This involves the use of advanced statistical and mathematical modelling techniques to map vector-borne diseases including how they vary over time in response to environmental changes. These methods also have broad applications in predicting and preventing emerging infectious disease spread.



**Paul Brindley,**

The University of Sheffield, UK

Paul is a postdoctoral researcher at the University of Sheffield. He is currently investigating the relationships between health inequality, deprivation and green space ([www.iwun.uk](http://www.iwun.uk)).

He graduated in geography at the University of Sheffield (1999) and holds a Masters in Geographic Information Science from the University of Nottingham (2000). He completed his PhD in the school of Computer Science at the University of Nottingham (2015). His doctoral work was concerned with the automatic generation of vague geographic units extracted from big data. Techniques were applied to form fuzzy neighbourhood boundaries and probabilistic settlement classifications.

Paul has worked on over fifty projects as a researcher at the University of Sheffield, including England and Wales' official Rural-Urban Definitions and investigating the relationship between air pollution and health using small area statistics. His research interests focus on the socio-economic applications of Geographic Information Science (GISc) and in particular with mapping spatial inequalities and understanding places.



**Pietro Ceccato,**

The International Research Institute for  
Climate and Society, NYC, USA

Pietro Ceccato trained originally as an agronomist and soil science scientist. He spent two years in Central African Republic working with local communities to improve agricultural practices.

He obtained a master's degree in environmental management using decision-support systems and worked as a research scientist at the Natural Resources Institute in United Kingdom. He developed remote sensing products to monitor active fires and vegetation status for the purpose of assessing the risk of fire occurrence. He worked at the European Commission Joint Research Centre (Ispra, Italy) on the use of remote sensing to monitor vegetation status and used this work to obtain his PhD in remote sensing from the University of Greenwich, UK. Ceccato then joined the UN Food and Agriculture Organization in Rome to develop an early warning system for desert locust monitoring. He developed remote sensing products and geographic information systems to be used operationally by the Ministries of Agriculture in 21 countries in Africa and Asia.

Ceccato joined the IRI in 2004. His current research activities include the development and integration of environmental remote sensing products into early warning systems for human health, agriculture, pest management and natural disasters.

**Rachel Lowe.**

London School of Hygiene & Tropical Medicine, UK and Barcelona Institute for Global Health (ISGLOBAL), Spain

Rachel is a Postdoctoral Scientist at Institut Català de Ciències del Clima - IC3. Her research involves modelling climate-sensitive disease risk and finding novel ways to communicate probabilistic forecasts to public health decision makers.

Rachel is also involved in the IC3 Climate Services Strategy for Health. Rachel graduated from the University of East Anglia in 2004 with a First Class Honours BSc in Meteorology and Oceanography with a year in Europe. She spent one year at the University of Granada in Spain reading Environmental Science. In 2007 she completed an MSc with distinction in Geophysical Hazards at University College London where she received a Graduate Masters Award. She then went on to obtain her PhD in Mathematics at the College of Engineering, Mathematics and Physical Sciences, University of Exeter (PhD Thesis: Spatio-temporal modelling of climate-sensitive disease risk: towards an early warning system for dengue in Brazil). Alongside her PhD, Rachel was Network Facilitator for the Leverhulme Trust funded project EUROBRISA. As part of the project she collaborated with climate scientists and public health experts at CPTEC/INPE and the Oswaldo Cruz Foundation (Fiocruz) during long-term visits to Brazil, which resulted in her ongoing participation in the innovative Brazilian Observatory for Climate and Health. Rachel was also a Visiting Scientist at the International Centre for Theoretical Physics, Italy, where she worked closely with the Ministry of Health in Malawi towards the development of predictive models for malaria and a platform to integrate climate information and rural telemedicine.



**Renato Assunção.**

Federal University of Minas Gerais, Brazil

Renato Assunção is Professor in the Department of Computer Science, Universidade Federal de Minas Gerais (UFMG) in Brazil.

He received his Ph.D. in Statistics in 1994 from the University of Washington, Seattle, USA. His current research is focused on the development of new algorithms and statistical methods to analyse spatial and space-time data. He is primarily concerned with the spatial analysis of risk appearing in such fields as epidemiological surveillance, geosensor networks, environmental problems, spatially variable risk.

**Robert Deardon,**

Faculty of Veterinary Medicine, University of  
Calgary, Canada

Robert Deardon is an Associate Professor of Biostatistics with a joint position in the Faculty of Veterinary Medicine and Department of Mathematics & Statistics at the University of Calgary.

Most of his recent work has been in the area of infectious disease modelling, but he is also interested in Bayesian & computational statistics, experimental design, disease surveillance methods, spatio-temporal modelling, and statistical modelling in general. He currently has a research group of around 10 postdocs and graduate students. Previous to his post at Calgary he had a 8-year long faculty position at the University of Guelph and postdoctoral positions at the Universities of Cambridge and Warwick.



**Robert Haining.**

University of Cambridge, UK

Robert Haining retired as Professor of Human Geography at the University of Cambridge in September 2015. He has long-standing research interests in the quantitative analysis of geographical data.

He has authored or co-authored over 150 articles and has published two books with Cambridge University Press: *Spatial Data Analysis in the Social and Environmental Sciences* (1990) and *Spatial Data Analysis: Theory and Practice* (2003). These books have provided an overview of the challenges facing those working with spatial data including; what it means to “think spatially”; problems of data collection and spatial representation; spatial sampling; exploratory data analysis; and relevant areas of statistical theory for small area estimation and hypothesis testing. One of his primary areas of applied interest includes the geography of health. He has worked in collaboration with colleagues at the University of Sheffield on evaluating the impact of air pollution on health status using small area statistics.

The growing availability of small area statistics has been made possible by the digital revolution, the development of Geographical Information Systems (GISs) together with organizational changes that have made the collection of geocoded data by many public and private agencies today a matter of routine. But small area statistics raise many challenges for statistical analysis and the drawing out of robust conclusions from what is often “noisy” small area data. In recent years he has had the opportunity to work on the analysis of crime data in collaboration with various police forces in England and Wales and with Home office funding. Most recently, he and colleagues have worked on the development of new methods for evaluating the effectiveness of small area targeted police interventions. He has taught courses on spatial data analysis and spatial econometrics at the undergraduate and graduate levels both at Cambridge and at other universities around the world.



**Sandra Alves,**

ESTSP.IPP, i3S/INEB, Portugal

Sandra Maria Ferreira Alves graduated from Faculty of Sciences and Technology, University of Coimbra in Mathematics (2001) and has a MSc (2005) and PhD (2013) in Biomedical Engineering from Faculty of Engineering of University of Porto. She is interested in statistical modeling of health events, epidemiology and spatial analysis. She is a Professor at the School of Allied Health Technologies Polytechnic Institute of Porto (ESTSP.IPP), since 2002, in the scientific area of Biomathematics, Biostatistics and Bioinformatics. She has been a member of the Biomedical Engineering Institute - INEB since 2003, first as a student and since May 2013 has a researcher in GeoEpidemiology.



**Sandra M. Hurtado Rua.**

Cleveland State University, USA

Sandra Hurtado Rúa completed her Ph.D. at the University of Connecticut under the supervision of Dr. Dipak Dey. Her thesis topic was "A New Class of Bayesian Survival Models and Beyond." She was a postdoctoral associate from 2011 - 2014 in the Division of Biostatistics and Epidemiology at Weill Medical College of Cornell University where I did consulting as well as methodological research related to biological and clinical applications. She previously had completed an M.S. in Mathematics from Northern Illinois University and a B.S. in Engineering from the National University of Colombia.



**Sebastian Meyer,**

University of Zurich, Switzerland

Sebastian Meyer is a postdoctoral researcher at the Friedrich-Alexander-Universität Erlangen-Nürnberg, Germany.

He is the current maintainer of the R package *surveillance*, which implements statistical methods for the temporal and spatio-temporal modelling and monitoring of epidemic phenomena. He holds a BSc and MSc in statistics from the University of Munich, where he has subsequently worked as a research assistant at the Department of Psychiatry and Psychotherapy. He recently (July 2016) completed his PhD in Biostatistics at the University of Zurich under the supervision of Leonhard Held. His PhD thesis elaborates on endemic-epidemic modelling approaches for both individual-level (point pattern) and area-level (count time series) data of infectious disease spread.



**Sulochana Shekhar,**  
Kuvempu University, India

Dr. Sulochana Shekhar is currently an Associate professor in the Department of Geography, School of Earth Sciences at the Central University of Karnataka. She is the Dean of School of Earth Sciences & Head of Department of Geography and has more than 16 years of teaching & research experience. Her research interests are in urban geography and geospatial science. She is the proud recipient of Commonwealth Academic fellowship (2013) and Endeavour Research fellowship (2016). Her current research is the outcome of collaboration with Prof. R P Haining, Department of Geography, University of Cambridge.



**Susanna Cramb,**

Cancer Council Queensland, Australia

Susanna Cramb is a postdoctoral Spatial Modeller at Cancer Council Queensland with adjunct appointments at Queensland University of Technology and Menzies School of Health Research.

Her primary research interest is in using Bayesian spatial and spatio-temporal models to understand how cancer outcomes vary by location. Susanna has worked in epidemiological research for over a decade and her publications have been cited over 1400 times. Queensland Health utilised Susanna's research when setting their cancer care objectives. Susanna previously worked at the School of Population Health, University of Queensland and was involved with large epidemiological projects, including the 2003 Australian Burden of Disease study, among others. Susanna is an alumnus of Queensland University of Technology, James Cook University and the University of Queensland.

**Syed Ashfaq Ahmed,**

Central University of Karnataka, India

Prof. Syed Ashfaq Ahmed is currently Professor at the Department of Applied Geology, Kuvempu University, Karnataka. He previously headed the Department of Geology at Central University of Karnataka, Gulbarga. He has over two decades of teaching and research experience. A former Commonwealth Fellowship awardee at the University of Nottingham, England. His research interests lie in the fields of remote sensing and image processing.



**Theodoros Economou.**

University of Exeter, UK

Theo Economou is a joint University of Exeter/UK Met Office lecturer in Statistical Science.

He is an applied statistician with experience in a variety of fields, primarily environmental sciences (e.g. modelling of extreme European storms, prediction of hail events) but also in water engineering (e.g. modelling water pipe brekage), epidemiology (e.g. infectious disease modelling), public health (e.g. modelling occurrence of hip fractures), biology and social science. His specific research interests include applied Bayesian modelling, space-time modelling of environmental processes, the analysis of track data and decision analysis.



**Theresa Smith,**  
University of Bath, UK

Theresa Smith is a lecturer in statistics in the Department of Mathematical Sciences at the University of Bath.

She completed her PhD in statistics at the University of Washington in 2014, and until recently (July 2016) was a senior research associate in spatial epidemiology in the medical school at Lancaster University. Her research has focused on spatial-temporal models and computation for Bayesian methods. Her interests include point processes and small area estimation applied to public health issues including cancer epidemiology and gastrointestinal illness.



**Tom Clemens,**

University of Edinburgh, UK

A health geographer by background, Tom's career has focused on the social and spatial determinants of health.

He completed a BA(Hons) degree in Human Geography from Lancaster University followed by a Master of Research (MRes) (supervised by Professor Robin Flowerdew) and PhD degree in health geography at the University of St Andrews. His PhD, supervised by Professor Paul Boyle, examined the association between worklessness and mortality using causal modelling techniques. After completing his PhD, Tom began working as a postdoctoral research fellow at the University of St Andrews before moving to the University of Edinburgh to continue postdoctoral work with Professor Chris Dibben. Throughout his PhD and postdoctoral positions Tom has worked extensively with routinely collected administrative health and social data and has developed linkages between them and a variety of environmental datasets. Currently Tom is working on a number of projects in the area of environmental epidemiology and the social determinants of health including the effects of air pollution exposure during pregnancy on birth outcomes and fetal growth, effects of the housing environment for general health outcomes and the relationship between various characteristics of the residential environment during pregnancy for health related behaviours and birth outcomes.



**Trevelyan J. McKinley,**

Exeter University, UK

TJ obtained a PhD in Statistics (2007) at the University of Exeter and in October 2006 he joined the Cambridge Infectious Diseases Consortium at the University of Cambridge as a Research Associate in Statistics, and in January 2014 became a Senior Research Associate in the Disease Dynamics Unit at the Department of Veterinary Medicine. As of November 2014 he is a Lecturer in Mathematical Biology at the University of Exeter. He is interested in applying and developing statistical methodology for the study of infectious diseases. In his PhD thesis he explored the feasibility of using spatial survival analysis as a means of predicting the path of infection in large-scale infectious animal disease epidemics. More recently he has been investigating the use of Approximate Bayesian Computation (ABC), pseudo-marginal and nested sampling techniques as alternative means of estimating parameters in epidemic models where the calculation of the likelihood is often far from trivial. His most recent work has involved developing reversible-jump MCMC techniques for fitting large-scale models for the spread of bovine tuberculosis across the UK cattle movement network.



**Trevor Bailey,**

University of Exeter, UK

Trevor Bailey is Professor of Applied and Computational Statistics at the University of Exeter, UK.

His research interests are in spatial statistics (particularly: spatial epidemiology, spatial modelling, multivariate spatial methods) and also in applied statistical modelling more generally. Much of his research has been collaborative involving academics and professionals from a variety of different fields including medicine, public health, geography, computer science, commercial organizations and government agencies. He is a Fellow of the Royal Statistical Society and of the Higher Education Academy and a Chartered Statistician.



**Veronica Berrocal,**

University of Michigan, USA

Veronica J. Berrocal is an Associate Professor in the Department of Biostatistics at the University of Michigan.

Veronica obtained her Ph.D. in Statistics at the University of Washington in 2007 where she worked on probability weather forecasting with spatial dependence. Between September 2007 and August 2010, Veronica held a postdoctoral position at the US Environmental Protection Agency, Duke University and SAMSI, respectively, where she worked on spatial statistical models for air pollution, and environmental health studies linking air pollution to birth outcomes. In September 2010, Veronica joined the Department of Biostatistics at University of Michigan as an Assistant Professor where she is continuing her research in spatial, environmental and Bayesian statistics.



**Victor Alegana.**

Worldpop group, University of Southampton

Victor Del Rio Vilas is currently at the Dept of Epidemiology, School of Veterinary Medicine, University of Surrey (UK). Previously, he was a consultant with the Pan American Health Organization (PAHO/WHO), based in Rio de Janeiro (Brazil) with regional responsibilities. He advised Ministries/Departments of Health on epidemiology, surveillance and control measures for a number of diseases such as rabies, leishmaniasis, hydatidosis, and on zoonoses programmatic issues across the region. He previously worked in Uzbekistan implementing the Biological Threat Reduction Program (Defense Threat Reduction Agency, US DoD), and as veterinary advisor and epidemiologist for UK's Department for Environment, Food and Rural Affairs (Defra) and the Veterinary Laboratories Agency, respectively.

**Victor Javier Del Rio Vilas,**

School of Veterinary Medicine, University of Surrey, UK

Victor Del Rio Vilas is currently at the Dept of Epidemiology, School of Veterinary Medicine, University of Surrey (UK). Previously, he was a consultant with the Pan American Health Organization (PAHO/WHO), based in Rio de Janeiro (Brazil) with regional responsibilities. He advised Ministries/Departments of Health on epidemiology, surveillance and control measures for a number of diseases such as rabies, leishmaniasis, hydatidosis, and on zoonoses programmatic issues across the region. He previously worked in Uzbekistan implementing the Biological Threat Reduction Program (Defense Threat Reduction Agency, US DoD), and as veterinary advisor and epidemiologist for UK's Department for Environment, Food and Rural Affairs (Defra) and the Veterinary Laboratories Agency, respectively.



**Wang Yu,**

School of Public Health, Peking University,  
China

As a lecturer in Global Health, Dr Wang Yu joined School of Public Health, Peking University in 2014. His key research interests include health systems, global health governance, and applications of GIS in health studies. As the Principle Investigator, he leads the China Prosperity Fund Project on AMR education and training in China funded by UK's Foreign and Commonwealth Office, as well as a governmental evaluation programme on Chinese medical teams in developing countries, funded by Beijing Municipal Government. Dr Wang is also an active player in promoting the applications of GIS and spatial data analysis in public health studies at Peking University. He set up a research network in the University which brings young researchers working together to apply GIS and spatial data analysis techniques in several public health projects. He also delivers an undergraduate course on GIS and global health at the University. Dr WANG has a PhD degree (2014) in Human Geography and an MPhil degree (2008) in GIS and Remote Sensing from the University of Cambridge, as well as a first class honors BSc degree (2007) in Environmental Science from Imperial College London.



## Plenary Speakers



### Plenary Session I

**Cholera In London, 1854.**

**Zika In Brazil, 2015**

**Marília Carvalho,**

Oswaldo Cruz Foundation, Brazil

Marília Sá Carvalho is a Brazilian senior researcher working at Oswaldo Cruz Foundation.

She graduated in medicine at the Federal University of Rio de Janeiro (1979), has a Master in Public Health from the Oswaldo Cruz Foundation (1990), PhD in Biomedical Engineering from the Federal University of Rio de Janeiro (1997). Her main focus for some years has been on statistical models applied to epidemiology and public health problems, therefore she has published extensively on both infectious and chronic health conditions. Her main research interests now are in environmental epidemiology. She is involved in some of the studies about the recently emerged Zika virus. She is currently editor-in-chief of *Cadernos de Saúde Pública* and associate editor of *PLOS Neglected Tropical Diseases*.

## **Abstract**

Cholera and Zika. The first killed 12.8% of the infected people. The second, in the Northeast of Brazil, caused a severe congenital syndrome in about half of the first trimester infected mothers. Similarities and differences in the scientific approach to both are explored in this talk, in special, the role of the place, and the potential of the geo-medical tools, together with the central unanswered questions about Zika. Considering the ideas of “consequentialist” scientist, what could we have done and what we could and should do.



## Plenary Session II

### Space-Time Modeling Of Small Area Data In A Developing World Setting

**Jon Wakefield,**

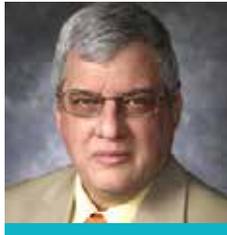
University of Washington, USA

Jon Wakefield is Professor of Statistics and Biostatistics at the University of Washington. Previously he has held positions in the Department of Mathematics (1990-1996) and the Department of Epidemiology and Public Health (DEPH, 1996-1999) at Imperial College, London.

At DEPH he was part of the small area health statistics unit (SAHSU) and worked on methods and applications in spatial epidemiology. More recently his research has moved from chronic disease spatial epidemiology to spatio-temporal modelling of infectious diseases and small area estimation. With respect to the latter, Dr Wakefield has a particular interest in estimation of outcomes in a developing world setting. He has a long-standing interest in Bayesian methods and computation and in 2013 published the Springer book "Bayesian and Frequentist Regression Methods". He is a member of the Statistical Genetics Program Faculty and is an Affiliate Member in the Vaccine and Infectious Disease Division at the Fred Hutchinson Cancer Research Center.

## Abstract

Many people living in low- and middle-income countries are not covered by civil registration and vital statistics systems. Consequently, household sample surveys with complex designs are often used to estimate health and population indicators. In this talk I will describe a hybrid model. We take as data the estimator of the quantity of interest (along with its variance). This data model is combined with a spatio-temporal smoothing model that alleviates problems of data sparsity. The result is a small-area estimation model. Issues that will be discussed include: accounting for the complex design; the simultaneous use of both point- and area-level data; how to make adjustments for HIV epidemics; the inclusion of so-called indirect data; and the effect of different space-time models including models that consider spatial modeling over discrete areas or over a continuous surface. The modeling of under-5 mortality in Kenya is used to motivate and illustrate the issues raised. Data come from a variety of sources including Demographic and Health Survey, and we produce estimates for the period 1980–2014.



### **Plenary Session III**

#### **An Integrated Vector Management (IVM) Surveillance System For Malaria Using Remote Sensing Based On Satellite And Unmanned Aerial Vehicle (UAV) Technologies**

**Daniel Griffith**, University of Texas, USA

Daniel Griffith is Professor of Geospatial Information Sciences and a faculty member in the School of Economic, Political and Policy Sciences. He has taught at UT Dallas since 2005.

His primary areas of research are in spatial statistics, quantitative urban and economic geography, and applied statistics. Griffith teaches courses about spatial statistics, urban economics and research design. His recent spatial statistical research has focused on public health, emphasizing geographic perspectives in environmental health, medical geography and health policy – more precisely, health environment issues associated with urban and social environments at the local level. Griffith is also a Fellow of the Regional Science Association International, and a past president of the North American Regional Science Council. Griffith was a faculty member at the University of Miami, Syracuse University, SUNY/Buffalo, and Ryerson Polytechnic University in Toronto. While at Syracuse University, he served as chair of the Department of Geography, director of the Interdisciplinary Program in Statistics, and deputy director of the New York State Program in Geographic Information and Analysis.

He also was an adjunct professor with the SUNY College of Environmental Science and Forestry, and a member of the Syracuse University Interdisciplinary Program in Statistics faculty. Griffith has published 17 books and monographs, and more than 200 papers, including articles in geography, regional science, statistics and mathematics journals, and 22 book chapters. He has given nearly 200 invited talks, including 46 keynote lectures, and convened/co-convened 27 spatial statistical workshops. He has been the editor of *Geographical Analysis* since 2008. Griffith was a Fulbright Research Fellow (to the University of Toronto), a Fulbright Senior Specialist (to the University of Alberta), a Guggenheim Fellow, an elected Fellow of the New York Academy of Sciences, an elected founding Fellow of the Spatial Econometrics Association, and a past president of the North American Regional Science Council. He also received Distinguished Research Honors from the Association of American Geographers in 2010. Most recently, the American Association for the Advancement of Science (AAAS) elected Griffith as a Fellow for his contributions to spatial statistics and quantitative geography.

## **Abstract**

Human-induced changes in both urban and natural ecosystems contribute substantially to the potential risks associated with malaria transmission. The pattern and extent of land use land cover (LULC) change can provide insight about factors affecting the overall dynamics of malaria transmission as they relate to the human host populations or numbers of parasites per individual, and the geographic distribution and abundance of malaria mosquito vectors.

One essential element leading to eradicating malaria is a surveillance system capable of providing real time and detailed information about the human host, the malaria parasite, and the vector mosquito. Integrated Vector Management (IVM) is a decision-making process for linking current information or evidence with operational protocols and tools that would make a significant impact in reducing malaria transmission.

The application of remote sensing techniques and drone technologies can make a significant contribution for the implementation and operation of a timely yet accurate surveillance system. Such surveillance needs to be based on georeferenced, sub-meter resolution, satellite data (e.g., World View 3) for optimally identifying landscape features, including urbanization, elevation, vegetation, bodies of water, and infrastructure features, such as roads, highways, bridges and paths. Satellite data support the construction of a working grid matrix for ground logistics to identify the geographic location of mosquito sampling zones, and the location of sampling devices. Official local, national, and global reports identifying LULC and delimitation of the mosquito control boundaries for a IVM program would constitute the core of the necessary GIS location based database.

Satellite data then can be used to locate and georeference mosquito aggregation sites, both aquatic and adult, within a defined area or landscape. Meanwhile, unmanned aerial vehicle (UAV) technologies can be employed to autonomously navigate and monitor specific areas of interest designated with remotely sensed satellite data. The UAVs can be programmed to survey mosquito aggregation sites based on need (e.g., daily, weekly, monthly, rainy or dry season), and provide a real time stream of infrared and red, green, and blue (RGB) video to mosquito control personnel. Because this system streams live footage, it furnishes mosquito control personnel with the ability to identify additional sources or aggregations of malaria mosquito vectors.

The described IVM surveillance system would fly quad-copter UAVs within localized and complex environments at low altitudes to visually confirm the presence of mosquito habitats or aggregations identified during the surveillance phase. Compared to fixed-wing aircraft, quad-copter UAVs are better suited and more maneuverable, for localized, low altitude flights in complex environments, which may contain buildings, trees and shrubs, and for visually detecting the presence of mosquito habitats. The described IVM system would include the development of an intelligent GIS using spectral signature algorithms in ArcGIS to safely navigate quad-copters to and from mosquito habitats. These algorithms are of particular importance in densely wooded areas where a UAV initially would fly above trees, but then must descend below the canopy in order to get to its destination. The UAV would need to include obstacle avoidance algorithms in ArcGIS to safely avoid obstructions as it navigates a sampling area. Because a UAV may lose the DGPS signal (with 10cm locational accuracy) as it navigates below the tree line, the system requires the construction of multiple maps in ArcGIS.

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# Oral Communica- tions

## Parallel Session 1 GIS In Public Health

### Oral Communication 01 | Invited Speaker

#### Mapping urban scale air quality using big data: Accounting for uncertainty

**Eun-Hye Enki Yoo**

Department of Geography, University at Buffalo, The State University of New York (SUNY), Buffalo, NY, USA

Recent advances in sensing technology enable investigators and communities to collect air quality measurements at times and locations of interest. The low-cost and real time sensing capability of portable sensors increase spatial and temporal resolution and data availability, although the reliability and quality of measurements often need improvement. Similarly, computer simulation models, such as community multiscale air quality models (CMAQ), and remote sensing provide information on air quality with exhaustive spatial coverage, whereas these data are not directly compatible with ground air quality measurements. For instance, CMAQ outputs are subject to error in input data on sources and sensitive to the spatial resolution of outputs, which are typically in the range of 4 to 100 km.

In this presentation, we investigate the impact of spatially and temporally correlated multiple data sets, available at different spatial and temporal resolutions with varying levels of uncertainty, on spatiotemporal model prediction performance. To illustrate our point, we assess the contribution of each data source on the quality of the reconstructed PM<sub>2.5</sub> concentration surface at a fine scale using a simulation example. The three data sets --- 24-hr PM<sub>2.5</sub> measurements from four fixed monitoring stations, CMAQ modelled values of PM<sub>2.5</sub> at a grid at 12 km resolution, and portable sensor measurements collected from randomly selected points and time instants---were generated from realistically simulated daily PM<sub>2.5</sub> concentration surfaces in Erie and Niagara counties in New York States, US, for 60 days. The three sets of

sample data were extracted from each simulation, and bias were added to both CMAQ outputs and mobile sensor measurements to account for the uncertainty present in both data sets. We used Fixed Rank Kriging (FRK) as a spatiotemporal predictor, which takes into account the mismatch of spatial and temporal resolutions among data sources, while explicitly accounting for different levels of reliability in each data source by separately modelling measurement error and fine-scale variation. FRK is also capable of handling large datasets with relatively easy computation. Model performance was evaluated using three metrics, specifically root mean square prediction error (RMSPE), correlation coefficients between predictions and reference values, and the percent of reference values that fell within the generated 90% confidence intervals at each location (90% coverage).

Our preliminary results indicate that the FRK predictions with all three datasets performed better in reducing RMSPE and in yielding high correlations compared to using two or one data set. In terms of percent of reference values falling within the 90% confidence intervals, results showed that FRK prediction with a single data set performed the best. We suspect that the latter result was due to the large FRK prediction error variance estimate at each location. Our finding on the performance of FRK depends on the quantity and quality of the mobile sensor measurements, as well as the spatial and temporal variability of underlying PM<sub>2.5</sub> concentration surface. Further analyses will be conducted to evaluate the sensitivity of the prediction performance with respect to an alternative sampling design for mobile sensors, as well as a simulation of more realistic PM<sub>2.5</sub> surfaces whose spatial and temporal variability reflect the topography, the proximity to major highways of the study area, or the day of the week.

## Oral Communication 02 | Invited Speaker

### A Geospatial Analysis of Factors Influencing Maternal Hospital Delivery in Rural China: a Case Study from Sichuan Province

**Yu Wang,**

School of Public Health, Peking University, China

**Background:** Hospital delivery is a safe delivery way highly recommended by the World Health Organization, since giving birth at a medical institution equipped with medical facilities and healthcare professionals can effectively reduce maternal and infant mortality rate. However, there are occasions when hospital delivery is not available to pregnant women in undeveloped remote areas, making it important to explore the influencing factors so that measures can be taken to increase the rate of hospital delivery in those areas. Research in the past has shown that hospital delivery in different areas of China could be associated with socio-economic and cultural factors; whereas very few studies explored the association between hospital delivery and possible geographic factors. This study explores influencing factors of hospital delivery for pregnant women in rural areas of Sichuan Province of China, which is one of the largest provinces of China with a complex feature of landscapes.

**Method:** The samples of this study are from the China National Pre-pregnancy Physical Examination Project in 2014. A total number of 109,181 live births in the rural areas of Sichuan Province

were taken into analysis. Multi-factor logistic regression was applied to investigate the association between hospital delivery and various types of possible influencing factors. Geographic Information System (GIS) techniques was used process the geographic data of the study for exploring how landscape and travel distance could influence the rate of hospital delivery.

**Results:** The rate of hospital delivery of the total samples in this study reached up to 99.5%. It was found that the number of giving birth in the past, mother's age, parent's ethnicity, education level and income level were highly associated with the rate of hospital delivery. The landscape where the parents live and the travel distance to nearest hospital were also found to strongly affect the rate of hospital delivery. Mothers with no experience of pregnancy (OR=1.3, 95% CI:1.1, 1.5), mothers under the age of 25 (OR=1.5, 95% CI:1.2, 1.8), parents inhabiting at plains (OR=3.4, 95% CI:2.6, 4.5), mothers live closer to the nearest hospitals (OR=1.4, 95% CI:1.1, 1.7), couples both being the Han ethnicity (OR=10.0, 95% CI:8, 13), couples at least one having education level above junior high school (OR=2.0, 95% CI:1.6, 2.5), couples with at least one having high income level (OR=2.0, 95% CI:1.4, 3.0) tend to have a greater rate of hospital delivery than the others.

**Conclusion:** Improving the awareness of safe delivery among pregnant women, strengthening the maternal healthcare infrastructure, and improving the people's accessibility to hospitals in rural areas are important measures to raise the rate of hospital delivery in rural China.

## Oral Communication 03

**Urban green spaces in the proximity of residences may reduce the effect of socioeconomic inequalities in the practice of sports among teenage girls**

**Alexandre Magalhães<sup>1,2</sup>, Debora Castiglione<sup>3</sup>, Elisabete Ramos<sup>4,5</sup>, Maria Fátima Pina<sup>1,2,6,7</sup>**

<sup>1</sup>I3S - Instituto de Investigação e Inovação em Saúde, Universidade do Porto. Rua Alfredo Allen, 208, 4200-135 Porto, Portugal.

<sup>2</sup>INEB - Instituto de Engenharia Biomédica, Universidade do Porto. Rua Alfredo Allen, 208, 4200-135 Porto, Portugal.

<sup>3</sup>ENSP/FIOCRUZ - Escola Nacional de Saúde Pública Sérgio Arouca, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil

<sup>4</sup>Departamento de Epidemiologia Clínica, Medicina Preditiva e Saúde Pública, Faculdade de Medicina da Universidade do Porto. Al. Prof. Hernâni Monteiro, 4200 - 319 Porto, Portugal.

<sup>5</sup>EPIUnit - Instituto de Saúde Pública da Universidade do Porto. Rua das Taipas 135, 4050-600, Porto, Portugal.

<sup>6</sup>Instituto de Comunicação e Investigação Científica e Tecnológica em Saúde, Fundação Oswaldo Cruz - ICICT/FIOCRUZ, Rio de Janeiro. Av. Brasil, 4365 - Manguinhos, Rio de Janeiro - CEP: 21040-900 Brasil.

<sup>7</sup>CARTO-FEN/UERJ - Departamento de Engenharia Cartográfica, Faculdade de Engenharia, Universidade do Estado do Rio de Janeiro. Rua S. Francisco Xavier - Rio de Janeiro, Brasil.

**Introduction:** Availability of urban green spaces (UGS) can influence the sports practice (SP) among teenagers, but it is not clear how this influence is affected by the socioeconomic status.

**Objective:** to analyse if proximity of UGS to residences reduces the socioeconomic inequalities in SP among 17 years old girls.

**Methodology:** We evaluated 722 teenagers' girls born in 1990, living and studying in Porto in 2007/2008, Portugal (EPITeen cohort). The shortest routes from residences to UGS were calculated using the street network from GIS. Distances were classified as:  $\leq 400\text{m}$ ;  $>400\text{m}$  to  $\leq 800\text{m}$ ;  $>800\text{m}$ . We used parent's higher education level as a proxy of SES, classified as low (elementary school), medium (secondary school) and high (college). We used chi-square test to compare proportions of teenagers practicing sports per SES, stratified by classes of distances to UGS and logistic regression to estimate the association between SP and SES through Odds Ratio (OR) and 95% confidence intervals (95%CI).

**Results:** Regarding the effect of proximity according SES, as the distances decrease the proportion of sports practitioners' increases, being this trend not significant in girls from low and high SES and much accentuated in girls from medium SES. Using higher SES as reference, girls from lower SES have 75% lower odds of SP regardless the distance to UGS. However, for girls from medium SES the odds of practice sports varies according the distances to UGS, being the Odds Ratio 0.42(0.22-0.80) at  $> 800$  meters, 0.51(0.24-1.09) at  $>400\text{m}$  to  $\leq 800\text{m}$  and 0.63(0.29-1.37) at  $\leq 400\text{m}$ . Conclusions: The proximity to UGS decreases the social inequalities in the practice of sports among girls from high and medium SES, in Porto city, however, it seems to be insufficient to raise the low level of SP among girls from low SES.

## Oral Communication 04

### Spatial hotspots of dementia risks: an approach to inform policy

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We have a poor understanding of whether dementia clusters geographically, how this occurs, and how dementia may relate to socio-demographic factors. To shed light on these important questions, first, this study aimed to compute a dementia risk score for individuals using general practices (or family physician) data. Second, assess spatial variation of dementia risk across the communities to identify significant clusters (hotspots) in spatial pattern of dementia risk and explore their association with socioeconomic status.

We used clinical records from 16 general practices with a population of 14,746 aged 65 years and over from west Adelaide, Australia for the duration of 1<sup>st</sup> January 2012 to 31<sup>st</sup> December 2014. Dementia risk was estimated using The Australian National University- Alzheimer's dementia Risk Index (ANU-ADRI). Spatial variation of dementia risk was assessed by generating choropleth maps across at small area level (statistical area level 1). Local spatial clusters at the statistical area level 1 (SA1) with high or low dementia risk were examined using the Getis-Ord  $G_i^*$  technique. We also used the Local Moran's  $I$  statistic to identify local spatial clusters of dementia risk at SA1 level. The statistic identifies hotspots (high-high), cold spots (low-low), and spatial outliers (high-low and low-high) in the pattern of dementia risk across communities.

Significant hotspots were observed in eastern and southern areas while cold spots were observed in the western area in west Adelaide. Additionally, significant hotspots were observed in low socio-economic communities. We found dementia risk scores increased with age, sex (female), high cholesterol, no physical activity, being alone (widow, divorced, separated or never married), and co-morbidities such as diabetes and depression. However, dementia risk scores were higher in underweight and normal weight individuals compared with obese and overweight individuals. Similarly, smoking was associated with a lower dementia risk score.

To the best of our knowledge, this is the first study to investigate the spatial heterogeneity of dementia risk in an urban setting using routinely collected medical data at the primary health care level. The robustness of our research findings were demonstrated by linking a number of spatial data explorations and statistical methods with GIS techniques. Our study findings will aid policy makers to target prevention strategies in areas with high dementia risk to reduce or delay the onset of dementia in Australian communities.

**Keywords:** dementia, general practice data, dementia risk score tools, geospatial analysis, hotspots, spatial variation.

## Oral Communication 05

### Evaluating the impact of residential mobility on health care accessibility for children with birth defects.

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Children with birth defects is a subset of children with special health care needs (CSHCN) who face significant barriers to accessing care compared to children without special needs. Conversely, timely diagnosis is a critical element to provide treatment if appropriate and increase chances of survival. Beyond the first four weeks, infants typically require long-term health care and may be referred to other multidisciplinary specialty care, which may be located far away. Such transfer may result in long distances between care center and place of residence and could be interpreted as a high travel burden, however parents with health knowledge and resources may select a more distant hospital for their child's care.

In maternal and child health, most studies assume that residential mobility does not occur during pregnancy or infancy. However, this assumption may not be valid for a longer period of time (e.g., throughout childhood). Families will likely relocate when long-term intensive care is needed for their children at a specialty center that is not in the vicinity of their residence. As such, the use of maternal residence at birth may result in biased estimates of association and imprecise risk estimation. Ignoring residential mobility during infancy and beyond will bias the true travel estimate (including costs) and consequently lead to wrong identification of regions with poor geographic access.

In this research, we evaluate the impact of residential mobility for infants diagnosed with Spina Bifida in the state of Florida, using the Florida Birth Defect Registry (FBDR) - a state-wide, population-based, passive surveillance system- and hospital discharge information, from 1998 to 2007. We estimate the percentage of children with SB where the maternal zip code at birth matches the zip code of hospital discharge records. We then impute the new geographic location when the zip code is different from the maternal zip code. This is an important step to estimate the travel time, distance, and costs from the place of residence to the hospital where care was received. Lastly, we compute the difference in geographical accessibility prior and post imputation.

The results suggest that ignoring residential mobility overestimate actual travel distances as parents tend to move closer to the health care center where the child receives care. These findings are particularly informative for public health officials, and/or health services researchers to identify and target underserved areas and improve health service delivery.

## Parallel Session 2 Spatial Health Surveillance I

### Oral Communication 01 | Invited Speaker

#### Spatio-temporal modelling and probabilistic forecasting of infectious disease counts

**Sebastian Meyer**

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Routine surveillance of notifiable infectious diseases gives rise to weekly counts of reported cases stratified by region and age group. A well-established approach to the statistical analysis of such surveillance data are endemic-epidemic time-series models (hhh4) as implemented in the *R* package **surveillance** (Meyer, Held, and Höhle 2017). Autoregressive model components reflect the temporal dependence inherent to communicable diseases. Spatial dynamics are largely driven by human travel and can be captured by movement network data or a parametric power law based on the adjacency matrix of the regions. Furthermore, the social phenomenon of "like seeks like" produces characteristic contact patterns between subgroups of a population, in particular with respect to age. We thus incorporate an age-structured contact matrix in the hhh4 modelling framework to assess age-specific disease spread while accounting for its spatial pattern (Meyer and Held 2017),

improve probabilistic forecasts of infectious disease spread (Held, Meyer, and Bracher 2017).

We analyze weekly surveillance counts on norovirus gastroenteritis from the 12 city districts of Berlin, in six age groups, from week 2011/27 to week 2015/26. The following year (2015/27 to 2016/26) is used to assess the quality of the predictions with proper scoring rules. We compare final size forecasts as well as multivariate forecasts of the total number of cases by age group, by district, and by week across different models of varying complexity.

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## Oral Communication 02 | Invited Speaker

### Multivariate Bayesian hierarchical models for the analysis of zoonoses

**Ana Corberán-Vallet<sup>1</sup>, Andrew B. Lawson<sup>2</sup>, Raymond M. Boaz<sup>2</sup>, Victor Del Rio Vilas<sup>3</sup>,**

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We present here two case studies where veterinary and human health data are combined in an effort to better understand diseases that are transmitted from animals to humans. In particular, we show an application to leishmaniasis data in Brazil, where dog and human case data are jointly analyzed through multivariate Bayesian hierarchical models to improve identification of areas at greater risk of disease. The second case study shows an application to echinococcosis data in Rio Negro, Argentina. Here we have annual data corresponding to human counts as well as counts of cases in lambs and dogs. The results obtained in both analyses are critical for the prioritization of control measures.

## Oral Communication 03 | Invited Speaker

### Bayesian surveillance reproduction number for infectious diseases

**Chawarat Rotejanaprasert**

Mahidol University, Bangkok, Thailand

New infectious diseases are public health concerns in which policy makers have to make decisions in the presence of enormous uncertainty. This is an important challenge in terms of emergency preparation requiring the operation of effective surveillance systems. A key concept to investigate the dynamic of infectious diseases is the basic reproduction number. However it is difficult to be applicable in real situations due to the underlying theoretical assumptions. Alternatively we present a robust and flexible methodology for estimating disease strength using the surveillance reproduction number. Withstanding the issues of context-specific conditions, our method provides practical advantages and can be applied to simultaneously estimate disease transmissibility at each location and time for real-time assessment of new emerging diseases.

## Oral Communication 04

### Identification of hotspots of rat abundance in a Brazilian slum community using indirect abundance metrics

**Poppy Miller<sup>6</sup>, Kathryn Hacker<sup>1</sup>, Amanda Minter<sup>7</sup>, Mike Begon<sup>2</sup>, Peter J. Diggle<sup>1,2,6</sup>, James E. Childs<sup>1</sup>, Mitermayer G. Ries<sup>3,4</sup>, Federico Costa<sup>1,2,4,5</sup>, Albert I. Ko<sup>1,4</sup>**

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<sup>7</sup>Life Sciences, University of Warwick

Rodent control measures have so far been largely ineffective at reducing the burden of leptospirosis in slum environments where Norway rats (*Rattus norvegicus*) are the primary reservoir hosts. A critical barrier to mounting adequate rodent control is reliable estimation of rat abundance and distribution in complex urban settings. We developed a tracking plate method to quantify the abundance and distribution of rats using rat-specific marks on lampblack coated tiles laid over the study region. The study design was a spatially continuous constrained random sample (340 points) at locations throughout a Brazilian urban slum community (0.46 km squared). An additional 100 random points were added at close range, to distinguish between short range spatial variation and underlying noise. This design allowed identification of hotspots at very small ranges (<30m). We performed environmental surveys and used satellite imagery to derive spatially relevant covariates (distance to open sewers and public trash, rainfall, and the proportion of area in the nearby vicinity that is an impervious surface, soil or vegetation).

Data collection was repeated for multiple campaigns during the wet and dry season. We analysed the data using a generalised linear spatio-temporal model to create high-resolution predictive maps of relative rat abundance that can be decomposed into explained (covariate-dependent) and unexplained (stochastic) components. This revealed marked spatial heterogeneity in both the microenvironment and rat abundance, which may offer an opportunity for more targeted rodent control for leptospirosis.

Additionally, a cohort of participants (usually resident in the same study area as above) had their leptospirosis titres measured before and after each of the rat tracking campaigns. Each participants time series of titres can be used to estimate the probability that their immune system was challenged (perhaps resulting in clinical disease) by leptospire in the intervals between testing. A spatio-temporal model was developed for the titres incorporating individual risk factors (gender, age, illiteracy, household income, informal employment, and cumulative exposure to rainfall), environmental risk factors (contact with flood water, sewers, and mud) and household related risk factors (elevation, proportion of area in the vicinity of the house that is an impervious surface, soil or vegetation, and distances to open sewers and public trash).

The rat tracking and leptospirosis infection models were combined to form a fully joint model which concurrently estimates the spatio-temporal surface of rat abundance and human leptospirosis infection. This allowed quantification of the spatio-temporal effect of rat abundance on the number and spatio-temporal distribution of human cases of leptospirosis.

## Oral Communication 05

### Spatio-temporal modelling of the number of calls to Saúde24 line to assess hospital savings

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Urgency admission is one of the most important factors regarding hospital costs, which can possibly be mitigated by the use of national health lines such as the Portuguese Saúde24 line (S24).

S24 intends to improve accessibility and to rationalize the use of existing resources, by directing users to the most appropriate institutions of the public national health services. Aiming a future development of decision support indicators in a hospital savings context, based on the economic impact of the use of S24, rather than hospital urgency services, this study investigates spatial dependencies in the number of calls to S24 in each Portuguese municipality, accounting at the same time for temporal correlations.

Different space-time structures are investigated under both a hierarchical and an autoregressive perspective in the study of S24 data set, over the period 2010-2016. The spatio-temporal structure is modelled with a set of autocorrelated random effects, in terms of a Poisson bayesian hierarchically model, using Car-Bayes-ST for implementation. Additionally, resorting to Integrated

Nested Laplace Approximations (INLA) methodology, temporally structured effects are implemented within a spatial lag Poisson bayesian model, which considers a spatial autoregressive way of accounting for areal similarities, based on a neighbourhood or a distance criteria. This is implemented in R-INLA.

The bayesian methods are greatly developed being now widely used in many research areas, including health economic assessment, growing in importance in several econometric analyses. Through this study, we implement temporal effects both on bayesian hierarchical and autoregressive models for count data, reaching an interesting spatio-temporal bayesian econometric alternative approach for these.

**Keywords:** Bayesian; Poisson; Hierarchical model; Autoregressive model; Space-time Correlation.

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## Parallel Session 3 Spatial Health Surveillance II

### Oral Communication 01 | Invited Speaker

#### Crime victimization and the implications for individual health and wellbeing

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Public health and criminology have developed largely independently of one another at the research and policy levels so that the links between crime victimization and health status are not well understood. The health sector is unavoidably drawn into dealing with many of the consequences of crime. By definition, violent crime impacts directly on health, while the health effects of non-violent crime may be more indirect or psychological. However, identifying crime as a public health issue remains a relatively new idea, despite the close proximity of both sectors.

Research and policy making in the area of public health adopt a broad, interdisciplinary perspective focusing on population health as the outcome of many factors affecting the lives of individuals, families, and communities via many pathways. The social model of health articulates these factors within a multidimensional definition of health that includes human well-being, human development, and quality of life, whilst emphasizing a community approach to promoting public health.

Although it is not difficult to support the idea of crime as a threat to the health of individuals and the wider community, the difficulty lies in quantifying the impact of crime on public

health, while controlling other variables, including gender and ethnicity. The primary goal of this research is to explore and to better understand the impacts of crime on individual health and wellbeing drawing on the social model of health. Specific objectives are to develop an understanding of the conceptual foundation underlying the links between crime (violent and non-violent) and health status, to explore the effect of the victimization experience on quality of life and physical and psychological wellbeing, and to investigate the role of social and demographic factors in the health-crime relationship.

The study is based on 840 responses from a postal survey administered to 4,100 households in Sheffield, England, located primarily in deprived areas where overall crime rates were high. Non-violent crimes were more frequently reported than violent crimes and in general, inner city neighbourhoods were associated with higher violent crime rates compared to suburban areas. Out of 392 victims of crime, 27% of individuals detailed physical injuries resulting directly from a crime event and 31% had taken some medical steps to treat a crime-related injury. 86% experienced at least one psychological or behavioural change, including stress, sleeping difficulties, loss of confidence, and depression. Logistic regression models estimated victimization risk based on various social and demographic variables. Violent crimes were consistently linked with higher odds of seeking medical treatment and a higher likelihood of experiencing psychological ill health effects or behavioural changes. In comparison, victims of non-violent or property crimes were not significantly associated with mental health or behavioural/lifestyle effects.

## Oral Communication 02

### Spatio-temporal variation of county-level rates of very low birth weight in the United States, 1989–2010

**Monica P. Shah, MPH<sup>1</sup>, Miriam E. Van Dyke, MPH<sup>1</sup>, Michael Kramer, PhD<sup>1</sup>**

Monica P. Shah, MPH<sup>1</sup>, Miriam E. Van Dyke, MPH<sup>1</sup>, Michael Kramer, PhD<sup>1</sup>

Background: Infants with very low birth weight (VLBW, <1,500 grams) are at substantially increased risk of neonatal morbidity and mortality compared to normal weight babies. Past research has documented consistent associations between environmental and social factors and cross-sectional VLBW prevalence, but little research has examined the determinants of the rates of change – either increases or decreases – through time. We characterize the spatial structure of cross-sectional VLBW prevalence, and estimate ecologic correlates of the absolute change in VLBW prevalence in the United States between 1989 and 2010.

Methods: Vital records data from singleton live births from all states except for Alaska and Hawaii were pooled into three year windows at each of two time periods: 1989 to 1991 and 2008 to 2010. County-level rates of VLBW by mother's race (White and Black) were estimated using spatial empirical Bayes smoothing to stabilize rates, and the absolute change from initial period (1989-1991) to follow up period (2008-2010) was calculated. Area-level predictors included: percentage below the poverty line (1990), percentage with a college education or higher (1990), social capital index (1990), violent crime rate (1986), proportion of women receiving adequate prenatal care (1989-1991), and density of physicians (1990). Global Moran's I and spatial econometric regression models were used to characterize spatial structure

and dependencies between area-level predictors and change in VLBW.

Results: Absolute change in VLBW rates varied from -43.3 to 102.1 per 1,000 live births across 3,109 counties. Moderate spatial autocorrelation in absolute change in VLBW was detected overall (Global Moran's I: 0.27, pseudo  $p=0.001$ ) and among Black mothers (Moran's I: 0.34), but minimal spatial autocorrelation was observed among White mothers (Moran's I: 0.16). Social capital index (Moran's I: 0.31), percentage with a college education or higher (Moran's I: 0.30) and percentage below the poverty line (Moran's I: 0.44) were also spatially clustered. After adjustment for area-level predictors in a spatially lagged model, higher physician density in 1990 ( $\beta=0.12$ ,  $p<0.001$ ) and lower social capital index in 1990 ( $\beta=-0.26$ ,  $p=0.006$ ) were associated with significant reductions in rate of VLBW among White mothers, with a significant spatial lag ( $p=0.35$ ,  $p<0.001$ ). Among Black mothers, greater percentage with a college education in 1990 ( $\beta=0.18$ ,  $p<0.001$ ) was significantly associated with declines in VLBW rates, with a significant spatial lag ( $p=0.67$ ,  $p<0.001$ ).

Conclusions: Considerable spatial variation in county-level rates and magnitude of change in rates of VLBW were observed across the United States between 1989 and 2010. Public health surveillance and prevention can be enhanced by understanding not only correlates of point-in-time prevalence, but social and environmental predictors of progress through time or worsening of prevalence by race and through space.

## **Oral Communication 03 | Invited Speaker**

### **Statistical inference from infectious disease modelling: guiding rabies control and elimination programmes**

#### **Katie Hampson**

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Models of infectious disease dynamics informed by surveillance data have considerable utility for guiding policy decisions and practice. However for rabies, traditional models that assume fully-mixed populations fail to capture patterns of infection limiting their utility. Using highly resolved spatiotemporal data on rabies incidence and host populations show that susceptible depletion at the population level is negligible, explaining why neither classical density-independent or density-dependent models generate realistic dynamics. Using an Approximate Bayesian Computation (ABC) approach we fitted an individual-based model to these data to explore the structures and processes that give rise to population-level patterns of infection. Across all spatial scales we identified a ridge in parameter space that reproduced temporal patterns of incidence that spanned from frequency-dependent to density-dependent functional forms of transmission.

Additional ABC fitting criteria relating to case densities were required to resolve the spatial scale of transmission and post-posterior checks simulating from the best fit parameters were needed to identify the transmission function. We conclude that observed population-level patterns emerge only when the scale of transmission is appropriately captured and for rabies, these patterns arise from local processes of disease-induced mortality and re-exposure. As surveillance data is aggregated, often at crude spatial scales, inference of these underlying mechanisms is difficult. Nonetheless, armed with these insights, we demonstrate how classical epidemiological models can be adapted to approximate these mechanisms thereby increasing their utility when applied to aggregate rabies surveillance data. We discuss insights from these different modelling approaches to informing rabies control and elimination policy and practice.

## Oral Communication 04 | Invited Speaker

### An Information-theoretic Portfolio Model for Disease Surveillance Evaluation

**Matteo Convertino<sup>1</sup>**, **Victor Del Rio Vilas<sup>2</sup>**, **Ana Riviere-Cinnamond<sup>3</sup>**, **Gilberto Montibeller<sup>4</sup>**, **Laura Streichert<sup>5</sup>**, **Honore Peggy<sup>6</sup>**

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Surveillance information is crucial for better understanding of disease dynamics, improving situational awareness, and for the identification of optimal control strategies. Despite surveillance systems' (SS) critical role, current approaches to their evaluation fail to properly consider and propagate the uncertainty around the evidence that informs standard surveillance performance attributes such as sensitivity. As a result, decision quality based on surveillance information may be compromised possibly leading to inadequate public health responses.

With this motivation we combine multicriteria decision analysis (MCDA) and a predictive information-theoretic model to comprehensively assess the Value of (Surveillance) Information (Vol) over different geographies and time. Specifically, we generate surveillance scenarios to derive aggregated MCDA scores for the actual state of the SS, and other potential states including the optimal surveillance state. This is done by calibrating the information-theoretic model with a subset of surveillance data and considering the uncertainties around the input data. After calibration, the model is evaluated by considering its ability to predict, on validation datasets, the health outcomes of interest. We apply our evaluation framework to cholera data from Haiti in the period 2010-2016. Maximization of the Vol leads to an increase in prediction accuracy of 50%, 47%, 30% and 27% for the four outcomes of interest: outbreak peak time, outbreak geographical spread, total # cases, and outbreak peak magnitude, respectively. Vol maximization also results in a 45% increase in the prediction accuracy of the outbreak infection sources. Our information-theoretic model does not contain any explicit biological mechanism or assumption as it relies entirely on the amount of disease information (e.g. incidence) generated in multiple areas and area interdependencies (inferred via maximum and transfer entropy functions). Thus, the model can be applied to any disease of interest or to multiple diseases simultaneously.

## Oral Communication 05 | Invited Speaker

### Efforts to integrate evidence: a multi-dimensional challenge

**Del Rio Vilas VJ<sup>1</sup>, Montibeller G<sup>2</sup>, Attema A<sup>3</sup>, He L<sup>4</sup>, Convertino M<sup>5</sup>, Shindo N<sup>6</sup>**

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Basic problem structuring identifies two types of complexities for most problems and decision settings: technical, and organizational. The West Africa Ebola outbreak, and the international response that ensued, highlighted the critical importance of the latter. Other emerging problems, such as the ongoing epidemic of yellow fever in Brazil has also brought to light critical organizational limitations to optimally identify, plan and properly resource disease response efforts.

Organizational complexities may result in vulnerabilities that, together with risks, should be combined in an integrated business management planning process for disease preparedness and response. The World Health Organization's Health Emergencies Programme (WHE) recognises the widespread occurrence of process related limitations and has as key priorities i) the development of robust and timely risk assessment and response mechanisms to health hazards; ii) the consolidation of coordinated action, and iii) the strengthening of national prevention and preparedness action plans. In this work we review ongoing efforts by WHE to integrate risks and vulnerabilities. In light of this review, we argue that whereas substantial work has been conducted on spatially explicit risk maps, similar work on capacity assessment is lacking. This limitation extends to spatially specific efficient resource allocation models, and methodologies to systematically capture the dynamic and spatially varying behaviours by the multiple stakeholders, either involved in response or benefiting from it. In this context we consider ongoing studies on vulnerabilities mapping, and the design challenges to mapping stakeholders and communities risk attitudes.

## **Parallel Session 4 Spatial Survival And Registry Data Analysis I**

### **Oral Communication 01 | Invited Speaker**

#### **Spatially-explicit Survival Modeling with Discrete Spatial Grouping of Cancer Predictors**

**Andrew B. Lawson<sup>1</sup>, Georgiana Onicescu<sup>2</sup>**

<sup>1</sup> Medical University of South Carolina, USA;

<sup>2</sup> Western Michigan University, USA

In this paper, the spatially explicit survival model, which broadens the definition of the survival, density and hazard functions by explicitly modeling the spatial dependency using direct derivations of these functions, is extended by allowing the relation with the explanatory covariates to be spatially adaptive using a threshold conditional autoregressive (CAR) model, allowing the inclusion of multiple threshold levels. The model is applied to prostate cancer survival based on Louisiana SEER registry, which holds individual records linked to vital outcomes and is geocoded at the parish level.

## Oral Communication 02 | Invited Speaker

### Joint spatial frailty model for modeling multiple time to events data

**Cindy Feng**

School of Public Health, the University of Saskatchewan, Canada

Survival analysis methods can be used to describe the occurrence and time to a series of events subject to censoring: for instance, age at diagnosis, and time from diagnosis until death in AIDS study. It is often of interest to investigate the effect of key clinical or environmental risk factors. Models that account for the effect of such key risk factors and how they may operate differently on various events through the stages of a disease, can assist in understanding the nature of the disease and aid in prognosis. Jointly modeling the multiple time to events allow us simultaneously investigate the effect of key risk factors on the related event outcomes while accounting for random errors linking events. Additionally, geographical variation may exist in the multiple events. To account for possible spatial correlation in these outcomes among subjects from the same geographical region, frailty terms employed in the survival model. We propose a joint spatial survival model for modeling times to multiple events. Our proposed method is evaluated by a simulation study and a motivating application will be used to demonstrate the utility of the proposed model.

## **Oral Communication 03 | Invited Speaker**

### **A transformation class for spatio-temporal survival data with a cure fraction**

**Sandra Hurtado Rúa**

Department of Mathematics, Cleveland State University, USA

We propose a hierarchical Bayesian methodology to model spatially or spatio-temporal clustered survival data with possibility of cure. A flexible continuous transformation class of survival curves indexed by a single parameter is used. This transformation model is a larger class of models containing two special cases of the well-known existing models: the proportional hazard and the proportional odds models. The survival curve is modeled as a function of a baseline cumulative distribution function, cure rates, and spatio-temporal frailties. The cure rates are modeled through a covariate link specification and the spatial frailties are specified using a conditionally autoregressive model with time-varying parameters resulting in a spatio-temporal formulation. The likelihood function is formulated assuming that the single parameter controlling the transformation is unknown and full conditional distributions are derived. A model with a non-parametric baseline cumulative distribution function is implemented and a Markov chain Monte Carlo algorithm is specified to obtain the usual posterior estimates, smoothed by regional level maps of spatio-temporal frailties and cure rates. Finally, we apply our methodology to melanoma cancer survival times for patients diagnosed in the state of New Jersey between 2000 and 2007, and with follow-up time until 2007.

## Oral Communication 04

### In My Time of Dying: A Spatial Epidemiological Re-analysis of John Graunt's Observations Made Upon the Bills of Mortality

**Olaf Berke**

Department of Population Medicine, University of Guelph,  
Canada

**Introduction and Objective:** In 1662 John Graunt laid the foundations for statistics and epidemiology when he reported about the London Bills of Mortality. The Bills of Mortality are an early example of health surveillance systems using registry data, and are also regarded as the origin of disease classification. One of Graunt's objectives was a spatial analysis of the plague mortality during the plague year 1625. Here, modern spatial epidemiological methods are applied to his data to reveal further insight into a medieval plague epidemic: household density (a miasma indicator) and percentage of substantive households (a socio-economic indicator) per parish are tested as predictors of proportional plague mortality.

**Material:** The Bills of Mortality for London's 97 parishes within the wall of 1625 as reported by Graunt are analyzed together with socio-economic census data of the time.

**Methods & Results:** A choropleth map highlights five negative and positive plague mortality cluster as detected by the flexible spatial scan test. Testing for spatial dependence using Moran's I demonstrates the presence of clustering, i.e. a non-random spatial pattern of parish-level plague mortality. Spatial regression modeling reveals that plague mortality is negatively correlated with the socio-economic status at parish population level but not with the miasma indicator: the density of households or population per acre.

**Summary, Discussion & Conclusion:** Plague mortality across the 97 parishes within the wall of medieval London showed distinct spatial patterns: clustering, clusters and a decreasing trend with socio-economic status. However, no evidence was found for a relation between the parish plague mortality and household density as an indicator for crowding and key to the miasma paradigm of Graunt's time.

Although Graunt saw the signs of overpopulation and social inequality among London's parishioners, but he discussed the cities' healthfulness in relation to stench and coal smoke, i.e. miasma. The birth of social epidemiology had to wait another 150 years for Louis-René Villermé and its pioneering studies relating mortality to poverty across the twelve arrondissements of Paris.

## Oral Communication 05

### Bayesian cure-rate survival model with spatially structured censoring

**Georgiana Onicescu**

Department of Statistics, Western Michigan University, USA

We propose a Bayesian spatial model for time-to event data in which we allow the censoring mechanism to depend on covariates and have a spatial structure. The survival model incorporates a cure rate fraction and assumes that the time to event follows a Weibull distribution, with covariates such as race, stage, grade, marital status and age at diagnosis being linked to its scale parameter. With right censoring being a primary concern, we consider a joint logistic regression model for the censoring indicator, allowing dependence on covariates and including a spatial structure via the use of uncorrelated and correlated random effects. We apply the models to examine prostate cancer data from the Surveillance, Epidemiology, and End Results (SEER) registry, which has a marked spatial variation.

## **Parallel Session 5 Spatial Survival And Registry Data Analysis II**

### **Oral Communication 01 | Invited Speaker**

#### **A new approach to small area cancer survival estimation**

**Susanna Cramb**

Cancer Council Queensland, Canada; ARC Centre of Excellence for Mathematical and Statistical Frontiers, Queensland University of Technology (QUT), Canada

Net cancer survival is commonly estimated via cause-specific or relative survival. However, there are few spatial relative survival models. This talk will present a recently developed method that can be applied to either net survival estimate: a Bayesian spatial flexible parametric survival model, and its application to the development of a National Cancer Atlas for Australia.

## Oral Communication 02

### Spatial patterns in multiple sclerosis: A case-control study using Danish register data 1971-2013

**Kristine Bihrmann<sup>1</sup>, Nete Munk Nielsen<sup>2</sup>, Rikke Baastrup Nordsborg<sup>1</sup>, Annette Kjær Ersbøll<sup>1</sup>**

School of Public Health, the University of Saskatchewan, Canada

**Background:** Multiple Sclerosis (MS) is a chronic disease of the central nervous system. Most MS patients experience their first clinical symptoms between 20 and 40 years of age and MS is considered a leading cause of disability among young and middle-aged adults in the developed world. Its aetiology is largely unknown, but commonly assumed to be a complex interaction between genes and environment. Previous studies have suggested that the first two decades of our life could be a period of particularly high susceptibility to environmental risk factors relevant for MS, and environmental exposures *in utero* and during puberty could be of specific importance. Studying spatial patterns in the occurrence of MS may potentially lead to identification of environmental risk factors for development of MS.

The aim of this study was to investigate the spatial pattern in the occurrence of MS in Denmark with focus on residential addresses prior to onset of disease, more specifically at date of birth and 15 year birthday. The spatial pattern was evaluated by 1) assessing the spatial variation in the risk of later in life developing MS, and 2) assessing spatial clustering of later MS cases.

**Materials and Methods:** Data were based on linkage between the Danish Multiple Sclerosis Register and the Civil Registration System with current and historical residential addresses. The study included 14,300 persons with clinical onset of MS in the period 1971-2013, and 5 age- and sex-matched controls per MS case. Spatial variation in risk was estimated by kernel regression, and *K*-function analysis was used to evaluate spatial clustering

**Results:** Significant spatial variation in the risk of later in life developing MS was found, and the risk estimates based on residence at birth and age 15 were similar. A significantly lower risk of later in life developing MS was found in Lolland, the central Jutland, Northern Jutland and the capital Copenhagen, whereas a significantly higher risk was found in Eastern Jutland and in some local areas in Funen and Zealand. The estimated risk in areas with the highest risk was about 2 times higher than the estimated risk in areas with the lowest risk.

Later MS cases showed no spatial clustering.

**Conclusion:** The risk of later in life developing MS according to residence at birth and age 15 varied across Denmark which may reflect one or more risk factors in the aetiology of the disease. Further studies are needed to confirm that. No spatial clustering of later MS cases was found, suggesting that potential risk factors are not related to having lived very close together.

## Oral Communication 03

### Acute Myocardial Infarction Via Verde (AMI-VV): A geographical approach to assess its impact on in-hospital mortality

**Francesca Fiorentino, Pedro Cabral**

Centro de Estudos de Medicina Baseada na Evidência (CEMBE)-  
Faculdade de Medicina da Universidade de Lisboa, Portugal

**Introduction:** Since 2005, a program named acute myocardial infarction (AMI) *via verde* (VV) which organizes a fast track in emergency department for AMI cases was gradually introduced in the Portuguese National Health System hospitals. This study aims to investigate whether hospital admissions for AMI via emergency department are characterized by higher mortality rate when patients live further from hospitals with VV.

**Methods:** Pooled data from the 2011, 2012, 2013 and 2015 Diagnostic-Related-Group database were analysed. The analysis was restricted to patients resident in Lisbon and Tejo Valley region, which is subdivided into 526 parishes (*freguesias*) where approximately a third of Portuguese population lives. Patients admitted via emergency department with main diagnosis of AMI, aged 60 and over were included in the analysis (N=14,075). The road network of the region was downloaded directly from the OpenStreetMap (OSM) archive, freely accessible online. It was estimated the distance in travel time between the expected patients' residence and the closest hospital with AMI VV. Each patient was expected to live in the mean centre of the geographic unit (*freguesia*) where he/she had residence.

The mean centre of each *freguesia* was computed after distributing the population within each of the 526 geographic units applying a dasymetric mapping method. Multivariate logistic regression was used for determining the association between distance from the hospital with VV and in-hospital mortality. Control variables included: indexes of episode complexity and demographic characteristics.

**Results:** The in-hospital mortality was found to not significantly depend on the distance between patients' residence and the closest hospital with AMI VV at a 5% significance level. Further research is needed to assess the impact of the program on the health outcomes of Portuguese population experiencing an AMI.

## Oral Communication 04 | Invited Speaker

### From politics to mathematics: Exploring optimal air ambulance base locations in Norway using advanced mathematical modeling

**Røislien J<sup>1,2,3</sup>, van den Berg PL<sup>4</sup>, Lindner T<sup>2,5</sup>, Zakariassen E<sup>2,6</sup>, Aardal K<sup>4,7</sup>, van Essen JT<sup>4,7</sup>**

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<sup>3</sup> Department of Biostatistics, Institute of Basic Medical Sciences, University of Oslo, Oslo, Norway;

<sup>4</sup> Delft Institute of Applied Mathematics, Delft University of Technology, Delft, The Netherlands;

<sup>5</sup> SAFER (Stavanger Acute Medicine Foundation for Education and Research) and Stavanger University Hospital, Stavanger, Norway;

<sup>6</sup> Department of Global Public Health and Primary Care, University of Bergen, Bergen, Norway;

<sup>7</sup> Centrum Wiskunde & Information, Amsterdam, The Netherlands.

Norway has a nationwide physician manned air ambulance service with 12 bases, established through historical local engagement from the 1970s. The service is considered essential in order to achieve the desired equality in healthcare, and has long been a topic of public debate. Government requirements state that 90% of the population should be reached within 45 minutes. Using the Maximal Covering Location Problem (MCLP) facility location optimization model we estimate optimal helicopter base locations, both in green field scenario and conditioning on the existing base structure. Results indicate that the whole population could be reached in 45 minutes or less using nine optimally placed bases. The current base structure could be improved upon by moving or adding one or two select bases.

## Oral Communication 05 | Invited Speaker

### Geographical clustering of service goal fulfillment for emergency ambulances in the capital region of Denmark

**Annette Kjær Ersbøll**

Statens Institut for Folkesundhed, Syddansk Universitet, Denmark

**Background:** Ambulance response time (RT) is a common quality indicator in Emergency Medical Services (EMS). Service goals have been developed to increase the EMS quality, including RT target values. Target values were: 13 min and 25 min for 90% of the ambulances dispatched with highest priority 1 and priority 2, respectively. We aimed at examining and identifying areas with significantly higher proportion of calls with RT above the recommended target values.

**Methods:** A total of 146,256 calls were included in the analysis from the Capital Region of Denmark with a catchment area of 1.7 mill individuals. Data were electronically collected and included geographical location of pick-up, priority response level, and RT. Small-area estimation methods were used to estimate smooth maps of the geographical distribution of the proportion of calls with RT above the target values. Spatial clustering was performed using spatial scan statistics to identify areas with significantly higher proportions of calls with RT above the target values.

**Results:** The median RT was 6:05 min and above the target value in 5.6% of priority 1 ambulances. For priority 2 ambulances, the median RT was 13:25 min and 12.4% were above the target value. Areas with significantly higher proportions of calls with RT above the target values were identified for both response priority levels with some overlap between the clusters.

**Conclusion:** Using geographical methods areas with a significantly higher proportion of long RT were identified and can be used to allocate resources to improve RT in certain areas.

## Parallel Session 6 Clustering Of Temporal Trends In Space-Time Disease Mapping

### Oral Communication 01 | Invited Speaker

#### A multivariate model for estimating the changes in health inequalities across Scotland over time

**Eilidh Jack, Duncan Lee, Nema Dean**

University of Glasgow

Disease risk is not constant over space and time and is often impacted by exposure to risk inducing behavior such as consumption of alcohol. Poverty and deprivation are major factors in the spatial variation observed in the risk of disease, with more highly deprived areas usually exhibiting elevated levels of disease risk. This difference in disease risk between social groups and population areas is known as a 'health inequality', and these are caused by a fundamental inequity in the distribution of income, power and wealth across Scotland. Although there was a major reduction in health inequalities in Scotland between 1920 and 1970, there still exists gaps between Scotland's most affluent and most deprived areas, and in some cases these gaps are still widening.

National Health Service (NHS) Scotland consists of 14 regional NHS Health Boards, which are responsible for the protection and improvement of their population's health and for the delivery of frontline healthcare services. It is therefore of interest to estimate the scale of health inequality in disease risk over Scotland and between these Health Boards and investigate how this is changing over time.

Our objective is to propose a multivariate spatio-temporal model and apply this to data containing hospital admissions for four of Scotland's biggest killers, namely, coronary heart disease, cancer, stroke and respiratory disease. This will allow us to answer the following three key questions. First of all, are there health inequalities between Scotland's 14 regional Health Boards? If there are inequalities, have they remained constant or changed over time? Finally, what impact do the covariates have on disease risk?

## **Oral Communication 02 | Invited Speaker**

### **Spatio-temporal log-Gaussian Cox processes for public health data**

**Theresa Smith**

University of Bath, UK

Health data with high spatial and temporal resolution are becoming more common, but there are several practical and computational challenges to using such data to study the relationships between disease risk and possible predictors. These difficulties include lack of measurements on individual-level covariates/exposures, integrating data measured on different spatial and temporal units, and computational complexity. In this talk, I outline strategies for jointly estimating systematic (i.e., parametric) trends in disease risk and assessing residual risk with spatio-temporal log-Gaussian Cox processes (LGCPs). LGCPs are a type of inhomogeneous Poisson point process where the log intensity surface is a GP. I will present and compare computational tools for using spatio-temporal LGCPs to investigate the roles of environmental and socio-economic risk-factors in the incidence of *Campylobacter* in England.

## Oral Communication 03 | Invited Speaker

### Understanding the mortality burden of air pollution in Michigan accounting for preferential sampling

**Veronica J. Berrocal<sup>1</sup>, Graciela Mentz<sup>2</sup>, Amy J. Schulz<sup>2</sup>**

<sup>1</sup> Department of Biostatistics, University of Michigan, School of Public Health, USA;

<sup>2</sup> Department of Health Behavior and Health Education, University of Michigan, School of Public Health, USA

The deleterious effect of exposure to ambient air pollution on human health has been recognized in several environmental epidemiological studies. Linking ambient air pollution exposure to health outcomes is often problematic as ambient air pollution is not measured everywhere or where health data is available. To address this issue, several strategies have been proposed, including using spatial statistical models to predict (or impute) the unobserved air pollution levels at the needed spatial locations and resolution. However, most of these model do not take into account the fact that air quality monitors are preferentially located at sites where pollution levels are expected to be high (preferential sampling). In this talk, we focus on fine particulate matter, as air pollutant, and mortality in Michigan during years 2001-2010, as health outcome, and we propose spatio-temporal statistical models that: (i) address the preferential placement of monitors, (ii) combine different data sources on air pollution, and (iii) evaluate the impact of the preferential placement of air quality monitors on the estimated mortality burden of PM<sub>2.5</sub> in Michigan over a 10-year period.

## Oral Communication 04

### Using Hierarchical clustering of timeseries for variable selection in Dengue forecasting

**Flavio Codeço Coelho**

School of Applied Mathematics, Getulio Vargas Foundation

Forecasting of dengue incidence timeseries is a difficult task due its complex dynamics. These dynamics are the result of many exogenous factors which include but are not limited to seasonal weather patterns, unpredictable arrival of new cases, variations of the immunological structure of the population,etc.

The InfoDengue system ([info.dengue.mat.br](http://info.dengue.mat.br)) is an online data analysis system focused on the dynamics of arboviroses. It integrates meteorological and epidemiological data, as well as social network data, to provide nowcasting of cases and a 4-level alert system, for Dengue and Chikungunya. Currently Infodengue services more than 500 Brazilian cities in three states.

The nowcasting provided by InfoDengue is already of great value to health authorities since the recording of reported cases may experience delays of up to 3 months. Nevertheless, Forecasting of the weekly incidence series has been a goal of InfoDengue since the beginning, and a hot request by many stakeholders.

It is well established that the spatial dimension is very important for the understanding of the dynamics of infectious diseases. Many infectious diseases display clear spatial patterns of spread, which when properly monitored, may provide early warning to certain localities on the path of this spatial spread. Even for endemic diseases with seasonal dynamics such as dengue, the spatio-temporal dynamics of exogenous factors such as weather, can also help to anticipate the increase in seasonal incidence.

Since the InfoDengue system maintain hundreds of continually updated incidence time series It makes easy to use non-local timeseries as exogenous variables for the forecast of any given timeseries. However, the problem of choosing which series are informative for the dynamics of one series is not a simple one. The full model, i.e., using all the other series to predict each one, is not a good idea, for obvious reasons.

In this paper we discuss the use of hierarchical clustering of all the timeseries in Infodengue to determine an optimal set of exogenous series for the forecast of each locality. We clustered the incidence timeseries within each state, using the correlation between the series as the distance metric and complete linkage as the clustering algorithm. The clustering led to the formation of well defined clusters with 2 to 15 cities each.

A Poisson Generalized Autoregressive Score (GAS) model was then used to generate forecasts for each city using the cities in its cluster as exogenous series. The models are then inspected to see whether each exogenous variables has any predictive power and the model is reduced to retain only those which are significantly associated with the series being modelled.

5-week forecasts are generated from each model and compared to the forecast of a univariate GAS model, in terms of MASE and coverage.

We found that the proposed method of variable selection is both light enough to be used on an online forecasting system and can propose models which are better for incidence forecasting than the univariate base model.

## Oral Communication 05

### A Bayesian Space-Time Model for Clustering Areal Units based on their Disease Trends

**G. Napier<sup>1</sup>, D. Lee<sup>1</sup>, C. Robertson<sup>2;3;4</sup>, A. Lawson<sup>5</sup>**

<sup>1</sup> School of Mathematics and Statistics, University of Glasgow;

<sup>2</sup> Department of Mathematics and Statistics, University of Strathclyde;

<sup>3</sup> Health Protection Scotland;

<sup>4</sup> International Prevention Research Institute, Lyon;

<sup>5</sup> Department of Public Health Sciences, Medical University of South Carolina

Disease risk varies in space and time, and a large amount of research has identified clusters of areal units exhibiting elevated risks. However, almost no research has extended the clustering paradigm to identify groups of areal units exhibiting similar temporal disease trends, which is the methodological contribution of this work. We present a novel Bayesian hierarchical mixture model for achieving this goal, with inference based on a Metropolis coupled Markov chain Monte Carlo ((MC)<sup>3</sup>) algorithm. The effectiveness of the (MC)<sup>3</sup> algorithm compared to a standard MCMC implementation is demonstrated in a simulation study, and the methodology is motivated by an important case study in Scotland. It concerns respiratory related hospitalisations, and investigates over a 10 year period which parts of the city of Glasgow have shown an increased risk, which have shown a decreased risk, and which have shown no change. Software has been developed in conjunction with this work, and will be made freely available as part of the R package CARBayesST.



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## **Parallel Session 7 Data Science Applied To Health: Strategies And Tools For Big Data, Machine Learning And Data Mining**

### **Oral Communication 01**

#### **Mining big data for environmental epidemiological analyses**

**D. Fecht<sup>1</sup>, R. Ghosh<sup>1</sup>, A.F. Sterrantino<sup>1</sup>, M. Chadeau<sup>2</sup>**

<sup>1</sup> UK Small Area Health Statistics Unit, School of Public Health, Imperial College London, London, UK;

<sup>2</sup> MRC-PHE Centre for Environment and Health, School of Public Health, Imperial College London, London, UK

Traditionally, environmental epidemiology analysis has aimed to analyse associations between one or multiple pollutants and a single health outcome. Recent advances in computing power and statistical methodology have made multi-level analysis of complex disease aetiologies realistic, but so far, "big data" health analyses have mostly focused on the analysis of -omics data.

We aim to agnostically investigate the associations between air pollution exposure (nitrogen dioxide and particulate matter) and all hospital admissions in England (2009-2012) using a range of biostatistical techniques including clustering and classification approaches that easily scale to a large number of participants.

The health databases of the UK Small Area Health Statistics Unit (SAHSU) contain well over half a billion routinely collected health records with over 500 million in NHS Hospital Episode Statistics (HES) alone. This readily available data source within SAHSU offers a unique and exciting opportunity to go beyond traditional environmental epidemiological analysis and simultaneously investigate a multitude of exposures and health outcomes.

Applying data mining techniques to analyse health outcomes associated with a common environmental exposure may help validate previously identified associations and identify new combinations of health effects. Potential clustering of certain health outcomes, both within and between individuals, could help to elucidate potential mechanistic pathways involved in the association between health and environmental exposure, highlight areas of future research needs and generate new hypotheses.

## Oral Communication 02

### Relative risk estimates from spatial and space-time scan statistics: Are they biased?

**Marcos Prates, Martin Kulldorff and Renato Assunção**

Universidade Federal de Minas Gerais, Brazil

The main goal of the scan statistic is to detect and evaluate the statistical significance of spatial or space-time clusters that cannot be explained by the assumption of spatial or space-time randomness. Suppose we observe a number of events located within a geographical region. Naus introduced the notion of a spatial scan statistic with a rectangular window of fixed size, scanning over the space for an unexpectedly large cluster of observations. With the increase of computational power, many alternative methods were proposed in the literature and spatial and space-time scan statistics have been widely applied in a variety of fields as infectious diseases, cancer epidemiology, parasitology and others.

Inference is performed using Monte Carlo hypothesis testing for each cluster detected by the spatial and space-time scan statistics resulting in a p-value that is adjusted for the multiple testing inherent in the many cluster locations and sizes considered. That is, if the null hypothesis of no clusters is true, then the probability of detecting any statistically significant cluster anywhere on the map is 0.05 for an alpha level of 0.05. While the p-values are the main results of a scan statistic, researchers often look at the observed relative risks of the detected cluster to better understand and interpret the results. However, it is not clear how the observed relative risk works as an estimate of a true underlying relative risk of the area in the detected cluster. Intuitively, the estimates of the relative risk

returned by a scan statistic may be upward biased, since it cherry picks areas with high rates and excludes those with low rates when determining the detected cluster.

Using the purely spatial scan statistic and the prospective space-time permutation scan statistic has been conducted a study to investigate if there is any bias in the estimated relative risk, its direction and its magnitude, to date no formal study on the behavior of the relative risk of these methods have been investigated. For the prospective space-time permutation scan statistic we introduce two novel relative risk definitions and describe how they can be estimated.

The results are that the relative risks observed for the spatial scan statistic indeed has an upward bias but the bias becomes negligible, tending to zero, when the true underlying relative risk increases and there is enough power to correctly detect the cluster. This asymptotic behavior is not observed for the prospective space-time permutation scan statistic, for which there is a conservative downward bias, so that the observed relative risks tend to be smaller than the true relative risks. When interpreting the results of spatial and space-time scan statistics, it is important to be aware of these properties of the observed relative risk in the detected clusters.

## Oral Communication 03 | Speaker Invited

### Big Data and Healthcare

#### **João Gama**

INESC TEC, University of Porto, Portugal

We are living in a world of digital data. We routinely collect digital data in most of our daily activities. The advent of the Internet of Things - IoT will connect millions of devices to the internet. Recent reports refer to healthcare as one of the domains where big data technologies might have more impact. Healthcare is a domain that requires decisions supported by knowledge. Healthcare is one the domains that most benefit from machine learning and the technologies to analyse, extract knowledge, and understand data. We collect electronic medical records at large scale. Medical images, reports of lab analysis, all type of sensor measurements, physician reports, etc. are the ingredients for big data. Making sense from data requires cross-checking all different types of data. The benefit is a much broad view, more detailed studies for identifying sub-groups, predicting trends, anticipating unexpected lateral effects, anomalies, etc. In this talk, we will present the main tasks and approaches to extract knowledge from data. We will present healthcare illustrative examples and real-world applications of machine learning to medicine.

## Oral Communication 04 | Speaker Invited

### Spatial Aspects of Collaborative Demography via Genealogical Data

**Arthur Charpentier<sup>1</sup> & Ewen Gallic<sup>2</sup>**

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Population dynamics examines the evolution of size and age of populations through theoretical models and simulations. With the emergence of the Web 2.0, new ways of massively collecting and sharing data have emerged, therefore allowing to provide applications to the theory using real data. In this paper we rely on genealogy data collected on GENEANET, an online site for family history records. With more than 3 billion records in Europe, GENEANET provides the most important European genealogy database. We focus on a sample of one hundred individuals born in a small French town and track their offspring, their mortality, as well as their geographic movements.

## **Oral Communication 05 | Speaker Invited**

### **Anomaly detection in the Brazilian Health Care Payment System**

**Renato Assunção**

Federal University of Minas Gerais, Brazil

We describe INFOSAS, a modern, interactive and automatic outlier detection in the payment system to the Sistema Único de Saúde (SUS) services providers for subsequent audit and verification. We apply statistical data mining algorithms to SUS data covering 269 groups of medical procedures in 5570 municipalities and more than 23,000 health care providers, summing up more than 1.5 million time series. We found 6811 providers with amounts considered excessive and discrepant. This group of providers is quite uneven. The surplus value concentrated in the 100 most critical providers is 210 million of reais, or 51% of the total surplus estimated. The INFOSAS system can be used to point out to cases for auditing process, improving their quality and reducing the frequency of unnecessary audits.



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## Parallel Session 8 Modifiable Areal Unit Issues And Methods

### Oral Communication 01 | Invited Speaker

#### Multiscale spatiotemporal models for aggregated small area health outcomes

**Andrew Lawson**

Medical University of South Carolina, Charleston, USA

One of the main interests in modifiable areal unit problems is the scaling effect caused by data aggregation from a fine into a coarse scale level. Although many studies adjust for this scaling effect using multiscale spatial models, there are limited methods that account for scaling and spatiotemporal effects simultaneously. Here, we propose novel multiscale spatiotemporal models to describe spatiotemporal risk variations across scales. Our approach uses joint models that link the risks across scales through shared random effects. The proposed models can also address contextual effects that arise from the classification of areal units into larger areal units. We applied these models to data on incidence of sepsis in the state of Georgia across the counties as well as the public health districts that are created for the regulation of public health resources. We found that applying models that adjust for contextual, scale, and spatiotemporal effects result in a better model fit and a more unbiased spatiotemporal risk variation than other models that ignore those effects.

## Oral Communication 02

### Promoting understanding of the modifiable areal unit problem in public health and epidemiology with dynamic geovisualization

**Brittany Krzyzanowski**

University of Minnesota

Epidemiological investigation of health and disease across space relies heavily on the use of predetermined regions (e.g., school district boundaries, census tracts) as their unit of analysis, but--because these delineations are arbitrary and not built with a research question in mind-- the outputted coefficients are vulnerable to the effects of the MAUP. This is especially concerning knowing that the MAUP effects are more prevalent in complex, multivariate, cross-correlated data which characterizes most public health data. The effects of the MAUP are potentially dramatic for studies relying on geographic units for analyses, and therefore study outcomes are largely dependent on choice of zoning system and level of aggregation. Many epidemiologists are not trained to engage in "spatial thinking" and may be unaware of the effects of the MAUP on aggregated data. Often geographic studies of health neglect to discuss MAUP effects in their limitations.

Therefore, in order to shed light on the pervasiveness of MAUP in spatial epidemiologic research we created a dynamic geovisualization that illustrates MAUP effects on the relative risks outputted from Poisson regression in both simulated and real epidemiological data. To our knowledge, no such animation exists or is being used to promote spatial thinking in epidemiology. We relied on the well-established Automated Zoning Procedure (AZP) to create districts within the Minneapolis metro area, using block groups as the basic spatial unit of aggregation, and Windows Movie Maker to build the geovisualization from 10 different solutions of redistricted zones. Additionally, this project engages with the innovative domain of CyberGIS to manage the computationally intensive regionalization strategy by utilizing parallel processing to execute the algorithm within a Python script. The geovisualization serves as a research instrument and instructional tool for facilitating understanding of MAUP, and encourages geographically meaning regionalization and appropriate use of our automated zoning script. Our primary goal is to make our results accessible to others and therefore we intend to host the geovisualization and parallelized Python script on an informational web resource tailored for broader public health research audiences.

## Oral Communication 03

### The effects of spatial resolution in disease mapping: A simulation study

**Garyfallos Konstantinoudis<sup>1</sup>, Christian Kreis<sup>1</sup>, Dominic Schuhmacher<sup>2</sup>, Ben D. Spycher<sup>1</sup>**

<sup>1</sup> Institute of Social and Preventive Medicine, University of Bern, Switzerland;

<sup>2</sup> Institute for Mathematical Stochastics, University of Goettingen, Germany

**Introduction:** The main goal of disease mapping is to identify areas with elevated risk. Such analyses are often hampered by the limited geographical resolution of the available data (aggregation by administrative areas). If precise geocodes are available it is natural to use methods for point pattern data. However, these methods are computationally demanding and their advantages over traditional disease mapping of areal data are unclear. In this study we investigated the effect of spatial resolution on the mapping of a rare disease.

**Methods:** We simulated data mimicking childhood leukaemia incidence over a 31-year period in the Canton of Zurich, Switzerland. Geocoded residence was available for the entire population at risk from the 2000 national census. We included 3 circular areas (5km radius) with twofold higher risk differing in population density (urban, semi-urban and rural). We analysed the simulated point pattern data (case locations) using log Gaussian Cox processes (LGCP) and as area count data aggregated to 500x500m, 1x1km and 2x2km grid cells and to the municipality level using conditional autoregressive (CAR) models. We used Markov Chain Monte Carlo (MCMC) and Integrated Nested Laplace Approximation (INLA) for inference.

**Results:** We found that LGCP fitted to point pattern data were more sensitive in identifying high-risk areas than CAR models using area count data. While all methods identified the urban high-risk area, none of them detected the rural high-risk area. For LGCP, the mean estimated RR in the high-risk areas compared to the remaining areas was 1.50, 1.17, 0.96 in the urban, semi-urban and rural areas, respectively. The CAR models tended to over-smooth and underestimate the risk in high-risk areas. Corresponding numbers for CAR models were 1.067, 1.004, 0.980 using 500x500m grid cells and 1.017, 1.002, 1.000 using municipality level data. Convergence and mixing of the log Gaussian Cox processes depended strongly on the selected priors.

**Conclusion:** Disease mapping based on aggregated data of a rare disease may fail to identify areas of increased risk, particularly in rural areas. While LGCP based on precise residential locations are more sensitive to localised risk increases, fitting these models is technically more challenging and the choice of priors requires careful consideration.

## **Oral Communication 04 | Invited Speaker**

### **Using Change of Support (COSP) approach in disease mapping: an application to mapping malaria in low transmission settings.**

#### **Victor Alegana**

Geography and Environment, Worldpop group, University of Southampton, UK

Fine scale multi-temporal mapping in low malaria transmission settings remains a challenge, as most surveillance data is assembled at administrative level or representative of a hospital catchment. In the past, areal-level models have been proposed, but the problem of modifiable areal unit (MAUP) persists. Here, we demonstrate how malaria incidence can be modelled via the change of support platform as a special case of misalignment. We derive fine spatial and temporal maps of incidence from administrative level malaria case data, incorporate metrics of health care use and environmental factors via a Bayesian approach. We then combined the predicted incidence estimates with population maps to estimate clinical burdens to increase the operational application in identifying areas and seasons that can be targeted for improved surveillance and interventions. Fine spatial resolution maps produced using this approach have been used to target resources to specific local populations, and to specific months of the season. This remote targeting can be especially effective where the population distribution is sparse and further surveillance can be limited to specific local areas.

## Oral Communication 05 | Invited Speaker

### Investigating aggregation effects in small area health data using synthetic microdata and automated zone design

**David Martin<sup>1,2</sup>, James Robards<sup>1</sup> and Chris Gale<sup>2</sup>**

<sup>1</sup>National Centre for Research Methods

<sup>2</sup>Administrative Data Research Centre, University of Southampton, Southampton, UK

Many population health studies involve small area aggregation. Confidential individual health records may be referenced by address or property identifiers which permit the calculation of spatial measures such as distances to health service locations or exposure to environmental conditions. However, population denominators and contextual variables, such as social deprivation indicators, are generally directly reliant on published data aggregated over small areas. Publication or mapping of analysis results will also generally require spatial aggregation as a statistical disclosure control mechanism to protect the identity of individual records. The design of these spatial aggregations often reflects administrative boundaries and is rarely under the control of the researcher.

Previous research has sought to investigate the modifiable areal unit effects present in such data using automated zone design methods, which are able to rapidly generate multiple alternative zonations with specified statistical properties, but have generally been limited to the reaggregation of small areas containing already-published data. In particular, it has not been possible to assess the implications of aggregation for the representation of individual and household-level spatial measures. It would

not be permissible or acceptable to use real record-level data for the purpose of producing potentially disclosive small area aggregations.

This paper presents progress on a current research agenda concerned both with disclosure control and modifiable areal unit challenges, particularly focusing on self-reported health and access to services. It is based on a purpose-built synthetic microdataset for England and Wales in which individual records from a census microdata sample have been duplicated and allocated into household structures, matched to known marginal values for a series of geographical units and constrained to fall within a high resolution model of the true spatial distribution of households. AZTool automated zone design software is used to recombine these records into multiple alternative area aggregations. We here exploit these synthetic data to explore the impact of zone design decisions on observed associations between health status, distance calculations and small area indicators.

This research being jointly undertaken at the UK Economic and Social Research Council's National Centre for Research Methods and Administrative Data Research Centre for England, using synthetic microdata from the Consumer Data Research Centre.

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## **Parallel Session 9**

### **Social Networks And Spatial Epidemiology: Tools, Opportunities And Challenges**

## **Oral Communication 01 | Invited Speaker**

### **On the promises, challenges and risks of Pokémon Go and similar geosocial (location-based) exergames**

**Maged N. Kamel Boulos**

University of the Highlands and Islands, Scotland, UK

Physical activity (in the right amount) is a key ingredient of a healthy lifestyle. It improves physical and psychological well-being, reduces stress, decreases a person's risk of developing major diseases, such as type 2 diabetes, heart disease, stroke and cancer, and lowers the risk of pre-mature death. Introduced in July 2016, Pokémon Go, a mobile location-based social exergame with potential and documented health benefits, is perhaps the most popular ever example of geosocial (location-based) exergames, with an added augmented reality twist. Created by the same experts behind Google Earth, Pokémon Go relies heavily on the location services of smartphones (GPS[Global Positioning System], Wi-Fi, and mobile networks) to deliver its multiplayer experience, but not without documented and potential misuses or safety and privacy concerns. This presentation will discuss the health merits and risks of Pokémon Go and similar geosocial exergames.

## Oral Communication 02 | Invited Speaker

### Support Vector Subset Scan for Spatial Pattern Detection

**Dylan Fitzpatrick and Daniel B. Neill**

Event and Pattern Detection Laboratory Carnegie Mellon University, Pittsburgh, USA

We present the support vector subset scan (SVSS), a new method for detecting localized and irregularly shaped patterns in spatial data.

SVSS builds on the fast subset scan, which detects significant spatial patterns by efficiently maximizing a log-likelihood ratio statistic over subsets of points. SVSS introduces soft spatial constraints to the fast subset scan in the form of penalties to the log likelihood ratio statistic, learned iteratively based on distance to a high-dimensional kernel support vector machine decision boundary. These constraints result in detected patterns that are spatially compact and irregular in shape. In simulated experiments, SVSS outperforms competing methods on the task of detecting randomly generated and irregular patterns. We demonstrate the real world utility of SVSS on West Nile virus outbreak detection in Chicago, IL and crime hot-spot detection in Portland, OR. This work was partially funded by NSF grant IIS-0953330.

## Oral Communication 03

### Going beyond with social network data: from disease accounting to identification of risk zones

**Roberto C.S.N.P. Souza<sup>1</sup>, Renato Assunção<sup>1</sup>, Daniel B. Neill<sup>2,3</sup> and Wagner Meira Jr.<sup>1</sup>**

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<sup>3</sup> H.J. Heinz III College – Carnegie Mellon University

Health surveillance systems usually identify high risk zones based only on the residence address or the working place of diseased individuals. This approach ignores a multitude of exposures the individuals are daily subject to and therefore provides little information about the actual places where people are infected, the truly important information for disease control. In this context, the recent availability of spatial information provided by geo-tagged social media data offers a unique opportunity: By identifying and following diseased individuals, we obtain a collection of sequential geo-located events that approximately describe the spatial distribution of each individual over time, as they drift on the map. This data may constitute a more precise source of information to detect high risk regions. Standard techniques for spatial cluster detection fail to address this new setting as they require a single location to each individual under analysis.

In this work, we discuss a more general problem of detecting regions that increase the risk of infection by a given disease when the input data consists of individuals' movement patterns. In particular, we present three different models for this task. Each of these models combines two main components: the mobility of the target population and the risk associated to each candidate region. We discuss how the presented models take each component into account in the search for anomalous patterns. In order to better illustrate the discussion, we present results obtained by each of the three models in different simulated scenarios. We also demonstrate the effectiveness of our models by applying them to a large collection of geo-located Twitter messages from Brazil. In particular, we target the identification of regions that increase the risk of infection by dengue, a vector-borne disease that affects millions of people in Brazil annually, and billions worldwide. Identifying the most risky places would be valuable because health officials could focus the expensive and diffuse preventive efforts undertaken until now. We present results for a set of large Brazilian cities and discuss how our approach can help in this challenging task.

## Oral Communication 04

### Developing a web-based survey application to collect contextually-relevant geographic data with exposure times

**Abby E Rudolph<sup>1</sup>, Karin Tobin<sup>2</sup>, Carl Latkin<sup>2</sup>**

<sup>1</sup>Boston University School of Public Health, Department of Epidemiology, Boston, Massachusetts, USA;

<sup>2</sup>Department of Health Behavior and Society, Johns Hopkins Bloomberg School of Public Health, Baltimore MD, USA

**Background:** Although studies that characterize the "risk environment" by linking contextual factors with individual-level data have led to advancements in HIV/HCV and substance use research, there are opportunities to refine how relevant neighborhood exposures are defined to reduce the potential for exposure misclassification. For example, for those who do not inject at home, injection risk behaviors may be influenced more by the environment where they inject than where they live. Similarly, among those who spend more time away from home, a measure that accounts for different neighborhood exposures and weights each according to the time spent in each location may better predict health service use than one's residential environment. To address this gap, we developed a web-based tool that interacts with Google Maps APIs to collect locations and the time spent in each location. Our analysis will examine the extent of overlap across different location types and compare different methods for measuring neighborhood exposure.

**Methods:** 340 persons who use drugs in Baltimore (5/14-1/16) completed an interviewer-administered web-based survey to collect information about where they were recruited, worked, lived, socialized, and injected drugs. For each location type,

participants gave an address/cross-street and then navigated to and confirmed each location with the map and street views. Geographic coordinates (and time/location) were joined to neighborhood data (walk score, vehicle ownership, unemployment, crime, % vacant lots) at the tract-level. We computed neighborhood exposures based on 1) injection location, 2) residential location, and 3) a weighted cumulative exposure and compared the measures using t-tests.

**Results:** Participants spent 89% of their at home, 71% where they injected, 22% where they worked, 30% where they socialized, and 11% where they were recruited. Residential locations were most likely and injection locations were least likely to overlap with other location types. The majority used public transportation (80%) or walked (10%) to get around, and among those who injected drugs, the median amount of time traveled to get drugs was 30 minutes. Compared with one's weighted cumulative neighborhood exposure, participants reported injecting in areas with more vacant houses (18% vs. 15%;  $p=0.03$ ), higher unemployment (19% vs. 18%;  $p=0.04$ ) and lower vehicle ownership (53% vs. 58%;  $p=0.01$ ). People lived in areas with lower walk scores than the areas where they injected ( $p=0.05$ ).

**Conclusions:** This analysis revealed significant differences in one's neighborhood exposure when it was defined by injection location vs. residential location vs. when all locations were considered relevant. Future analyses are needed to determine which exposure measures are most strongly correlated with risk behaviors and health service use and to explore whether associations between individual-level behaviors and neighborhood exposures are modified by exposure times.

## Oral Communication 05

### Georeferenced Twitter data to estimate the temporal variation of the density of people in each sample area in Madrid using GIS technology

**Dr. Francisco Javier Escobar Martínez<sup>1</sup>, Juan Luis Bermúdez González<sup>2</sup>**

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Epidemiological studies are often based on government data on population and density, and assume that people are in their respective place of residence throughout the day. Given the acknowledged impact that urban conditions exert over population health, environmental epidemiological studies have focused on the relationship between place of residence and characterization of residential area. However, most people are also influenced by environmental conditions of work, leisure, education or other places they visit.

Taking advantage of this line of work and supported by the current availability of geolocated Twitter data our objective is to develop a GIS-based method to estimate actual spatial-temporal presence of people in urban areas. This includes knowing the occupation during the day for any of the study areas in Madrid, and as a secondary result the relationship between the place of the Tweet and the place of origin contained in the user registry.

The study has been conducted in the city of Madrid, with a population over 3 million people. Knowing the real data on the number of Twitter users is not easy because there are ghost users, duplicate accounts and other issues that can influence,

but in the worst case can be estimated that at least 5% of the population in Madrid are active users of this social network. Selected geolocalized information contained in Twitter has been downloaded and cleaned to then be integrated with contextual geospatial information of the city in a GIS environment. Web mapping technology has then been adopted to freely disseminate the information to the largest possible amount of users.

Results allow to estimating number of people present in Madrid administrative units at different times of the day and different days of the week. This in turn permits the estimation of people affected by health-related environmental conditions characterising each urban administrative unit. These results are disseminated under a freely available web-based interactive application.

Given that low populated areas are at times occupied by a high number of people, and inversely some high populated areas are empty during certain hours, the produced cartographic tool provides the basis for prioritising areas under need of intervention in order to improve environmental health conditions in Madrid.

Despite limitations inherent to Twitter data, this tool also will allow to estimating the actual impact of the environmental conditions over population health and will serve as the basis for population estimation when facing emergency procedures after eventual environmental accidents.

## Parallel Session 10 Modelling Climate- Sensitive Disease I

### Oral Communication 01 | Invited Speaker

#### The climatic constraints on the present and future global spread of dengue and Zika

**Oliver Brady**

London School of Hygiene & Tropical Medicine

Over the past 30 years we have seen the global expansion of the arboviruses with dengue, chikungunya and now Zika. However, as mosquito-borne diseases primarily transmitted by *Aedes aegypti*, spread of these arboviruses is inherently limited by the climatic constraints imposed on their vectors.

The principle method through which these climatic constraints act is through vector and virus survival. Hotter temperatures generally speed up viral replication in the mosquito, and improve mosquito survival, but temperatures that are too high can have the opposite effect on mosquito survival.

Mosquito abundance is also highly dependent on precipitation patterns as *Ae. aegypti* typically lays its eggs in small peri-domestic containers, filled either by rainfall or through water storage in times of drought.

These behaviours place key limits on the long term and seasonal distribution of these diseases and in doing so, affect the routes by which they can spread around the globe.

In this talk I will illustrate how models of *Ae. aegypti* suitability and transmission potential can be used to map the seasonal limits of transmission of dengue and Zika. Pairing these maps with data on human movement via air travel allows us to predict how pandemics spread which I will illustrate in the context of the 2015 Zika epidemic. Finally, I will talk about the effect of climate and future urbanization trends on the potential future limits of these diseases and their vectors, with implications for new areas and populations at risk.

## Oral Communication 02 | Invited Speaker

### Dengue spatial diffusion in Brazil. How far will this go? Will zika follow the same steps?

**Christovam Barcellos<sup>1</sup>; Rachel Lowe<sup>2</sup>**

<sup>1</sup>Oswaldo Cruz Foundation, Brazil;

<sup>2</sup>IC3 Catalan Climate Sciences Institute, Spain

Vector-borne diseases, specially dengue, zika and chikungunya, are prevalent in tropical countries and consist in a major public health issue that can be aggravated with global warming. Changes in temperature and precipitation patterns may alter the seasonality of these diseases in regions where the transmission currently occurs, as well as the expansion of transmission areas towards temperate regions and high altitude zones. The objective of this work is to examine the spatial and temporal patterns of the expansion of dengue transmission area in Brazil (2001–2014) with the aim to identify pathways and constraints to dengue diffusion, and compare it to zika recent diffusion along the country.

Synthetic indicators were calculated to characterise timing (year of first dengue outbreak), permanence (number of years with dengue outbreaks) and intensity (outbreak occurrence). The indicators were used to map dengue diffusion and compare cities within different climatic zones, with varying population densities. Currently, a large portion of the country comprises a dengue transmission area, but cities situated in the mesothermal zone, in the south, and remote areas, in the Amazon, are relatively exempt.

Long-term permanence of dengue transmission depends on the existence of a favourable climate, abundant population and connectivity. Large and warm cities sustain and spread dengue viruses, for which specific dengue control measures must be developed. The concentration of outbreaks along climate transition fringes indicates a boundary between two transmission regimes and raises awareness to the effects of ongoing climatic and socio-economic changes.

## **Oral Communication 03 | Invited Speaker**

### **Google Earth Engine: Health Applications of Google's Cloud Platform for Big Earth Data**

**Allison Lieber**

Google

The volume of satellite and other Earth data is growing rapidly, as is the urgent demand for information that can be derived from such data to inform decisions in a range of areas including food and water security, disease and disaster risk management, biodiversity, and climate change adaptation. Google's platform for planetary-scale geospatial data analysis, Earth Engine, grants access to petabytes of continually updating Earth and climate data, programming interfaces for analyzing the data without the need to download and manage it, and mechanisms for sharing the analyses and publishing results for data-driven decision making. This talk will describe Earth Engine and other Google tools and planetary-scale examples such as global monitoring of forest loss and gain and global surface water availability. On a more local scale, multiple sources of data can be combined and deep stacks of temporal imagery analyzed to estimate crop yield, malaria risk, and street-level air pollution.

## **Oral Communication 04 | Invited Speaker**

### **Use of GEE for climate, environmental and disease modelling**

#### **Pietro Ceccato**

The International Research Institute for Climate and Society, NYC,  
USA

Google Earth Engine provides the possibility to analyze Big Data from the new generation of sensors such as Sentinel 1, Sentinel 2. The processing capabilities of GEE allow users to analyze in real time data at high spatial resolution to map environmental and climatic data that can be integrated with disease data. This presentation will showcase the use of GEE to map precipitation, temperature, vegetation, floods in conjunction with disease data.

## Oral Communication 05 | Invited Speaker

### Spatial-temporal analysis of climate factors effects on hospitalization due to falls

**Oliveira CM<sup>1,2,3</sup>, Alves SM<sup>1,2,3</sup>, Bessa AC<sup>1,2</sup>, Pina MF<sup>1,2,4,5</sup>**

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<sup>2</sup>INEB - Instituto de Engenharia Biomédica, Universidade do Porto, Portugal;

<sup>3</sup>ESS/IPP - Escola Superior da Saúde do Porto, Instituto Politécnico do Porto, Portugal;

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**Introduction:** A higher risk of falls in winter, when compared to summer, has been reported, although climatic factors as risk factors for falls have been little studied. Our aim is to identify the effects of climatic factors (CF) on the spatial-temporal distribution of hospitalization for fall-related injuries in older adults (2000-2010).

**Methods:** From the National Hospital Discharge Register we selected admissions of patient's  $\geq 65$  years-old, with diagnosis of fall-related injuries. Data from meteorological stations were obtained from national institute of meteorology ("Instituto Português do Mar e da Atmosfera"). An exposure inference for Portugal was performed by a geostatistical procedure: first, a suitable semivariogram was selected to characterize the spatial dependence, based on the geographical coordinates of the stations, of the year/monthly mean of daily precipitation

(Prec, mm), mean temperature (meanTemp, °C), relative humidity (RelHum, %), sunshine daily hours (SunDur, hours) and atmospheric pressure (AtmPres, hPa); second, a kriging technique was used to interpolate data to each of the places of interest. A spatio-temporal generalized Poisson additive model was used to estimate the relative risk (RR) of fall-related injuries associated with variation in CF adjusting for seasonal pattern, socioeconomic status, rural condition and age-group. A stepwise procedure was used to select the final model based on the smallest Akaike Information Criterion (AIC). Models without and with CF were assessed.

**Results:** We selected 192,422 hospitalizations for fall-related injuries episodes (69.4% in women). On average, women were older than men 80.337.7 vs 77.937.7 years ( $p < 0.001$ ) at admission. Model with better performance (lowest AIC) was the one with all the CF and with interaction between space and time. Seasonality pattern was observed. An increase risk over time and an increase of areas at higher risk was observed in the study period. A significant inverse association between CF and falls was found in women:  $RR_{Prec} 0.916$  (0.896-0.935) per 10 mm,  $RR_{meanTemp} 0.977$  (0.967-0.988) per 5°C,  $RR_{AtmPres} 0.925$  (0.923-0.927) per 10 hPa and in men:  $RR_{Prec} 0.894$  (0.869-0.920) per 10 mm,  $RR_{DurSun} 0.991$  (0.985-0.998) per 1 hour,  $RR_{HumRel} 0.997$  (0.996-0.998) per 1 % and  $RR_{AtmPres} 0.923$  (0.921-0.926) per 10 hPa.

**Conclusion:** The risk of falls has been increasing over time and across regions and the pattern of seasonality continues to be observed even after adjusted for the weather factors. Policy measures should be taken to lock this increase in falls in individuals over 65 years of age.

## Parallel Session 11 Modelling Climate- Sensitive Disease II

### Oral Communication 01 | Invited Speaker

#### Probabilistic dengue predictions based on ensemble seasonal climate forecasts

**Rachel Lowe<sup>1,2</sup>, Anna M. Stewart-Ibarra<sup>3</sup>, Desislava Petrova<sup>2</sup>, Markel García-Díez<sup>4</sup>, Mercy J. Borbor-Cordova<sup>5</sup>, Raul Mejía<sup>6</sup>, Mary Regato<sup>7</sup>, Xavier Rodó<sup>2,8</sup>**

<sup>1</sup> London School of Hygiene & Tropical Medicine, UK;

<sup>2</sup> Barcelona Institute for Global Health (ISGLOBAL), Spain;

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<sup>4</sup> Predictia Intelligent Data Solutions, Spain;

<sup>5</sup> Escuela Superior Politecnica del Litoral (ESPOL), Ecuador;

<sup>6</sup> National Institute of Meteorology and Hydrology (INAMHI), Ecuador;

<sup>7</sup> National Institute of Public Health Research (INSPI), Ecuador;

<sup>8</sup> Institució Catalana de Recerca i Estudis Avançats (ICREA), Spain

El Niño and its impact on local meteorological conditions potentially influences interannual variability in dengue fever transmission in southern coastal Ecuador. El Oro province is a key dengue surveillance site, due to the high burden of dengue fever, co-circulation of all four dengue serotypes, proximity to an international border and major port, and the recent introduction of chikungunya and Zika viruses. In this study, we used ensemble climate forecasts to predict the evolution of the 2016 dengue season in the city of Machala, following one of the strongest El Niño events on record. We incorporated precipitation, temperature and El Niño forecasts in a Bayesian hierarchical mixed model to predict dengue incidence.

The model was initiated on 1 January 2016, producing monthly dengue forecasts until November 2016. We accounted for misreporting due to the introduction of chikungunya virus in 2015, by using active surveillance data to correct reported dengue case data. We then evaluated the forecast retrospectively with available epidemiological information. The predictions correctly forecast an early peak in dengue incidence in March 2016, with a 90% chance of exceeding the mean dengue incidence for the previous five years. Accounting for the proportion of chikungunya infections that had been incorrectly recorded as dengue cases in 2015 improved the prediction of the magnitude of dengue incidence in 2016. The main advantage of this dengue prediction framework is the use of long-lead seasonal climate and El Niño forecasts, which permits a prediction to be made at the start of the year for the entire dengue season. Combining active surveillance data with routine dengue reports improved not only model fit and performance, but also the accuracy of benchmark estimates based on historic seasonal averages. This study advances the state-of-the-art of climate services for the health, by demonstrating the potential value of incorporating climate information in the public health decision-making process in Ecuador.

## Oral Communication 02 | Invited Speaker

### Climate and malaria analysis for national decision-making. Data, methodologies and tools.

#### **Madeleine Thomson**

International Research Institute for Climate and Society and  
Department of Environmental Health Sciences, Mailman,  
Columbia University, New York;

Malaria has long been understood as a climate sensitive disease. In this presentation we explore how this sensitivity may be exploited to improve malaria prevention, control and elimination. Climate information including historical, current and forecast products and services, can support a wide range of malaria intervention decisions. For example, malaria control programme staff can use climate information to better understand the dynamics of the disease and to heighten routine planning and surveillance and preparedness activities through improved:

- *understanding of the underlying mechanisms that determine how climates impact malaria outcomes*
- *identification of the spatial distribution of populations at risk of malaria (e.g. riskmaps)*
- *identification of the seasonality of malaria (best timing of routine interventions)*

- *monitoring and prediction of short term and seasonal or year-to-year variations in malaria incidence (providing early warning systems for epidemics).*
- *monitoring and prediction of longer term malaria trends (which can be used in climate change impacts and vulnerability assessments)*
- *assessment of the impact of malaria interventions.*

However, to fully exploit the currently available information, and identify where improvements need to be made in the development of new data sources, methodologies and tools it is essential to understand the sources of uncertainty that limit our capacity to explain and forecast malaria transmission dynamics based on climate driven models. Uptake of climate information by decision-makers must be based on a sound knowledge of the strengths and limitations of the information provided.

## Oral Communication 03

### The influence of air temperature on hospital admissions due to mental disorders in Lisbon

**Ricardo Almendra<sup>1</sup>, Adriana Loureiro<sup>1</sup>, João Vasconcelos<sup>2</sup>, Paula Santana<sup>1</sup>**

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<sup>2</sup>Centre for Geographical Studies (IGOT), Universidade de Lisboa and Polytechnic Institute of Leiria

**Background:** Individuals with mental disorders are often susceptible to the effects of extreme ambient temperatures. Temperature has long been considered a health determinant for psychotic exacerbation of core symptoms for many specific mental and behavior disorders (McMichael et al., 2006). Thus, the aim of this study is to assess the short-term impacts of daily mean temperature on hospitalizations due to mental disorders in Lisbon (NUT III region).

**Data and methods:** Daily number of hospital admissions with primary diagnosis of mental disorders (ICD-9: 291-293; 295-298; 300; 3071; 3075; 3078; 303-305; 308-309; 311; 316) or with main external cause of suicide and self-inflicted injury (ICD 9: E95) was collected from the Diagnosis Related Groups general database, provided by the Portuguese Health System Central Administration. Meteorological variables (average temperature and relative humidity) were gathered from the NNDC climate data online for the Gago Coutinho meteorological station. Air

pollutants concentration (PM10 and O<sub>3</sub>) were collected from the background stations of the study area. A seven years period (2008-2014) of daily data was analyzed.

A quasi-Poisson generalized additive model combined with a distributed lag non-linear model was applied to analyze the lag-exposure-response relationship between daily mean temperature and hospital admissions due to mental disorders. The model was adjusted for day of the week, air pollution, relative humidity, time trend and seasonality.

**Results:** During the study period, 30,139 hospital admissions were recorded (daily average of 11.8 hospitalizations). Using the median temperature (16.8 °C) as reference, a significant positive association between the temperature and hospital admission due to mental disorders was found above the threshold of 24°C at a lag of 0-1. The relative risk for 28.8°C (99% percentile), when compared to the reference temperature, was 1.26 (95% confidence intervals: 1.09-1.47). The effect of high temperatures at the other lags tested was not significant.

Cold weather is not significantly associated with the increase of hospital admissions for mental disorders.

**Conclusion:** The findings of this study are in conformity to similar studies applied in different locations. The results suggest that high temperatures are a significant risk for mental disorders.

## Oral Communication 04

### Modelling climate and non-climate impacts on malaria in Malawi for effective control interventions

**J. Chirombo<sup>1,2</sup>, P. Ceccato<sup>3</sup>, R. Lowe<sup>4</sup>, D.J. Terlouw<sup>2,5</sup>, M.C. Thomson<sup>3</sup>, D. Kathyola<sup>6</sup>, P.J. Diggle<sup>1</sup>, J.M. Read<sup>1</sup>**

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<sup>5</sup>Liverpool School of Tropical Medicine, Liverpool, UK;

<sup>6</sup>Ministry of Health, Malawi

**Background:** Climate variation is thought to be a significant driver of vector-borne disease transmission, such as malaria. Quantifying the impact of climate on transmission could inform control interventions. Non-climate factors also affect transmission. Consequently, it is important to understand the relative role of climatic and non-climatic drivers of malaria incidence, and how these may change over time and across space.

**Methods:** We use a spatio-temporal generalized linear mixed model and a Bayesian inferential framework to quantify the contribution of climatic, environmental and socio-economic factors to district-level variation in malaria infection risk in Malawi. The model incorporates spatio-temporal random effects. We produce malaria risk maps for Malawi.

**Results:** We find that average monthly air temperature anomalies are a significant predictor of malaria incidence, while average monthly rainfall anomalies are not. Population density is negatively associated with incidence. Vegetative cover, as given by the normalized difference vegetative index (NDVI) shows a strong relationship with malaria incidence. Areas with a high density of health facilities have a higher malaria risk compared to areas with fewer facilities.

**Conclusion:** By considering important climatic and non-climatic factors, our modelling approach can identify locations likely to have unusually high or low risk of malaria incidence across Malawi. This information could be exploited for public health purposes, to direct surveillance and intervention efforts.

## Oral Communication 05 | Invited Speaker

### Space-time modelling of mosquito densities: application to *Aedes albopictus*, vector of viruses, in Reunion Island

**Roux E<sup>1</sup>**, **Tran A<sup>2</sup>**, **Herbreteau V<sup>1</sup>**, **Réveillion C<sup>3</sup>**, **Demarchi M<sup>4</sup>**, **Mangeas M<sup>1</sup>**, **Degenne P<sup>2</sup>**, **Dehecq J-S<sup>5</sup>**

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**Context:** *Aedes albopictus* mosquitoes transmit many viruses like those responsible of Chikungunya, Dengue fever and Zika, which are diseases of major concern worldwide. Accurate understanding and prediction of the spatial and temporal distributions of their densities are needed to optimize surveillance and control of several important arboviroses. Among the environmental drivers of their distribution and abundance, meteorological conditions significantly determine their dynamics.

**Objectives:** Taking the example of *Aedes albopictus* in Reunion Island, this study had three main objectives i) modelling the densities of *Aedes albopictus* mosquito in time, as a function of meteorological data; ii) extrapolating the model throughout the island using a land cover characterization; iii) providing operational tools for surveillance and control of vector populations, in order to optimize surveillance and control of mosquito-borne diseases.

**Methods:** Different models were developed, using process-based and data-based approaches linking meteorological variables (daily temperature and rainfall) and entomological collections of *Aedes albopictus* larvae from 9 sites located around the Island.

A land cover classification derived from SPOT-5 imagery allowed to spatialize an environment-dependent parameter of the process-based model and consequently the prediction of the mosquito densities at the island scale. Eventually, a user-friendly interface was developed in order to make the models and their results easily operational by the vector-control actors.

**Results.** The predicted abundance of *Aedes albopictus* fit well with field observations, with Spearman's correlation coefficients ranging from 0.45 to 0.90. Higher correlations were obtained in places with a higher seasonality of the mosquito population dynamics.

**Conclusions:** A flexible and efficient tool that predicts mosquito abundance based on local environmental and meteorological factors was developed. It is operational with a simplified user-friendly interface and used by vector-control agencies to target surveillance areas on Reunion Island.

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## Parallel Session 12 Agent-Based Modelling

### Oral Communication 01 | Invited Speaker

#### Using agent-based models to investigate the impact of firearms disqualification criteria based on alcohol abuse on firearm-related homicide and suicide

##### Magdalena Cerdá

Department of Emergency Medicine, University of California, Davis; Sacramento, California.

**Background:** Approximately 500,000 people die every year from firearm violence. The strong link between alcohol abuse and firearm violence suggests that restricting access to firearms for persons with a documented history of alcohol abuse may be a promising firearm violence prevention measure. Yet little information exists on the impact that disqualifying this high-risk group from owning firearms would have on firearm-related violence. In this presentation, I illustrate how agent-based models can be used to simulate the change in firearm-related homicide and suicide that would result from disqualifying people from owning a firearm given a range of alcohol abuse-based disqualification criteria. We investigated a range of criteria, from the most feasible yet restricted (having been convicted of at least one Driving Under the Influence (DUI) charge in the past 5 years) to the most unfeasible yet broad (history of alcohol abuse in the past year).

**Methods:** We created a population of 260,000 agents reflecting a 5% sample of the adult population of New York City (NYC). Agents were placed into a grid representing the size, demographics, and location of NYC neighborhoods. Agents could interact, use alcohol, be arrested and convicted for various crimes, purchase or illegally obtain firearms, and engage in violence or self-harm. The model was based on more than 20 national and city-level data sources.

**Results:** Among the general population, a 5-year disqualification based on having been convicted for at least one DUI in the past 5 years reduced firearm-related homicide by 2.6% (95% CI -8.3-9.2%) and suicide by 10.3% (95% CI -6.9-26.2%). In contrast, a 5-year disqualification based on having met criteria for alcohol abuse in the past year reduced firearm-related homicide by 5.5% (95% CI -0.5-17.4%) and suicide by 27.4% (10.2-44.6%).

**Conclusions:** Even broad and infeasible disqualifications based on alcohol abuse history may have limited impact on firearm-related homicide. Broad expansions of firearms prohibitions could substantially reduce firearm-related suicide, but this raises concerns about feasibility and stigma. Future research is aimed at using agent-based models to identify the types of firearm policies that can produce the largest reduction in firearm violence.

## **Oral Communication 02 | Invited Speaker**

### **Why Integrating Environmental Modelling and Spatially-explicit ABM? Revisiting Max Sorre's Ideas can be the Answers of Why and How.**

**Antonio Miguel V. Monteiro**

Brazilian National Institute for Space Research (INPE), Brazil

The living earth is the natural support where complex relations evolve over time. It has great influence in how we set up and maintain relations, because we are grounded to places with unique characteristics and dynamics. The human being has always changed its environment. Changes can occur at the physical, social, and economic levels, individually and collectively. The inherent complexity of the processes involved in these changing system shows non-linearity, displayed by a complex behaviour that presents thresholds, positive and negative feedback loops, lags in time and space, resilience, heterogeneity, and, above all, surprises. As the complexity of these relations and the rate of the transformations increase new methods for studying the dynamics of the health-disease processes have been searched for. Modeling complex interactions is a hard task. It involves collecting data, building up a conceptual approach, implementing, calibrating, simulating, validating, and possibly repeating these steps again and again.

There are different conceptual approaches proposed in the literature to tackle this problem. Agent-Based Modelling (ABM) comes as an approach for addressing these issues broadly. However, these changing relationships need an integrated and non-fragmented view, in which biology, entomology, epidemiology, medicine, human geography, physical geography, ecology and the new disciplines that study environmental changes can establish a conceptual scope for this dialogue. In the epidemiology field the ABM use have lacked a theoretical-conceptual framework in which it can address this issue in an integrated way, observing the nature of the interactions between the human being and his environment. These interactions are those that produce his living space of everyday life, and thus also produce landscapes for the potential breeding of health-disease processes, Pathogenic Landscapes. In this talk I will argument that a seminal work of the early twentieth century, originated in the Geography domain, with the French geographer Max Sorre can be very helpful as a conceptual basis for working the new and old complexities of health relations in a context of intensified environmental changes using ABM. I will show some progress we have made in producing an ABM toolkit that allow for landscape grounded agents and its relations oriented for health-disease processes modelling.

## Oral Communication 03

### A comercial airline network model for chikungunya spread in the Caribbean

**Carlos Dommar and Xavier Rodó**

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A commercial airline database has been used to set a human mobility network model. This network model has in turn been coupled to a SEIR epidemic model in order to simulate the first stages of the CHIKV spread that started in the end of 2013 in the Caribbean region. The fitted model explores the role of the topology of the particular flight network of the Caribbean -and thus the mobility of infectious hosts- on the initial spatial and temporal patterns of incidence of CHIKV in the set of the firstly affected islands and mainlands of the outbreak. Several scenarios has been investigated for such purpose. And finally simulations of the fitted model of a simple intervention measurement demonstrate the appearance of a limit time horizon where any level control efforts later than it will have null effect to lessen the epidemic severity. The model reveals that, for interventions strategies to be useful in controlling outbreaks of emergent infectious diseases in naive populations such as CHIKV in the Americas in 2013, the understanding of the dynamics of the initial stages is crucial.



## Parallel Session 13 GIS In Public Health II

### Oral Communication 01 | Invited Speaker

#### An interactive Spatial Decision Support System to manage Public Health in Gulbarga taluk, Karnataka, India

**S.A. Ahmed<sup>1</sup>, S. Shekhar<sup>2</sup>, R. Haining<sup>3</sup>, S. Kadannolly<sup>2</sup>, E-H. Yoo<sup>4</sup>**

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<sup>2</sup> Department of Geography, Central University of Karnataka, India;

<sup>3</sup> Department of Geography, University of Cambridge, United Kingdom;

<sup>4</sup> Department of Geography, State University of New York, Buffalo, USA

India is experiencing a rapid health transition; there is a strong emphasis on building an interoperable health information system for public health. Technically, some major issues still remain relating to health data visualization, spatial processing of health data, health information dissemination, data sharing and the access of local communities to health information.

A study was carried out in the Kalaburagi taluk, situated in the Northern Part of Karnataka state in South India. The study area is characterized by complex spatial variations in climatic conditions. It is one of the most vulnerable areas to vector borne diseases especially malaria. The combination of climatic and socio economic conditions, the livelihoods of local communities and the lack of mosquito control measures have all contributed to a significant increase in the number of infected cases.

The occurrence of common vector borne diseases including Malaria, Dengue, Chikungunya, represent a major health problem in Kalaburagi district which is closely related to environmental, climatic and socio-economic conditions. Though its prevalence has been reduced, for the past couple of years there has been a growing risk of these diseases re-emerging in susceptible communities living in remote regions. Most research into malaria has focused on malaria epidemiology which has achieved many results that have helped in malaria prevention. But the disease is not adequately addressed due to lack of research on disease management, monitoring, detection and early treatment of patients among local communities. A mechanism to share health information throughout communities is an important route to addressing nation-wide public health issues. This research used the case of malaria distribution as the example data for applying spatial pattern detection tools.

Knowing about geographical distribution patterns enables health practitioners to understand the area-specific underlying mechanisms of disease development over time and the driving factors behind changes. Therefore, the identification and measurement of patterns is an important step in analysing geographic information. Results from this work was reported in an earlier study. The present work deals with building a practical Spatial Decision Support System (SDSS) to manage and support the delivery of public health.

The SDSS-framework is a platform to: rapidly collect, store and extract essential data through key phases of program implementation; effectively manage and ensure essential services are delivered at optimal levels of coverage in target areas; actively locate and classify transmission to guide swift and appropriate responses. The integral role of malaria program personnel, and transitioning from traditional styles of monitoring and evaluation to active surveillance-response using minimal essential data integrated in modern SDSS technology, are two important features of the current programme of work.

In the first phase of work mapping and cluster detection (identifying areas of excess risk) including evaluating the temporal persistence of excess risk and the local conditions with which high counts are statistically associated were undertaken. In the second phase of work, a conceptual spatial decision support system was designed and was implemented practically through a web based interactive system.

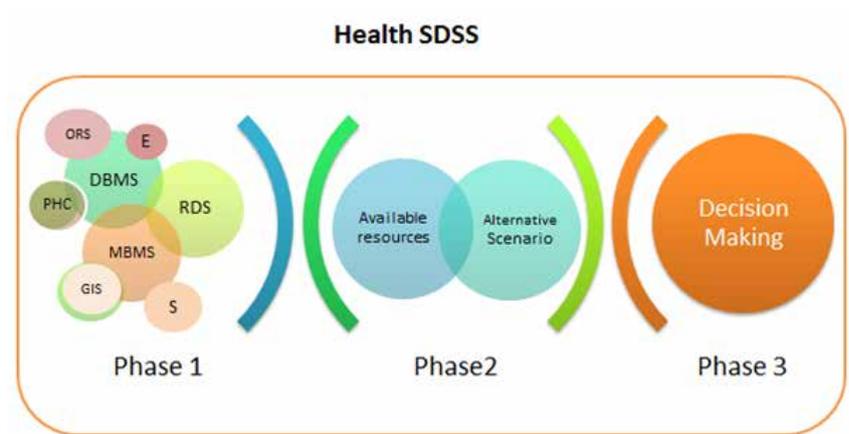
**Conceptual Health SDSS:** Conceptually, a SDSS can be thought of as an integrated set of flexible capabilities (Amstrong, Densham and Rushton 1986; Densham and Armstrong 1987; Shekhar, 2014).

In the present structure, there are five major components and they have been grouped into three phases depending on the process (Figure 1).

In Phase 1, the Data Base Management System (DBMS), the Model based Management System (MBMS) and the Result Display System (RDS) perform the primary activities such as data management, analysing the data by using Statistical software and GIS software and displaying the results in the form of graphs and maps.

The second phase deals with the assessment of available resources with the results of data analysis. Based on that it is possible to develop different scenarios.

In the third phase, the decision will be taken leading to implementation. This may happen in any of three different ways. The first way is to take a decision based on the most suitable/viable scenario. The second way is to go back to Phase 2, make changes to the existing infrastructure, and create new scenarios and take decisions based on the new scenario. The third way is to repeat the entire process from Phase 1, incorporate the necessary changes and finally take the decision.



**Figure 1:** Structure of a Health SDSS

*DBMS: Data Base Management System*

*MBMS: Model base Management System*

*RDS: Result Display System*

*PHC: Primary Health Centres (Data input)*

*ORS: Other Relevant Sources (Data Input)*

*E: Environmental factors (Data Input)*

*GIS: Geographic Information System/Science (Software for analysing the data)*

*S: Statistical analysis (ER, SIR)*

*Available Resources: Available Infrastructure, connectivity to Hospitals, Measures for controlling the disease*

*Alternative Scenario: Based on the data input, hot spots and available facilities different scenarios will be generated.*

*Decision making: The viable solution to manage the epidemic Vector borne disease will be selected by the Decision Maker.*

The present work tries to assist the stakeholders in controlling the diseases, keeping the incidence at a permanently low level within the regional population. This should be possible if the health SDSS is taken into account when designing and implementing epidemiological surveillance policies.

## Oral Communication 02 | Invited Speaker

### Is more always better? Exploring indicators of quality of green space in relation to self-reported general health

**Brindley, P.<sup>1</sup>, Cameron, R. W.<sup>1</sup>, Ersoy, E.<sup>2</sup>, Jorgensen, A.<sup>1</sup>, and Maheswaran, R.<sup>3</sup>**

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There has been a growing body of research exploring the health benefits of green space. Most, however, treats green space as homogenous. There remains a need to move away from simply measuring the extent or area of green space and instead focus on measures of 'quality'. To date, few studies have explored the role of the quality of green space when exploring the health benefits of the natural environment. Quality may be a substantial determinant for both use and activity within green spaces. This paper will examine a variety of measures of quality of green space in relation to self-reported general health. A small-area level ecological study is undertaken within the city of Sheffield, UK. Health data are drawn from the general health question within the 2011 UK Census of Population which is a self-assessment of a person's state of health.

A diverse collection of quality measures are explored, ranging from the more traditional on-site surveys and biodiversity evaluation; secondary data proxies such as local crime statistics; to more novel approaches extracting estimates from social media sources. These quality measures generated from social media include the number of photographs taken within green spaces and uploaded to popular internet photography sites (such as Flickr and Geograph); the sentiment of these photograph captions; and an analysis of geo-referenced Tweets from Twitter. Exploring these different measures of quality and their potential value in understanding the relationship between self-reported general health and green space will enable us to inform the debate regarding quality versus quantity of green space.

## Oral Communication 03

### An activity space approach to assessing food-related spatial behavior of urban African-American women in Atlanta, GA, USA

**I.G. Raskind<sup>1</sup>, M.R. Kramer<sup>1</sup>, R. Landon<sup>1</sup>**

<sup>1</sup>Rollins School of Public Health, Emory University, Atlanta, Georgia, USA

**Introduction:** New directions in food environment research recommend assessing individual spatial behavior beyond the residential neighborhood to accurately capture the food sources people regularly encounter and utilize. We use an activity space approach to measure the routine destinations of socioeconomically diverse, pregnant African-American women, and assess whether food-related spatial behavior varies by individual and neighborhood attributes.

**Methods:** We present initial results (n=38) from an ongoing cohort study recruiting women from antenatal care clinics in Atlanta, GA, USA. Data are collected using a web-based activity space questionnaire, the Visualization and Evaluation of Routine Itineraries, Travel destinations, and Activity Spaces adapted for use with maternal and child health populations (VERITAS-MCH). Three environment types are defined from these data: residential census tract (CT), and convex hull polygons of *overall* and *food-*

*specific* activity spaces. Linear regression was used to identify associations between individual/neighborhood attributes and 1) environment size (area in km<sup>2</sup>), and 2) proportion of food sources utilized within each environment. Stacked multilevel models (environment types nested within women) were used to assess predictors of discordance between environment sizes.

**Results:** Lower income women had smaller *overall* activity spaces ( $\beta=-405.7$ , SE=245.8,  $p=0.11$ ). Women living in food deserts had smaller *food-specific* activity spaces ( $\beta=-46.5$ , SE=29.7,  $p=0.13$ ). A small proportion of utilized food sources fell within the boundaries of women's CTs (mean=12.7%, SD=18.6), compared to their overall activity spaces (mean=45.9%, SD=32.9). Lower income women had a smaller proportion of utilized food sources fall within their overall activity spaces ( $\beta=-25.4$ , SE=13.4,  $p=0.07$ ). Lower income women ( $\beta=-567.8$ , SE=266.2,  $p=0.03$ ) and women living in tracts with higher neighborhood deprivation index scores ( $\beta=-171.8$ , SE=112.1,  $p=0.13$ ), had a smaller degree of discordance between overall activity space size and CT size. Women living in food deserts had a smaller degree of discordance between overall ( $\beta=-354.8$ , SE=179.3,  $p=0.05$ ), and food-specific ( $\beta=-50.0$ , SE=23.0,  $p=0.03$ ) activity space sizes and CT size.

**Discussion:** Disadvantaged women had smaller overall and food-specific activity spaces, and lower discordance between environment sizes, suggesting that the extent of their spatial behavior may be constrained by factors like access to transportation. At the same time, a higher percentage of lower income women travelled *outside* of their overall activity spaces to utilize food sources. Findings suggest that disadvantaged women may face a double burden of constrained spatial behavior and constrained food access. As study recruitment progresses through 2017, next steps include linking geospatial and retail food environment data to assess discordance in food source density and relative healthfulness between environment types.

## Oral Communication 04

### Spatial and temporal analysis of malaria and risk factors in the Brazilian Amazon, 2010-2015

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<sup>2</sup>Johns Hopkins Bloomberg School of Public Health, Baltimore, USA;

<sup>3</sup>Global Public Health Observatory, Baltimore, USA

**Introduction:** Malaria is a problem in the Americas, Brazil accounted for 37% of the cases in 2015 and of these 99.5% are located in the Brazilian Amazon. Despite the mobilization of resources from Brazilian National Plan for Malaria Control, there are still too many municipalities with moderate and high transmission levels. Several factors modify the dynamic of malaria transmission, however, there is no consensus on the importance of each one in the transmission, although there are indispensable for planning effective interventions. Spatiotemporal statistics have been used to understand better the transmission of malaria.

**Aim:** To analyze spatially and temporally the malaria autochthonous incidence and its risk factors in the municipalities of the Brazilian Amazon, in the period 2010 to 2015.

**Methods:** Malaria data were stratified by the annual parasite incidence (API), over the six years and by municipality. Environmental and socioeconomic risk factors were obtained from remote sensing and the 2010 census and analyzed with the help of Geographic Information Systems. Time-series and spatial analysis were performed to analyze the API. LISA indicators were used to explore autocorrelation. General linear models (GLM) were used to assess the relationship between selected risk factors and malaria incidence. Geographic Weighted Regression (GWR) was applied to assess the spatial relationships between the risk factors and malaria incidence.

**Results:** Malaria API has declined 61% from 2010 to 2015, and there was a 40% reduction of municipalities with high transmission (API higher than 50). This represents 9.4% of all the municipalities in the study site and 63% of all cases, in 2015. The time-series analyses showed different incidence patterns by region after 2012; some States have minimized the effect of the seasonality in their incidence rates. LISA indicators showed spatial autocorrelation locally and globally. GLM and GRW presented space-time divergences in the influence of risk factors.

**Conclusion:** The use of spatial statistics has been proved useful to understand malaria dynamics and its risk factors. However, it is necessary that strategies to control and prevent malaria include the use of these spatial statistics to plan more effective interventions that take into account the epidemiological profile of every municipality or local context since environmental and socioeconomic risk factors presented different dynamics in the Brazilian Amazon. Nevertheless, spatial statistics applied to area data in Amazon forest context might lose specificity since population and thus, malaria cases are not homogeneously distributed in the territory.

## Parallel Session 14 Modelling And Inference In Infectious Disease Epidemiology

### Oral Communication 01

#### Spatiotemporal heterogeneity in leptospirosis transmission in northeastern Thailand

**Katharine A. Owers<sup>1</sup>, Soawapak Hinjoy<sup>2</sup>, James E. Childs<sup>1</sup>, Vincent Herbreteau<sup>3</sup>, Peter J. Diggle<sup>4</sup>, Albert I. Ko<sup>1,5</sup>**

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Leptospirosis is an environmentally transmitted zoonotic infection that causes nearly 60,000 deaths and one million severe cases per year. Thailand experienced an explosive country-wide outbreak of leptospirosis in the late 1990s, and while incidence has subsided, it remains above pre-epidemic levels. The majority of cases, both during and since the epidemic, occurred in the northeastern region of the country, a largely rural farming area. Exploratory analysis revealed heterogeneous incidence in both space and time, and our lack of knowledge about the factors underlying this heterogeneity has been a key barrier to effective control. We sought to formally characterize the complex disease transmission dynamics during the epidemic to endemic transition in northeast Thailand, with the overall goal of guiding public health professionals working to prevent outbreaks.

To cause disease the bacterium must be deposited in soil or water via the urine of a mammalian host, such as rodents or livestock, and survive in the environment long enough to infect a human. We therefore hypothesize that characteristics of the agricultural system, such as land use and livestock density, as well as environment features related to bacterial survival and contact with humans (rainfall, temperature, and flooding propensity) are important determinants of incidence.

Using data from the Thai passive notifiable disease surveillance system (R506), we created a spatiotemporally explicit Poisson model of weekly leptospirosis cases geocoded at the level of the 320 districts in northeastern Thailand between 2000 and 2014. The model used 6-month and 12-month harmonics to capture region-wide seasonality, time-constant environmental and agricultural covariates to account partially for variation between districts, and geostatistically smoothed weather data from 28 stations across the study region to generate concurrent and lagged rain and temperature covariates for each week in each district. We also included a linear spline to represent the region-wide transition from the epidemic to the endemic state.

We found that while incidence in the region as a whole settled into an endemic pattern, individual districts continued to experience outbreaks. In accordance with our hypothesis, environmental and agricultural characteristics were strongly associated with incidence, as were concurrent and lagged rainfall and temperature. The residuals from this model showed evidence of unexplained variation that could be due to stochastic events such as new introductions of the bacterium or unmeasured covariates. At the meeting, we will report progress on modelling this residual unexplained variation as a latent spatio-temporal Gaussian process.

## **Oral Communication 02 | Invited Speaker**

### **Modelling human mobility for respiratory pathogen transmission**

#### **Jonathan Read**

Centre for Health Informatics, Computing and Statistics,  
Lancaster Medical School, Lancaster University, United Kingdom

Respiratory infections, such as pandemic and seasonal influenza, depend on the co-location or close interaction of susceptible and infectious individuals. Such interaction patterns play out in geographical space, driven by the movement of individuals and their travel behaviour. This talk will summarise human mobility models and, using human movement patterns collected in China, identify the most suitable model forms for modelling the spatial distribution of interaction patterns relevant to the spread of influenza.

## **Oral Communication 03 | Invited Speaker**

### **Individual level infectious disease models incorporating aggregate level spatial structure**

**Rob Deardon**

Faculty of Veterinary Medicine, University of Calgary, Canada

Numerous examples exist of infectious disease models that incorporate spatial distance and other covariates at the individual level. This has been most noticeable perhaps in agricultural case studies such as the UK 2001 foot and mouth disease epidemic. However, both in agriculture and public health, many salient covariates that display spatial structure are collected at a regional level. Here, we extend individual level infectious disease models to incorporate such spatially structured regional/aggregate level information. This is done primarily within the context of regional data from the public health system of Alberta, Canada. We discuss issues of both inference and computation.

## Oral Communication 04

### Using Genotyping and Geospatial Analyses to Study Multi-drug Resistant Tuberculosis Transmission and Migrants

**Erjia Ge**

Division of Epidemiology, Dalla Lana School of Public Health, University of Toronto

**Background:** Multi-drug resistant tuberculosis (MDR-TB) is a form of tuberculosis (TB) infected by bacteria resistant to treatment with at least one of the two most powerful first-line anti-TB medicines: isoniazid and rifampicin. WHO estimated that there were 480,000 new cases and 190,000 deaths of MDR-TB worldwide in 2015, among which over 50% of these cases occurred in India, China, and the Russian Federation. MDR-TB has caused large economic and disease burden worldwide and developing countries particularly. However, the transmission of MDR-TB is complex and highly dynamic, which remains little explored, especially in cities with large migrants such as Shanghai, China.

**Objectives:** We investigated MDR transmission and its association with migrants.

**Methods:** This population-based molecular and spatial epidemiological study included all patients aged 15 years or above with culture-confirmed MDR-TB cases reported by Shanghai CDC between January 1st 2009 and December 31st 2012. MDR-TB isolates were divided by genetic clustered and non-genetic groups using genotyping. The transmission rates were estimated with respect to patients' residential status (i.e. migrants or local residence). Spatial statistics *K*-Function and *LISA* were used to estimate the spatial patterns of the two

groups across multiple space scales. Auto-logistic regression were employed to model the associations between TB transmission and migrants with patients' gender, age, living districts, treatment history, sputum smear result, lineage type, and spatial infection effects adjusted.

**Results:** A total of 367 (4.6%) MDR-TB patients were identified from 7,982 culture positive cases, while 299 (81.5%) had both genotyping and geocoding information. Among the 299 MDR-TB cases, 110 (36.8%) sharing genetic similarity clustered were considered as people-to-people "recent transmission", while non-cluster stains were initially acquired from improper treatment for ordinary TB, called "acquisition". The odds of the MDR-TB transmission rate in local residents to migrants was 3.36 (95% CI, 1.86-6.09). The MDR-transmission rate in central urban was 29.5% and 1.87 (95% CI, 0.88-1.96) higher than that of rural 15.8%. MDR-TB cases demonstrated clustering at community level over around 3 kilometers, within which the cases were more likely to share genetic similarity than outside with adjusted odds 4.47 (95% CI, 1.19-17.6). Within the same spatial scale, the odds ratio of genetic clustering in local patients to migrants was 4.11 (95% CI, 2.15-8.09).

**Conclusion:** Local patients have played important roles in the recent transmission of MDR-TB. Although migrants were suspected to TB prevalence, MDR-TB demonstrated a specific model of people-to-people transmission among local residents in Shanghai. Such information provides an opportunity to MDR-TB control, such as through targeting specific neighborhoods or local subgroups rather individual contacts, especially with surveillance and health resources limited.

## Oral Communication 05

### Delay in diagnosis of Pulmonary Tuberculosis: space matters!

**C. Nunes<sup>1</sup>, D. Gomes<sup>2</sup>, P. Filipe<sup>2</sup>, B. Sousa<sup>3</sup>**

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<sup>2</sup>Universidade de Évora, Portugal;

<sup>3</sup>Faculdade de Psicologia e de Ciências da Educação, Universidade de Coimbra, Portugal

The goals of this article are: (i) to understand how individual characteristics affect the delay between symptoms and diagnosis of pulmonary tuberculosis (PTB); (ii) to quantify the predictive capacity of these risk factors; and (iii) to quantify and map spatial variation in the risk of higher delays. We used generalized additive models with a spatial component to model the delay across continental Portugal. We focused on new PTB cases, diagnosed between 2000 and 2013, and included some individual information (sex, age, residence area, alcohol abuse, intravenous drug use, homelessness, HIV, imprisonment status). We found that the global default rate was 55 days, higher in females and not statistical significant for other individual covariates.

Of specific epidemiological interest was that our geographical analysis found that Lisbon and Alentejo have higher default rates compared to the rest of the country, after adjusting for the previously mentioned risk factors, areas that not overlap with high incidence areas of PTB. The challenge of understand (and if possible, decrease) the delay, considering other individual non-measured characteristics, healthcare system failure or patient recalcitrance requires further analysis in the spatiotemporal domain. Our findings suggest the presence of significant within-country variation in the delay that cannot be explained by these classical individual risk factors alone. Applied methods are simple to implement, results are easily interpreted and could definitely be applied to other diseases.

## **Parallel Session 15**

### **The Use Of Linked Data In Spatial Epidemiology**

## **Oral Communication 01 | Invited Speaker**

**Using people's spatial movement as 'natural experiments' for environment-health effects – possibilities and problems using large scale administrative data studies**

**Chris Dibben**

University of Edinburgh, UKI

Studies of environment-health relationships typically have to be based on 'observational' studies because it is difficult or impossible to design experiments where people are randomised to environmental situations. In these types of designs peoples' exposure and health can often be measured accurately however the variation in exposure is outside the control of the research team, typically related to peoples 'normal' life. This means that the environmental exposure may be associated with other factors that in turn may affect the health outcome of interest and therefore confound the relationship of interest. Statistical adjustment may be used, however problems of unmeasured and poorly measurement variables will hinder this. One potentially helpful approach is to use individuals as their own controls. If an individual's environmental exposure has varied overtime, it is possible to carry out a 'within individual' analysis in which all individual non-time varying factors will be constant and therefore ignorable.

This then simplifies the problem of unmeasured confounding considerably, focusing it mainly on controlling for factors that change over time and in particular are related to the change in the environmental exposure (e.g. the environment exposure may have changed with a residential location change or job) and indeed it may be possible to argue that the change is 'as if' random. This approach however requires large sample sizes and therefore may only be a practicable approach using linked administrative data. In this paper we discuss a number a case studies of within person designs using administrative data and highlight the strengths and weaknesses of this approach.

## **Oral Communication 02 | Invited Speaker**

### **The Exposome: Use of linked data to build a whole life course approach to environmental and social exposures**

#### **Clive Sabel**

Department of Environmental Science, University of Aarhus,  
Denmark

The Exposome represents the totality of exposures from conception onwards, simultaneously identifying, characterising and quantifying the exogenous and endogenous exposures and modifiable risk factors that predispose to and predict diseases throughout a person's life span (Wild, 2005; Jacquez et al 2015). Unravelling the exposome implies that both environmental exposures and genetic variation are reliably measured simultaneously.

The EU Horizon2020 HELIX, EXPOsOMICS, and HEALS projects and US initiative HERCULES are four large current five year studies investigating the Exposome. This paper reports ongoing efforts within HEALS (Health and Environment-wide Associations based on Large population Surveys). HEALS brings together a comprehensive array of novel technologies, data analysis and modelling tools that support efficient design and execution of exposome studies. The HEALS approach brings together and organizes environmental, socio-economic, exposure, biomarker and health effect data; in addition, it includes all the procedures and computational sequences necessary for applying advanced bioinformatics coupling advanced data mining, biological and exposure modelling so as to ensure that environmental exposure-health associations are studied comprehensively. The overall approach will be verified in a series of population studies across

Europe, tackling various levels of environmental exposure, age windows and gender differentiation of exposure, and socio-economic and genetic variability.

There are substantial challenges in attempting to rebuild whole lifecourses and exposures for ethnically and socio-economically diverse populations across the whole of Europe. Its a good example of a truly Big Data initiative. For practical and scientific reasons, attention needs to be focussed on critical life periods. There are substantial challenges integrating diverse multiple sources of data, including national registers, health surveys, birth and death certificates and biomarkers. Practise varies by country. The Scandinavian tradition of population registers isn't replicated elsewhere. Some countries have comprehensive local geography censuses, others don't. Trying to overcome these data challenges, we are investigating using social media, smart micro sensors and smartphone apps to track mobility and exposure. This brings its own challenges around the ethics of tracking individuals, the acceptibility of fine geographical locating 24/7; who uses technology, and who doesn't.

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## **Oral Communication 03 | Invited Speaker**

### **Using linked individual health data to study air pollution and pregnancy outcomes: a bayesian spatial modelling approach**

**Tom Clemens**

School of Geosciences | University of Edinburgh

Ecological studies of the effect of air pollution for health suffer from spatial autocorrelation, where spatial units that are closer together are more similar than those further apart. In a regression model, this results in residuals that are correlated violating the independence assumption necessary for valid inference. Though some of these problems can be mitigated by including covariates, residual autocorrelation is inevitable and thus additional techniques are required typically involving the estimation of a set of random effects to account for these underlying dependencies. A growing number of studies are now utilising individual level data (particularly administrative health records) together with area based estimates of air pollution exposure. Here, area and individual level information is combined resulting in a multilevel data structure where the effect of an area level air pollution exposure variable is estimated for individuals as the units of analysis.

Despite the same issues of spatial autocorrelation being present in these data, there has been relatively little attempts to extend the techniques described in the ecological literature to individual level analyses, including those analyses linking air pollution exposure with adverse pregnancy outcomes. In this study, we examine the effect of air pollution exposure (NO<sub>2</sub>, PM<sub>10</sub>, PM<sub>2.5</sub>) for pregnancy outcomes (low birthweight, risk of premature birth) in the city of Glasgow, Scotland. We do so using administrative maternity inpatient records linked by residential postcode to estimates of air pollution concentrations for the 9 month period of pregnancy. An extension of the localised Bayesian conditional autoregressive model is used to incorporate the multilevel structure of the data with random effects for both area and mother. The talk will discuss the methods and present some initial findings.

## Oral Communication 04

### Can the geographical patterns in acute myocardial infarction in Denmark be explained by the sociodemographic structure of the population?

**T. M. Kjærulff<sup>1</sup>, K. Bihrmann<sup>1</sup>, G. Gislason<sup>2</sup>, M. Lytken-Larsen<sup>3</sup>, A. K. Ersbøll<sup>1</sup>**

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**Introduction:** Geographical patterns in incident acute myocardial infarction (AMI) have been found and regions with high risk of AMI are characterized by low neighborhood and individual socioeconomic position (SEP); however, it remains unknown whether the geographical variation in the sociodemographic structure fully explain the geographical patterns in AMI. This study aimed to examine to which extent the geographical patterns in AMI can be explained by the sociodemographic structure including individual- and neighborhood-level SEP.

**Methods:** The study is an open cohort study of AMI-naïve adults ( $\geq 30$  years) with residential location in Denmark between 2005 and 2014. Data were obtained from Danish national population registers: National Patient Register, Central Registration System, the Causes of Death Register and the Databases on buildings in Denmark. Poisson regression of incidence rates of AMI with

and without a geographical component as a random effect was performed in R by use of the Bayesian Integrated Nested Laplace Approximations (INLA) method. The analysis included the variables age, sex, ethnicity, calendar year, cohabitation status, disposable household income, education, and median household income, population turnover, and ethnical composition in the neighborhood.

**Results:** The study population consisted of 4,218,932 adults out of whom 104,303 experienced incident AMI between 2005 and 2011. Persons in the lowest income quintile had an incidence rate ratio (IRR) of 1.40 (95% confidence interval (CI)=1.36-1.44) for AMI compared to persons in the highest income quintile and persons living in low SEP neighborhoods had an IRR of 1.13 (CI=1.10-1.16) for AMI compared to those living in high SEP neighborhoods. Models including SEP indicators performed better than models only including age, gender and calendar year and SEP can explain part, but not all of the geographical variation in AMI.

**Conclusions:** Geographical patterns in AMI persist when taking individual and neighborhood SEP into account. Further studies are needed to examine determinants of the remaining geographical differences in AMI, including studies focusing on availability of health services across the country and the geographical variability in the use of these services.

## Oral Communication 05

### State-level Minimum Wage and Heart Disease Death Rates in the United States, 1980-2015

**M. E. Van Dyke<sup>1</sup>, K. A. Komro<sup>2</sup>, M. P. Shah<sup>1</sup>, M. D. Livingston<sup>3</sup>, M. L. Casper<sup>4</sup>, M. R. Kramer<sup>1</sup>**

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**Introduction:** Despite substantial declines since the 1960's, heart disease remains the leading cause of death in the United States (US), and geographic and racial disparities in heart disease death rates and magnitude of declines across states persist. Spatio-temporal variation in heart disease death rates across US states may be driven in part by differences in various state-level socioeconomic factors. This study examined the association between state-level minimum wage and trends in heart disease death rates among Blacks and Whites from 1980 to 2015 in the US.

**Methods:** Annual, inflation-adjusted state and federal minimum wage data were extracted from legal databases and annual state-level heart disease death rates for Blacks and Whites were obtained from the National Vital Statistics System for 1980-2015.

Conventional multivariable regression models and marginal structural models adjusting for time-varying confounding estimated the association between each \$1 increase in state-level minimum wage above the federal minimum wage and heart disease death rates for Blacks and Whites. Models were adjusted for state-level unemployment, education, and income and included year and state fixed effects to account for temporal trends and unobserved state-level confounding.

**Results:** From 1980-2015, US states on average adopted a state-level minimum wage of \$0.25 above the federal minimum wage, although there was variation by US geographic region (average range: Midwest: \$0.10 - Northeast: \$0.46). States adopting a minimum wage level of \$1 or more above the federal minimum wage had lower heart disease death rates for both Blacks ( $\beta = -98.78$  per 100,000, 95% CI: -128.4, -69.16) and Whites ( $\beta = -83.7$  per 100,000, 95% CI: -101, -66.8) than states maintaining the federal minimum wage.

**Conclusions:** Compared to states maintaining the federal minimum wage, states with increases in the minimum wage of \$1 or greater above the federal minimum wage had lower heart disease death rates for both Blacks and Whites. State-level minimum wage increases above the federal minimum wage may be an important factor for spatiotemporal variation in heart disease death rates for Blacks and Whites in the US.

## Parallel Session 16 Joint Modelling With Spatial Variation

### Oral Communication 01 | Invited Speaker

#### Bayesian joint modeling of longitudinal and spatial survival AIDS data

**Rui Martins<sup>1</sup>, Giovani L. Silva<sup>2,3</sup>, Valeska Andreozzi<sup>2,4</sup>**

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Joint analysis of longitudinal and survival data has received increasing attention in the recent years, especially for analyzing cancer and AIDS data. As both repeated measurements (longitudinal) and time-to-event (survival) outcomes are observed in an individual, a joint modeling is more appropriate because it takes into account the dependence between the two types of responses, which are often analyzed separately. We propose a Bayesian hierarchical model for jointly modeling longitudinal and survival data considering functional time and spatial frailty effects, respectively.

That is, the proposed model deals with non-linear longitudinal effects and spatial survival effects accounting for the unobserved heterogeneity among individuals living in the same region. This joint approach is applied to a cohort study of patients with HIV/AIDS in Brazil during the years 2002–2006. Our Bayesian joint model presents considerable improvements in the estimation of survival times of the Brazilian HIV/AIDS patients when compared with those obtained through a separate survival model and shows that the spatial risk of death is the same across the different Brazilian states.

## **Oral Communication 02 | Invited Speaker**

### **Joint modeling of longitudinal biomarkers and recurrence in breast cancer with spatial effects**

**Inês Sousa**

CMAT and Dept of Mathematics and Applications - University of Minho

Joint modeling of longitudinal responses and time to event is necessary when these outcomes are known to be associated. In patients diagnosed with breast cancer, biomarkers are measured after first treatment for monitoring a possible recurrence of the disease. Therefore, time to recurrence and biomarkers response should be analyze under a joint modeling approach. In this work we consider a data set of 526 patients from a central hospital in the North of Portugal, where patients residence is known. Spatial location of patients it is a possible risk factor for progression of biomarkers and time to recurrence, as patients from rural areas maybe diagnosed at later stages of the disease. In this work we propose a shared random effect joint model with a spatial effect.

## **Oral Communication 03 | Invited Speaker**

### **Joint Modeling of Spatial Outcomes: Benefits to Understanding the Underlying Process and Power Gains**

**Charmaine Dean**

University of Waterloo, Canada

This talk discusses joint outcome modeling of multivariate spatial data, where outcomes include count as well as zero-inflated count data. The framework utilized for the joint spatial count outcome analysis reflects that which is now commonly employed for the joint analysis of longitudinal and survival data, termed shared frailty models, in which the outcomes are linked through a shared latent spatial random risk term. We discuss these types of joint mapping models and consider the benefits achieved through such joint modeling in the disease mapping context. We also consider the power of tests for common spatial structure and develop recommendations on the sort of power achievable in some contexts, as well as overall recommendations on the utility of joint mapping. We illustrate the approaches in an analysis of lung cancer mortality as well as an ecological study of Comandra blister rust infection of lodgepole pine trees.

## Oral Communication 04

### Bayesian Inference for High Dimensional Dynamic Spatio-Temporal Models

**Sofia Maria Karadimitriou, Kostas Triantafyllopoulos and Timothy Heaton**

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Spatio-temporal processes are geographically represented, i.e. in space, either by being a point, a field or a map and also they vary in time. We would like to make inference on the spatial and temporal change of certain phenomena which for instance could be the air pollution increasing or decreasing in time and ranging in a city or a country. Today high dimensional datasets can be available, where measurements are observed daily or even hourly at more than one hundred weather stations or locations along with many predictors. Therefore, what we would like to infer is high dimensional and the analysis is difficult to come through due to high complexity of calculations or efficiency from a computational aspect.

The first reduced dimension Dynamic Spatio-temporal Model (DSTM) was introduced by Wikle and Cressie (1999) to jointly describe the spatial and temporal evolution of a function observed subject to noise. A basic state space model is adopted for the discrete temporal variation, while a continuous autoregressive structure describes the continuous spatial evolution. Application of Wikle and Cressie's DTSM relies upon the pre-selection of a suitable reduced set of basis functions and this can present a challenge in practice.

In this paper we propose an estimation method for high dimensional spatio-temporal data based upon DTSM which attempt to resolve this issue allowing the basis to adapt to the observed data. Specifically, we present a wavelet decomposition for the spatial evolution but where one would typically expect parsimony. This believed parsimony can be achieved by placing a Spike and Slab prior distribution on the wavelet coefficients. The aim of using the Spike and Slab prior, is to filter wavelet coefficients with low contribution, and thus achieve the dimension reduction with significant computation savings. We then propose a Hierarchical Bayesian State Space model, for the estimation of which we offer an appropriate Forward Filtering Backward Sampling algorithm which includes Metropolis-Hastings steps for the spatial covariance inference. We describe a process to simulate medium and high dimensional spatial-temporal data. Simulations from that process are used in order to judge and evaluate the performance of the proposed methodology.

**Keywords:** dynamic spatio-temporal models; wavelets; spike and slab prior; pollution;

### Reference

- 01 Wikle, C. K., & Cressie, N. (1999). A dimension-reduced approach to space-time Kalman filtering. *Biometrika*, 815-829.

## Oral Communication 05

### An evaluation of multi pollutant profiles and respiratory mortality in London and Oxford

**A. Freni-Sterrantino<sup>1</sup>, D. Morley<sup>1</sup>, D. Fecht<sup>1</sup>, M. Blangiardo<sup>2</sup>, S. Liverani<sup>3</sup>, A.L. Hansell<sup>1</sup>, J. Molitor<sup>4</sup>**

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<sup>4</sup>Department of Public Health and Human Sciences, Oregon State University, United States

Traffic-related air pollution exposure is often highly correlated, both at the individual and small-area level. Due to the inadequacy of classical statistical methods to analyze joint effects of correlated covariates, different air pollutants are commonly analyzed separately. In this study, we analyze the joint effect of air pollution exposure, socio-economic status and the relative risk of respiratory mortality, in London and Oxford.

We estimated air pollution exposure (particulate matter (PM) of different fraction sizes, nitrogen dioxide [NO<sub>2</sub>] and nitrogen oxides [NO<sub>x</sub>]) for each postcode using European Study of Cohorts for Air Pollution Effects (ESCAPE) land use regression models and aggregating these to 7,849 Lower Layer Super Output Areas (LSOA average population size of 7,787). Respiratory mortality counts (2008-2011) provided by the Office for National Statistics were compiled for each LSOA.

We collected data on the confounders smoking (weekly tobacco expenditure), percentage of Asian population and an area-level measure of socio-economic status (Index of Multiple Deprivation 2010). We used a Bayesian approach: the Profile Regression Mixture Model using Dirichlet Process. The profile regression assembles a mixture of two sub models: a multi-dimensional Gaussian density for the covariates profiles and a Poisson distribution for disease rates. The method identifies clusters, composed of geographical areas of similar profiles in covariates and disease rate.

In preliminary analysis, correlations among exposures were all positive: particulate matters PMs Concentrations ranged between 44% and 88%. The lowest correlation was 40% between PMcoarse and NO<sub>2</sub>, while NO<sub>2</sub> and NO<sub>x</sub> correlated at 97%. We identified 16 clusters which range in size from 31 to 1560 LSOAs. Six of the 16 clusters covered 80% of the study area. From the Poisson regression, we estimated an increase in mortality relative risk associated with the deprivation index 1.013 (CI 95%: 1.011, 1.015) and weekly tobacco expenditure 1.043 (CI 95%: 1.028, 1.057).

From graphical inspection, the random effects for the clusters within Greater London are lower in when compared with the rest of study area.

In this study, using profile regression, we were able to identify clusters of geographical areas characterized by joint patterns of exposure profiles and risks. We also identified areas drifting from global trend and evaluated information of each single variable, unlike classical approaches which combine correlated variables in a unique score.

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## **Parallel Session 17**

### **Remote Sensing Applications In Health**

## **Oral Communication 01 | Invited Speaker**

### **Remote sensing for studying and modelling infectious diseases: advances and challenges**

**Emmanuel Roux**

IRD, UMR ESPACE-DEV, Montpellier, France

The interest in remote sensing for understanding, modeling and/or monitoring health issues goes back to the late 70's. However, since its first application in the health domain, remote sensing generated many promises and some frustrations depending, notably, on the data availability, cost and quality; the progresses in data science and modeling, as well as in technologies and software tools; the skills of people who work in the domain. Nowadays, new emerging remote sensing products allow significant progresses to be envisaged, by exploiting very high spatial and temporal resolution images. However, new challenges arise, both from scientific and technological points of view.

The talk will briefly present different existing or forthcoming remotely sensed data and how these data are (or could be) used to response health issues related to vector-borne diseases. Some of the promises and frustrations encountered in the past will be presented, as well as how advances in landscape characterization and spatialized data analysis strengthened the interest for the use of remote sensing to address health issues. Eventually, the most challenging issues that will be encounter in order that the health actually and efficiently benefit from the current remote sensing advances, will be discussed.

## Oral Communication 02 | Invited Speaker

### CNES activities in tele-epidemiology

#### **Cécile Vignolles**

CNES, Toulouse, France

Emerging/re-emerging infectious diseases such as dengue, Zika or malaria, with high epidemiological potential risks, lead public health managers to adapt their policies. Adaptation includes early knowledge of risks. The latter requires new tools to prevent re-emerging risks.

The key factors, involved in the emergence of these infectious diseases, can be environmental, climatic, demographic, socio-economic and/or behavioral. Some can be identified from space, which requires the development of effective methods to use remote sensing for risk factor characterization, mapping and monitoring. Data from Earth observation satellites do not directly concern the pathogens causing the disease, but their environment – they will therefore be used to measure these favorable factors.

In this framework, the French Spatial Agency (CNES) with its partners has developed a conceptual approach called tele-epidemiology which consists in studying the links between the environment, ecosystems and etiological agents responsible for diseases in human, animal and plant populations, based on space products truly adapted to the needs of health actors. This multidisciplinary approach is based upon the study of the key

mechanisms favoring the surge and spread of those diseases. Analysis of those processes is a key step in the development of new and original risk mapping using Earth observation satellite data. The primary mission is to provide to public health actors additional tools/services helping them in diseases surveillance and in the implementation of strategies to diseases control. The overall objective is to attempt predicting and mitigating public health impacts from epidemics.

This concept has been applied with success for examples such as the Rift Valley Fever (RVF) in the Ferlo region in Senegal and the Dengue fever in La Martinique. The project objectives were to provide and validate dynamic entomological risk maps, then to study adaptation processes for controlling management. For those two examples, results will be presented. CNES and its partners have worked with the countries' health authorities and with scientists to develop tools to compile entomological risk maps for some infectious vector-borne diseases (presence/absence of water points, presence/absence of larvae breeding sites, larval densities and adult mosquito densities) with high spatial and temporal resolution. The effectiveness of risk prevention could be improved by providing health authorities with these maps predicting "when and where" there will be a risk of emergence of the disease vectors and the risk level. If regularly updated, risk maps could provide useful data to optimize vector control measures.

**Keywords:** tele-epidemiology, public health, infectious diseases, climatic and environmental factors, remote sensing, risk mapping, spatio-temporal dynamics

## **Oral Communication 03 | Invited Speaker**

### **How the Earth Observation (EO) Community can help Bridging the Gap between Research and Services in Public Health Operational Programs? The Joint INPE and FIOCRUZ Experience**

**Antonio Miguel V. Monteiro**

Brazilian National Institute for Space Research (INPE), Brazil

In the last July, 23rd we have completed 45 years of a very successful Earth Observation Satellites Programs around the world. In that exact day the ERTS (Earth Resources Technology Satellite), later known as Landsat 1, was launched. It was the first in a series of Earth-observing satellites designed for studying and monitor our domo communi, the planet Earth. And although, since the very first Earth-observing satellite mission, the Public Health was amongst the four (4) key applications planned for it, together with Forests, Agriculture and Geology it was the only one that did not develop like the others. Why did it happen? In this talk, I will try to build up an argument line that lies on the assessment of a joint experience of INPE - the Brazilian National Institute for Space Research and FIOCRUZ- the Oswaldo Cruz Foundation in the search of the lost time when dealing with Earth Observation resources and Health issues.

## **Oral Communication 04 | Invited Speaker**

### **Integrating Remotely-Sensed Climate and Environmental Information into Public Health**

#### **Pietro Ceccato**

The International Research Institute for Climate and Society, NYC, USA

A number of the major human infectious diseases that plague the developing world are sensitive to inter-seasonal and inter-decadal changes in environment and climate. Monitoring variations in environmental conditions such as rainfall, temperature, water bodies and vegetation helps decision-makers at Ministries of Health to assess the risk levels of malaria epidemics and evaluate the impact of control measures. The International Research Institute for Climate and Society (IRI) has developed products based on remotely sensed data to monitor those changes and provide the information directly to the decision-makers. This presentation will present recent developments which use remote sensing and available ground-based observations to monitor climate variability, environmental conditions and their impacts on the dynamics of infectious diseases.

## Oral Communication 05

### Environmental changes and the incidence of visceral leishmaniasis in Teresina, Brazil through 1996 to 2007

**GL Werneck<sup>1,2</sup>, A Almeida<sup>3</sup>, E Braga<sup>1</sup>.**

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<sup>2</sup>IESC, Federal University of Rio de Janeiro, <sup>3</sup>Fundação Oswaldo Cruz, Rio de Janeiro

**Background:** In Brazil, visceral leishmaniasis (VL), a zoonotic infectious vector-borne disease was, originally, restricted to rural regions, but found in urban areas suitable conditions for its occurrence. Environmental transformations associated to migration, urbanization and poor socioeconomic living standards have been implicated with the emergence of VL in urban areas of Brazil.

**Objective:** To evaluate the association between environmental changes and the incidence of VL across time in the neighborhoods of Teresina, Brazil.

**Methods:** Study area: Teresina is located at 05°05' South and 42°48' West. The climate is tropical, with a dry winter and rainy summer, with a mean annual temperature of 26.8°C. The current population is >800 thousand.

*Design:* This is a mixed ecologic study in which the unities of analysis are the 102 neighborhoods of Teresina in the years of 1996-2007.

*Outcome:* VL cases as reported to City's Health Department were geocoded at the neighborhood level by using GPS and topographic maps. Outcome was defined as the number of cases of VL for each year and neighborhood.

*Exposure variables:* Annual changes in environmental variables derived from remote sensing imagery from the years of 1995, 1997, 2000, 2003, 2005 and 2007.. The following annual changes were evaluated:

a) Relative changes in the mean NDVI (Normalized Difference Vegetation Index)

b) Changes in the following land use/cover classes

- Percentage of the area covered by dense vegetation, grass or shrubs that changed to residential, commercial or industrial;

- Percentage of the area covered by dense vegetation, grass or shrubs that changed to bare soil;

- Percentage of the area covered by bare soil that changed to residential, commercial or industrial;

- Percentage of the area covered by green residential areas that changed to dense residential, commercial or industrial.

*Statistical analysis:* A random intercept multilevel negative binomial regression (the  $\ln(\text{population})$  as the offset) was used to assess the association between annual changes in the exposure variables and changes in incidence rates from 1995 to 2007. Associations expressed as rate ratios (RR) and 95% confidence intervals (95%CI). We used IDRISI and Stata 13 softwares for the analyses.

**Results:** From 1995 to 2007, around 15% of the city's area covered by vegetation was substituted by residential/commercial structures, with some neighborhoods with >50% of their area with such changes. The incidence rates increased by 15% (RR=1.15, 95%CI: 1.01-1.30) for each annual increase in 1% of the area covered by bare soil changing to residential, commercial or industrial area. On the other hand, the incidence rates decreased by 7% (RR=0.93, 95%CI: 0.89-0.96) for each annual increase in 1% of the area covered by green residential areas changing to dense residential, commercial or industrial.

**Conclusion:** Along the years, the city of Teresina experienced significant environmental changes with a substantial increase in urban features. Annual changes in land use and cover were important factors in defining neighborhoods at higher risk of VL. These variables might be used to predict high risk areas for guiding interventions against the disease.

## **Parallel Session 18 Challenges And Advances In Spatio- Temporal Disease Modelling**

### **Oral Communication 01 | Invited Speaker**

#### **Global Estimation of Air Quality and the Burden of Disease associated with Ambient Air Pollution**

**Gavin Shaddick**

Department of Mathematical Sciences, University of Bath

Air pollution is a major risk factor for global health, with both ambient and household air pollution contributing substantial components of the overall global disease burden. One of the key drivers of adverse health effects is fine particulate matter ambient pollution (PM<sub>2.5</sub>) to which an estimated 3 million deaths can be attributed annually. The primary source of information for estimating exposures has been measurements from ground monitoring networks but, although coverage is increasing, there remain regions in which monitoring is limited. Ground monitoring data therefore needs to be supplemented with information from other sources, such as satellite retrievals of aerosol optical depth and chemical transport models. A hierarchical modelling approach for integrating data from multiple sources is proposed allowing spatially-varying relationships between ground measurements and other factors that estimate air quality. Set within a Bayesian framework, the resulting Data Integration Model for Air Quality (DIMAQ) is used to estimate exposures, together with associated measures of uncertainty, on a high resolution grid covering the entire world.

Bayesian analysis on this scale can be computationally challenging and here approximate Bayesian inference is performed using Integrated Nested Laplace Approximations. Based on summaries of the posterior distributions for each grid cell, it is estimated that 92% of the world's population reside in areas exceeding the World Health Organization's Air Quality Guidelines. Estimated exposures from the model, produced on a high-resolution grid (10km x 10km) covering the entire globe, are combined with risk estimates to produce a global assessment of exposures to PM<sub>2.5</sub> and to estimate the associated burden of disease attributable to air pollution.

## **Oral Communication 02**

### **A spatio-temporal process-convolution model for quantifying health inequalities in respiratory prescription rates in Scotland**

**Duncan Lee**

University of Glasgow, UK

The rates of respiratory prescriptions vary by GP surgery across Scotland, suggesting there are sizeable health inequalities in respiratory ill health across the country. The aim of this paper is to estimate the magnitude, spatial pattern and drivers of this spatial variation. Monthly data on respiratory prescriptions are available at the GP surgery level, which creates an interesting methodological challenge as these data are not the classical geostatistical, areal unit or point process data types. A novel process-convolution model is proposed, which extends existing methods by being an adaptive smoother via a random weighting scheme and using a tapering function to reduce the computational burden. The results show that particulate air pollution, poverty and ethnicity all drive the health inequalities, while there are additional regional inequalities in rates after covariate adjustment.

## Oral Communication 03 | Invited Speaker

### TB or not TB?

**Trevelyan J. McKinley**

University of Exeter, UK

Bovine tuberculosis (bTB) is one of the most serious diseases of livestock and wildlife in Great Britain; currently costing the UK government upwards of £100 million per year in testing and compensation, notwithstanding the additional impacts on the livelihoods of farmers affected by the disease. Despite intensive surveillance the disease is still persisting in the national herd. It is also one of the most challenging disease systems to model. Large data sets on animal movements and trading are available, as well as the results of routine herd surveillance testing; nonetheless, there are myriad hidden states and large degrees of missing information, compounded by the potential presence of a wildlife reservoir of infection that varies across space and time. In this talk we present some work aiming to use state-of-the-art data-augmented Markov chain Monte Carlo methods for fitting a spatio-temporal dynamic model of bTB infection to these data, and discuss the challenges faced and those still to overcome.

## Oral Communication 04

### Spatial tracking of a Measles outbreak in England and Wales using data assimilation

**Loren Cobb<sup>1</sup>, Ashok Krishnamurthy<sup>2</sup>**

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We present a spatial variant of the time series SIR (TSIR; Time series Susceptible–Infected–Recovered) stochastic population-based model to capture the spatial transmission dynamics of an infectious disease outbreak in England and Wales.

Many infectious diseases show seasonal patterns of incidence. Specifically, we explore how the basic dynamical features of the long-term pattern measles outbreak with a seasonal forcing of transmission acts as a major driver of a long-term epidemic behavior. We use a 20-year pre-vaccination era biweekly time series data (births by year and incidence of measles) from 60 towns and cities in England and Wales to capture the spatial spread of measles.

“Data Assimilation” is a general class of techniques for tracking state variables (in our case, time series of susceptibles AND infected), using Bayesian updates applied to a dynamic model. Without data assimilation, the TSIR model would only be able to blindly forecast the outbreak without any correction from real-world data.

The prediction is expected to improve as data is assimilated over time. The posterior thus provides a realization of the state variables conditioned on all prior data and newly arrived data. The projected number of newly infected cases are estimated and presented. From the simulation, we recover spatiotemporal maps of the incidence of the infection. We compare simulated time-series graphs with real data compiled by Grenfell and others.

## **Oral Communication 05 | Invited Speaker**

### **Modelling reporting delays of surveillance data**

**Leonardo Bastos**

Fundação Oswaldo Cruz, Rio de Janeiro, Brasil

One difficult for real-time tracking of epidemics is related to reporting delay. The reporting delay may be due to laboratory confirmation, logistic problems, infrastructure difficulties, etc. However, some notification systems report not only the case date but also the data entry date. Based on this two dates, we developed a hierarchical dynamic linear model that update the total notification cases by estimating the delayed cases. Inference was done under the Bayesian approach through an efficient algorithm based on integrated nested Laplace approximation (INLA). We apply the proposed method in dengue notification data from Rio de Janeiro.



# Posters

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### Poster 01

#### Data Integration for high-resolution, continental- scale estimation of air pollution concentrations

[Matthew L. Thomas](#), Gavin Shaddick and Kees de Hoogh

### Poster 02

#### Public management of the Basic Sanitation Using Analyses of System of Geographical Informations (SIG). Case study Macaé - Rio de Janeiro

[Almeida, Janimayri Forastierj](#); [Nunes-Da-Fonseca, Rodrigo](#); [Medeiros, Márcio José De](#); [Ribeiro, Enoque Gonçalves](#).

### Poster 03

#### Mapping Temporal and Geographic Variation in Suicide Rates in the U.S., 2005-2015

[Diba Khan](#), Lauren M. Rossen, Holly Hedegaard, and Margaret Warner

### Poster 04

#### A two-step procedure to model discontinuities in spatio-temporal disease mapping

[Adin, A.](#), [Lee, D.](#), [Goicoa, T.](#), [Ugarte, MD](#)

### Poster 05

#### Spatiotemporal regressions to explore suicide mortality in Germany

[Marco Helbich](#), Paul L. Plener, Sebastian Hartung, Victor Blüml

### Poster 06

#### Mortality trend due to traffic crashes in young in Brazil, 2000 to 2014

[W. A. Melo](#), [M. D. B.Carvalho](#)

### Poster 07

#### Yellow fever: tragedy announced by disasters and political negligencias

[Anselmo Romão](#), [Christovam Barcellos](#), [Ricardo Antunes Dantas de Oliveira](#), [Renata Gracie](#)

### Poster 08

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##### Data Integration for high-resolution, continental- scale estimation of air pollution concentrations

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<sup>3</sup> Swiss Tropical and Public Health Institute, Basel, Switzerland;

<sup>4</sup> University of Basel, Basel, Switzerland

Air pollution represents one of the most important environmental risk factors to human health globally with a number of pollutants associated with adverse health outcomes. Epidemiological studies designed to estimate the risks associated air pollution require accurate measures of concentrations with comprehensive coverage of a study area. Traditionally, these have been based on measurements from ground monitors but this may not provide information of sufficient quality and coverage to allow accurate spatial (and temporal) prediction at all locations at which estimated concentrations are required. Ground monitoring data may therefore need to be supplemented with information from other sources, such as estimates from satellite remote sensing, chemical transport models, land use and topography. Here, we integrate data from multiple sources within a Bayesian hierarchical modelling framework, allowing the biases and uncertainties associated with the different sources of information related to air quality to be incorporated.

Within the modelling framework, downscaling models are used to align data generated at different geographical resolutions, including point locations and a series of (potentially non-aligned) grids of varying resolutions. The proposed modelling approach is used to predict concentrations of nitrogen dioxide, together with measures of uncertainty, at high-resolution (up to 100m x 100m) throughout the European Union by integrating data from 2400 ground monitoring locations, remote sensing satellite retrievals together with land-use information. Performing complex Bayesian inference combining potentially very large datasets is computationally challenging and here we perform approximate Bayesian inference using Integrated Nested Laplace Approximations.

## Poster 02

### Public management of the Basic Sanitation Using Analyses of System of Geographical Informations (SIG). Case study Macaé - Rio de Janeiro

**Almeida, Janimayri Forastieri; Nunes-Da-Fonseca, Rodrigo; Medeiros, Márcio José De; Ribeiro, Enoque Gonçalves.**

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Currently Brazil relives outbreaks of arboviruses (viruses transmitted by arthropods), especially those related to mosquitoes. In search of solutions, public and private projects in basic sanitation are developed.

One of the instruments used to prioritize Basic Sanitation is the legal requirements, such as the Federal Basic Sanitation Law 11.445 / 2007, which provides for the treatment and supply of drinking water, collection and treatment of sanitary sewage, storm drainage and collection and Disposal of solid waste, services that should be offered to the entire population. This law establishes that each municipality is responsible for the execution of the aforementioned services and that they present a Basic Sanitation Plan considering short, medium and long term measures for their adaptation. However, many Brazilian municipalities claim difficulty in drawing up this plan given the need for specific manpower.

A geographical information system (GIS) -based management tool powered by local diagnosis of sanitation, health, education, and others, as well as general characteristics by neighborhood, generating indicators and prognosis, directing investments, works and sanitation projects, will help municipalities in the preparation and monitoring of the implementation of the Basic Sanitation Plan required by federal law. This tool will also assist the management of public services in several other areas of municipal administration such as health, construction and education, as they present different indexes of the cross-referencing of the diagnosed information.

Thus the implantation of this tool can be recognized as a method of controlling or even eliminating outbreaks of diseases generated by lack of basic sanitation works and services offered to the population, as it can be one of the causes of arbovirus outbreaks.

This work aims to propose and implement a computational tool for Municipal Basic Sanitation using a GIS, helping public management in decision and making promoting quality of life to the population. To illustrate the use of the tool, the Municipality of Macaé, Brazil, was listed as a case study.

## Poster 03

### Mapping Temporal and Geographic Variation in Suicide Rates in the U.S., 2005-2015

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Over the past several years, suicide rates (SRs) have increased in the U.S. Geographic variation in SRs at the state level has been reported, however county level SRs are rarely examined. Due to concerns about statistical reliability and confidentiality, county-level mortality rates based on fewer than 20 deaths are suppressed based on Division of Vital Statistics (NCHS) statistical reliability criteria, precluding an examination of spatiotemporal variation in SRs at the county level using direct estimates. We used mortality data from 2005-2015 to explore spatiotemporal variation in SRs, applying small area estimation methods to predict year and county-specific SRs. Specifically, hierarchical Bayesian spatio-temporal models were implemented with spatially structured and unstructured random effects, correlated time effects, time varying confounders and space-time interaction terms via Integrated Nested Laplace Approximation (INLA) in R, borrowing strength across both counties and years to produce smoothed county level SRs.

This method allows examination of spatiotemporal variation across the entire U.S., even where data is sparse. Model-based estimates of SRs were mapped to explore geographic variation for the years 2005 and 2015. In 2005, just under 10% of counties had estimated SRs less than 10 per 100,000, while only 2% were below this rate in 2015. While 8% of counties had estimated SRs in excess of 20 per 100,000 in 2005, 31% surpassed this rate in 2015. The majority of counties in the western part of the U.S., with the exception of southern California and parts of Washington, had predicted SRs in excess of 20 per 100,000 in 2015. Findings highlight U.S. counties where SRs are higher or lower than the national average, which may help guide suicide prevention policies and programs.

## Poster 04

### A two-step procedure to model discontinuities in spatio-temporal disease mapping

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<sup>3</sup>School of Mathematics and Statistics, University of Glasgow, United KingdomP

Maps have been and still are crucial tools to detect inequalities in health among different small areas within a larger region. A vast majority of the research in disease mapping has been focused on developing models to smooth risks in space and time and to unveil the geographical and temporal patterns. However, when discontinuities are present, that is when there are groups of areas with high (low) risk surrounded by areas with low (high) risk, an excess of smoothing may impede the detection of these hotspots (coldspots) and their evolution in time.

On the contrary, techniques specifically designed for detecting hotspots (coldspots) do not provide risk estimates for the small areas and consequently, the geographical and temporal patterns are missed. In this work, a two-stage approach is proposed to smooth risks in space and time and to model discontinuities simultaneously. The procedure deals with spatial clusters that grow or shrink in time. In the first step, a set of cluster configuration in space and time is elicited using an agglomerative algorithm on training data. In the second step, a set of spatio-temporal models are fitted using integrated nested Laplace approximations (INLA). The procedure is illustrated with stomach cancer data in Spain and brain cancer in two Spanish regions: Navarre and Basque Country.

## Poster 05

### Spatiotemporal regressions to explore suicide mortality in Germany

**Marco Helbich<sup>1</sup>, Paul L. Plener<sup>2</sup>, Sebastian Hartung<sup>3</sup>, Victor Blüml<sup>4</sup>**

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**Introduction:** Suicide is a serious public health issue throughout the world: Each year, more than one million people commit suicide. After years of constant or declining suicide rates across Germany, the number of suicide cases is on the rise again. The German-wide suicide rate displays a constant upward trend from 11.4 deaths per 100,000 persons in 2007, to 12.6 deaths per 100,000 persons in 2011. Of similar importance, it seems that there are regional variations within the country, which also change over time. However, comprehensive knowledge about the underlying reasons is inconclusive.

**Methods:** Therefore, the present study utilized an ecological research design based on 402 districts to investigate suicide risk across space and over time (2007-11), and to identify relevant risk and protective factors through space-time regression models using INLA.

**Results:** The results show that the higher the district-specific unemployment rate, the more pronounced the suicide risk. In contrast, higher average income seems to be a protective factor diminishing the risk. Variables referring to mental health service provision (e.g., the number of psychiatrists and psychotherapists per 100,000 persons) were not associated with suicide risk. Significant urban–rural differences were observed. We found a significant increase in suicide risk over time for Germany as a whole, whereas district-specific deviations occurred. Striking spatial patterns also emerged across Germany.

**Conclusion:** The findings are crucial for the National Suicide Prevention Program of Germany supporting place-based prevention strategies focusing on the identified areas under high risk.

**Keywords:** Suicide, mental health, spatiotemporal analysis, risk factors

## Poster 06

### Mortality trend due to traffic crashes in young in Brazil, 2000 to 2014

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**Introduction:** Considered a major global public health problem, traffic accidents especially affect people aged between 15 and 29 years [1], one of the most productive population age groups. This has significant economic, social and emotional repercussions [2]. Objective: The aim of this study was to analyze the trend in mortality from road traffic crashes among young in Brazil between 2000 and 2014.

**Methods:** It is an ecological time series and cross-sectional study of deaths from road traffic crashes among young adults (15-24 years old) residing in Brazil from 2000 to 2014. Secondary mortality data was obtained from the Mortality Information System (MIS), containing information on all cases of death occurred in the Brazil, and the population data were obtained from the Brazilian Institute of Geography and Statistics (IBGE) [14]. Trend analysis was performed using polynomial regression models. A polynomial model attempts to find the curve that best fits the data, in order to describe the relationship between the dependent variable Y (mortality rate) and the independent variable X (year of study). The linear polynomial regression ( $Y = \beta_0 + \beta_1 X$ ), quadratic ( $Y = \beta_0 + \beta_1 X + \beta_2 X^2$ ) and cubic ( $Y = \beta_0 + \beta_1 X + \beta_2 X^2 + \beta_3 X^3$ ) models were tested. A trend was considered significant when the estimated model obtained a p-value < 0.05.

**Results:** The total cases studied were 203,404 deaths, being 83.1% males. The linear polynomial regression analysis showed a significant and growing trend for accident mortality rates of motorcyclists ( $y=10.0+1.13x$ ;  $R^2=0.94$ ;  $p<0.001$ ), car ( $y=9.22+0.43x$ ;  $R^2=0.9$ ;  $p<0.001$ ) and pick-up truck occupants ( $y=0.29+0.01x$ ;  $R^2=0.4$ ;  $p=0.01$ ), and a decreasing trend for accidents involving pedestrian deaths ( $y=4.71-0.21x$ ;  $R^2=0.8$ ;  $p<0.001$ ). There was a significant increasing trend for the motorcyclist and car occupant categories in Brazil, as well as a significant decreasing trend in the pedestrian category and increased mortality for all years and all categories, especially among motorcycles and car occupants. The results of the present study suggest that public authorities have not satisfactorily assumed their responsibility for the control and reduction of crashes and mortality from road traffic, especially those involving motorcycles.

**Conclusion:** The need to prevent injuries and deaths from crashes is an increasingly important public health issue in Brazil and around the world.

**Keywords:** Mortality rate, Trends, Traffic accidents, Epidemiology.

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## Poster 07

### Yellow fever: tragedy announced by disasters and political negligencities

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The yellow fever is an infectious disease transmitted by vectors, which has occurred in vast tropical regions in South America and Africa since the 17<sup>th</sup> century. With the development of vaccines and vector control campaigns, a considerable reduction of the occurrence of this harm took place, especially in urban areas. However, the wild cycle of transmission still a challenge, keeping it endemic in some areas in Brazil.

Dissemination scenario of wild yellow fever in the 1930's, the Canaã valley located in the south part of Doce river basin was an object of a pioneer study of this zoonosis, that has reemerged recently in the same hydrographic basin. This objective of this work is to show the distribution of occurrence area of yellow fever, comparing the last cases in 2016, relating it to environmental changes.

Initially the yellow fever cases were selected in the period of 2007 to 2016 and maps were built with the occurrence distribution of this harm considering the data collected at DATASUS and by the Health' secretaries of States and Municipalities. It was observed that between 2007 and 2015, the occurrence of human cases of yellow fever was reducing its incidence and coverage area. From 2016 there is an increase in the number of cases and of the yellow fever occurrence coverage area.

A great part of the new transmission area is concentrated along the Doce river basin, where in the end of 2015 a big environmental disaster happened, caused by the spill of mining tailings, which affected the whole river during various months. The disaster that occurred at Mariana's dam altered in a significant way the dynamics of the hydrographic basin, compromising the existing interaction between aquatic life and the other surrounding ecosystems, resulting in a new environmental, ecological and social configuration that still to be understood.

The effects of the changes of the environmental conservation policies, as the 2012 alteration of Brazilian Forest Code, also need to be considered. These environmental changes resulted in landscape and ecology changes in places where there was not favorable characteristics to yellow fever transmission. There was an increasing occupation of rural areas, the fragmentation of remaining areas of tropical forests and urbanization of small and medium cities. All of these events are related to the fact that various policies that should have been taken to protect the population were not adequately implemented.

## Poster 08

### Intra-regional comparison of primary care quality in Portugal using prevention quality indicators

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**Background:** Primary care is a cornerstone of the Portuguese National Health System. The quality of primary care services can be evaluated by several methods, such as identifying hospitalizations for conditions that should be treatable or less severe if appropriately treated on an outpatient basis. In this line, the Agency for Healthcare Research and Quality (AHRQ) developed 13 prevention quality indicators (PQIs) plus 3 composite indicators and an overall composite indicator. As comparison of performance of healthcare services between countries, regions and other geographical areas are a major input in healthcare decision making, our aim was to compare PQIs in Portugal across regions.

**Methods:** We performed a retrospective study, analyzing all adult hospitalizations between 2011 and 2015 in Portugal. PQI rates were computed using AHRQ specifications. We considered only the overall composite PQI (PQI 90) and the three composites (i.e. 91 – acute, 92 – chronic, 93 – diabetes). We compared the PQI rates between regions of residence by NUTS II. Descriptive and inferential statistics were used.

**Results:** Of all adult hospitalizations occurred between 2011 and 2015, 11.9% (407,792 hospitalizations) were included in the selected PQIs. The national rate of the PQI 90 was of 997.4 hospitalizations per 100,000 inhabitants, with 535.3 hospitalizations per 100,000 inhabitants for PQI 91, 468.4 hospitalizations per 100,000 inhabitants for PQI 92 and 106.4 hospitalizations per 100,000 inhabitants for PQI93. Statistically significant differences between regions were found, with Norte having the lowest overall PQI rate (i.e. 889.9 hospitalizations per 100,000 inhabitants) and Centro the highest (i.e. 1273.2 hospitalizations per 100,000 inhabitants). Moreover, there was an increase with time (e.g. overall PQI rate increased from 999.5 hospitalizations per 100,000 inhabitants in 2011 to 1231.0 hospitalizations per 100,000 inhabitants in 2015).

**Discussion:** A significant variation of composite PQIs between regions was observed. As a proxy of primary care quality, we should assess and study more carefully these possible differences of provided primary care and healthcare policies should be designed to improve it.

### **Acknowledgement**

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## Poster 09

### Strong Spatial Inequalities In The Nutrition Status Of Elderly (Portugal)

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**Introduction:** Within Nutrition UP 65 study nutritional health problems of the elderly Portuguese population were described, but it of major relevance to identify target vulnerable groups for public health interventions. This analysis aims to identify clusters of priority intervention in the improvement of the nutritional deficit in this population.

**Methods:** Data was provided by a cluster sampling of 1500 individuals with 65 or more years, representative of the elder people living in Portugal, according to the age, gender, education level and NUT2 regional area of the country. Using an interview as the inquiry procedure, information about lifestyle, health and nutritional status was individually collected. Serum vitamin D and 24-hour urine were also evaluated. A spatial scan statistic was obtained, using SaTScan software and the Gaussian model for quantitative variables and the Bernoulli model for dichotomous variables, to assess possible clustering of individual nutritional status such as frailty, obesity, sarcopenia, hydration, vitamin D status and salt consumption. A Log Likelihood Ratio (LLR) test was used to identify significant clusters of higher than expected (hotspot) or lower than expected (coldspot) nutritional status and p-value less than 0.05 was considered statistically significant.

**Results:** SaTScan analysis detected two hotspot of fragility on the northwest (LLR = 23.32; p-value<0.05) and center coast (LLR = 10.59; p-value<0.05); one hotspot of hipohydration on the northwest (LLR = 33.50; p-value<0.05); one hotspot of Vitamin D on the center (LLR = 14.67; p-value<0.05); two hotspot of salt consumption the northwest (LLR = 11.86; p-value<0.05) and center coast (LLR = 9.83; p-value<0.05), which means that the nutrition status of the elderly in these regions is more likely to be impaired. No clusters of better nutritional condition were detected (coldspot).

**Conclusion:** This analysis showed that northwest and center are priority regions for intervention to improve the nutrition status of the Portuguese older adults.

## Poster 10

### Hospitalisations with obstructive lung disease in Portugal, from 2011 to 2015

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Obstructive lung disease (OLD), a category of chronic respiratory diseases characterised by airway obstruction, includes chronic obstructive pulmonary disease (COPD), asthma, and bronchiectasis. COPD alone is predicted to be the third cause of death by 2030. A previous study on hospitalisations in Portugal between 2000 and 2010 showed a considerable decrease in in-hospital COPD mortality over years, with hospitalisations and length of stay not changing substantially. In this context, we aimed to update and analyse trends in OLD hospitalisations in Portuguese hospitals, between 2011 and 2015, including an analysis by region.

This retrospective observational study was carried out using data from hospital discharges, provided by the Central Administration of the Health System (ACSS). OLD episodes were selected considering ICD-9-CM coded diagnoses, either principal or secondary. Specifically, we included all inpatient episodes in mainland Portuguese hospitals with a discharge between years 2011 and 2015, with age of 18 years and over, and with a diagnosis of OLD, i.e., ICD-9-CM codes 491.x for chronic bronchitis, 492.x for emphysema, 493.x for asthma, 494.x for bronchiectasis, and 496 for chronic airway obstruction not elsewhere classified (COPD includes codes 491.x, 492.x and 496). We studied patients' gender, age and residence region (NUTS II).

A total of 293 627 inpatient episodes with OLD were identified. These inpatients had an average age of 70 years old, 55.6% were male, and 18.6% of them (n=54 479) had a principal diagnosis of OLD. Of all hospitalisations in 2011, 6.8% had a diagnosis of OLD, with a continuous increase to 8.8% in 2015. OLD as principal diagnosis remained stable, with 1.4% in 2011 and 1.4% in 2015. Considering the geographic location of the patient residence, Norte was the region with highest absolute annual frequency of hospitalisations with a principal diagnosis of OLD, with 4 595 on average (42.3% of the total). Norte also had the highest incidence, with 153 cases per 100 000 inhabitants, followed by Centro, Lisboa, Algarve and Alentejo, with 148, 112, 92 and 89 cases per 100 000 inhabitants, respectively. Comparing 2011 with 2015, there was a global increase of 4.2% in the incidence of hospitalisations with a principal diagnosis of OLD, with the highest variation in the Norte region with +17.7%, and the lowest in Lisboa with -10.2%. The region with highest in-hospital mortality in hospitalised patients due to OLD was Alentejo with 10.6%, whereas the lowest was observed in Lisboa with 5.7%. COPD alone was responsible for 76.4% of all discharges with a principal diagnosis of OLD.

In the last years, the overall number of inpatient episodes with OLD increased in Portugal. Considerable geographic differences were observed, which need to be further studied.

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## Poster 11

### Reducing the sample size of surveillance system for the dengue vector *Aedes aegypti* in Rio de Janeiro via genetic algorithms

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Concerns about the spread of diseases affect both the population in their daily life and public health policy in Brazil and worldwide. The Brazilian Ministry of Health estimates that 2.5 billion people across the globe live in regions where dengue fever is an endemic disease, and approximately 50 million people are infected each year. In Brazil, new disease outbreaks occur every 3 to 5 years, generally associated with the introduction of a new serotype in the country. The last outbreak occurred in 2013 with the introduction of the so-called type-4 dengue virus.

Surveillance of mosquito reproduction and infestation includes, among other methods, the use of ovitraps – traps where mosquitoes lay their eggs, which are considered one of the best alternatives for detecting dengue and yellow fever outbreaks.

The aim of this study is to reduce the sample size of the system for capturing dengue mosquito eggs used by the city of Rio de Janeiro. With this, it will be possible to increase the frequency of data collection from a monthly to a weekly basis without increasing costs, while maintaining the quality of estimates obtained from the sample.

The sampling grid reduction problem is associated with a combinatorial optimization problem belonging to the NP class where, given a sample of size  $n$ , a subset of elements of size  $n^*$  needs to be found such that the estimation error is less a preset limit. From this definition, it is possible to turn the sample reduction problem into a case of the *0/1 knapsack problem*. Using this association, this paper proposes objective functions that incorporate spatio-temporal dependence effects as well as an approach using biased random-key genetic algorithms.

**Keywords:** sampling design reduction; genetic algorithms; combinatorial optimization.

## Poster 12

### Geographic distribution in canine rabies and possible environmental conditions associated with its incidence in Peru, 2010 – 2016.

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Rabies is still a serious public health concern in developing countries. In Peru the number of cases of canine rabies has increased in recent years, due to the occurrence of a major outbreak in the southern region of the country. Although the number of cases has decreased significantly in the last decades as the result of the commitment made in the 1980s by all the member states of the Pan American Health Organization. The maintenance of the transmission of the rabies virus (VR) and the emergence of this important outbreak have increased the efforts by the surveillance program to control its dissemination to other areas. The aim of the study was to describe the spatial distribution of canine rabies between 2010-2016 in Peru and to describe possible environmental factors associated with its incidence.

**Material and Methods:** Official database of canine rabies were analysed from 2010 to 2016, geospatial information was used to estimate the spatial distribution, also were evaluate epidemiological indicators such as the incidence and frequency. An environmental characterization in the regions affected was performed.

**Results:** According to the data evaluated and the literature reviewed, the southern region of the state of Puno is an endemic region of canine rabies in the country, that also reports human rabies cases, and more recently the state of Arequipa if the outbreak is not managed, is on the process of becoming another national endemic region. The environmental conditions are similar, both belong to the Andean region, but Arequipa has an important coastal area, and is crossed by many important roads which connect it with other regions including the city capital of Lima, which would represent a potential risk for the dissemination of urban rabies to other states.

**Conclusions:** The spatial distribution of canine rabies shows that the southern region of the country is endemic. It is necessary to improve the prevention and control measures in the region with an outbreak of canine rabies. Studies are necessary to investigate the hypotheses presented.

**Keywords:** Peru, canine, rabies, Puno, Arequipa.

## Poster 13

### Human Visceral Leishmaniosis In Brazil: An Analysis Spatial From 2001 To 2015.

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Visceral leishmaniasis (LV) is a very common zoonosis in Brazil with 90% lethality when untreated. However, its spatial distribution does not occur at random, and it is essential to analyze the LV behavior in Brazilian municipalities. The objective of this study was to analyze the incidence of human visceral leishmaniasis in Brazil during the period from 2001 to 2015. It was an observational, descriptive epidemiological study based on secondary data from the Department of Informatics of the Brazilian National Health System - DATASUS. The mean incidence was calculated per quinquennium for each municipality. Spatial analysis was performed using QGIS software version 2.14.11 and TerraView version 4.2.2. LV is unevenly distributed throughout Brazil. In the period from 2001 to 2005, of the 1,581 (28%) municipalities that registered cases the average incidence ranged from 0.01 to 76.64 cases per 100,000 inhabitants. The Northeast region had the highest average incidence with 0.77 cases per

100,000 inhabitants, with the municipalities of Cacimbinhas, Carneiros and Campo Grande (Alagoas), with incidence of 27.8; 21.6 and 19 cases / 100,000 inhabitants, respectively. During this period no municipality in the southern region registered cases. From 2006 to 2010, 1,619 (29%) municipalities registered cases of VL, the Northeast remained the largest number of cases. However, the Central-West region presented an increased incidence, with the municipalities of Araguaína, Pequizeiro and Araguatins (Tocantins) with incidence of 110.17; 78.48 and 77.7 cases / 100,000 inhabitants, respectively. 18 municipalities registered cases in the South region. Between 2011 and 2015, of the ten municipalities with the highest average incidence, seven were from Tocantins, the municipality of Carmolândia had an average incidence of 179 cases / 100,000 inhabitants. Of the 1,807 (32%) municipalities with case records, 1,038 (57%) are in the Northeast region. During this period, progress was observed in the municipalities of northern Minas Gerais and western São Paulo. In the southern region, only eight municipalities had cases. Visceral leishmaniasis is a disease of high incidence in municipalities in the Northeast region, with progress in the Midwest and Southeast regions, more specifically in the north of Minas Gerais and in the west of São Paulo. Brazil has LV as a public health problem, with more than 3 thousand cases per year. Thus, it is necessary, on the part of the municipalities, the implementation and intensification of the control actions recommended by the Ministry of Health.

**Keywords:** visceral leishmaniasis, Brazil, Municipalities, Public health

## Poster 14

### Disaster risk management in the Brazilian Unified Health System

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Disasters are among the factors that influence living conditions and have an impact on the health of the population and on health services. Its occurrence shows vulnerability conditions related to social, economic and environmental inequalities, mainly affecting the populations of poorer areas as well as the capacity to reduce risk and build resilience.

The disaster risk management process involves actions of risk reduction, management and recovery where looking at the territory is essential to know the scenario, its hazards and vulnerabilities. It is thus possible to identify the problems and resources available and necessary to address them. In this context, this work aims to present the distribution of floods in Brazil with a focus on Amazonas and the diagnosis of the capacity of health secretariats in these situations.

For the analysis, data from the federal government from 2003 to 2015 were used. The SUS data are from Fiocruz research grouped into three levels. Priority was given to those who demonstrate the institutionalization of the theme. The data were tabulated in Excel and spatialized using Qgis.

The most recurrent disasters in Brazil are floods and drought. Between 1991 and 2010, 31,909 natural disasters hit all regions and 32.7% from floods. The country has more than 1,000 municipalities at risk. In the Amazon there are more than 49% of them, where the greatest vulnerability is along the Solimões

and Amazonas rivers, which are submerged for six months and change the community dynamics and the adaptation of services and where there is less capacity to act in disasters. There are information limitations and there are no management mechanisms for actions.

In the Amazon, it is common for communities to adapt their homes by raising the level of the floor with boards so that they remain there, even flooded, increasing the risks of exposure. For the circulation of people, wooden walkways are built and health care and garbage collection, for example, are carried out in floating units.

Disaster risk reduction is one of the essential public health functions since they can cause death, illness and disruption of health services. Therefore, knowing the risk scenario and preparing these services to act in a timely manner is essential to reduce damages to the population.

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## Poster 15

### Combining social and built environment dimensions to categorize the territory - testing a multivariate statistical methodology in Lisbon municipality

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Territory integrates several dimensions namely geographical, anthropological, cultural, social, economical and bioecological. This study is based on a geographical view of territory: the result from a set of processes in which the material, physical and social aspects of human action are inseparable and interdependent. Public health studies often categorize territory using deprivation indices to identify priority areas to tackle health inequalities. Deprivation is multidimensional so composite indices better reflect the reality instead of a single indicator. This study aimed to test a methodologic approach to territory categorization using census data and was carried in Lisbon Municipality.

Data was collected from the 2011 census at the statistical sections level (area of 3300 dwellers). Sixty-one sociodemographic, economic and building variables were collected on the National Statistics Institute website and 11 variables on land use collected on the Territory General Directorate website. Data were grouped in Physical Aspects (PA) -data on buildings and land use- and Social Aspects (SA) -demographic and socioeconomic data. Statistical analyses were performed using SPSS and Moran I computed in ArcGIS.

Principal Components Factor Analysis (PCA) was used to reduce the number of indicators. PCA on PA initially resulted in 12 factors but factors were reduced to 6 by excluding information according to their initial loading value. PA 6 factors accounts for almost 75% of the variance in this group. Factor 1 is related to housing conditions, factor 2 concerns housing dimension, factor 3 is mainly non residential, factor 4 relates to urban land use, factor 5 is associated with construction material, and factor 6 is exclusively agricultural. PCA on SA resulted in 5 factors that account for almost 82% of this group variance. Factor 1 has a low socioeconomic level, factor 2 is socioeconomically stable, factor 3 concerns families with under 15 y/o children, factor 4 is related with residents' gender and, factor 5 concerns families with over 15 y/o children.

An Ascending Hierarchical Classification, also known as cluster analysis, performed with the 6 PA factors and the 5 SA factors, resulted in 4 clusters: (1) joins sectors similar in housing size, low socioeconomic level and families with under and over 15 years old individuals; (2) consists of urban sections with good housing conditions, families with over 15 years old individuals and employees in the tertiary sector; (3) sections are characterized by small house size, mainly non-residential buildings and low socioeconomic level; (4) is agricultural area. Moran's I confirmed that the clusters' distribution was spatially autocorrelated and significant.

This methodology proved its applicability. Despite territory categorization complexity it is crucial to the development of more strategic planning interventions.

## Poster 16

### **Comprehensive Area-Level Measures for Studying Tobacco Use Disparities: The 2015 Neighborhood Determinants of Tobacco Use among Young Adults Study**

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Disparities in health outcomes can be traced to myriad factors at different levels of organization ranging from social circumstances, cultural factors, environmental exposures, and the characteristics of the neighborhoods in which people live, to lifestyle behaviors and biology.<sup>1,2</sup> Perhaps no other agent of disease better illustrates the complexity of the determinants of disparities at these multiple levels than tobacco. Racial/ethnic and socioeconomic disparities in health behavior and outcomes, such as tobacco use and lung cancer, have long been documented on a broad scale in the public health literature.<sup>3,4</sup> Not only is tobacco use the single most important etiologic factor in overall U.S. mortality, but it is also the major cause of death for cancer and one of the primary factors in death and disability from cardiovascular disease, the major sources of premature mortality in the United States.<sup>5</sup>

Tobacco use often begins in adolescence and intensifies in young adulthood, with young adults continuing to smoke at higher rates than any other age group in the U.S., and rates of alternative

tobacco use rising even as cigarette smoking declines.<sup>6</sup> Within this age group already at higher risk for tobacco use, there are also persistent disparities that exacerbate the risk. Latino and Black young adults, as well as those of lower socioeconomic status (SES), have been shown to use cigarettes, menthol cigarettes, cigars, blunts and e-cigarettes at higher rates than Non-Latino Whites and Asians and those of higher SES.<sup>7</sup> These populations also have more difficulty quitting tobacco use later in life.<sup>8</sup> Young adulthood is therefore a critical time to intervene on tobacco use behavior, especially because cessation prior to the age of 30 has the potential to eliminate long-term damaging effects from tobacco use.<sup>9</sup>

As health disparities research has evolved over the last two decades, researchers have increasingly recognized the importance of salutogenic factors that may promote or obstruct healthy behavior among individuals.<sup>10</sup> In particular, neighborhoods or local urban environments have emerged as important contexts for the study of health disparities as well as behavioral and chronic disease outcomes generally. Differences in tobacco use and exposure are likely as subject to context as other well studied behavioral measures, such as physical activity. However, there is a sparse literature surrounding neighborhood characteristics and tobacco use as yet. The bulk of existing research focuses on locally aggregated measures of neighborhood SES or material deprivation.<sup>11,12</sup> Nevertheless, a few recent studies have emphasized place as determinant of tobacco use and smoking behavior – for example, Osypuk et al.<sup>13</sup> theorize differences in smoking patterns by state and race/ethnicity for the U.S. population and find significant variation between nationally reported smoking prevalence rates by race/ethnicity and state-level prevalence rates by subgroup. Henriksen

and colleagues<sup>14,15</sup> find that the density and proximity of tobacco retail outlets in relationship to high schools in the San Francisco Bay Area are associated with the smoking prevalence rate among high school students, and Rodriguez et al.<sup>16</sup> in a national analysis of tobacco outlet density by census tract find higher density in tracts characterized by lower socioeconomic status and higher proportions of nonwhite residents.

Additionally, Pearce et al.<sup>17</sup> conceptualize place as determinant of smoking along two primary pathways: 1) place-based practices, including social capital, social norms, contagion and neighborhood disorder; and 2) place-based regulation, referring to smoking cessation policies, access to and availability of tobacco products, targeted tobacco advertising and urban regeneration, or efforts to make environmental modifications designed to promote healthy behavior in urban areas characterized by lower SES. Other theoretical models of smoking behavior emphasize similar themes.<sup>18,19</sup>

Following Pearce et al.'s model<sup>17</sup>, in the area of place-based practices Christakis and Fowler have found social network behavior to influence a variety of health behaviors including smoking<sup>20</sup> – individuals who have a friend, sibling or spouse quit smoking are much more likely to do so themselves, while those whose networks continue smoking are more likely to continue smoking themselves. This tendency to model behavior may be more diffuse at the neighborhood level, but there is evidence to suggest that collective behavioral norms are associated with the

probability of smoking. For example, Ahern et al.<sup>21</sup> found higher odds of smoking in neighborhoods with permissive smoking norms where collective efficacy was high, while neighborhoods that had high collective efficacy with strong anti-smoking norms had much lower odds of smoking. Kandula et al.<sup>22</sup> also found that living in ethnic enclaves decreased the likelihood of smoking for Asians in California, which the authors surmise may be related to cultural norms and social cohesion that buffer stress and reduce the propensity to use smoking as a coping behavior. Additional research has found neighborhood social cohesion and civic participation to reduce smoking risk<sup>23,24</sup> while low levels of cohesion and trust are associated with higher smoking rates.<sup>25-27</sup>

More of the research on smoking and neighborhoods has focused on the neighborhood disorder facet of Pearce et al.'s framework along with social inequality and material deprivation. Disorder can be characterized in a number of ways; the neighborhoods and health literature has focused mostly on three issues – perceived safety, crime incidence and physical disorder theorized along the lines of Wilson and Kelling's "broken windows" hypothesis<sup>28</sup>, i.e. the idea that well-kept neighborhoods may help deter crime. With respect to smoking, perceived neighborhood safety appears to be protective against smoking behavior<sup>18,23</sup> while perceived neighborhood disorder predicts smoking.<sup>29</sup> The limited studies that have examined neighborhood crime and smoking found that higher crime rates were positively associated with both smoking duration<sup>30</sup> and the likelihood of smoking currently.<sup>31</sup>

Lower neighborhood-level socioeconomic status and greater social disadvantage appear to have clear relationships with smoking behavior. Perceived neighborhood disadvantage has been shown to be positively associated with smoking<sup>32</sup> and a number of studies have found positive relationships between smoking and low SES or greater material deprivation.<sup>24,33-37</sup> Additionally, Miles<sup>18</sup> found neighborhood population density, often used as a proxy for area SES, to be positively associated with smoking and Chuang et al.<sup>38</sup> found in Taiwan neighborhoods that neighborhood-level education was positively associated with smoking for low income women, while it was negatively associated with smoking for higher income women, lending support to the idea that relative deprivation may have a powerful influence on health behaviors.<sup>39</sup>

While these findings establish an important foundation for investigating the complex interactions between neighborhoods and tobacco use, much work remains to gain a more comprehensive understanding of the ways in which neighborhood characteristics may differentially influence tobacco use. In particular, area-level social measures and place-specific triggers may be crucial to understanding when and whether individuals begin using tobacco, how much they smoke or otherwise use tobacco and whether they find success in attempts to quit. Furthermore, insofar as smoking may be an expression of stress, individual propensity to smoke will be partially contingent on environmentally-induced stressors, ranging from crime to noise to disputes with neighbors.

In addition, features of neighborhoods such as income gradients, crime rates and physical disorder likely influence not only the propensity to smoke but also the extent to which residents engage in other health behaviors, such as physical activity or alcohol consumption that may buffer or exacerbate the effects of smoking.

In order to address some of the gaps in the existing literature and approach tobacco use among young adults from a comprehensive area- and individual-level perspective, we undertook a multiyear study in the San Francisco Bay Area in which we collected a series of data on young adult tobacco use and neighborhood and tobacco retail outlet characteristics that may influence tobacco use and health. We further combined these data with previously compiled data on land use, health care access and utilization and parcel information along with U.S. Census Bureau data to generate an extensive database including spatial and individual-level information allowing us to interrogate various aspects of tobacco use in context. For this study, we employ our young adult survey and neighborhood audit data and American Community Survey (ACS) data at the block group level to demonstrate our approach to random neighborhood sampling for collecting health-related data and how a random selection of neighborhoods within a larger study area can be weighted, similar to probabilistic individual-level survey data, to draw representative conclusions about the entire area.

**Data & Methods:** Between 2014 and 2017 we collected five sets of data in San Francisco and Alameda Counties in California – three at the neighborhood and two at the individual level. At the individual level, we completed (1) a survey of young adult tobacco use (n=1,363) and (2) an ecological momentary assessment study (n=150) of young adults followed on their smartphones for a period of 30 days. At the area level we collected information on neighborhood characteristics at the block group level (n=135) with a neighborhood audit instrument (3) and by collecting spatial video information<sup>40,41</sup> (4), and finally collected data in tobacco retail outlets (n=242), including all outlets located in the 135 selected block groups as well as sample of those outlets outside. For this study, we use the individual survey and neighborhood audit data.

The 2014 San Francisco Bay Area Young Adult Health Survey (BAYAHS), funded by the National Cancer Institute (NCI) and the National Institute for Minority Health and Health Disparities (NIMHD), was a probabilistic multi-mode (mail, telephone, face-to-face) household survey conducted among adults aged 18-26 (n=1,363). The study was designed to capture a representative number of observations from four race/ethnic groups – 1) non-Latino whites (nffi300); 2) non-Latino blacks (nffi300); 3) non-Latino Asian and Pacific Islanders (nffi300); and 4) Latinos (nffi300) – in order to investigate disparities in exposure to and use of tobacco products. The sample frame consisted of 16,136 households in which there was an approximately 20-40 percent probability of finding an eligible 18-26-year-old

participant. These households were identified using address lists developed by Marketing Systems Group and by analyzing block-level population data from the 2010 decennial census. Figure 1 above illustrates the distribution of selected housing units in the household survey by census block (identified in green).



**Figure 1.** Census Blocks Comprising Bay Area Young Adult Household Survey Sample Frame (n=6,353). Green indicates the distribution of selected housing units by census block.

After completion of data collection and reduction for the BAYAHS (in 2015), we used our survey data and 2009-2013 ACS summary file and TIGER/Line shapefile data in Stata 14 and ArcGIS 10.3 to generate a neighborhood sample frame consisting of Census block groups in our survey sample area in which at least three of our survey respondents resided. To emulate random sampling procedures used in our survey, we drew a proportionate random sample of eligible block groups, or “neighborhoods.” First, we classified all block groups in the two counties into three groups using ACS data and the Grouping Analysis tool in ArcGIS 10.3. We created a layer file in ArcGIS aggregated by the geolocated points of each survey respondent’s home address, then identified all those block groups with their population centroid in the aggregated point layer. From this we limited the sample frame to those block groups in which at least three survey respondents resided for reasons of multilevel data analysis, and finally, we randomly selected a set of block groups from this frame, proportionate to the number in each of the three classification groups (i.e. highest income, most homogeneity to lowest income, least homogeneity; n=135). To increase efficiency of data collection, we further generated a random selection of 30 percent of the streets or edges in each of the selected block groups. Research assistants (RA), working in pairs, were commissioned to walk the entirety of the selected roads in the sample area and complete a neighborhood audit instrument while in the field. We designed the instrument using Qualtrics and RAs completed the audits on Apple iPad mini devices once they had completed their walk of the block group. Categories of measures included in the audit instrument are shown in Table 1 below.

**Table 1.** Categories of items included in neighborhood audit instrument

NEIGHBORHOOD CONSTRUCT	ITEM EXAMPLES
Composition	Tree cover, foot traffic
Disorder, Decay	Street litter, vacant lots
Walkability	Sidewalk maintenance, connectivity
Sights, Sounds, Smells	Noise, smell pollution
Streets & Parking	Traffic speed, parking restriction
Green Space, Recreation, Land Use	Access, proximity to green space, amenities
Advertising	Bus shelters, billboards, storefronts with public health messaging or tobacco/nicotine, alcohol, sugar-sweetened beverage ads

Ultimately, we collected neighborhood audit data in 135 block groups, or 17% of those for which we had survey data (n=793), accounting for approximately 30% of our survey respondents' neighborhoods. The neighborhood sample was designed to maximize efficiency of time and cost while also providing an opportunity for later extrapolation or "weighting" of the neighborhood variables such that we can utilize our area-level results in combination with our full set of survey data in order to draw conclusions about neighborhood-tobacco use associations for young adults throughout the two county study area. In this paper we detail the steps taken to generate a weighted neighborhood data set and compare results using the original data set and the weighted data to evaluate individual young adult tobacco use behavior as it relates to neighborhood characteristics.

In particular, we address the following steps: 1) neighborhood sampling using Stata 14 and ArcGIS; 2) data collection and reduction; 3) principal components analysis (Stata) of neighborhood measures for purposes of consolidation; 4) spatial analysis (ArcGIS) of consolidated and single item neighborhood measures to evaluate distribution and uniformity; 5) assignment of area-level weights; and 6) testing of weighted data against individual outcomes and demonstration of results.

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## Poster 17

### Spatial pattern of hospitalizations due to low impact falls in Portugal: exploratory analysis

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**Introduction:** Low impact falls result from low energy (falling from a chair or tripping on a mat), Female sex (up to 60/70%) and increase age (mean age of 80.3 years  $\pm$  8.7) are identified as risk factors falling. The continual increase of the elderly population worldwide poses as a problem to healthcare systems as theoretical there will be more individuals needing health assistance after suffering a fall. Despite extensive research and preventive efforts, accidental falls continues to be a massive health problem as in the elderly falls are a leading cause of severe injury requiring acute care or causing death. It is important to identify the spatial pattern to understand what is causing the increase and to plan awareness campaigns. We aim to identify the spatial pattern of hospitalizations due to low impact falls, in individuals over 65 years old in Continental Portugal (2000, 2007 and 2013).

**Methods:** The study area was Continental Portugal. Hospitalizations (2000, 2007, 2013) caused by low impact falls (classified according to International Classification of Diseases, 9th Revision, Clinical Modification) were retrieved

from the National Hospital Discharge Register, mandatory for public hospitals. Population data was retrieved from Statistics Portugal. Counts of hospitalizations were used to calculate age-standardized Empirical Bayesian incidence rates (AEB) by municipality, per 1000 inhabitants (direct-method, 5-years age groups: 65-69; 70-74; 75-79; 80-84; 85+ and Portuguese population from 2011 census as the standard). The AEB rates were calculated (Bailey and Gatrell, 1995) with shared border as the criterion to define neighbors. Rates were calculated for 2000, 2007 and 2013, for both genders and separately for females and males. The spatial pattern was compared, the Moran's I calculated and spatial clusters were determined using Local Moran's I.

**Results:** For the three years, the mean number of hospitalizations was 17422.7 (SD 3181.8), the percentage of women was, respectively, 68.3%, 70.2%, 68.7% for 2000, 2007 and 2013. The annual crude rates were similar in the three years assessed; both genders: 10 per 1000 inhabitants in the three years, female: 11, 12, and 12 per 1000 inhabitants in 2000, 2007 and 2013 (respectively) and male: 7 in 2000, 7 in 2007 and 8 in 2013 (1000 inhabitants).

The Moran's I (respectively for each year) was 0.61, 0.63 and 0.74 for men, 0.57, 0.67 and 0.72 for women and 0.58, 0.68 and 0.76 ( $p$ -value<0.001). A similar overall spatial pattern was observed in both genders: clusters of high incidence in the north and low incidence in the south. Over time a marked northeast to southwest pattern was accentuated.

**Discussion:** Marked spatial patterns in hospitalization due to low energy falls were identified in both genders. The pattern observed is similar to the two main climatic regions of Portugal; north region more humid and cold (high-high clusters) south region more dry and hot (low-low clusters) suggesting that environmental factors may play important role in explaining the spatial pattern.

## Poster 18

### The Territory And Territorialities Of The Viral Hepatitis In Brazil

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Viral hepatitis are infectious diseases caused by different etiological agents (viruses) that particularly affect the liver and have similar epidemiological, clinical and laboratory characteristics, but with important peculiarities according to each type. In Brazil, viral hepatitis are very important because it affects a large number of individuals and the possibility of complications of the acute and medium and long term forms. At present, it is not known what the territory of viral hepatitis in Brazil is, ie, how viral hepatitis are distributed by the units of the federation and what relations explain this distribution. In addition, the use of maps for this presentation is also unknown. The objective of this study was initially to discuss the distribution of viral hepatitis in the federation units with the use of maps,

considering the territory of viral hepatitis as the site with the highest number (confirmed cases, incidence rate, chronicity rate and rate of mortality) and the territorialities of viral hepatitis as the historical and social characteristics of each territory linked to the sources of contamination and modes of transmission of viral hepatitis. For this, we used quantitative data for the manipulation of secondary data on the viral hepatitis A, B, C and D reports and transformation into incidence rates, from 2010 to 2014, obtained from the Notification of Injury Information System and the Mortality Information System. Finally, treating viral hepatitis as territories is to understand the importance of these diseases in certain spaces of some societies and to present them on maps is their own identification and individualization. These actions sought reflection from space and its characteristics and relations (territorialities), believing that any type of action that aims to prevent and combat these diseases should start from that point. These historically established social relations are present in the northern region of Brazil and that is why this is the main territory of viral hepatitis presenting the highest incidence rates. In particular, the state of Acre presented the highest incidence in almost all etiologies except type C, for which the state of Rio Grande do Sul was registered. Knowledge of this information, when applied to teaching in educational processes, may contribute For the promotion of health by at least two means: a) public sector, in the punctual application in the proper territories of the policies according to each territoriality; And b) the population in general, who better understand the reality of the territory and territoriality that is inserted can create a reflexive attitude and behavior change.

**Keywords:** viral hepatitis, territory, territoriality, map.

## Poster 19

### Spatio-temporal modelling of cryptorchidism in France

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**Context:** There is an increasing concern that congenital malformations of the male urinary tract, and in particular cryptorchidism (undescended testis), are becoming more prevalent. Cryptorchidism is part of the testicular dysgenesis syndrome, which includes other male reproductive disorders such as hypospadias and testis cancer. It is especially suspected to be related to a precocious exposure to endocrine disruptor chemicals [1]. Therefore, it is of interest to describe the geographical and temporal variations of this disease. The aim of our study was to describe the spatial and temporal pattern of the risk of cryptorchidism in France.

**Methods:** Data for cryptorchidism were obtained from the French National Hospital Discharge Database for the 94 mainland French *departments* for the period 2002 to 2014. Surgical procedures of cryptorchidism among male children under the age of 7 were selected.

Spatio-temporal disease mapping models were used to describe the pattern of disease counts and to identify departments with unusual incidence levels, time trends or both. We fitted different models: the parametric model proposed by Bernardinelli et al. [2] and the nonparametric models proposed by Knorr-Held [3]. As cryptorchidism is a rare disease, we considered it appropriate to model the number of cases with a Poisson distribution.

The population of boys under the age of 7 according to year, department and age was included in the model as an offset term. A logarithmic link was used. The Integrated Nested Laplace Approximation approach (INLA) was used to compute the posterior marginals of all parameters of interest. Model fit was measured by the Deviance Information Criterion and the effective number of parameters.

**Results:** The global estimated temporal trend shows an increase in the risk of cryptorchidism between 2002 and 2014 in France. Maps of the estimated risk show evidence of spatial heterogeneity with higher estimated risk of cryptorchidism in some departments. The estimated temporal trend is not different for these areas than the global estimated trend apart for a few years. No strong evidence of a space-time interaction is observed.

**Conclusions:** A significant rise in cryptorchidism has taken place over the last years in France with higher estimated risks observed in some departments. Further studies should be undertaken to determine the risk factors that might be causing this.

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## Poster 20

### Confounding between exposure and spatial random effect: An illustration on Parkinson's disease and air pollution in France

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**Context:** Recent studies have linked particulate exposures to brain pathologies associated with Parkinson's (PD) and Alzheimer's disease.

A spatial ecological study was carried out to investigate the potential impact of air pollution on Parkinson's disease. Air pollutant concentrations present spatial variability and that could be correlated to spatial random effects. Thus, the main objective of this study was to assess the sensitivity of the air pollution effect in regards of spatial random effects control. Different models were considered to adjust on remaining spatial autocorrelation in the disease data after accounting for the known covariates.

**Methods:** Health data were obtained from the French National Health Insurance Inter-Regime Information System. Parkinson's disease patients were identified through antiparkinsonian drug claims at the canton scale (1972 units) for 2010-2012.

A Poisson log-linear model was defined to estimate the effects of air pollution exposures, represented by  $PM_{2.5}$ ,  $PM_{10}$  and  $NO_2$ , on PD. The model includes known covariates, the socio-economic deprivation score, tobacco consumption and exposure to pesticides, and spatially autocorrelated random effects. We modeled these random effects as part of a hierarchical Bayesian model with a conditional autoregressive prior distribution, the

Besag-York-Mollié (BYM) model. For comparison, the model proposed by Leroux et al, the modified BYM proposed by Riebler et al [1], the orthogonal smoothing proposed by Hughes and Haran [2] and the localized CAR proposed by Lee and Sarran [3] were also considered. These models differ either in their control for residual spatial autocorrelation, from a single global level of spatial smoothness to localized smoothing, either in their parameterization of the BYM model.

**Results:** The localized CAR model fitted the data best. While the orthogonal smoothing resulted in a poorer fit to the data (in terms of the Deviance Information Criterion). The spatial parametrization affects differently the estimate of air pollution. This could reflect differences in their spatial variability, as shown by variograms.

**Conclusions:** Residuals spatial confounding needs to be carefully adjusted, to avoid vanishing or overestimating the air pollution effect.

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## Poster 21

### Malaria along urban-rural gradient in the Amazon

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In the Amazon, malaria is found in a variety of landscapes, from agricultural frontiers, to peri-urban and urban areas. Each landscape has specific determinants and their combination form a complex mosaic with fuzzy boundaries distributed along an immense territory. Malaria transmission within and between these landscapes is mediated by socioeconomic, environmental and political factors affecting individual, household, and local vulnerability. Here, we report results from a study developed to investigate the determinants of malaria and its association with socio-economic, demographic and geographic factors in an important malaria hotspot in Latin America (Alto Juruá, Acre, Brazil). We hypothesize that malaria is maintained in these village-rural systems as a source-sink dynamics. A household survey was conducted in 2015 in 40 localities (n=520).

The questionnaire contained questions on previous malaria episodes, sociodemographic data, house structure and goods, habits related to exposure to malaria. Multiple correspondence analysis (MCA) was used to visualize the associations between the socioeconomic, behavioral, demographic parameters and malaria prevalence at household level and infer gradients. The dimensions elicited from the MCA were considered as covariates in a mixed logistic regression model, having as response variable: “at least one malaria episode among dwellers in the last 12 months”. The first three MCA dimensions accounted for almost 50% of the variability. The first dimension defined a urbanization gradient, the most influent variables being household accessibility via road or river, access to public services, frequency at which householders entered the forest, worked in agriculture, had a boat, and had crevices in the house wall. We found a significant association between this axis and the probability of malaria at the household level. The second dimension described a gradient from rural settlements in agricultural areas to forested areas. Accessibility via dirt road or river, access to electricity powergrid services and aquaculture were important factors. Odds of having malaria was significant associated with agricultural-type areas. The third axis did not correlate with malaria. Overall, our results show that living conditions in the Amazonian municipalities are strongly geographically structured. Although malaria is found throughout all the landscapes, household traits can explain part of the variation found in the odds of having malaria. Still, there are strong effects at the locality level not accounted for by the household traits. We hypothesize that these high-scale effects are driven by spatial and environmental factors as well as by the interdependence of the localities not taken into account in the analysis. We expect these results will stimulate further discussions on modeling approaches targeting a more systemic and multi-level view of malaria dynamics.

## Poster 22

### Surveillance of CKD epidemiology in the US - a joint analysis of NHANES and KEEP

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Chronic Kidney Disease (CKD) is a public health concern in the United States due to its high prevalence, excessive healthcare costs and association with increased morbidity and mortality. Epidemiological systems for surveillance of CKD such as the CDC's surveillance system, rely on population data that are based mainly on the NHANES survey, which may not include many patients with the most severe and less frequent forms of CKD. We investigate the feasibility of estimating CKD prevalence from the large-scale community disease detection Kidney Early Evaluation and Program (KEEP). We used NHANES to estimate the probability of participation in KEEP and used these selection weights to reduce bias in state and county level prevalence estimates for CKD. Our main outcomes of interest were CKD Stage 3-5 (estimated glomerular filtration rate  $<60$  mL/min/1.73m<sup>2</sup> (eGFR)) and CKD Stage 4-5 (eGFR  $<30$  mL/min/1.73m<sup>2</sup>).

NHANES data were used to reconstruct a nationally representative reference sample with covariates including CKD stage and risk factors that were part of targeted recruitment messaging for KEEP (e.g., age, sex, race/ethnicity, diabetes, obesity, smoking, hypertension and family history of CKD, cardiovascular disease or hypertension). Logistic regression was used to predict KEEP participation relative to the NHANES reference sample using these covariates plus education and insurance status. Selection probabilities were converted to inverse probability weights for KEEP participants. Generalized mixed model regression (GMM) with inverse probability weighting and post-stratification was used to estimate national CKD rates overall and by year. We then added county random effects with exponential spatial covariance to make state estimates. The data were self-selected participants in KEEP surveys (N=127,149) and participants in NHANES (N=27,565), 2001 – 2012. Relative to NHANES (0.51%, 95% CI: 0.43-0.59%), the unweighted prevalence of Stage 4-5 CKD (<30 mL/min/1.73m<sup>2</sup> estimated glomerular filtration, eGFR) was much higher in KEEP (1.00%, 95%CI: 0.94-1.05%). Application of a selection model resulted in prevalence estimates with reduced bias and overlapping confidence intervals (0.55%, 95% CI: 0.50-0.60%) with NHANES. Weighted prevalence of Stages 3-5 CKD (<60 mL/min/1.73m<sup>2</sup> eGFR) in KEEP was 8.95% (95% CI: 8.72-9.19%) compared to 6.75% (95% CI: 6.30-7.19%) for NHANES. Using a GMM approach we computed state-level CKD estimates. Additional work is underway to develop county-level estimates using integrated nested Laplace approximation and other approaches.

## Poster 23

### Adaptive Geostatistical Design (AGD) Enables More Efficient Identification of Malaria Hotspots in Rural Chikwawa, Malawi.

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Adaptive geostatistical designs (AGDs) allow collection of geostatistical data over time to depend on information obtained from previous information to optimise data collection towards the analysis objective. AGDs are becoming more important in spatial mapping, particularly in poor resource settings where uniformly precise mapping may be unrealistically costly and the priority is often to identify critical areas where interventions can have the most health impact. Two constructions are: *singleton* and *batch* adaptive sampling. In singleton sampling, locations  $x_i$  are chosen sequentially and at each stage,  $x_{k+1}$  depends on data obtained at locations  $x_1, \dots, x_k$ . In batch sampling, locations are chosen in batches of size  $b > 1$ , allowing each new batch,  $\{x_{(k+1)}, \dots, x_{(k+b)}\}$ , to depend on data obtained at locations  $x_1, \dots, x_{kb}$ . In most settings, batch sampling is more realistic than singleton sampling. We proposed specific batch AGDs and assess their efficiency relative to their singleton adaptive and non-adaptive counterparts using simulations.

We then conducted repeated cross-sectional surveys guided by batch AGD sampling design to monitor malaria parasitaemia and anaemia prevalence in children aged 6–59 months in the communities living around Majete Wildlife Reserve in Chikwawa district, Malawi. We fitted a geostatistical model to predict malaria prevalence in the area. We conducted five rounds of sampling, and tested 876 children from 1,377 households over a 12-month period. Malaria prevalence prediction maps showed spatial heterogeneity and presence of hotspots; predictors of malaria include age, socio-economic status and ownership of insecticide-treated mosquito nets. Continuous malaria prevalence surveys using adaptive sampling increased prevalence prediction accuracy. Results from the surveys were readily available after data collection. The tool can assist local managers to target control interventions in areas with the greatest health impact and is ready for assessment in other diseases.

## Poster 24

### Summer 2013: Mainland Portugal District vulnerability to extreme temperatures?

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**Background:** Direct effects of ambient temperature on human health are known and, in the case of elevated temperatures, can range from moderate skin irritations to the so-called heat stroke. Excess temperature can also have adverse effects on health by aggravating preexisting diseases such as cardiovascular and cerebrovascular diseases, respiratory diseases, diabetes, among others (1, 2).

In Portugal, similarly to other countries, the effects of excess heat on health are known, specifically on mortality, in situations of sudden and intense temperature increase, ie during the so-called heat waves (2, 3, 4, 5, 6, 7).

The objective of this work is to study the vulnerability of mainland Portugal districts to extreme temperatures using data from the summer of 2013.

**Methods:** The study period was the summer of 2013 (between may 1<sup>st</sup> and September 30<sup>th</sup>), on a daily base, and restricted to mainland Portugal (18 districts).

Mortality data was provided by VDM (Vigilância Diária da Mortalidade) system hold on Instituto Nacional de Saúde Doutor Ricardo Jorge (INSA), and meteorological data by Instituto Português do mar e da Atmosfera (IPMA).

Firstly a descriptive analysis of data was performed.

Secondly a geoadditive Regression with BayesX was applied to mortality rate (/100000 inhabitants) considering as explanatory variables daily maximum temperature, a spatial function, and the day of the week.

Results:

In summer of 2013 mean daily mortality rates by districts vary between 1,85 and 3,93 / 100 000 inhabitants. The minimum and maximum daily mortality rate registered was 0 and 11,93 / 100 000 inhabitants.

Mean temperature in mainland Portugal was 27°C and the maximum temperature registered was 42°C on Santarém (07-07-2013) and Setúbal (08-07-2013).

Based on the mean temperature, three districts share the higher predicted mortality rates. Using the highest registered temperature, these three districts maintain the higher predictions, and they do not all belong to the interior of mainland Portugal.

Analyzing one of the hottest day of June July heat wave 2013 period (07-07-2013) it is possible to verify that although one district presented the higher temperatures it has not the higher mortality rate. In contrast it is possible to see that another district registered a higher mortality rate observed than predicted considering the temperatures registered on that day.

**Conclusions:** The inclusion of spatial dimension in models for study relations between mortality rates and temperature is very important.

The extreme heat impacts are not equal all over mainland Portugal, and although the higher predicted mortality rates were found on interior, there is also a coast district with high possible impacts.

The study only take into account data from 2013 and should use more data, since this is the first geoaddivitive approach to this issue.

**Keywords:** Mortality, Extreme heat, ICARO, Mainland Portugal, District level

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## Poster 25

### The R package *scanstatistics*

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This poster presentation will introduce *scanstatistics*, a new R package that offers a free and open-source implementation of many scan statistics found (sometimes only) in the literature. Its detection capabilities and ease-of-use will be demonstrated on real-world disease data, showing how the regression and visualization tools available in other R packages can be integrated into the analysis. The package is thus a flexible alternative to the popular but closed-source **SaTScan™** software, which provides several long-established scan statistics and is employed by many public health agencies as part of routine surveillance for disease outbreaks.

The current (and first) version of the *scanstatistics* package is readily available on **CRAN**, and implements multiple spatio-temporal scan statistics based on the Poisson [1], negative binomial [2], and zero-inflated Poisson distributions, with multiple options for the type of spatial clusters to be searched. The next version of the package, scheduled for release in June 2017 and available in development form on **GitHub**, adds many more features and methods, including but not limited to:

- Multiple algorithms from the Fast Subset Scan [3] and Penalized Fast Subset Scan [4] frameworks, suitable for multivariate space-time data modeled by an exponential family distribution.
- Kulldorff's prospective space-time Poisson scan statistic [5].
- The space-time permutation scan statistic [6].
- Gumbel p-values [7], which can reduce the computational burden of hypothesis testing by orders of magnitude.

To encourage collaboration and dissemination of ideas, authors are welcome to submit their R or C++ code for integration into the package.

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- [02] DOI:10.1186/1476-072X-9-61
- [03] DOI:10.1002/sim.5675
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- [05] DOI:10.1111/1467-985x.00186
- [06] DOI:10.1186/1476-072X-9-61

## Poster 26

### A spatio-temporal vector surveillance system for sleeping sickness control

**Michelle Stanton**

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Human African trypanosomiasis (HAT), more commonly known as sleeping sickness, is a very serious neglected tropical disease affecting populations in sub-Saharan Africa. The most common form of the disease, Gambian HAT (gHAT) affects populations in Central and Western Africa, and is predominantly transmitted by riverine species of tsetse fly. Control of gHAT is achieved through both active and passive case detection plus vector control to reduce the tsetse population. An effective way of reducing the tsetse population is to deploy small insecticide-treated targets ("tiny targets") in high transmission risk areas. These tiny targets have been shown to cost-effectively reduce the tsetse population by up to 90% in small scale studies.

At present, tiny targets are being deployed along rivers located within high transmission risk areas in countries including Uganda and Democratic Republic of Congo (DRC). Once deployed, the progress of the intervention is monitored using a network of tsetse traps to assess the abundance of tsetse over time. Monitoring sites are selected based on expert opinion, and data are collected on paper. As the intervention continues to geographically scale up, it is becoming increasingly challenging to manage monitoring activities using this approach. The goal of this project was therefore to develop and implement a spatio-temporal vector surveillance system in tiny target intervention areas. The aims of the project were two-fold: (1) to develop

data collection tools that would enable monitoring data to be rapidly collated and disseminated to the project team, and (2) to use this data, plus additional ground-based and remotely sensed environmental information to identify areas that require additional control efforts.

To address (1), an electronic system was developed which included a smartphone app developed using OpenDataKit for collecting georeferenced tsetse monitoring data, and a Shiny app in R which displayed interactive maps and time series plots of the resulting data in a web browser. These tools were developed in collaboration with tsetse control implementers in Uganda and DRC. To address (2), existing tsetse monitoring data were used to identify spatio-temporal trends in tsetse counts. Environmental variables associated with tsetse presence and abundance e.g. land cover type and habitat fragmentation were derived using high resolution (10m) publicly available remotely sensed data, and validated using field observations. A range of spatial and spatio-temporal statistical models were fitted to existing monitoring data, and were used to derive spatially and temporally varying tsetse count prediction intervals. The final objective of this project is to integrate these outputs into the electronic surveillance system as a tool to identify areas where future observed tsetse counts are higher or lower than expected. This will enable the field team to respond to potential problems with the control intervention in near real time.

## Poster 27

### Geographical distribution of Human and dog lymphomas in “Large area of Porto” – a case study at Porto city.

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Lymphomas are a widely heterogeneous group of neoplasms which originate from lymphoid cells. Canine lymphoma is one of the most common neoplasms in dogs and its increasing frequency mimics a trend in human oncology in which non-Hodgkin’s lymphoma (NHL) represents 5% of all new cancer cases and is one of the top five leading cancer-related deaths. Epidemiological studies on companion animals have been increasing, defining the dog as sentinels of potential risk factors to human health, mainly due to shared environments, shorter disease latency, spontaneous disease and more specifically to the similarity between canine lymphoma and NHL in humans. The negative outcomes of modern lifestyle upon health seem to show strong scientific evidence of environmental and socioeconomic

injustices and they represent an extraordinary motivation to rethink and restructure urban planning. Lymphomas can be a good testbed to evaluate this hypothesis. The aim of this study is to geographically compare the data of human and canine lymphomas and to associate them with environmental factors.

Postal Codes of NHL´s patients, diagnosed between 2005 and 2010, resident in the Large area of Porto, Portugal, were obtained from RORENO and ROR-Centro. Also, data of canine lymphomas diagnosed from 2005 to 2016 in several veterinary centers were collected. Kernel density estimation (KDE) was performed and associated with environmental factors.

The results show that human and canine geographical distribution of lymphomas are quite similar and present the highest values in the Porto city center. It seems that there is a close relationship between the socioeconomic and environmental backgrounds and the prevalence of the disease in humans and animals. The typical and common artificial urban elements that ensure 21<sup>st</sup> century "life style", impervious soil, lack of green spaces, electrical and communications network, traffic pollution, soil contamination, among others, seem to be spatially coincident with the peaks of the density of this disease.

The spatial analysis evidences the geographic association between human and canine lymphomas and it highlights the importance of a surveillance of cancer in pet animals as an efficient tool to predict, prevent and control hazards for humans as well as the need of adopting and implementing healthier urban policies.

## Poster 28

### Kernel maps and arboviruses in Recife, Pernambuco-Brazil

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The control of *Aedes aegypti* proliferation, a known vector of diseases, has been an important challenge for the developing countries. Therefore, the use of Geographic Information System (GIS) has been assumed an increasingly role in public health policies decisions. These systems stand out in the capacity to efficiently implement mathematical models that represent a spread of diseases. One of the software applications based on these systems, the Kernel Density Estimation (KDE), may help in the best interpretation of punctual data. It's an interpolation technique originally developed to obtain a smoothed estimate of a univariate or multivariate probability density from a sample of observed data. The objective of this work is to present the pattern of distribution of dengue cases from 2013 to 2016, and zika and chikungunya, in 2015 and 2016 in the city of Recife, located in the state of Pernambuco - Brazil, through Kernel Maps. The study period chosen for zika and chikungunya is justified by the fact that the Brazilian governmental authorities don't have relevant records of these diseases in this city in before 2015. In addition, it was also analyzed the relation between the dissemination of these diseases and regional factors of climate

and precipitation. To date, the data used to perform this research has been obtained mostly of the governmental institutions: State Agency of the Environment ([www.cprh.pe.gov.br](http://www.cprh.pe.gov.br)), State Agency of The Water and Weather ([www.apac.pe.gov.br/](http://www.apac.pe.gov.br/)), Brazilian Institute of Geographic and Statistics ([www.ibge.com.br](http://www.ibge.com.br)), National Institute of Metrology ([www.inmet.gov.br](http://www.inmet.gov.br)), Open Data Portal of The City Hall of The Recife ([www.dados.recife.pe.gov.br](http://www.dados.recife.pe.gov.br)) and The Geographical Information Service of The City of Recife (<http://www.recife.pe.gov.br/ESIG/>). The data that have the addresses of confirmed cases of diseases were inserted in ArcMap application of the ArcGIS v10.5 platform, by batch geocoding and, posteriorly, Kernel Maps derived from the processing of this data were created. From data obtained A01/00 from rainfall stations located at strategic locations around the city, average precipitation tables were created in Microsoft Excel 2013, using the Thiessen Polygons Tool of the ArcMap. The climatic data obtained from a meteorological data collection station located in the city, were processed in Microsoft Excel 2013, using methods indicated by the INMET (National Institute of Metrology), to obtain values of average temperature and relative humidity of the air, referring to the studied period in this research. Finally, these pieces of information were crossed by geostatistical analysis, aiming to search for intrinsic relationships that may offer new pieces of information of the diffusion of these diseases by the *Aedes aegypti*.

## Poster 29

### Geographically weighted regression and geostatistical uncertainty to model local relations between health and air pollution

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In this research, we combine known methods to present a new approach to assess spatial uncertainty of associations between air pollution and health. We use geographically weighted generalized linear models (Chen and Yang, 2012) to estimate local associations of air pollution on birth weight, and use geostatistical methods (Goovaerts, 1997) to integrate spatial uncertainty of associations in the models.

The geographical dataset analysed includes air pollution measurements collected at sampling sites and health data collected at birth addresses within a studied region. Because air pollution data do not match the health data locations, we use a Kriging interpolator to predict air pollution in unsampled locations and to assign exposures during gestation. Moreover, we incorporate Kriging within a geostatistical simulation algorithm, to provide a measure of spatial uncertainty of exposures. From exploratory spatial analysis performed with geographically weighted generalized linear models, we draw the distribution of local parameters to estimate the associations of air pollution exposure with birth weight.

The proposed methodology copes with non-stationary spatial processes and incorporates spatial uncertainty on the associations estimated locally, providing an additional tool for uncertainty analysis of the impacts of place in health.

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## Poster 30

### High resolution age-structured mapping of measles vaccination coverage in low and middle income countries

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Expanding access to childhood vaccination has been one of the most successful public health interventions of recent decades. Indicators of the performance of intervention programmes such as coverage rates and numbers covered are typically measured through national statistics or at the scale of large regions due to administrative convenience. These mask inequities and hotspots of low coverage that may allow diseases to persist, even if overall coverage is high. Hence, to achieve parity and accelerate progress towards disease elimination goals, fine-scale variations in coverage should be well understood. Focusing on measles as an example, we use cluster-level Demographic and Health Survey (DHS) data to map vaccination coverage at 1 x 1 km spatial resolution in Cambodia, Mozambique and Nigeria for varying age-group categories of children under five years using Bayesian geostatistical techniques implemented via Markov Chain Monte Carlo (MCMC) methods, built on a suite of geospatial covariates. Our results show strong predictive power, as well as considerable spatial heterogeneities and geographic clustering of low vaccine coverage areas, which highlight risks for measles outbreaks despite high levels of national coverage in some cases. We show how estimates of numbers covered changes substantially through these spatially refined mapping approach. We also highlight areas where there is a confluence of high population density and low vaccination coverage that may have the potential to sustain measles transmission regionally despite robust vaccination campaigns in surrounding areas. Finally, spatially aggregated coverage maps are produced to support decision making in targeting of scarce resources in order to maximize the utility of interventions.

## Poster 31

### Temporally dependent accelerated failure time model for capturing the impact of events that alter survival in disease mapping

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The introduction of spatial and temporal frailty parameters in survival models furnishes a way to represent unmeasured confounding in the outcome of interest. Using a Bayesian accelerated failure time model, we are able to flexibly address a wide range of spatial and temporal options for structuring frailties as well as examine the benefits of using these different structures in certain settings. Our results suggest that it is important to include these temporal frailties when there is a true temporal structure to the confounding and including them when a true temporal structure is absent does not sacrifice model fit.

Additionally, the frailties are able to correctly recover the confounding ground truth in simulated data without affecting the fixed effect estimates. In the case study involving Louisiana breast cancer-specific mortality, our temporal frailty played an important role in representing the unmeasured confounding related to improvements in disease knowledge and education as well as the impact of Hurricane Katrina. In conclusion, the incorporation of spatial and temporal frailties in survival analysis can lead to better fitting models and improved inference by representing spatially and temporally varying confounding that could impact survival, e.g. health disparities and environmental events respectively.

**Keywords:** breast cancer; accelerated failure time; survival; spatio-temporal; spatial frailty

## Posters Abstracts

### Poster Session 2

#### Poster 32

##### Comparing how well residential neighbourhood delineations and 'enhanced' neighbourhood delineations capture where children spend time

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**Background:** An exclusive focus on measuring residential environments is a known problem in place and health research. While tracking data (e.g. GPS) can be used to identify and measure exposure to environments beyond the home neighbourhood, methods of delineating places people spend time that do not require detailed tracking data are now needed.

New delineation methods require an appropriate assessment of how well these capture daily activity. However, published research has only assessed overlap (how much of the time/area visited by a participant is captured). This ignores potentially important errors of commission (i.e. extent of the delineation measured but not visited by participants) and omission (i.e. extent visited by participants but not included in the delineation).

This study aimed to address these two related gaps by 1) assessing the spatial extent of children's daily activity captured by common GIS methods of delineating residential neighbourhoods, and 2) applying a more nuanced test of how well residential neighbourhoods and an 'enhanced' home-school neighbourhood better captured the places where children spent time.

**Methods:** Seven-day GPS data from 236 children (9-13 years) were sourced from the Kids in the City Study. Daily path areas were calculated for each child by buffering GPS points by 50 m to represent where children spent time. Residential neighbourhoods were delineated for each child using road network buffers at nine scales from 400-2000 m. Enhanced buffers were developed by combining home and school road network buffers at multiple scales. GPS derived time spent in a location and the spatial overlap, errors of commission, and errors of omission between daily path areas were calculated for both the residential and enhanced buffers.

**Results:** On average, 18% of the daily path area and 30% of the time spent in those places were captured by the 400 m residential buffer. The 2000 m residential buffer captured 53% and 46% respectively. The 400m enhanced home-school buffers captured 31% of the daily path area and 47% of the time, and the 800m enhanced home-school buffers captured 44% and 50% respectively. In comparison to the residential buffer, the enhanced home-school buffer had fewer errors of omission and commission.

**Conclusions:** Places that children spent time were not adequately captured by common GIS residential neighbourhood delineations. Enhanced home-school buffers better captured places children spent time. Similar enhanced buffers may help to better measure the environments children and other population groups are exposed to.

## Poster 33

### Geographic distribution of infant mortality in Brasília, Brazil. A hierarchical spatial model

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Introduction: Infant Mortality Rate (IMR) remains a considerable public health problem, especially in low-income populations. In many cases, the identification of this population at risk is not easy, especially when the unit of analysis is polygons. The monitoring and studies on inequalities in the risk of infant death in the Federal District (FD) justified for to broaden the debate on health inequities in these territories.

Objective: analyze the spatial and factors common to declarations of live births associated with IMR in the DF, 2009.

Methods: Spatial case control study, cases were defined as live births in 2009 from the FD and who died under 1 year of age (identified in the Mortality Information System - SIM). Controls were considered live births in the same population not identified in SIM. For the point patterns analysis of the data was used additive regression model (GAM) to estimate spatial distribution effects of odds to infant death. This database was analyzed using hierarchical logistic regression to estimate the factors associated with IMR.

Results: Regarding the study of the spatial distribution of infant mortality in DF, the following results were observed: The risk of infant death in the population of births in 2009 was 12.21 ‰ live births, where 62.9% of deaths was to preventable causes and 36.5% for unavoidable causes. Socioeconomic variables were associated with the spatial distribution of infant deaths from preventable causes ( $p < 0.05$ ) but not with non-preventable causes ( $p > 0.05$ ). The variables related to health care and maternal biological characteristics were associated with both outcomes ( $p < 0.05$ ). The explanatory power of space in relation to infant mortality lost significance after inclusion of variables related to characteristics of the child in the all models studied.

**Conclusion:** High-risk ("hot spot") were identified for infant mortality in the peripheral areas and less low-risk in the more central, suggesting the existence of inequalities in health care and the persistence of unmet need for Population groups. Regions of high risk of infant death in FD incompatible with the current economic development presented nationally and locally in the capital of Brazil were identified. These results may to support public health policies aimed at improving health and reducing inequalities in the risk of infant mortality in these territories.

## Poster 34

### Geographic database and WebGIS in Recife, Pernambuco, Brazil

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*Aedes aegypti* is the vector of dengue, zika and chikungunya, diseases that can result in epidemics and even lead to death. In the 80's, when there was a great circulation of the virus in Brazil, the adoption of methodologies for the surveillance of this vector was started. The evaluation of vector density through oviposition traps and larval collection traps has become an applicable methodology when the objective is to estimate the egg density of the mosquito. This trap, commonly known in Brazil as ovitraps, has been shown to be superior in relation to larval research, to verify the occurrence of the vector. In this context, this article aims to describe the current stage of development of a geographic information system for the monitoring of ovitraps installed in a cemetery in Várzea neighborhood, in the city of Recife, Pernambuco, Brazil, and the availability of these data via the web (SIGWeb). This work has two lines of research: the first one is the structuring of a geographic database that gathers information plans with climatic, environmental and social data of the neighborhood in order to find spatial relationships in function of the distribution of arboviruses cases in the Neighborhood.

The data acquisition was based on the consultation of online services of Brazilian governmental institutions and surveys in loco. The data obtained were processed and processed in the ArcMap application of the ArcGIS v.10.5 platform. The geographic database also has monitoring of the thirty ovitraps distributed in the cemetery, which has been carried out every 15 days since 2014. The results are preliminary, however, it was observed that the neighborhood of Várzea, (in Recife-PE- Brazil) presented many cases of Dengue, Zika and Chikungunya in the last three years and it is investigated the influence of several factors on the distribution of arboviruses cases. The second part of this work concerns to the development of a web platform for the availability of monitoring data on the ovitraps and climatic A01/00 data of the neighborhood. PostgreSQL was chosen as a database management system because it was a free platform and supported along with the PostGIS extension to geographic databases. An entity-relationship model was created to define the tables, the data that should be stored in them, as well as the proper relationships between these tables. The database model has been defined with six tables which store important data for the system. After the finalization of the entity-relationship model with the definition of all tables, relationships and attributes, the script for the creation of the database was implemented. This bank was created and it has already been in operation locally. In the future, we intend to strengthen ties with the Municipal Health Secretaria of Recife and expand the project to insert other monitoring points of the vector with ovitraps and make SIGWeb available to the city.

## Poster 35

### Tuberculosis in urban space: the case of Rio de Janeiro

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Tuberculosis is a disease directly linked to poor living conditions<sup>1</sup>. The central idea of the use of spatial analysis is to incorporate space for traditional analysis and measuring properties and relationships of the variables under study. Several techniques Spatial Statistics can be applied in these cases, including the spatial regression models, which as the classical regression model, seeks to adjust statistical models to describe a particular variable in relation to the others, however incorporating the spatial dependence between observations. The aim of this study is to analyze the spatial pattern of tuberculosis identifying relevant socioeconomic variables for the occurrence of tuberculosis through spatial statistical models. Spatial analysis was performed using the strategy of data analysis area and the census tract was chosen how unit aggregation. TB cases were geocoded by address of residence and then quantified by census tract<sup>2</sup>. Incidence rates were calculated and to eliminate the instability of these smoothing of the incidence rates was applied using the Bayesian Local Empirical method. A classical multivariate regression model was used and then compared the spatial global regression models: Spatial Lag and Spatial Error. The spatial dependence was detected using Moran's index. At

the end of the process variables responsible Proportion with income between 1 and 2 minimum salary, illiterate proportion, proportion of households with people living alone and average income of the responsible were best fitted model. And the model with the best parameters was the Spatial Lag with R<sup>2</sup> of 0.3215, log likelihood = -9228.39, AIC and SBC = 18468 = 18512.2. And the Moran index of the residuals was -0.018. Overall, the statistical methods used in this work showed to be efficient in identifying spatial patterns of tuberculosis and the definition of some determinants for the occurrence of the disease, however it should be noted that the 11% loss in the geo cases may cause a possible bias in the results.

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## Poster 36

### Herd-level spatial cluster analysis of bovine cysticercosis in the state of Paraíba, northeastern Brazil

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Bovine cysticercosis is a tropical zoonotic disease caused by the larval stage of *Taenia saginata* in cattle. Data on bovine cysticercosis in Brazil is available only from veterinary inspection records at slaughterhouses, and some cases may be unnoticed, especially in mild infections. Thus, the use of serological tests with sensitivity higher than the routine postmortem inspection has been recommended as an option for ante-mortem detection of bovine cysticercosis, allowing a more accurate early identification of infected animals. Positive findings for bovine cysticercosis based on absolute numbers of occurrences may lead to misinterpretation of the disease spatial distribution, since regions with high concentrations of these events are not always the areas with the highest risk. Therefore, epidemiological maps of disease risk have been produced in order to correlate disease data with environmental features at sites known to harbor bovine cysticercosis. However, studies on the distribution of bovine cysticercosis in Brazil have only taken postmortem inspections into account and not serological tests. Thus, so far, no surveys involving herd-level spatial clustering analysis on bovine

cysticercosis seroprevalence in Brazil have been conducted. The aim of this survey was to identify spatial clustering of bovine cysticercosis-positive herds in the state of Paraíba. The state was divided into three sampling groups: sampling stratum 1 (Sertão mesoregion), sampling stratum 2 (Borborema mesoregion) and sampling stratum 3 (Zona da Mata and Agreste mesoregions), and 2382 cows aging  $\geq 24$  months from 474 farms were sampled. Serological diagnoses of bovine cysticercosis were initially done by means of indirect ELISA, and positive serum samples were confirmed by a immunoblot test. Herds were deemed positive for cysticercosis if they presented at least one positive animal in herds of up to 29 females, and two positive animals in herds with more than 29 females. The spatial clustering was assessed using the Cuzick-Edwards  $k$ -nearest neighbor method and spatial scan statistics. A significant clustering of positive herds was detected in the southern part of the Borborema mesoregion. Given that serological tests for bovine cysticercosis are not widely available, and also that replacement and maintenance of herds through animal purchases is common in the region, it can be concluded that prevention measures should be applied at herd level.

**Keywords:** Cattle, epidemiology, cluster analysis, bovine cysticercosis.

## Poster 37

### Spatial non-stationarity and geographic scale in models of canine cancer incidence

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Epidemiological studies are often concerned with the spatial distribution of disease incidences. This requires analytical methods accounting both for the data attribute and its relative location. Further, these methods need to consider that relationships between incidences and independent variables may vary as a function of the location, thus exhibiting spatial non-stationarity. Related to that but often ignored, the size of the geographic extent under consideration may also play a crucial role in determining these relationships. In order to explore these issues, several spatial modeling methods have been developed so far. An example is geographically weighted regression (GWR) that estimates model coefficients locally, by fitting incidences across geographic extents of different size—or kernels—for locations within the study area. Thus, local coefficient estimates may be scale-dependent somehow, because different patterns

of spatial non-stationarity can emerge at different kernel sizes. To account for such scale effects, GWR allows for testing different kernel sizes. Still, interactions between spatial non-stationarity and scale can also be more intricate, as scale effects may also vary across the study area. To better understand these complex interactions in models of canine cancer incidence, we developed a case study based on data aggregated within Swiss municipalities between 2008 and 2013. We adapted and extended an existing regional-scale modeling approach for robust analysis and diagnosis of spatial nonstationarity in an epidemiological context. Unlike most local estimators, this technique makes use of the structure of a well-established non-spatial modeling framework. Spatial non-stationarity and scale are implicitly incorporated through the geographic extents to which the regional-scale models are fit. In a simulation approach, we fit these models to regions centered at each municipal unit within the study area for different geographical extents, defined by the number of  $k$ -nearest neighboring units. For each central unit and  $k$ -value, we collect a rich set of model diagnostics, and summarize them through measures of central tendency and spread. Finally, we present these summaries by means of two powerful visualization techniques: scalograms and alpha-by-value maps. Preliminary results reveal that scalograms could allow us to gain insights into scale effects amongst the different diagnostic summaries. Alpha-by-value maps are expected to help us to develop a deep understanding of the complex interactions between spatial non-stationarity and scale. The latter appears to be of high relevance in our model of canine cancer incidence.

## Poster 38

### The 'local trap' or spatial entrapment? Spatial behavior among pregnant, African American women in an urban environment

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**Introduction:** Explanation of socio-spatial variation in population health often relies on theories of 'deprivation amplification' wherein the health consequences of low individual social status are amplified by exposure to deprived environmental conditions. However empirical measurement of environmental resources are often derived from residential areas leading some to argue that the 'local trap' - reliance on a single geographic scale centered on residence - mischaracterizes the experienced environment. We use an activity space approach to characterizing the spatial behavior of socioeconomically diverse, pregnant African American women in an urban environment. Recognizing the anchoring role of residence, we assess variations in spatial behaviors as a function of women's residential location and attributes.

**Methods:** To date n=45 of an anticipated 300 women have been recruited from routine antenatal care clinics in Atlanta, GA, USA; recruitment and data collection will continue through 2017 and results will be updated as data becomes available. Routine activity space was measured with a web-based survey instrument, the Visualization and Evaluation of Routine

Itineraries, Travel destinations, and Activity Spaces adapted for use with maternal and child health populations (VERITAS-MCH). 27 indicators of spatial behavior including number and type of destinations, road network distances, areas of convex hull polygon and perceived residential neighborhood, and density and distribution of destinations were summarized into spatial behavioral typologies with aspatial principal components analysis (PCA). Linear regression of principal component scores on individual and neighborhood factors characterized determinants of behavior. Geographically weighted PCA was carried out to assess for spatial variation in principal component loading.

**Results:** Two principal components—reflecting spatial size and extent of activity space (PC1), and density of activity in perceived residential area (PC2) – explained 35% of total variance. Low versus high income women had smaller activity space size and extent (PC1) ( $p=0.01$ ), and women from neighborhoods with higher violent crime had greater destination density near home (PC2) ( $p=0.05$ ). PCA loadings vary spatially with more homogenous behavior in historically more segregated southwest Atlanta, and more diverse behavior in more suburban northeast Atlanta.

**Discussion:** Nearly all women have routine behavior beyond the bounds of their local neighborhood suggesting that reliance on residential neighborhood measures alone – the ‘local trap’ – may be incomplete. However the spatial diversity and extent of visited locations varies by individual and neighborhood social characteristics suggesting that local spatial entrapment may modify women’s spatial behavior. Amplification of residential deprivation may be more important for women constrained due to family demands or access to transportation.

## Poster 39

### Patient choice and proximity: the case of the outpatient services of an Italian region

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The Italian National Health Care System is a public health system that provides universal coverage for comprehensive and essential health services through general taxation, recognizing health as a fundamental right of individuals and a collective interest of society. In the early 1990s, national reforms started transferring several key administrative and organizational responsibilities from the central government to the 20 Italian regions. In this scenario, a rational investigation of the choices taken by the patients will allow the care managers to operate on the basis of reliable observations in order to better allocate the resources and make the system more efficient.

Most of the literature focuses on inpatient system studying hospitals' choices in competitive contests. Competition is not one of the principles that characterizes NHS, but thanks to the decentralization strategy of the 1990s, some of the Italian regions implemented a reform that gave patients freedom to choose, thus stimulating competition between the services. This study focuses on outpatient clinic system of Tuscany Region, characterized by a non-competition system, addressing the research question:

“In a health care system without competition what are the drivers the address patients' choice of outpatient services?”.

The dataset used is the 2015 individual-level administrative care outpatient, from which we extracted the first elective non-emergency cardiological visits data, characterizing each patient by age, sex, and nationality. We considered factors such as the patient mobility that could be limited by distance from home of the hospital, travel costs and difficulties of getting informal support. Considering the spatial accessibility as the balance between supply and demand connected in space, we choose the 2step floating catchment area method to compute a synthetic value of how many services can be reached within a minimum travel distance of 15 minutes. To better estimate the distribution of the population, we used the dasymetric modeling, while a two-level multinomial logistic regression with random effects has been chosen to identify which variables affect most the choices.

To our knowledge, this is the first study of this kind carried on in Italy and in spite of its early stage, we already can individuate the waiting time as one of the most influential aspects of the patients' choice.

The research idea arises from the need of an outpatient system able to meet the population's needs at a more local level. With this study, we want to rationally analyze the choices of the patients in order to put their needs to the center of the entire health care system. Moreover, this analysis can be used to optimize the allocation of resources, reduce inequities in access care services and increase the responsiveness and quality of outpatient systems.

## Poster 40

### Mapping vector distribution for public health risks: the need to account for uncertainty

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**Background:** Vector-borne diseases (VBD) are an important public health concern, affecting a large number of people globally. Models for the spatial distribution of vectors have proven to be an important tool in the assessment of the risk of VBD enabling better targeting of surveillance and control. However, the modelling and mapping of species distribution possesses intrinsic uncertainties. In spatial statistical models, uncertainty arises due to the raw distributional data inputs, and the model and mapping processes used. Nevertheless, maps are frequently presented as certain fact, without an indication of uncertainty. As uncertainty plays an important role in risk assessment, management and communication, it should be recognized and presented as a study output, leading to transparency in the communication process, and helping the public or decision-makers better understand the risk present.

Lyme borreliosis (LB) is the most prevalent arthropod-borne disease in the temperate regions of the Northern Hemisphere and is increasingly reported in Scotland. The complex ecology of the disease, which is carried by *Ixodes ricinus* ticks and maintained by multiple host species, makes it challenging to understand, predict and control.

**Objectives and Methodology:** Using LB as an example, the aim of this study was to assess uncertainty of models and maps of tick distribution in Scotland using two different tick datasets, collected using different methodological approaches. Both models used the same statistical methodology (a Bayesian approach using INLA R package) and the same set of climatic, environmental and host variables.

**Results:** The models produced different predicted distributions with different levels and distributions of uncertainty. These were used to determine the environmental factors associated with uncertainty, in order to understand the relative strengths and biases of each dataset, and inform future data collection. Tick distributions and uncertainty were mapped to provide users with visual representation of the uncertainty of the maps, an important tool in risk communication to the public or decision-makers.

**Conclusions:** We demonstrate that the outputs of a model are critically dependent of the inputs, raising questions about what data are sufficient to produce a reliable output that can be used for public health decision-making. We conclude that the degree and spatial distribution of uncertainty should be assessed when creating vector distribution maps to inform public health risks, and not only their overall accuracy.

## Poster 41

### Spatial dependence of body mass index and exposure to night-time noise in the Geneva urban area

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Obesity is a public health challenge worldwide: by 2025 the global prevalence could reach 18% in men and 21% in women (NCD-RisC 2016). High body-mass index (BMI) is an important risk factor for diabetes, cardiovascular disease and cancer (NCD-RisC 2016). The increase of noise from traffic can be considered a contributory cause (Mueller et al 2017). Exposure to high noise levels may be associated with high BMI in the population (Christensen et al 2016) or in population subgroups (Ofstedal et al 2015). Reasons are that a high noise level may discourage physical activity and boost energy intake (Parrish&Teske 2016) with a consequent weight gain, but also that sleep disorders may in turn cause metabolic troubles favouring obesity (Miedema&Vos 2007). While high values of BMI may be clustered and spatially dependent in dense urban areas (Joost et al. 2016), the spatial co-dependence of high BMI and noise values has not clearly been shown yet.

In this study, we calculated the night-noise mean (SonBase 2014, compatible with the EU Environmental Noise Directive) for the 5 classes obtained after computation of Local Indicators of Spatial Association (LISA; Anselin et al 1995) on the BMI of the participants in the Bus Santé study, a cohort managed by the Geneva University Hospitals (N=15'544; Guessous et al 2014). We expected the mean of dBs to be significantly higher in the group showing spatial dependence of high BMI values (high-high class).

We ran an ANOVA and multiple T-tests to compare the dB means between LISA clusters. The approach was applied to the participants of the whole State Geneva cohort, and to a reduced set of individuals living in the urban environment of the municipality of Geneva only.

With a significance level of 95%, 45% of participants belong to LISA clusters in the State and downtown Geneva. In the latter area, a low-low BMI cluster on the left bank of the river is characterized by a mean of 51.7 dB, and a high-high cluster on the right bank by a mean of 49.5 dB. Using the whole State data, the same clusters are observed and show respectively 48.7 dB (low-low) and 46.3 dB (high-high). The 5 clusters obtained show significantly different night-noise means.

Our study confirms the existence of spatially dependent BMI clusters on the two scales investigated, but our hypothesis is rejected as it does not show a significantly higher night-noise level in high-high BMI clusters than in the other classes. Socio-economic factors mainly explain the results obtained.

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### Predictive spatial models of obesity as risk factor for diabetes type 2 in Mexico

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The prevalence of non-communicable diseases is rising rapidly throughout the world, and it is expected to be the leading cause of mortality in Latin America [1]. The increases of obesity and metabolic syndrome is a worldwide phenomenon and Mexico is not the exception, also, both conditions are the main risk factors for type 2 diabetes and cardiovascular diseases [2]. Obesity is the main modifiable risk factor for the development of chronic non-communicable diseases, such as diabetes mellitus and cardiovascular diseases, which are the two main causes of general mortality in Mexico. For type 2 diabetes a complex gene-environmental interaction for which several risk factors, such as age, sex, obesity and hypertension, are well documented [3]. In Mexico, by the year 2025, close to 11.7 million Mexicans are expected to have diabetes [4]. Moreover, there is a lack of spatial studies examining the association of diabetes or cardiovascular diseases with the distribution of obesity or others socio-economic indicators. Although non-communicable diseases cannot be characterized by an infectious agent, the observed spatial pattern of incidence (new events) or prevalent cases could provide information on the underlying mechanisms

of the disease [5]. We assess this relationship with a Bayesian spatial models for urban and rural localities in Mexico for examine obesity and others factors of risk for diabetes type 2.

We used the data from National Health Survey to Mexico (2012) and socio-economic indicators from National Institute of Geographic and Statistics. We applied an exploratory analysis with area-to-area kriging for obesity, metabolic syndrome and diabetes [6]. Also, Bayesian generalised mixed models (GLMMs) using Markov chain Monte Carlo were used to model non-transmissible diseases prevalence. Multivariable models including all seven lifestyle covariates were fitted to the diabetes data.

The intrinsic conditional autoregressive (CAR) prior were fit to the spatially correlated residual terms in the two previous equations.



**Figure 1.** Distribution of Body Mass Index of municipalities in the states of Mexico.

The preliminary results indicated a weak relationship between obesity (Body Mass Index) and marginality index. This result will contribute to the analysis of data for making informed decisions regarding the diagnosis, planning and evaluating prevention programs of the major non-communicable diseases at national level. Likewise, it will formalize a protocol for the integration of this type of analysis in the planning of policies related to the health sector. The greatest impact will be the link with users and decision makers at more local levels of government through incidence probability maps and the relationship with local variables.

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## Poster 43

### High-complexity care in Brazil - what changed in the territory in 15 years (2000 and 2015)? Trajectories and determinants

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**Objectives:** Analysis of the evolution of the use of high complexity (tertiary) services in oncology and cardiovascular surgery, and of the geographic displacement of patients demanding those services, in the years 2000 and 2015, to evaluate the effects of regionalization policies in the period.

**Methods:** Ecological study of high-complexity care in the Unified National Health System (SUS) network, based on data from the Hospital Information System (SIH) for hospital in-patient admissions in Brazil in the years 2000 and 2015. Analysis of the networks of attention in oncology and cardiovascular surgery was based on the dominant flows (the largest outflow of patients from a municipality), and on the distance traveled in search of care, using public-domain software: R, TabWin and TerraView.

**Results:** Between 2000 and 2015, access improved, with increases both in the number of municipalities and of patients treated. Overall, displacement patterns did not change significantly. Despite the expansion of coverage in the North, and parts of the Northeast regions, people living in those areas still have to overcome long distances. In the South and Southeast regions, on the other hand, with greater provision and distribution of service units, distances to care have shrunk.

**Conclusions:** Regionalization of access to oncological care and to cardiovascular surgical interventions made marked progress in the period analyzed. In regions with higher socioeconomic levels, the provision of services is also present in regional centers; in the others, State capitals are the main service hub. The expansion of the coverage facilitated patient access: hospitalizations increased by a factor close to 3 in the period, and distances covered are, as a rule, smaller.

**Advances / applications of the study:** The investigation of coverage areas of SUS units through the identification of the networks established by actual use, and indications of possible alternative regionalizations given by the cross-flows, are tools with potentially important application in planning and improving the distribution of services according to Need of the user population.

**Financing:** National Council for Scientific and Technological Development (CNPq) - grants 309692 / 2013-0 and 309728 / 2012-6

## Poster 44

### Rural Health Mapping The Reconcavo Of Bahia-Brazil

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The magnitude of waterborne diseases is higher and impossible to quantify, particularly in remote regions of the planet, as the Reconcavo of Bahia, where the population usually uses private reservoir of water, such as artesian wells without water treatment and quality control. The present study aimed to collect data regarding the conditions of the rural sanitation in the Bahian Reconcavo region and compare them with the specific federal and international regulations. In addition, sanitary maps were prepared in order to visualize, geographically, the polluted areas. The study area comprised the 20 municipalities that compose the Bahian recôncavo, which are: Cabaceiras do Paraguaçu, Cachoeira, Castro Alves, Conceição do Almeida, Cruz das Almas, Dom Macedo Costa, Governador Mangabeira, Maragogipe, Muniz Ferreira, Muritiba, Nazaré, São Felipe, São Felix, São Francisco do Conde, São Sebastião do Passe, Sapeaçu, Saubara, Santo Antônio de Jesus, Santo Amaro and Varzedo. From each municipality a maximum number of 100 alternative sources of water, existing in the rural environment, was chosen for water collection, totaling 2000 samples.

After collection, the samples from wells were transported to the Laboratory of Animal Microbiology of the Center for Agricultural, Environmental and Biological Sciences (CCAAB) of the Federal University of Recôncavo da Bahia (UFRB), where they were processed. The determination of the Most Likely Numbers (NMP) of *Enterococcus*, total coliforms and *Escherichia coli* and Colony Forming Units (CFU) of Mesophilic Microorganisms was performed according to global and official methodologies. In order to determine the physicochemical parameters of color (UHazen), turbidity (UNT) and free residual chlorine (ppm), the following devices were used: colorimeter, turbidimeter and chlorimeter. The microbiological and physico-chemical results were evaluated according to the standard values established by national and international laws. The groundwater samples analyzed were highly polluted with high concentrations of total coliforms (> 2,000 NMP/100mL), *Escherichia coli* (> 2,000 NMP/100mL), *Enterococcus* (> 2,000 NMP/100mL) and Mesophilic (10<sup>6</sup> to 10<sup>9</sup> CFU / mL), and not safe for human consumption, considering national and international laws. The values of color, turbidity, free residual chlorine were also exacerbated and above the maximum permissible values. Despite the great efforts made by national and international development programs, communities researched this inquiry are still exposed to poor quality water and urgent steps must be performed on the entire chain of water, with the aim of establishing this region sanitation

## Poster 45

### Methods for addressing neighbourhood self-selection in studies of neighbourhood effects on health

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**Introduction:** Self-selection into residential neighbourhoods and related bias is a widely acknowledged but under-studied phenomenon in research investigating neighbourhood influences on health. Our aim was to identify methods used to account for self-selection, and to identify possible approaches for future research.

**Methods:** In this scoping review, articles in PubMed which used the terms “neighbo(u)rhood” and “self-selection” were identified to determine methods used to address neighbourhood self-selection.

**Results:** Sixty-one articles were identified; 31 (50.8%) accounted for self-selection in neighbourhood and health associations. Approaches used to address neighbourhood self-selection varied but most studies adjusted for neighbourhood preference items. Common approaches were model adjustment for multiple variables using principal components or factor analysis (22.6%), or propensity scores (9.7%). One study used instrumental variables. In longitudinal research, fixed effects models were used to account for time-invariant self-selection.

**Conclusions:** Methods used thus far to account for self-selection assume that the factors underlying neighbourhood self-selection have been assessed and accurately measured. Fixed effects models, while useful for longitudinal research, do not adjust for time-varying self-selection. Instrumental variables may provide a promising avenue for future work. This approach, however, requires identifying a candidate variable that predicts the health outcome through the particular neighbourhood exposure of interest.

## Poster 46

### Hepatitis A Outbreak in Europe: what about sexual transmission?

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**Introduction:** Hepatitis A is an acute, usually self-limiting infection caused by the hepatitis A virus (HAV). Transmission is predominately by the faecal-oral route, through contaminated water or food-products or through direct contact with an infectious person (1). Transmission through sexual exposure has been associated with outbreaks in men who have sex with men (MSM) since the 1970s (2). The main risk factor is related to direct oral-anal contact during sexual activity (3).

**Results:** Between 1 June 2016 and 16 May 2017, 15 EU countries (Austria, Belgium, Denmark, Finland, France, Germany, Ireland, Italy, the Netherlands, Norway, Portugal, Slovenia, Spain, Sweden and the United Kingdom) have reported three clusters involving 1 173 HAV confirmed cases, associated with three different HAV genotypes. Each of these clusters involve between ten and fifteen different EU Member States. Most cases are reported among HAV-unvaccinated adult MSM, although evidence already exists for secondary cases among the general population. The extent of these outbreaks is likely to be underestimated, as reported cases are limited to those attending healthcare facilities and for which sequencing was performed (3).

**Discussion:** The multinational dimension of these clusters may be explained by the highly interconnected sexual networks among MSM in Europe. The main prevention measure in the context of the current outbreaks is hepatitis A vaccination of MSM (3). The actual level of immunity among the MSM population in Europe is unknown. It has been estimated that a level of immunity greater than ~70% among the MSM population would prevent sustained transmission and future outbreaks (4).

**Conclusion:** Further transmission resulting from these clusters may be prevented by vaccination of MSM and post-exposure prophylaxis in identified contacts. However, limited vaccine availability in some countries may have an impact on the implementation of such control measures (3).

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## Poster 47

### Measles situation in Europe: is elimination a mirage?

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**Introduction:** Measles is an acute, highly contagious viral disease capable of causing epidemics. Infectivity is close to 100% in susceptible individuals and in the pre-vaccine era measles would affect nearly every individual during childhood. Immunisation has dramatically reduced the incidence of measles in Europe, but despite overall high immunisation coverage, measles continues to cause frequent outbreaks. Globally, measles remains a leading cause of childhood deaths and an estimated 160000 children die each year from complications of the disease<sup>1</sup>.

**Results:** Between 1 April 2016 and 31 March 2017, 30 EU/EEA Member States reported 6597 cases of measles. The highest number of cases was reported by Romania (3072), Italy (1314) and Germany (711) – respectively 47%, 20% and 11% of the EU/EEA cases in the 12-month period. In 11 EU/EEA Member States the number of cases reported in just 3 months in 2017 has exceeded the number of cases reported during the entire 2016<sup>2</sup>.

Of all cases with known age (5876), 2426 (41%) were children less than 5 years of age, while 2208 (38%) were aged 15 years or over. Of all cases with known vaccination status (6133), 88% were unvaccinated and 8% were vaccinated with one dose. The proportion of unvaccinated cases was highest among children below one year of age (95%). In the target group for the first dose of routine childhood MMR vaccination (1-4 year-old), 85% of the cases were unvaccinated and 11% were vaccinated with

one dose. Sixteen deaths due to measles were reported during the 12-month period, all in Romania<sup>2</sup>. In April and May 2017, 2 additional deaths occurred due to measles: 1 in Germany and 1 in Portugal<sup>3</sup>.

**Discussion:** Measles continues to spread across Europe because the vaccination coverage in many EU/EEA countries is suboptimal. The vaccination coverage of measles was below 95% in 12 of 27 EU/EEA countries for the first dose and, for the second dose, in 15 of 23 EU/EEA countries. Infants are particularly vulnerable to complications of measles and are best protected by herd immunity which is achieved when population coverage for the second dose of a measles-containing vaccine is at least 95%<sup>2</sup>.

**Conclusion:** Immunisation is the only effective preventive measure against acquiring measles. If the elimination goal is to be reached, the vaccination coverage rates for children targeted by routine vaccination programmes will have to be increased. Routine immunisation needs to be strengthened by facilitating access to vaccination, and mechanisms to identify people who are not or are incompletely vaccinated are needed. Strengthening and ensuring timely surveillance of measles helps guide public health actions and is critical to disease control<sup>2</sup>.

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## Poster 48

### Conceptualising, selecting, assessing and reporting public open space exposure measures in health research

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**Introduction:** Public open space (POS) has been found to be associated with a variety of health and behavioural outcomes. Although POS is frequently used as an exposure measure in policy-relevant research, the specific exposure measure can vary across studies. Furthermore, assessment of POS can be complicated due to the under-reporting of key aspects, limiting the comparability of findings across studies. The aim of this study is to highlight important methodological considerations for reporting and assessing POS exposure measures and to make recommendations for consistent data reporting.

**Methods:** A discussion of the key methodological issues related to the reporting of POS exposure measures, including the definition, data source, availability measure and treatment in statistical analysis, is provided. These issues are illustrated through a review of Australian studies published between 2005 and 2015 that examined associations between POS availability and health or health-related behaviour outcomes.

**Results:** A number of key methodological issues were identified. Definitions of POS exposure measures varied between studies and there was limited information about the sub-types of POS included or excluded. Many studies did not report on key data source information (e.g. year of data collection). While it was typically clear how POS exposure was defined, with many studies using proximity measures, specific details were sometimes lacking, such as the POS access point. Furthermore, the studies showed differences in the treatment of POS exposure measures in analysis, including using percentile categorisation rather than continuous exposure measures. This limits direct comparison between studies.

**Conclusions:** There is a lack of consistency in the reporting of POS exposure measures in health research, highlighted in this review of Australian literature. While only Australian studies were reviewed, the issues covered are unlikely to be restricted to Australia and are internationally transferable. A reporting checklist was developed to assist researchers in reporting on the key aspects of POS exposure variables necessary to include to enable comparison of study findings and replication in the creation of exposure variables.

## **Poster 49**

### **A GIS based investigation of spatial accessibility to dental services in Scotland**

**Zhiqiang Feng**

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Utilization of dental services is determined by many demographic and socioeconomic factors. Geographical dimension is also important in affecting utilization of dental services. Distance to dental service providers is widely accepted as a significant barrier to utilization of the service. As a result dental services should be geographically distributed in such a way that allows people to access a provider at relative ease. Inequalities in access to dental care services may have negative influence on taking up dental services and further lead to poor outcomes in oral health. Over years the Scottish government has introduced incentives encouraging dentists to work in remote and deprived areas. Thus it is important to provide evidence in relation to spatial accessibility to and utilization of dental care services.

In this paper we used the 2011 dental patient registration data and the population census data to investigate variation in spatial accessibility to dental services. Also we explored what socioeconomic factors were associated with spatial accessibility to dental services. The dental patient registration data were extracted from ISD which include locations of registered patients and NHS dental practices. The census data were extracted from the 2011 census covering demographic, socioeconomic characteristics at the data zone level. The Ordnance Survey Integrated Transport Network (ITN) Road Links were obtained from EDINA. We calculated drive times and road network distances from each patient to the registered dental service using the Network Analyst in ArcGIS 10.2. We summarise the variation of road travel distances and drivetimes by areal deprivation and urban-rural types at the data zone level. We fit regression models to explore what factors explained variations of spatial accessibility to dental services. Our descriptive results show that there was a considerable variation of travel distances and times across different types of areas. The modelling results show residential location was still a significant predictor after controlling for demographic and socioeconomic factors.

## Poster 50

### **An exploratory analysis of the effects of crime on health and quality of life at the neighbourhood level in Toronto, Canada**

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The impacts of crime on health are complex and varied. Violent crimes can cause significant physical and psychological harm to victims with potentially long-lasting and permanent effects. Property crimes can also result in psychological impacts, which may significantly affect an individual's daily routines and quality of life. Victims may suffer from a wide range of psychological and behavioural changes, such as mental illness, depression, work absenteeism, substance abuse, and smoking. However, such impacts are difficult to assess and quantify, since conventional police-recorded crime statistics do not collect data on people's perception of their risk of crime and health impacts from victimization.

This study is based on a conceptual social model of crime and health that identifies the relationships between crime, deprivation, health, and healthcare services. This model is investigated through empirical results from a questionnaire survey administered to selected neighbourhoods in Toronto, Canada, which collected information about previous crime experiences, awareness of crime in the neighbourhood, and impacts on physical health, psychological wellbeing, and quality of life. Based on statistical approaches including chi-square tests and logistic regression models, this study evaluates victimization experience as an explanatory variable for physical and mental health conditions in Toronto neighbourhoods.

Our study findings suggest that violent crime offences, which inherently have physical health consequences, are less frequently occurring in Toronto neighbourhoods than property-related crimes. Survey results indicated that victims suffer from physical and psychological harm to various degrees after experiencing a crime, whether the incident was violent or non-violent by nature. Psychological effects, such as stress, panic attacks, depression, and lack of confidence were commonly cited among victims of violent crimes, while psychological impacts and behavioural changes were more prevalent in victims of property-related crimes. Both violent and property crimes were associated with psychological effects, including avoidance behaviours and becoming more vigilant and watchful of neighbourhood crime. Relationships between crime occurrences and neighbourhood characteristics were assessed, such as socio-demographic and location-based characteristics, including income and marriage status.

This study emphasizes the importance of addressing health impacts of crime beyond immediate physical harm, recognizing long-term consequences of victimization, and providing health care services from a victim support perspective. This study provides empirical evidence for understanding the effects of crime on health, thus underscoring the far-ranging health impacts that victimization can have within a community. \*presenting author  
Keywords: Violence, crime, victimization, public health, wellbeing, victim support, Canada

\*presenting author

**Keywords:** Violence, crime, victimization, public health, wellbeing, victim support, Canada

## Poster 51

### Predictive mapping of the cutaneous leishmaniasis vector (*Phlebotomus papatasi*) in Jordan using multi-criteria decision analysis

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**Background:** Cutaneous leishmaniasis (CL) is an endemic vector-borne disease in Jordan. It is highly pertinent because it is severely under-reported with estimated incidence in some years being 47 times that of officially reported cases in the Mid Jordan Valley. Despite inaccurate reporting, the number of cases has increased by 149% between 2012 and 2015; from 103 cases to 257. This change in CL epidemiology could partially be due to the influx of refugees from Syria (over 250,000 in 2017), which is part of a coalition with five other countries where over two thirds of all new CL cases occur. Furthermore, CL outbreaks have been described in areas adjacent to Syrian refugee camps in Lebanon and Turkey highlighting the challenges of cross-border health. In addition to the inaccurate CL reporting there is a lack of robust Jordanian entomological data, including the CL sandfly vector *P. papatasi*, which hampers the possibility of creating accurate disease risk maps. In these cases, knowledge-driven methods using published scientific literature and expert opinion can provide an alternative.

**Aim:** Construct habitat suitability maps of the CL vector *P. papatasi* in Jordan using multi-criteria decision analysis (MCDA) in order to identify areas most prone to vector exposure and therefore, potential outbreaks. Special focus will be given to areas near refugee camps.

**Methods:** A review of the literature identified key predictor attributes influencing *P. papatasi* presence, and maps were sourced for each variable. These maps were standardised to a common scale of 0 to 1 using appropriate fuzzy membership functions that best defined the relationship between degree of suitability and *P. papatasi* presence. Analytical hierarchy process (AHP) was used to perform a pairwise comparison of the predictors, thereby generating predictor weights based on Eigen values. Predictor maps and variables were combined to generate a habitat suitability map for *P. papatasi* in Jordan.

**Results:** Relevant predictors included monthly temperature, monthly relative humidity, annual precipitation, vegetation index, presence of fat sand rats (rodent burrows provide shelter and food for sandflies), and monthly wind speed. The AHP generated predictor weights of 0.39 for fat sand rat habitat suitability; 0.36 for temperature; 0.13 for vegetation; 0.09 for precipitation and 0.04 for relative humidity. The combination of all the predictors for July, a month when sandflies are abundant, generated a suitability map that showed high suitability in the North-western regions close to the Jordan Valley and stretched down South bordering the Jordan Rift Valley. Low suitability corresponded to the Eastern and South-eastern desert regions. Four out of the five Syrian refugee camps (Azraq, Mrajeeb Al Fhood, Zaatari, King Abdullah and Cyber City) in Northern Jordan were in medium to high CL vector suitability areas.

**Discussion and conclusion:** MCDA can be useful in data-scarce environments like here where robust entomological information was lacking. Implications of identifying areas prone to disease-transmitting vector occurrence include the implementation of targeted surveillance systems and interventions, or land management planning that considers disease risk (e.g location of refugee camps). This is the first study, to our knowledge, that investigated CL vector distribution in Jordan using spatial analysis tools.

## Poster 52

### Spatial patterns of anaemia among young children in Burkina Faso: a Bayesian Geo-Additive Modelling

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**Background:** Anaemia remains a major public health problem in Burkina Faso (BF), a malaria-endemic country, mainly affecting children under five with major consequence for socioeconomic development. Despite the magnitude of anaemia in BF, knowledge about the geographic variability of haemoglobin (Hb) concentration, severity of anaemia and identification of risk factors within this country remains poor. Identifying spatial effects would however be useful to inform where greatest scaling-up efforts should be concentrated and to provide baseline data against which future scaling-up of interventions can be compared. The aim of this study is therefore to explore the spatial pattern and possible determinants of anaemia among young children in BF.

**Methods and materials:** Individual data on Hb concentration and severity of anaemia (Hb < 8.0g/dl) of 6225 children, aged 6–59 months and distributed across 45 provinces in Burkina Faso were obtained from the 2014 Malaria Indicator Survey. We used a Bayesian semi-parametric random effects model to examine the effect of different covariates and possible spatial variation.

**Results:** Overall, severe anaemia prevalence ranged from 6.1% to 49.3% across provinces. Spatial patterns evidenced significantly higher anaemia prevalence in the extreme north and west regions of the country. The fixed effects showed that young children and children belonging to households with lower wealth index or located in rural setting usually display lower Hb concentrations, corresponding to a higher prevalence of anaemia.

**Conclusions:** We observed a spatial heterogeneity between districts in child's health beyond the effects explained by the included fixed effects. Planning, implementation, and evaluation of programs for controlling anaemia should be based on province conditions, and they should take into account the specific aetiology and prevalence of anaemia.

**Keywords:** Anaemia, haemoglobin, Burkina Faso, Bayesian spatial analysis

## Poster 53

### Health problems in the amazon frontier expansion: spatial patterns of spread of diseases

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In the health sector, the Geographic Information Systems (GIS) allow to explain the interaction between physical environments with economic parameters in the interface of health problems. To observe the health conditions of populations as dynamic and complex phenomena, in isolation way are not innovation, but to consider the simultaneous occurrence of three health problems at different stages of time and space in regions of economic border can extract additional meanings to the conventional analyzes, aiding in the understanding of the dynamics of the

process health-disease. This ecological study discusses the implementation of the Geographically Weighted Regression (GWR) model in the identification of socioeconomic indicators more associated to places of larger occurrence for homicidal violence, malaria and dengue. The data of registration correspond to the time series of 1980-2010, aggregated by municipalities, in the Legal Amazon, Brazil. Initially, a model of regression classic multivariada was used OLS (Ordinary Least Squares Estimation) soon afterwards the model GWR was applied with the selected variables. In the model GWR, the associations between the occurrence of the diseases and socioeconomic factors were analyzed. The maps generated by the GWR allowed to analyze the distribution of each independent variable through the estimates and of their values of associated t. The results of the research attest that the occurrence of each one of the diseases is linked to productive activities, territorial fluidity and levels of urbanization, which confirms the possibility of application of pathogenesis theory in the regional scale (GRMEK, 1995), when a group of present illnesses in a given population, in certain time and place, indicates that the presence of a health problem depends on several endogenous and ecological factors, as well as, of the frequency of all the other diseases present in this same population.

**Keywords:** Homicide. Malaria. Dengue. Epidemiology. Spatial Analysis. GWR. Public Health. Frontier

## Poster 54

### Bayesian Health Impacts Analysis: estimating the health impacts of landfills in Europe

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The environmental and health impacts associated with the collection, transport, processing, and disposal of waste have the potential to adversely affect a substantial proportion of the population. Here, we perform a Bayesian analysis of the health impacts associated with landfills within the European Union, with particular focus on propagating the uncertainties that are associated with the inputs for the calculation of disability adjusted life years for a selection of health outcomes; low birth-weight, congenital abnormalities, respiratory diseases and annoyance from odour. Uncertainties associated with the risks of these outcomes and the underlying rates of diseases in different countries are incorporated within the Bayesian model as are uncertainties associated with the populations at risk. In the case of the latter, populations at risk around all landfills reported within the European Environment Agency 's European Pollutant and Transfer Register were estimated using a GIS based on downscaling CORINE land-cover information. As part of the analyses, we examine the sensitivity of results to the use of different exposure-risk relationships. The output of these analyses include both point estimates, of the total impacts associated with landfills, and estimates of uncertainty associated with those estimates.

## Poster 55

### Risk Assessment of Urban Schistosoma Infection Based on Precise Positioning by Using Portable GPS Combining with Google Earth in Wuhan, China

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**Background:** With effective control of schistosoma infection through snail control drug and engineering transformation on the marshland of Yangtze River in the past years, snail area has greatly reduced. But scattered distribution of snail is still a problem that may lead to urban schistosoma infection and transmission. So a precise positioning technology is urgently needed in urban schistosoma infection control and risk assessment.

**Objective:** Develop and apply a technology based on precise positioning by using portable GPS combining with Google Earth in the work of schistosoma infection control and risk assessment. Collect various types of risk sources data to make a scientific assessment of schistosoma infection risk level in different sections (Phrase I to Phrase IV) of the marshland of Yangtze River in Wuhan, China.

**Methods:** Utilized portable GPS combining with Google Earth to monitor sources of infection including snails, voles and wild feces, and identified them by laboratory testing. Social behavioral observational method was applied to investigate the spatial pattern of mainstream population in Yangtze River. According to the results of source of infection monitoring and demographic monitoring of each sections of Yangtze River marshland, Delphi method and risk matrix were used to evaluate the risk level from the aspects of harmfulness, possibility and controllable level.

**Results:** The average density of living snails and infected snails were 0.993/0.11 m<sup>2</sup> and 0.012/0.11m<sup>2</sup>. Snail infection rate was 1.18%. A total of 30 infected snails were captured in 27 sites in Phrase II to Phrase IV, and the quantities were 5, 5 and 20 respectively. A total of 67 voles were captured and 2 of them that were captured in phase III were positive, and the positive rate was 0.23%. A total of 248 pieces of wild feces were collected, and schistosoma eggs were founded in 2 pieces in Phrase III and Phrase IV with the infection rate of 0.81%. Flow monitoring results of gates of Hankou marshland showed that both the total flow and the ratio of people on the waterfront layer of phase I were the largest among the four phases. The harmfulness level of phase I was the highest of all, the possibility level and the controllable level were rising from Phrase I to Phrase IV.

**Conclusion:** Precise positioning technology by using portable GPS combining with Google Earth can play a great advantage in urban schistosoma infection control and risk assessment. The harmfulness of schistosoma infection in Phrase I of Hankou marshland of Yangtze River is serious, the possibilities of schistosoma infection in Phrase III and Phrase IV are large but relatively easy to control.

## Poster 56

### The development of a space positioning technique for detecting the occurrence of *Oncomelania* snails in the river beaches of the Yangtze River in China

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**Background:** Variation in the distribution of snails has always been a problem in scientific research. Traditional methods of snail surveying are imprecise, difficult to reproduce, and labor intense. This study aims to develop a space positioning technique as well as a more scientific approach to field surveys for detecting the occurrence of *Oncomelania* snails in river beaches.

**Methods:** Electronic map and positioning equipment were chosen by comparing their performance, operating system and accuracy, etc. The protocol for detecting snail distribution was established based on the specification for prevention and control of schistosomiasis in china and positioning technology articles, and improved through field demonstration and revision for three times. A comparison between this study and the traditional approach was performed to test for differences in accuracy, efficiency, the ability to geographically map information and figures, ease of data sharing, and economic effectiveness.

**Results:** The Garmin eTrex 20x hand-held GPS, Google Earth, BaseCamp, and Picasa were selected and applied to the trial beach. A total of 12 technical standards were proposed for the detection of *Oncomelania* snails in field. In the same area, the accuracy of positioning was increased by 16 fold, the efficiency of data processing was increased more than 10 fold and the ratio of frame with snail increased by 4.35 fold compared with traditional methods. A GIS platform of snail distribution which contributes to the monitoring and early warning was established. It showed the snail point of interest on Google Earth with geographic information, snail quantity and environment image, and could be easily shared and had good reproducibility. In addition, the economic effectiveness of snail control using our method was 1/6 of the compared traditional method.

**Conclusion:** The developed space positioning technique and protocol in this study are scientific and beneficial in detecting snails in river beaches. Specifically, they increase the accuracy and reproducibility of discovering snail spots, decrease the cost of snail control, and establish an effective sharing and dynamic monitoring platform.

**Keywords:** GPS; *Oncomelania* snails; field Survey; Schistosomiasis; Monitoring

## Poster 57

### Modelling of habitat suitability for mosquitoes breeding sites in Eastern Spain

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Mosquitoes are insects of high interest for public health due to their impact as potential vectors of several major diseases like malaria, West Nile, dengue, zika, chikungunya or yellow fever. There is a big consensus in the scientific community that the ongoing climate change will change distribution, behavior and phenology of these vectors in the next years. The identification of environmental variables that modulate the occurrence of mosquitoes is important to establish the risk areas of likely disease transmission, and consequently implement preventive surveillance and control programs. We employed the data collected during a comprehensive study of mosquitoes breeding sites that was carried out in the Valencian Community between 2005-2008 as a basis of our study.

In these surveys a total of 28 species of mosquitoes were recorded and several physical, chemical and environmental variables of these aquatic breeding sites were registered and analyzed. Hence, it is essential to understand the high complex interactions between environmental variables and the occurrence of mosquitoes. The random forest (RF) approach, a robust non-parametric ensemble learning technique, can predict multisource data with non-linear response variable. Concretely, RF is an improved Classification and Regression Tree, and allow to study the variable importance as a measure of the potentially influential parameters through the percent increase of the mean squared error. The principal aim of this study was to create predictive mosquito occurrence maps generated using the selected variables based on the RF algorithm. Another goal was to study, generally, the variable importance independently of potential spatial availability. The principal environmental variables used were temperature, rainfall, altitude, several physical, chemical parameters, terrain slope and orientation, ocean distance, latitude, longitude, topographic ruggedness and the normalized difference vegetation index (NDVI). The topographic ruggedness, the average elevation change, was identified as the most influential predictor variable due to the close relationship to the local microclimatic conditions in the mountainous areas.

**Keywords:** Mosquitoes, Vector-borne diseases, modelling, randomForest, environment

## Poster 58

### Operationalising the 20-minute neighbourhood

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**Background:** The 20-minute neighbourhood (20-MN) concept suggests neighbourhoods should contain services and places that support the everyday, non-work-related, activities within a 20-minute walk, cycle, or public transport trip from home. Whilst the concept of a 20-MN is now firmly embedded into many Melbourne planning documents, it has not been formally operationalised. The aim of this study is operationalise a working definition of a 20-MN which will be directly translatable to urban planners.

**Methods:** The concept of what constitutes a 20-MN has changed across the various iterations of the major planning strategy for Melbourne: "Plan Melbourne". The latest iteration, will be prioritised in the process of operationalising this measure, however our definition will also be informed by earlier versions of Plan Melbourne.

**Results:** Numerous data sources have been obtained to allow us to determine the location of services and places that make up a 20-MN. Indicators of quality are also being investigated to assess whether these can form part of the definition.

**Conclusions:** The operationalisation of a working definition shifts the 20-MN from a concept in planning documents to something that can be measured and assessed. Our measure will be utilised in future studies assessing the health benefits of a 20-MN.

## Poster 59

### **A rural/urban comparison of privacy and confidentiality concerns associated with providing sensitive location information in epidemiologic research involving persons who use drugs**

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**Background:** Analyses that link contextual factors with individual-level data can enhance our understanding of the “risk environment”; however, the accuracy of information provided by participants about locations where illegal and/or stigmatized behaviors occur may be influenced by privacy and confidentiality concerns which may vary by setting and/or data collection approach.

**Methods:** Thirty-five persons who use drugs were recruited from a rural Appalachian town and a Mid-Atlantic city to participate in in-depth interviews. Thematic analyses identified and compared privacy and confidentiality concerns associated with two survey methods that (1) collect self-reported addresses/cross-streets and (2) use an interactive web-based map to find/confirm locations (i.e., where participants live/sleep and use/purchase drugs) in rural and urban settings.

**Results:** Concerns differed more by setting than between methods. Rural participants valued interviewer rapport and protections provided by the Certificate of Confidentiality more, locations considered to be sensitive differed in rural (i.e., others' homes) and urban (i.e., where drugs were used) settings, and urban participants were more likely to view providing cross-streets as an acceptable alternative to providing exact addresses for sensitive locations and to prefer the web-based map approach.

**Conclusion:** Rural-urban differences in privacy and confidentiality concerns reflect contextual differences (i.e., where drugs are used/purchased, population density, and prior drug-related arrests). Strategies to alleviate these concerns include: (1) obtaining a Certificate of Confidentiality, (2) collecting geographic data at the scale necessary for proposed analyses, and (3) permitting participants to provide intersections or landmarks in close proximity to actual locations rather than exact addresses or to skip questions where providing an intersection or landmark would not obfuscate the actual address.

## Poster 60

### Dengue spatial dynamics in the Federal District-Brazil between 2007 and 2014

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Dengue fever is a viral disease transmitted by *Aedes aegypti* mosquito, whose incidence has been continuously increasing in Brazil. The Federal District (DF) is located in a region that until the early 1990s was considered a dengue-free area especially due to its altitude above 1,000m and its climate with a well-marked dry season. Though, already in the early 2000s DF had its first outbreak and after that the yearly number of cases has become increasingly bigger. Due to its polynucleated urban structure, analyzing dengue spatial dynamics in DF has been a challenge. DF is a Federation Unity with a single municipality (Brasília) and an administrative organization without formal neighborhoods and standard addresses. In this context, spatialization, disaggregation, and cross-referencing of spatial data are quite complex. In order to have a better detailing of the dengue spatialization, an important work was done delimiting urban and rural health center's coverage areas, which is used as a proxy of neighborhood boundary by DF Health Department. For this purpose, GoogleEarth and WikiMapia database were used.

Thus, it was possible to spatialize dengue cases available in the Information System of Notifiable Diseases (SINAN) in 110 areas and to analyze the relationship between dengue and socio-spatial inequalities through spatial analysis and socio-environmental indicators. The methodologies adopted were construction of maps of the number of cases and incidence rates, geostatistical analysis of Global and Local Moran's Indexes and construction of social and environmental indicators' thematic maps. The results pointed out that there is a recurrence of the areas with the highest number of cases and higher rates throughout the studied period and that there are high incidence rates also in rural areas. Results from the Global Moran's Index have shown that in the epidemic years (2010, 2013 and 2014) dengue incidence rates have a clustered pattern. In the other years, there is no spatial autocorrelation and the distribution is random. The results of the Local Moran's Index allowed the identification of significant clustered areas. Crossing these results with socioenvironmental indicators' maps, it was possible to verify that in the urban areas the indicators most related to dengue were low average income associated with a high number of people per household. In rural areas, the most related indicators were the percentage of households with no water supply. Using hypsometry, it was also possible to identify potential geographical barriers to disease's containment. It can be concluded that, in the DF, dengue is unevenly distributed, reaching more areas with lower income and less access to urban infrastructure.

## Posters Abstracts Poster Session 3

### Poster 61

#### From Theory to Practice: Integrating Spatial Statistics with Epidemiologic Methods to Advance the Study of Population Health

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Although the field of spatial epidemiology has evolved rapidly in the past two decades, the gap between theory and practice remains wide. In this presentation we will review methodological developments in spatial statistical science and epidemiological theory, and identify opportunities both to improve the utilization of advances in spatial statistics in epidemiologic studies on the one hand, and on the other hand to focus the attention of spatial statisticians on issues that address methodological concerns in epidemiologic research.

This presentation will build on our recent review of advances in spatial epidemiology and GIS (Kirby, Delmelle and Eberth, 2017), highlighting technical developments and opportunities to apply spatial analytic methods in epidemiologic research, focusing on methodologies involving geocoding, distance estimation, residential mobility, record linkage and data integration, spatial and spatio-temporal clustering, small area estimation, and Bayesian applications to disease mapping. It is our hope that through multidisciplinary collaboration, the lag between theory and practice in spatial epidemiology can narrow, enhancing the future work of spatial statisticians and population health scientists alike.

## Poster 62

### Spatially-dependent variable selection modeling for space-time health data

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In space-time epidemiological modeling, most studies have considered the overall variation of space and time in relative risk in order to better estimate the effects of risk factors on health outcomes. However, the association between risk factors and health outcomes may vary with space and time. The temporal patterns of the covariate effects may depend on space. Thus, we propose a spatially-dependent variable selection approach for space-time health data in order to capture the spatially-varying subsets of regression coefficients. A flexible Bayesian hierarchical modeling is applied to account for the complicated spatio-temporal dependency structures in variable selection approach. We provide a simulation study to investigate the performance of the proposed models, comparing to the competing models. A real data analysis is also conducted.

## Poster 63

### Development of Mosquito Activity Prediction System

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Mosquitoes are a public health concern because they are vectors of pathogen, which cause human-related diseases. Recent climate and environmental changes have resulted in increased frequency of contact with mosquitos and humans. It is well known that the occurrence of mosquitoes is highly influenced by meteorological conditions such as temperature, humidity, precipitation and urban land features such as artificial cover, natural grassland.

Mosquito activity prediction models have become simpler, it remains difficult to control many parameters and understand the knowledge. Therefore, it is necessary to develop a lighter prediction model, such as an empirical approach, for predicting mosquito. In this study, we developed a system for predicting the mosquito activity index based on the empirical model considering cumulated meteorological variables and 16 types of urban land features.

The empirical prediction model used the machine learning such as random forest method and the sliding window algorithm was applied to predict the mosquito activity index of the next day considering the mosquito activity of the last 30 days.

Random Forest model were applied to estimate mosquito index in 2-year observations in Seoul. As a result of comparing with observation data, accuracy of mosquito activity prediction was about 80 percentage. It has a plan to calculated the daily disease risk index and provide it to the citizens.

## Poster 64

### Multivariate spatiotemporal modeling with applications to stroke mortality and data privacy

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Geographic patterns in stroke mortality have been studied as far back as the 1960s, when a region of the southeastern United States became known as the “stroke belt” due to its unusually high rates. While stroke mortality rates are known to increase exponentially with age, an investigation of spatiotemporal trends by age group at the county-level is daunting due to the preponderance of small population sizes and/or few stroke events by age group. Our goal here is two-pronged: (1) to conduct a thorough surveillance of spatiotemporal trends in age group-specific stroke mortality rates for those aged 65+ and (2) to explore how these surveillance efforts could be used by data stewards to disseminate high-quality synthetic data for public use.

To conduct the surveillance of stroke mortality rates, we harness the power of a nonseparable multivariate space-time model which borrows strength across space, time, and age group to obtain reliable estimates of annual county-level mortality rates from US counties between 1973 and 2013. In particular, we find that rates of decline among those aged 65-74 throughout Texas and Oklahoma have been much slower than average, providing

evidence that the recent geographic “shift” in the stroke belt may be primarily driven by younger age brackets. Furthermore, unlike the vast majority of the nation, rates of decline among those aged 75-84 in much of the Deep South failed to significantly exceed the rates of decline among those aged 85 and older, indicating that the excess burden of stroke mortality in this region may yet worsen.

Following these disease surveillance efforts, we outline how the results of this model fit can be used to generate high-quality synthetic data for public use that preserve data confidentiality without sacrificing data utility. More specifically, we propose replacing small counts (which are often suppressed in public-use data) with draws from the posterior predictive distribution from our model fit. Because our model accounts for multivariate spatiotemporal dependencies, the resulting synthetic data also possess this same dependence structure, thereby increasing the utility of the synthetic data over more conventional approaches. Furthermore, the nature of our model yields synthetic data with known theoretical bounds on the risk of disclosure; these bounds can be adjusted to comply with agency-specific standards for data confidentiality as needed.

## Poster 65

### Bayesian spatio-temporal estimation of dengue fever: when areas are few

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**Introduction:** Spatio-temporal modelling when there are few (<20) small areas can be challenging. Bayesian methods can be beneficial in this situation due to the ease of specifying structure and additional information through priors. However, care is needed as there are often fewer neighbours and more edges, which may influence results.

Dengue fever is still a serious health problem in several countries including Indonesia. Makassar, Indonesia had 6882 new cases of dengue registered from 2002 to 2015, and there have been fluctuations over time. Previous Bayesian spatio-temporal modelling approaches for dengue fever when there were few areas included incorporating a linear temporal trend component (Mukhsar et al. 2016). Here we investigate Bayesian spatial and spatio-temporal model specification when there are few areas.

**Methods:** Annual dengue fever incidence data for Makassar, Indonesia (14 geographic areas) during 2002-2015 were obtained from the Ministry of Health of Sulawesi Selatan Province.

A range of Bayesian model specifications were considered, including the following (all with a Poisson likelihood):

- 01 No spatial component, only an unstructured (iid) random effect.

02 Spatial component (e.g. BYM (Besag, York & Mollié) model with spatial intrinsic conditional autoregressive (CAR) and iid random effects).

03 Spatio-temporal component (e.g. linear temporal trend (Bernardinelli et al., 1995), also a nonparametric dynamic trend (Knorr-Held, 2000)).

Models were run using R-INLA and compared using goodness-of-fit measures, such as Deviance Information Criterion (DIC) and Conditional Predictive Ordinate (CPO), as well as comparing the obtained estimates and their precision for each area.

**Results:** Using adjacent boundaries to define neighbours, the maximum number of neighbours was 6 and the minimum number was 1. The median annual number of cases observed in a district was 16 (range: 0 - 419). Across all models, the highest relative risk (RR) was observed in Rappocini in 2002 and the estimate ranged from 2.12 to 7.07 between models. The lowest DIC and -mean (log (CPO)) was seen for the nonparametric dynamic trend spatio-temporal model. The RR in each area and year from the dynamic model had wider 95% CIs than the linear time trend spatio-temporal model.

**Conclusion:** Model choice had a large impact on results, and the nonparametric dynamic trend spatio-temporal model had much better fit than other options. To ensure results are valid and reliable, careful exploration of a range of models is important, especially when there are few areas.

## Poster 66

### Crime Spatio-Temporal Modelling

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In 1996 the World Health Organization adopted Resolution WHA49.25 – Preventing violence: a public health priority, and declared “violence a leading worldwide public health problem”. With this resolution it was intended to call attention to the serious consequences of violence for individuals, families, communities and countries, and highlight the damaging effects of violence on public health.

The public health approach is science-based and multidisciplinary and complements criminal justice and human rights responses to violence.

In this perspective the study of the evolution of crime, whether in a temporal level or in a space level, presents a great importance in defining measures to improve the welfare of the population thus contributing to the public health approach to violence prevention.

Usually, to analyze the evolution of crime in a given region, it resorts to compare rates of several years. This work aims to extend this analysis and use spatial and temporal models that allow to characterize the trend of crime in the spatial level and in the temporal level. In other words, it intends to understand if over the years and across regions there have been changes in crime patterns. Also it aims to study the influence of population characteristics through some related covariates. To achieve these aims, hierarchical Bayesian models are used and to implement these models INLA methodology (“Integrated Nested Laplace

Approximations”) is used through the package R-INLA. These models are applied to data crime observed in the municipalities of the mainland Portugal, from 2011 to 2015.

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## Poster 67

### Study of the influence of climatic variables on the number of dengue cases and severe respiratory tract infections in Brazil in 2010

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This work study refers to the study of the climate and raises all the conventional climatic seasons existing in the Brazilian territory. We collected information on the variables of humidity, temperature, insolation, precipitation, cloudiness, evaporation and altimetry, and hospitalization data and results of patients registered by the Unified Health System (DATASUS portal,) for the year 2010, in order to identify Spatial relationship between the number of hospitalized patients with dengue and serious respiratory diseases and also the cases of deaths caused by these diseases and theses climatic clusters variables considering the annual study, semiannually and quarterly. We used the Beta-Scan model (Lima et al., 2015) to identify areas with spatial clusters related to humidity in the presence of covariates insolation, precipitation, minimum and maximum temperature, evaporation and cloudiness. In addition, since the stations are georeferenced points in all states of Brazil, for this, we use the Kriging method (Vieira, 2000) to predict the temperature and humidity scales continuously in space using the sampling points of the conventional climatic seasons and the Geoda software (Anselin, 2006) to perform spatial cluster analysis and to compare with the results obtained by the Beta-Scan method ,

which is a method of searching for clusters based on the Beta models (Ferrari and Cribari\_Neto, 2004) and statistical Scan (Kulldorff and Nagarwalla, 1995). There are many situations in which the interest variable is continuous and limited in the interval  $[0,1]$ , for these cases, the Beta-Scan model fits it is appropriately. The maps produced by the Beta -Scan statistic is presented below and shows the division into two clusters referring to the annual humidity of the year 2010 in Brazil. The parameters and other maps will be presented later



**Figure 1:** Distribution of annual average moisture rates in Brazil climatic seasons in 2010.

The dots in blue indicate the seasons with the highest average annual humidity the left and low at right, however, these same data analyzed per semester show another subdivision, but in both there is great spatial influence in the rates of diseases, hospitalizations and death mainly in children whit dengue and mainly respiratory causes

## Poster 68

### Spatial-temporal analysis of forest fires effects on hospitalizations for respiratory disease (2001-2010)

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**Introduction:** A notable increase in the prevalence of fires has been noticed in the last decades in our country, thereby increasing a wide range of organic fuels, which level of toxicity of particulate can lead to serious health problems. The short-term exposures to fine particulate generated from the fires have been associated with increased mortality and morbidity. Our aim is to identify the effects of forest fire (FF) on the spatial-temporal distribution of hospitalizations for respiratory disease in Portugal (2001-2010).

**Methods:** From the National Hospital Discharge Register we selected admissions of patients  $\geq 65$  years-old, with diagnosis of respiratory disease (codes ICD-10 460-66, 480-87, 491, 492, 493 e 496). Data from FF were obtained from the national Institute for Conservation of Nature and Forests (ICNF) and data from meteorological stations were obtained from national institute of meteorology (IPMAR). A spatio-temporal generalized Poisson additive model was used to estimate the relative risk (RR) of respiratory disease associated with variation of FF adjusting for mean temperature and relative humidity. Space and time covariates were used to control for differences that may arise due to weekly, year and space pattern. A stepwise procedure was used to select the final model based on the smallest Akaike Information Criterion (AIC). Models without and with FF were assessed.

**Results:** We selected 219 166 episodes (52% in men). During hospital admissions, we found higher mean age in women than in men (77.738.4 vs 76.137.2 years;  $p < 0.001$ ). Model with better performance (lowest AIC) was the one with FF adjusted for climate variables. Forest fire increase the risk of hospitalizations for respiratory disease in both sexes (women: RR 1.02 (1.01-1.03) and men: RR 1.03 (1.02-1.04)). There was a significant spatial effect ( $p < 0.001$ ) in the distribution of hospitalizations for respiratory disease, however no significant difference in space was observed when taking into account the forest fire.

**Conclusion:** Forest fire explains some of the hospitalizations for respiratory disease. Including the forest fire variable, no significant difference was observed in space, showing that forest fire did not explain the spatial distribution of hospitalization for respiratory disease.

## Poster 69

### Relationship between Respiratory Diseases like Asthma with PM2.5 Spatial Concentration data estimated with Landsat 8 satellite images in Quito, Ecuador

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Quito, Ecuador is a high-altitude region between 2800 meters over sea level, with a high cloud conditions and closeness to equatorial line, with a great variability in its weather; since sun in the morning to rain in the afternoon; with a high increase in some traffic and industry regions that can be considered the principal sources to produce PM2.5 (Secretaria del Ambiente de Quito, 2014) like big capital cities.

PM10 and PM2.5 are considered a problem in the air pollution, where some of the problems considered are respiratory diseases like Asthma, PM2.5 has been associated with adverse human health impacts such as asthma symptoms, missed school days, hospitalization and the frequency of asthma episodes (Fan, Li, Fan, Bai, & Yang, 2016).

Asthma is a chronic disease characterized by recurrent attacks of breathlessness and wheezing, which vary in severity and frequency from person to person. According to WHO estimates, 235 million people suffer from asthma. Asthma is the most common chronic disease among children (WHO, 2007).

The Landsat Program has provided over 40 years of calibrated high spatial resolution data of the Earth's surface to a broad and varied user community. Landsat-8 Operational Land Imager (OLI) is the latest in a continuous series of land remote sensing satellites that began in 1972. It was launched into space in February of 2013 providing data allow agricultural, forestry, geology, land use, air contamination and other uses (Department of the Interior U.S. Geological Survey, 2016).

Some works let estimate from Landsat 8 PM<sub>2.5</sub> and PM<sub>10</sub> in an urban area considering field data (Gupta et al., 2006; Han, Tong, Bai, Chen, & City, 2013; Weng, Xu, Hu, & Liu, 2013)

In this work, the data collection was conducted based on Landsat 8 imagery from years 2012, 2013 and 2014 in different dates to obtain an estimation in PM<sub>2.5</sub> with the field data obtained from Quito Environmental Secretary with equation 1.

$$PM_{2.5} = e^{\beta_0} * AOT^{\beta_{AOT}} * ALT^{\beta_{ALT}} * LST^{\beta_{LST}} \quad (1)$$

Where, the PM<sub>2.5</sub> data were collected from ground-based measurement, which are PM<sub>2.5</sub> concentration 24-hour average when the satellite overpasses. The predictor variables are as follows: the AOT are retrieved from Landsat 8 data, LST is land surface temperature (LST) retrieved from the thermal infrared band data (band10) of the Landsat 8 data using Image-based



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## Poster 70

**Analysis on the direction of play activities in the Coexistence Centers of the Municipalities of CISAMUSEP, aiming at the quality of life of the elderly. 2014.**

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The evidence shows that the world's society, each day, has an older population, a fact also found in Brazil. Individuals over 60 are part of the context of all cities and many of them participate in programs directly assigned to them in their municipalities. In these places, ludic activities, when well targeted, contribute to the quality of life of the elderly. In this perspective, this study seeks to respond to the challenges posed by the phenomenon of aging, a fact that has significant impacts on the various dimensions of the development and functioning of society. The objective is to analyze the direction of play activities in the Elderly Living Centers belonging to the Municipalities of CISAMUSEP and the possible referrals to be suggested, since it is not intended to direct activities that are not within reach of the actual social situations, physical space and Human and material resources.

This is a descriptive study carried out with a sample composed of 200 elderly people and 10 coordinators from 10 municipalities, who answered two questionnaires composed of open, closed and mixed questions in order to know the reality of the activities offered in the researched places. Data were analyzed through qualitative statistics, frequency and percentage. It is concluded that the activities, when well targeted according to the cultural, financial and religious reality of each municipality, contribute to the good development of the collective health of the elderly in the psychological, motor and socialization aspects, as well as, this will have repercussions on a smaller number of elderly people in queues to be attended at the health posts of the municipalities.

**Keywords:** CISAMUSEP; Center of Coexistence; Play activities; quality of life.

## Poster 71

### Evaluation of the technique of population estimate people in pixel and your potentiality in the studies of Dengue in the Federal District-Brazil

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The population estimates by geospatial data have been studied since the 1930s. The challenge that this development methods is to obtain population numbers in the inter census years, especially in the detail scales, where the census data do not have degree of detail enough to meet them. In health studies, is essential obtain spatialized population data on the detailed scale to understand the dynamics, density and location of the population, because this information's is important to analyzed the transmission and dispersion processes of the diseases and in calculating the incidence rate which are of highest importance for the definition of control strategies diseases.

Considering that dengue is one disease that have the most grown in Brazil, it's important adopt techniques that allow estimating the population, especially in detailed scale and in inter population census years. Due to the characteristics geophysiques (climate and altitude) until the years 1990 the Federal District (DF) is considered unlikely for Dengue, but in 2016 registered almost 20,000 cases. Besides, the population in this same period increased from 1 million and 600,000 to more than 3 million of

people. It is considered one of the highest growth rates in the country.

Several techniques the population estimates have been developed mainly with the advent of orbital satellites, seeking relate the occurrence and density levels of urban occupation with the quantitative of population. One of them is *People in pixel* of Cruz *et al.* (2007). Which consists of estimating the number of inhabitants for each urban area pixel in a satellite image, by disaggregating the population of the census tracts into the smallest area unit of an image. The proposed model, based on the dasimetric method, is given by:  $Hab / pix_{ij} = (totpop * weight) / \sum (weight * totpix)$ , where:  $i$  = occupancy class;  $J$  = sampling unit; Tot\_pop = population total of sample unit  $j$ ; Weight = weight relative to class  $i$ ; Pixel = number of pixels belonging to a given class  $i$  in a sample unit  $j$ . Among the advantages of the model is the estimation in different times and scales.

In this context, our objective is applying the *People in pixel* technique to estimate the population of the DF in the period from 2007 to 2014 and calculate the incidence of dengue in the level of the health care areas. To verifying, the degree of accurate, we will compare with the official data of population and evaluate if the technique constitutes an alternative to the traditional methods used in the dengue incidence studies. Let us use the mean square error (RMSE) and the correlation coefficient to calculate the precision. The first results in the test area, the Administrative Region of Ceilândia in 2010, showed a high correlation coefficient between the estimated and official population ( $R^2 = 0.93$ ) and RMSE for the test area was 3.33%. Indicating a good correlation of the real and estimated populations if we compare with other studies of the same nature.

## Poster 72

### Teeth aesthetic improvement using a Bayesian spatial joint analysis for independent regular lattices

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An important feature in dentistry is teeth brightness [1]. During the intervention the doctor has to apply a resin and then a polishing to achieve the final result, i.e, the highest gloss (brightness) and the lowest roughness possible. The smaller the roughness the greater the gloss. The aim of this study was to evaluate the effect of 4 polishing protocols in teeth surface roughness and gloss when considering 2 different resins.

Twenty discs of a nanofilled resin (Filtek Supreme XT) and 20 of a nanohybrid resin (Brilliant Everglow) were prepared as a surrogate for teeth surface. Sets of 5 discs were randomly assigned to each resin\*polishing group. We end up with  $N=40$  discs and 8 groups,  $\{g_1, \dots, g_8\}$ . Analysis of surface roughness was performed using an Atomic Force Microscope (AFM). A 4x4 regular lattice per disc was considered. 16 roughness measurements were obtained. The dimensions of each of the 16 squares were 10Qmx10Qm. A unique gloss measure per disc was evaluated using an appropriate meter with incidence at 60°.

Assuming independence of the discs the statistical model for the spatially correlated roughness measures within each lattice considers disc-specific random effects and spatially varying intercepts for different groups. The group spatial dependence is introduced through a CAR prior [2], which smooths the spatially correlated random-effects toward its neighbours. Neighbourhood is defined via an adjacency matrix. The model to analyse the observed gloss for each disk considers the impact of the disk-specific random-effects and the spatial variance of the roughness into the gloss, i.e., the model shares some parameters with the roughness model which allows us to interpret how the heterogeneity and the variability of the surface roughness impacts the tooth gloss.

The statistical model developed behaves quite well, indicating the best combination resin\*polishing, and is an alternative to the “traditional” two-way ANOVA used in dentistry journals.

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## Poster 73

### Spatial Modeling of Life Expectancy (LE) in Virginia using Geographically Weighted Regression (GWR) and Bayesian Geographically Weighted Regression (BGWR)

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For the past 20 years, the average LE in the United States has been increasing while aged populations also have been rapidly increasing. Although medical advancement have been contributing to an improvement in life expectancy, some studies indicated that the gap in LE between the rich and poor has been increasing recently. To better understand the associations between explanatory factors and LE at a local level, first the GWR model will explore the effects of the local explanatory factors on LE at the census tract level, and in return show that GWR models can be used to geographically differentiate the associations between LE and its explanatory variables. However, to provide a more robust approach, BGWR will also be conducted. The objective of this study is to compare two local spatial regression models, GWR and BGWR, and assess whether there is an improvement in the context of inference power.

In this study, census tract was the spatial unit and there were a total of 1853 census tracts within the state of Virginia. The LE at birth values was estimated based on the population and number of deaths from the U.S. Census Bureau for the period of 2009-2013. As for the explanatory variables, all of the information was estimated at the census tract level. LE of each census tract will be used as the dependent variable and explanatory variables or covariates will be healthcare access index, transportation cost, housing cost, median household income, cancer risk index,

respiratory risk index, average years of education, population churning index, food desert index, Gini coefficient, number of unemployed, segregation index, and walkability index.

As for developing local spatial regression models, a global model is usually adopted to assess the association between a dependent variable (i.e., outcome of interest) and explanatory variables that is based on the assumption that this association of spatial process is stationary. GWR model incorporates spatial heterogeneity, which includes only the nearby areal units (i.e., census tracts) in the local regression. And all of the census tracts will be given a weight based on its spatial distance to the corresponding census tract. And an exponential distance-decay function will be used to generate the weight matrix, where greater values of weights are assigned for observations nearer to the prediction area.

However, based on some spatial modeling literatures, GWR has its weaknesses and one of them is the susceptibility to outliers or aberrant observations. Thus, BGWR will be conducted to address this issue by down-weighting any outliers or aberrant observations, and ultimately smoothing them with the corresponding neighboring values. The Gibbs sampling method will be used to estimate BGWR, which is based on the Markov-Chain Monte-Carlo (MCMC) simulations.

Rather than using the conventional Ordinary Least Squares (OLS) regression, which computes a single regression output and summarizes the global relationship between the predictors and dependent variable, GWR and BGWR can identify spatial variation of the relationships in a model. In addition, GWR can generate maps to assess any spatial non-stationarity. The results of this study will provide explanations and insights for which specific areas need to be targeted for interventions in the context of explanatory factors so that improvements can be made in specific field, and ultimately enhance LE outcome.

## Poster 74

### Spatial Clustering Detection Of Human Development Index Of The State Of Minas Gerais – Brazil Through Beta-Scan Model (1991-2010)

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In this paper, methods for detecting spatial clusters that can incorporate information about a cluster location, such as the BetaScan model. We used data from the Human Development Index (HDI) in the state of Minas Gerais (BRA) from 1991 to 2010 and our goal was to verify a Beta\_ Scan methodology would be able to capture how changes in the configuration of cities as indicators. The study of hot spots and spatial clusters has been increasing. Among them, it stands out Scan-Space method (Kulldorff and Nagarwalla, 1995) and BetaScan (Lima et al., 2015) which was used in this paper. However, there are many situations in which the interest variable is continuous and limited in the interval [0,1].

We used the Scan Beta model proposed by Lima et al. (2005), which is based on the computed beta model (Ferrari and Cribari-Neto, 2004) to discuss the parameters of this model in the detection of spatial clusters using data from the Human Development Index (HDI) of the 853 cities of the State of Minas Gerais From 1991 to 2010. The results, in the year of 1991, showed that the more developed regions of the state formed a large cluster with 218 cities. However, in 2000, it was reduced to 47 cities within this same area of the 1991 cluster and in 2010 no clusters were formed. This result indicates that there may have been an increase in the quality of life and improved income distribution from the years 1991 to 2010. Therefore, we can conclude by means of the Beta-Scan method, that there has been general growth in municipal HDI index in the State of Minas Gerais over the last 20 years.

## Poster 75

### Modelling zero inflated biomass from fisheries in the Lower Amazon River

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Fishing, one of the most ancient human economic activities, has enormous significance in people lives because Fishing, one of the most ancient human economic activities, has enormous significance in many countries because seafood is an important staple in some people's diet. For this reason there is growing public concern about conservation of fishing resources. Government organizations and international committees seek to establish policies for the sustainable exploitation of fishing resources with a view to ensure the long-term viability of this economic sector and guarantee food production for future generations. Quantitative models, which allow us to make the best possible predictions based on the available data, are required for a formal and detailed stock assessment. Usually, catch and fishing effort data generated by commercial fisheries are the most common data available for stock assessment, apart from covariates related to the vessels and the fishing environment. Moreover, statistical modelling allows us to understand the variation in catches associated with variations in effort and environmental covariates. This study has been motivated by the difficulty facing researchers in applying conventional statistical models to analyse data for catch per unit of effort, from fisheries in the Lower Amazon River. Data fishery information is collated for each fishing trip. Namely, the coordinates of latitude and longitude indicating locations around which the fishing activity took place. In general, the total

catches are aggregated by species, month and location, which can lead to the occurrence of the zero inflation phenomenon in the observation of these totals. The zeros may occur for two reasons: i) because the locations are not visited by any vessel in that month, ii) There is more than one visit in those locations, but for all of the visits there is no success in catching a particular species. Moreover, the catches may be spatially correlated. In this study we aimed to develop a statistical model that was able to accommodate the zero inflation on catches allowing a better understanding of variations of catch in weight related to variations in effort and other covariates available. The data employed in this study was obtained from the fishing industry on the Lower Amazon River, where the catches were landed in Santarém-Brazil ports in 2004. This data set includes the number of fishing trips by location, the total weight caught by species, fishing effort and the fishing environment (river or floodplain lakes). In order to analyse this data, we developed a Bayesian three-stage hierarchical model, implemented in OpenBugs software. At the first stage we described the number of fishing trips per location ( $N$ ) according to a Poisson distribution, with the Poisson mean depending on the fishing environment. At the second stage, given  $N > 0$  we defined a Bernoulli variable  $X$  with probability  $q$  of success, where  $X$  assumes 1 if catches occurred for a particular species, and zero if naught is caught for that species. The logit of  $q$  was assumed to be dependent on the covariate 'fishing environment'. Eventually at the third stage we modelled the weight denoted by  $Y$ , which assumes zero when  $N=0$  or when  $X=0$  and  $N > 0$ . When  $X=1$  and  $N > 0$  we described  $Y$  according to a gamma distribution, where the mean was proportional to the number of visits  $N$ . This approach provided a useful tool to analyse the variation on catch per unit of effort as function of covariates when the data were inflated by zeros coming from both sources: abstinence of fishing activity and absence of catch in the presence of fishing activity.

**Keywords:** Zero-inflated data, fisheries, compound Poisson, Bayesian hierarchical modelling

## Poster 76

### Forecasting human health resources in Portugal

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Uneven supply and demand of the health workforce is a social concern and a worldwide longstanding problem. Understanding these imbalances is essential for policy-makers since human health resources are the largest contributors to the health expenditure. On the other hand, it largely contributes to the improvement of many health outcomes, such as equity access to health care services targeted by the United Nations Sustainable Development Goals in 2015. A lot of discussion has been devoted to this topic over the last forty years. . However, it remains nowadays a major concern in several countries, influencing them social and economically. On the social point of view, there are great differences in health outcomes, such as lower equity access and increasing waiting times, which might lead to a lower quality of health services. On the economic point of view, this situation may affect not only the productivity but the overall socio-economic development.

Among other countries, the planning of the health workforce in Portugal has been conducted in a reactive way lacking a prospective vision based on an integrated, comprehensive and valid analysis. This is even more critical given the expected shortage of the health workforce in the future. Furthermore, Portugal is facing an aging context of some professional classes (physicians and nurses), and it has one of the lowest nurse to physician ratio, 1.5, below the European Region and the OECD

averages (2.2 and 2.8, respectively). In this milieu, there is a need to develop a proper tool capable of forecasting the required Portuguese health workforce, by integrating all the different drivers affecting the healthcare needs' evolution, such as demography, citizens' illness profiles, technology, population's income and health public policies.

This study aims to embrace this issue, by proposing a Bayesian-based approach to estimate the required number of physicians and nurses in Portugal, by specialty and by quinquennium until 2040 (within the scope of a national funded project – Health 2040). The proposed methodology follows a socio-technical approach with the social component being characterized by meetings and workshops to gather experts' viewpoints (e.g. physicians, nurses and members of the Central Administration of the Health System) that will complement and enhance the available data, regarding the drivers of the healthcare needs' evolution.

The results of such methodology allow us to infer about the training needs of physicians and nurses, in the medium and long run, and the number of students that must be admitted into medicine and nursing training systems, each year and in each specialty. Besides that, these results can be used as a starting point to test the impact of different health public policies. Because this model considers the dependency of health care demand on population volume, age structure and per capita income, a regional distribution of health personnel may be estimated at NUTS III level.

**Keywords:** Bayesian estimation, Health economics, Health workforce planning, Spatial planning

## Poster 77

### A Bayesian spatial versus traditional approach to characterize areal socioeconomic deprivation: what is the impact on public health ecological studies?

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**Background:** Area-level socioeconomic deprivation is a well-established strong predictor of a wide range of health and social outcomes including mortality risk, asthma, substance overdose, and crime. In public health research, the traditional approach used in ecological analyses has been to use Principal Component Analysis (PCA) of the indicators and then aggregate the sum of the factor to the “area-level” variable, which can be ZIP-code, Census Tract, or some other administrative or geographic unit. There is substantial evidence now that spatial effects such as spatial autocorrelation can significantly bias our findings if not adequately modeled in regression analyses. However, while some studies adjust for or directly model spatial autocorrelation, few studies have used Spatial Factor Analysis (SFA) to create area-level measures. SFA is a technique that describes the correlation and variation of a set of observable and correlated indicators with a lower number of latent factors while simultaneously addresses the spatial autocorrelation within the indicators. Moreover, we do not fully understand the magnitude of bias on an outcome when a variable such as socioeconomic deprivation is created using SFA or PCA.

**Methods:** We used a Bayesian Spatial Poisson Model, including a spatial random effect ICAR, to examine the impact of socioeconomic deprivation created using SFA vs. PCA in association with alcohol-related police complaints across N=167 New York City (NYC) ZIP codes. Socioeconomic deprivation index included: % in poverty, % < high school diploma, % unemployed, median income, % of homes > \$300,000, from the American Community Survey 5-year estimates, 2009-2013. Alcohol-related complaints came from the NYC Open Data, 2010-2015.

**Results:** When characterized by quantiles, we found that SFA- and PCA-based socioeconomic deprivation produced different distributions in terms of which ZIP codes should be classified in the top quintile (20%). This discrepancy mainly locates in northern NYC as well as some ZIP codes in central NYC, and varies with different numbers of classification groups. Next, socioeconomic deprivation from SFA was significantly associated with higher alcohol-related complaints:  $\beta=0.365$ , 95% Credible Interval (CrI) [0.099, 0.638]. In contrast, socioeconomic deprivation from PCA was not significantly associated with the outcome:  $\beta=0.146$ , 95% CrI [-0.04, 0.334].

**Conclusions:** Our findings emphasize that in ecological studies it is paramount to utilize SFA when deriving indices such as socioeconomic deprivation at the area-level. If inappropriate methods are used, results can be misleading (especially when there is an effect), and can jeopardize resource allocation to respond to public health outcomes in areas with greater deprivation.

## Poster 78

### The effects of distance from major or minor road networks on prevalence of myositis and its major phenotypes in the United States

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**Importance:** Myositis comprises a group of rare, life-threatening, chronic systemic autoimmune disorders. Little is known about the impact of potential environmental exposures leading to these diseases.

**Objective:** Like other autoimmune diseases, there may be increased prevalence of myositis or its major phenotypes in association with exposure to pollution, as identified by residential distance to a major or minor roadway. This study assessed the effect of distance from residence at the time of myositis diagnosis to such roadways, and how the prevalence of myositis cases is associated with this distance after adjusting for other population characteristics.

**Design and Setting:** Retrospective cohort study of myositis cases extracted from a national myositis patient registry database. Only patients residing in the United States (US) and Canada at the time of diagnosis were eligible to enroll in the myositis patient registry.

**Participants:** Myositis cases diagnosed from 1985 to 2011 from the registry in contiguous US states, whose zip code at time of diagnosis matched the zip code of their address at the time of enrollment, were chosen for study.

**Exposure:** Distance from a major or minor roadway to residence where patients lived at the time of myositis diagnosis.

**Main Outcome and Measure(s):** The geocoded location of residential address where patients lived at the time of myositis diagnosis, in combination with census data, provides a means for assessing intensity of cases as a proxy for prevalence. Log Gaussian Cox Process (LGCP) statistical modeling was used with population density as an offset value for assessing the effect of distance to roads on myositis prevalence.

**Results and Conclusion:** There were trends of a higher risk of all myositis (n=1247), and the major phenotypes of polymyositis (n=358), dermatomyositis (n=484), inclusion body myositis (n=318), and those with lung disease (n=303) in those living within 50m of a major or minor road network relative to living beyond 200m (adjusted coefficient estimates of minimum distance from roadways were 0.39-0.94). However, none of these results reached statistical significance. More research is needed to understand the role of proximity to roadways as a surrogate for air pollution in the development of myositis and its phenotypes.

**Keywords:** Myositis; Major or minor road networks; Spatial point process models; Log-Gaussian Cox processes

## Poster 79

### Analysis of Space and Temporal Distribution of HIV between pregnant women in the State of Ceará, Northeast Brazil, 2007 - 2014

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Introduction: Continuous monitoring of HIV infection among pregnant women is an important indicator of infection in the sexually active female population, since it allows the early detection of changes in the epidemiological profile, as well as the planning of disease control actions. It is thus imperative to know the spatial and temporal distribution of HIV infection in this population. Objective: to describe the spatial and temporal distribution of HIV cases among pregnant women in Ceará between 2007 and 2014. Methods: ecological study with the spatial approach of confirmed cases of pregnant women with HIV, registered in the Notification of Injury Information System. The cartographic base of the state is the Brazilian Institute of Geography and Statistics; The characteristics of the municipalities were combined in order to configure the state's micro-regions of health as units of analysis. Data analysis was done through the Statistical Package for Social Sciences, version 20.0. The calculation of the Moran Global and Local Indices was performed in Geoda software. Results: 1,382 cases of pregnant

women with HIV were reported in the study period, with a mean age of 26.56 years (SD: 3 6.1). The race / brown color prevailed among the cases (n = 1,014, 73.4%), and schooling was concentrated in Elementary School II (n = 503, 36.4%). The coefficient of HIV detection in pregnant women increased from 1.15 / 100,000 live births to 1.54 / 100.00 live births, in a trend line with increasing linear adjustment ( $R^2 = 0.4421$ ). The Moran Global Index, after the Empirical Bayes correction, it presented a positive spatial association with statistical significance ( $I = 0.422941$ ;  $p = 0.01$ ). Moran Map and LisaMap showed clusters of high / high association ( $p = 0.01$ ) for the microregions of Fortaleza, Caucaia, Maracanaú and Cascavel, which compose part of the Metropolitan Region of Fortaleza and are naturally more populated regions, due to the proximity to the Tourism, higher concentration of jobs and greater supply of health services at different levels of attention. In the southern region of the state there is a predominance of clusters with low / low association ( $p = 0.05$ ), mentioned here: Tauá, Icó, Iguatu, Crato and Juazeiro do Norte. Conclusion: significant clusters were identified in the health microregions near Fortaleza, which makes this cluster a priority for health policies and actions aimed at prevention, early diagnosis and HIV control in this population.

**Descriptors:** pregnant women, space-time analysis, HIV, georeferencing

## Poster 80

### Spacial Analysis of Visceral Leishmaniosis in the State of Ceará, Northeast Brazil, 2007 to 2015

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**Introduction:** Human Visceral Leishmaniasis (LVH) is widely distributed throughout Brazil. Among the regions, the Northeast presents the highest number of cases. Thus, the importance of a study that identifies the patterns of distribution of Visceral Leishmaniasis in time and space is pointed out.

**Objective:** to know the spatial and temporal evolution of VL in the state of Ceará, Northeast Brazil, from 2007 to 2015.

**Methodology:** A descriptive study in the ecological modality, with a spatial approach, based on the confirmed cases of LVH recorded in the System database (SINAN) and cartographic base of the Brazilian Institute of Geography and Statistics (IBGE) with verification of the spatial correlation through the Global and Local Moran index in Geoda software. The municipality was designated as unit of analysis.

**Results:** There were 5,502 cases of the disease in the period, with a mean incidence of 3.91 cases / 100,000 inhabitants. There was positive and significant spatial autocorrelation (Moran Global Index = 0.135327;  $p = 0.01$ ), indicating the existence of neighboring municipalities with similar VL rates in the state of

Ceará. Lisa Map identified clusters of spatial dependence with significance of 95%, 99% and 99.9%. The Box-map showed a high-cluster type, with municipalities in the north and south of the state: Abaiara, Alcântaras, Barbalha, Barro, Coreaú, Crato, Forquilha, Juazeiro do Norte, Mauriti, Missão Velha and Mucambo, priorities for actions control and management of the disease. The Low-Low quadrant indicates municipalities, distributed in part in the central region of the state and in part near the capital Fortaleza and eastern region of the state: Umirim, Acoiara, Senador Pompeu, Alto Santo, Quixadá, Ibaretama, Aracati, Banabuiú, Morada Nova, Iracema, Pacajus, Guaiuba, Palmácia, Redenção, Baturité, and Capistrano. In the High-Low quadrant is the municipality of Barreira, near the capital Fortaleza, and in the Low-High quadrant are the municipalities of Groaíras, Cariré, Irauçuba, Miraíma, Massapê, Meruoca, Santana do Acaraú, Jardim and Altaneira, Near the northern region of the state and the Serra da Ibiapaba. Conclusions: the disease is widely distributed in the state with presence of high/high clusters in the North and South regions of the state; The municipality of Barreira concentrates around them a High/Low cluster. These municipalities need priority actions for prevention, early diagnosis and treatment of the disease.

**Keywords:** Visceral Leishmaniasis; Georeferencing; Space Analysis

## Poster 81

### Spatial Analysis Of Small Ruminant Brucellosis Occurrence In Trás-Os-Montes And Alto Douro (Portugal, 2010-2014)

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**Introduction:** Small ruminant brucellosis (SRB) is a zoonotic disease caused by *Brucella melitensis* responsible for economic losses from decreased productivity and lost trade in endemic regions. Although an ongoing national official disease control program is implemented, the efforts in eradicating the disease in Trás-os-Montes and Alto Douro, a region in Northeast of Portugal have not so far been successful, particularly in effectively eliminate new herds infection. Our aim is to analyse the spatial distribution of the prevalence and incidence at herd level of SRB and assess potential risk factors associated with the incidence using data of the control campaigns undertaken between 2010 and 2014.

**Methods:** From the Portuguese database PISA.net we selected all herds registered and enrolled in the special SRB eradication program in the regional administrative food and animal health services of Bragança, Chaves-Mirandela and Vila Real-Douro Sul, excluding the herds from the municipality of Mondim de Basto in Vila Real district due to lack of accessible information. A spatial regression model, using the Poisson distribution, was used to quantify the Relative Risk (RR) of SRB. Spatial autocorrelation of the prevalence and incidence of SRB at village level was assessed using Global Moran's I (GMI) and local clusters were identified using Local Moran's I (LMI) as a LISA.

**Results:** A spatial heterogeneity of the distribution of positive and infected herds was observed with clustering of villages of the study area. The incidence (new cases) of infected herds is widespread and there is not a cluster distribution pattern, except for 2013 (GMI=0.004, p-value=0.045), but prevalence was clustered during the five years. Furthermore, we found no significant association between clusters of high risk of prevalence and incident villages. The odds of brucellosis was significantly higher in large herd size ( $OR_{adj}$  1.006 and 95% CI 1.005-1.007) and lower through the years ( $OR_{adj}$  0.793 and 95% CI 0.729-0.863).

**Conclusion:** SRB herd prevalence varied significantly within villages in Trás-os-Montes and Alto Douro between 2010-2014. While annual herd prevalence is clustered in certain villages, annual herd incidence by villages seems to be randomly distributed across the region (the exception is 2013). These distinct patterns suggest difference in risk factors for the two measures. And may contribute to clarify the question whether the direct contact between flocks or the sharing of pastures play a determinant role in dissemination of the disease in the region. Additionally, the risk of infection was higher as herds increase in size and lowered as years pass by. This latter finding was expected, as a result of the eradication program applied in the region of study.

## Poster 82

### Using a Bayesian geostatistical model to understand local-scale heterogeneity of malaria risk: the example of Bunkpurugu-Yunyoo district in northern Ghana

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Bayesian methods have been used to generate country-level and global maps of malaria risk on a large geographical scale but these maps may lack the ability to identify smaller scale heterogeneity and thus may not be ideal for operational prevention and control of malaria. The aim of this research is to apply methods to high resolution malaria data to understand if we can better predict the micro-scale spatial heterogeneity. We will rely on existing malaria parasitemia survey from northern Ghana, consisting of 10,366 children from 438 GPS-located communities sampled between November 2010 and 2013 bi-annually. The Bayesian hierarchical model was chosen to account for individual and community level drivers whilst

accounting for both spatial correlation and random variation between communities. It also used both a Gibbs sampler and Metropolis Hastings algorithm. Prior to model runs, Gibbs variable selection was used to determine key variables selected based on availability of spatial information and were chosen to represent both environmental - such as elevation, temperature, NDVI, rainfall - and GIS-derived demographic factors such as distance to health facility, urban centres, roads and water bodies. Model selection revealed elevation, distance to urban centre and distance to health facilities to be important covariates. The geostatistical model showed that malaria prevalence varied between 19% and 90%, showing a north-east to south-west gradient of predicted risk with the highest prevalence rates found at lower elevation. The general distribution is heavily weighted between the two urban centres, showing lower risk in urban centres compared to rural areas, with some indication that a threshold distance to an urban centre exists for malaria risk. Model predictions revealed high variability in malaria prevalence in areas previously assumed to be homogenous, indicating important short-comings of country level spatial modelling from a programmatic perspective. These types of model can be useful for predicting on ground risk in similar regions for program planning.

## Poster 83

### Bayesian Logistic Regression Model for Down Syndrome Data in Kuwait

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In this paper we developed a series of Bayesian prediction algorithms using three different approaches, including logistic regression models, probit models and complementary log-log or cloglog models. These models were implemented from a Bayesian perspective using Gibbs sampling Markov Chain Monte Carlo (MCMC) methods available in the specialist software WinBUGS. The MCMC methods permit great flexibility in the specification of complex non-standard models and also facilitate the computation of model complexity and fit statistics for non-nested models.

Comparison was performed for the three models through an analysis of risk factors for Down Syndrome (DS), the most prominent genetic disease reported in Kuwait. The data consists of patients referred to Kuwait Medical Genetic Centre (KMGC) at Ministry of Health for the period (1979-2003) with different available covariates or factors.

We identified different possible risk factors. The covariates of interest were: ethnicity, sex, nationality, parental couple consanguinity, maternal age at child's birth, preconceptional history, gestational age, amniotic fluid, complications during pregnancy and age. The main purpose was to compare the three proposed models. The comparison was performed by applying the deviance information criteria (DIC), one of the most widely used model selection criteria in Bayesian inference.

**Keywords:** Bayesian methods; MCMC methods; Down Syndrome data; Logistic Regression; Probit model; Complementary log-log model; Deviance Information Criteria DIC.

## Poster 84

### Investigating the spillover effects on village-level malaria risk in Kalaburagi, Karnataka, India: a Bayesian spatial and spatio-temporal econometric approach

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Over the past few decades, the risk of malaria has been reduced dramatically worldwide. However, according to the latest WHO estimates, there were 212 million cases of malaria and 429000 deaths in 2015. Poor and developing countries/communities are affected most. As a vector-borne disease, effective prevention and control of malaria at the community/village level require an understanding of the complex interplay between the disease risk and various risk factors. For example, an effective vector control in a particular village can reduce the risk of malaria not only within that village but also in other (nearby) villages. In the spatial

econometric literature, the former effect is known as a direct effect whilst the latter is referred to as an indirect or “spillover” effect. Recognising such spillover effects has shown to play a crucial role in an effective implementation of malaria intervention (see, for example, Hawley et al. 2003). Using Bayesian spatial and spatio-temporal econometric models, this study seeks to examine the presence (or absence) of the spillover effects from a set of environmental and socio-economic risk factors on village-level malaria risk in Kalaburagi, India. This analysis also aims to quantify both the direct and spillover effects of these risk factors. Implications of the analysis results on the prevention and control of malaria at the community level will be discussed.

### Reference

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## Poster 85

### Spatial Autoregressive Models for Health Data with Application

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The article sought to highlight the importance of spatial analysis for health data; traditional regression methods require assumption of independence between observations, when the study is about diseases, for example, these assumptions are strong since they are not applicable in practice. Waldo Tobler (1979) says “Everything is related to everything else, but near things are more related than far things”. This law succinctly defines the statistical notion of (positive) spatial autocorrelation, in which pairs of observations taken nearby are more alike than those taken farther apart, which weakens the assumptions of independence. Spatial epidemiology and medical geography refer to a set of techniques that seek to relate the study of spatial patterns of disease incidence/mortality. Where people live can be of great importance in identifying patterns of disease. Spatial analyses in public health need not concern solely to geographical distributions of disease; the spatial distributions of the sociodemographic structure, occupational patterns, environmental exposures can provide insight into specific causes of the disease as mechanisms of transmission and identification of infectious agents (Waller & Gotway, 2004).

As an alternative to classical regression, two models able to capturing spatial dependence were considered: simultaneous autoregressive models (SAR) and conditional autoregressive models (CAR), which, through their spatial parameters, measure the present autocorrelation. The classic, SAR and CAR models were applied to dengue occurrence data in Rio Claro, located in the interior of the state of São Paulo-Brazil, in order to identify areas of higher incidence and to relate the disease to socioeconomic factors. The choice of the appropriate model, from the statistical point of view, is extremely important in the analysis; the most parsimonious model is sought. The selection criterion used in this analysis was the Akaike Information Criterion (AIC) and the Likelihood Logarithm (LIK). The classical linear regression model had AIC (1380.290) and LIK equal to (-684.145), SAR had AIC (1351.240) and LIK (-669.662), lastly the CAR had AIC (1352.800) and LIK equal to (-671.898).

The model that best fit the data was the SAR model, compared with the other two adjusted models, there was an increase in the LIK to -669.662; reduction in the values of AIC to 1351.240; the estimated spatial autoregressive coefficient  $\hat{\rho}$  was 0.43, a highly significant value ( $p < 0.0000001$ ); the likelihood ratio test, which compares the null hypothesis model (classic linear regression) with the alternative (SAR), resulted in the value 29.09 ( $p < 0.0000001$ ). The adjustments were obtained by GeoDA software. The models also contribute to the solution of random fluctuation, with smoothed maps, and in formulating hypotheses about the disease in relation to external factors. The generated maps are easy to interpret and can become useful tools for health planners.

## Poster 86

### Geostatistical inference in the presence of positional error: a composite-likelihood approach

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In almost any geostatistical analysis, one of the underlying, often implicit, modelling assumptions is that the spatial locations, where measurements are taken, are recorded without error. In this study we develop geostatistical inference when this assumption is not valid. This is often the case when, for example, individual address information is randomly altered to provide privacy protection or imprecisions are induced by geocoding processes and measurement devices. Our objective is to develop a method of inference based on the composite likelihood that overcomes the inherent computational limits of the full likelihood method as set out in Fanshawe and Diggle (2011). Through a simulation study, we then compare the performance of our proposed approach with an N-weighted least squares estimation procedure, based on a corrected version of the empirical variogram.

Our results indicate that the composite-likelihood approach outperforms the latter, leading to smaller mean-square-errors in the parameter estimates.

**Keywords:** composite likelihood, geomasking, geostatistics, positional error

**Reference**

- 01 Fanshawe, T. R. and Diggle, P. J. (2011). Spatial prediction in the presence of positional error. *Environmetrics*, 22(2):109-122.

## Poster 87

### Geostatistical Modelling of the Association between Malaria and Child Growth in Children 0-5 in Africa

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**Background:** Undernutrition among children under five years continues to be a public health challenge in many low- and middle-income countries (LMICs) and often leads to growth stunting. Infectious diseases, such as malaria, may also affect child growth. The association between malaria and stunting however remains unclear and has been a matter of debate, with previous studies showing significant positives, negatives, no associations and causality in both directions.

**Objectives:** We study the association between malaria and height-for-age z-scores (HAZ) using data from 20 Demographic and Health Surveys (DHS) conducted in 12 African countries. Our objective is to make inferences on the effect of malaria incidence during the first year of life on HAZ.

**Methods:** We develop a geostatistical model for HAZ as a function of both measured and unmeasured child-specific and spatial risk factors. Our study approach allows us to investigate differences in the Malaria-HAZ associations for the different surveys. We visualize stunting risk in each of the 20 analyzed

surveys by mapping the predictive probability that HAZ is below -2. Finally, we carry out a meta-analysis by modelling the estimated effects of malaria incidence on HAZ from each DHS as a linear regression on national development indicators from the World Bank.

**Results:** A non-spatial unadjusted linear regression of HAZ on malaria incidence showed a negative association in 18 out of 20 surveys. HAZ trajectories were non-linear in age and shown to depend on malaria exposure with, generally, children with lower malaria exposure showing better HAZ trajectories. However, after adjusting for spatial risk factors and controlling for confounding effects, we found a weaker association between HAZ and malaria, with a mix of positive and negative estimates, of which only 3 out of 20 are significantly different from zero at 5% level. The meta-analysis showed that such a variation in the estimated regression relationship between malaria incidence and HAZ is significantly associated with the amount of land under cereal production in the country and year of survey.

**Conclusion:** Our results indicate that confounding effects on the relationship between malaria and stunting vary both by country and over time. Among those, geo-political factors, such as those related to agriculture, might also play an important role. Our results further indicate that with better nutrition, malaria is less detrimental to linear growth.

#### **Paper Source**

Amoah B., Giorge E., Hayes D. J., van Buuren S., Diggle P. J., "Geostatistical Modelling of the Association between Malaria and Child Growth in Africa", *Unpublished article*.

## Poster 88

### Mathematical modelling of the West African Ebola virus epidemic

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The West African Ebola virus epidemic (2013–2016) was the most widespread outbreak in history—causing major loss of life in Guinea, Liberia, and Sierra Leone. The first cases were recorded in Guinea in December 2013; later, the disease spread to neighboring Liberia and Sierra Leone, with minor outbreaks occurring elsewhere.

We present a stochastic SEIHRD (Susceptible-Exposed-Infectious-Hospitalized-Recovered-Dead) compartment model of epidemiology to capture the spatial transmission dynamics of the Ebola epidemic. The model parameters were set based on the characteristics of Ebola and the road network of West Africa. The model is only able to blindly forecast the epidemic without any correction from real-world data and with no governmental or public health interventions to avoid transmission of Ebola. In historical fact, the effects of international, national, and local efforts to prevent Ebola began to be felt at about Day 200. This is where our model begins to diverge from the true history of Ebola.

“Data Assimilation” is a general class of techniques for tracking a state vector in time, using Bayesian updates applied to a dynamic model. Here we used a stochastic population-based model, but data assimilation can be applied to almost any type of model. The key is the Bayesian update, not the details of the model. Using registered Ebola disease incidence data from the World Health Organization (WHO) situation reports, we attempt to project the number of newly infected and death cases. We observe that the prediction improves as data is assimilated over time. The analysis thus provides a realization conditioned on all prior data and newly arrived WHO data. We compare simulated maps with real data map compiled by WHO.

## Poster 89

### Combining Extreme Learning Machines with Spatial Modeling to Improve Prediction of Disease Counts

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Feedforward Neural Networks (FNN) have shown to be efficient to find solution in problems with complex nonlinear mapping between the inputs and response, and also provide models for phenomena that are hard to be handle by parametric techniques. However, it is success and applicability it is well known that: (1) the traditional back propagation algorithm can stop in local minima providing undesired results; (2) the network can be over trained by the algorithm and (3) gradient based learning are computationally costly in most applications. To overcome these limitations extreme learning machines (ELM) were proposed as an much more efficient alternative to train single layer feed forward neural networks providing results as good as traditional FNN.

The application of machine intelligence in the medical and the biomedical areas is a new trend for large data applications. For example, most of the diagnosis techniques in medical field are systematized as intelligent data classification approaches. Recently, ELM have been used to solve problem in many medical situations as: predicting protein-protein interactions, epileptic EEG patterns recognition, EEG-based vigilance estimation, transmembrane beta-barrel chains detection , thyroid disease diagnosis and many others.

In this paper we combine the ELM framework with a spatial Bayesian modeling (SPELM) to improve disease count estimation when there is missing information. In order to do so, we implement the ELM using the INLA methodology and combine with the traditional spatial ICAR modeling. With INLA we keep the time efficiency of the ELM and takes advantage of Bayesian the framework to automatically performs a  $L^2$  penalization to the likelihood to improve generalization performance of the network.

The new methodology is applied to total count of people infected by Dengue fever in each municipality of the state of Rio de Janeiro in Brazil in the years of 2011 and 2012. Dengue fever is viral disease that become an important health issue in Brazil since it have already infected more than 50 million people in the country. Demographic information of each municipality is obtained by the 2010 Brazilian CENSUS and used as explanatory variables. A simulation study is performed to see the capability of the ELM and the SPELM methods to make such prediction. To do so, a Monte Carlo study with 5%, 10% and 20% of the disease counts were randomly treated as missing and prediction were performed. To compare the results the root mean square prediction error (RMSPE) was used to measure the predictive power of each method. From our findings we can see that after training and tuning the ELM and SPELM methods, the SPELM uniformly improves count prediction by the RMSPE criterion.

## Poster 90

### Use of tracking plates to identify hotspots of rat abundance in slum communities with high endemic leptospirosis infection.

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Spatial heterogeneity, where risk of disease is highly localized, is a broadly applicable problem to a variety of infectious disease systems, including rat-borne leptospirosis in urban slum settings. Rodent control is largely ineffective at reducing the burden of leptospirosis where Norway rats (*Rattus norvegicus*) are the primary reservoir hosts. Delineating the spatial heterogeneity of rat populations in the complex urban slum environment is a key barrier to controlling these pests and the diseases, such as leptospirosis, which they transmit.

We developed a tracking plate method and geostatistical-modeling framework to quantify the abundance and distribution of rats using rat-specific marks on lampblack-coated tiles. We used this method to create high-resolution risk maps for rat abundance and distribution throughout a Brazilian urban slum

community (0.17 km<sup>2</sup>) where leptospirosis sub-clinical infection is endemic (5.14% CI, 4.10 – 6.46). We first developed an interval-censored mixed model to evaluate environmental characteristics associated with rat intensity. We then used the significant variables to fit a generalized linear model with spatial effects to derive fine-scale prediction maps of rat intensity and distribution.

Of the 369 sampled points, 189 points (51.2%) had identifiable rat markings. The presence of rats was associated with domestic areas (OR 1.75 CI 1.41 - 2.17), areas with access to open sewers (OR 1.95 CI 1.57 - 2.44), and the proportional area of impervious surfaces (1.98 per percent CI 1.46 – 2.67). The distribution and intensity of rat activity was highly heterogeneous with identifiable hotspots located less than 20m from cold-spots. The 10m-resolution predictive maps demonstrated marked spatial autocorrelation at areas less than 40m apart indicating the existence of spatial variation in rat activity that was not explained by environmental covariates.

These findings emphasize both the importance of spatially explicit design and the ability of tracking plates to capture rat distribution in complex urban environments divorced from common environmental traits. Furthermore, we demonstrate an applicable approach to map spatial heterogeneous processes using the example of urban rats. The observed spatial heterogeneity in the microenvironment in urban slums may also offer an opportunity for targeted control of rat populations and rat-borne leptospirosis.

## Poster 91

### Mapping tuberculosis in Brazil: incidence estimation and spatial distribution, 2012-2014

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According to Global Plan to End Tuberculosis 2016-2020, the goal is to identify at least 90% of all people who need treatment worldwide. The case detection rate (CDR) for tuberculosis (TB) is the ratio between the number of cases notified in the information system of a region and the total cases estimated in this location. The World Health Organization estimated the TB-CDR in Brazil of 82% in 2014, which is below the target, and presents important variation between regions, microregions and municipalities.

This study aimed to estimate and map the TB incidence rate in Brazilian microregions (n=558) in the 2012-2014 triennium. A Hierarchical Bayesian Model was developed to estimate the TB incidence, in order to correct for the under-reporting of cases. The new cases followed a Poisson distribution with censoring in those microregions suspected of under-reporting. We used socioeconomic indicators as independent variables and included random effects spatially and non-spatially structured.

To identify the microregions with censored data, an evaluation of the tuberculosis surveillance system was carried out based on four attributes: completeness, consistency, opportunity and acceptability. The indicators of each attribute, as well

the cut-off points of attributes and indicators, were defined according to the literature and from the experts on the subject. The recommendations of five experts were obtained from the responses to a semi-structured and self-administered questionnaire.

The surveillance indicators were categorized as "good", "regular" or "poor", according to its value in the microregion compared with the established cut-off point. If more than 15% of the data to calculate an indicator were incomplete, the indicator was classified as "invalid" in the microregion. All microregions with poor median completeness (n=82) were considered censored. Consistency was not discriminant to infer the data quality.

To describe the microregions with "good" and "regular" completeness (n=476) we used Hierarchical Clustering for the attributes opportunity and acceptability. All microregions in clusters with inadequate data (n=69) were considered censored. Once we had categorical indicators, Multiple Correspondence Analysis (MCA) was used to process the data before cluster analysis.

The Brazilian surveillance system achieved acceptable data quality in many microregions. The opportunity of treatment, the proportion of cases tested for HIV and the proportion of cases who completed treatment must be improved. The estimation of the incidence rate by Bayesian model resulted in a clearer spatial pattern of the tuberculosis distribution through the country. The use of socioeconomic indicators and censoring in modelling was useful to improve tuberculosis incidence estimation and, hence, to identify areas for active search for tuberculosis. The results at local level allows to provide more effective recommendations to improve the tuberculosis surveillance system in Brazil.

## Poster 92

### Modelling Lyme disease risks in space and time

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**Background:** Lyme disease (LD) is a bacterial infection spread by ticks. It is the most common vector-borne disease in Europe and USA with increasing number of cases reported annually. The distribution of LD risk in the UK has been largely represented by mapping the distribution of *Ixodes ricinus* ticks considered to be the main vector of the bacteria *Borrelia burgdorferi* responsible for the disease. Environmental and climatic factors influence tick survival ability and abundance, leading to intra annual variations. Hence, variation in environmental and climatic factors between geographical areas implies heterogeneity in *Ixodes ricinus* distribution and consequently, differences in the spatial distribution of Lyme disease cases. Therefore, understanding the spatial epidemiology of the disease is a sine qua non for the development of appropriate statistical model to adequately predict the spread of the disease risk and is also useful for the disease surveillance, control and prevention. In this paper, we model the spatiotemporal distribution of LD risks in Scotland using laboratory confirmed cases with a view to understand the spatial and temporal patterns and assess spatial heterogeneity of the disease risk.

**Data and Methods:** Laboratory confirmed cases of LD between 2006 and 2015 were obtained from National Lyme Borreliosis Testing Laboratory (NLBTL) in Scotland and aggregated at county level for each year. Following Knorr-Held (2000),

we fitted spatiotemporal ecological regression models that accounted for the effects of temporal, socioeconomic and some ecogeographical variables on the number of diagnosed cases in each Scottish county. The structured temporal effect was represented as first-order random walk process to capture the impacts of variation in reporting and diagnostic protocols on temporal trend. Spatial dependencies were represented using Besag et al. (1991). Area specific effects were modelled as random effects. The models were implemented with INLA in R.

**Results:** Posterior estimates of the overall trend depict increasing number of cases over the years and spatially structured residual risks. Scottish highland had the largest risk and risk increased from South to North of Scotland. This spatial pattern of risks was associated, inter alia, with the spatial distribution of some covariates. Model estimates indicate statistically significant positive association between socioeconomic status, tick abundance and Lyme disease risk. Also, residing near woodlands increased the risk of infection.

**Conclusion:** Climatic, ecological and socioeconomic factors are strong predictors of LD. Heterogeneity in spatial risks reflects differences in distribution of these factors, as well as variation in diagnosis and reporting.

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