

# Biogeoinformatics

Stéphane JOOST

Lab of Geographic Information Systems (LASIG)

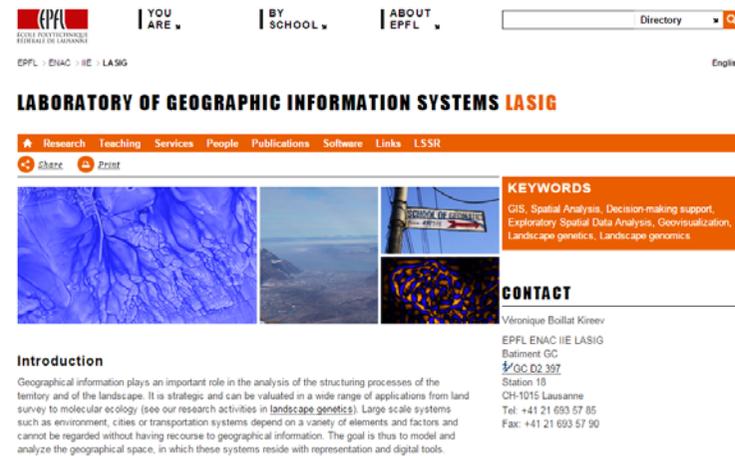
Ecole Polytechnique Fédérale de Lausanne



ÉCOLE POLYTECHNIQUE  
FÉDÉRALE DE LAUSANNE

# GIS Lab EPFL

- GIS application design
- Spatial Decision Support Systems
- Geospatial data infrastructures
- GIS for urban studies and design
  
- Spatial statistics and analysis



The screenshot shows the website for the Laboratory of Geographic Information Systems (LASIG) at EPFL. The header includes the EPFL logo and navigation links: 'YOU ARE', 'BY SCHOOL', and 'ABOUT EPFL'. Below the header, the text 'EPFL - ENAC - IIE - LASIG' is visible. The main title is 'LABORATORY OF GEOGRAPHIC INFORMATION SYSTEMS LASIG'. A navigation bar contains links for 'Research', 'Teaching', 'Services', 'People', 'Publications', 'Software', 'Links', and 'LSSR'. There are also 'Home' and 'Print' buttons. The main content area features three images: a blue-toned topographic map, a landscape view, and a network diagram. To the right, there are sections for 'KEYWORDS' (GIS, Spatial Analysis, Decision-making support, Exploratory Spatial Data Analysis, Geovisualization, Landscape genetics, Landscape genomics) and 'CONTACT' (Véronique Bollat Kireev, EPFL ENAC IIE LASIG, Batiment GC, GC D2 397, Station 18, CH-1015 Lausanne, Tel: +41 21 693 57 85, Fax: +41 21 693 57 90). An 'Introduction' section is also present, discussing the role of geographical information in landscape analysis.

## Computational Landscape Genetics Group

- Joost
- Widmer
- Leempoel
- Duruz
- Rochat
- Cesconeto

# Research goals

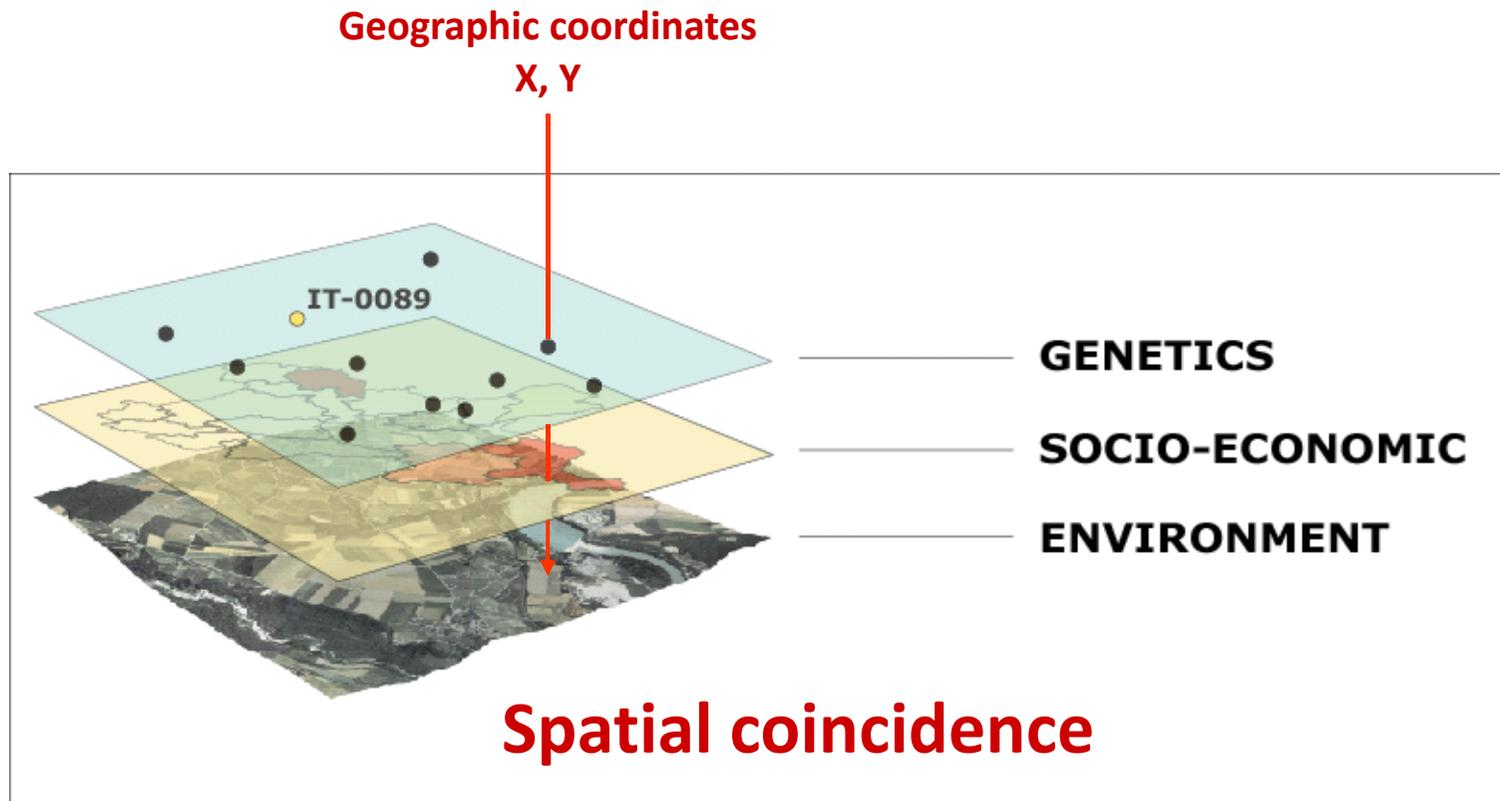
- Make use of GIScience methods and geodata to contribute to :
  - The elaboration of efficient decision-making support approaches to favor the conservation of plant/animal genetic diversity
  - The advancement of our understanding of mechanisms controlling the evolution of species (adaptation to local environment in particular)

# GIScience as insider

- Since 2001, immersion in the evolutionary biology community
- Close collaboration with biologists, geneticists, vets, etc.
- **Transdisciplinarity** vs interdisciplinarity
- A real appropriation of the research field
- Members of the team are biologists
- Projects submitted to life science divisions



# A key function



# **Conservation and monitoring of Farm animal Genetic Resources**

# FAnGR conservation

- Management and conservation of livestock genetic resources imply breed prioritization, and therefore **decision making**
- Decision making rests on the simultaneous analysis of several **criteria...**
- ... in order to identify and to favour sustainable breeding conditions

# Data categories

1. Population and evolutionary **genetics**
2. Animal **husbandry** practices
3. **Socio-economic** and **socio-demographic** data in the regions where animals are bred
4. **Environmental** information: climatic and geophysical characteristics of the places where animals are bred
5. Political and administrative boundaries: geographical units where **policies** have to be applied

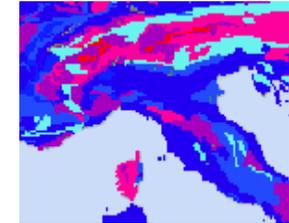


# Data integration

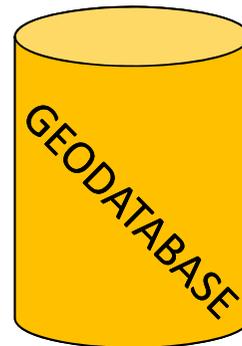


Administrative boundaries  
Socio-Economic data  
Socio-demographic data

Environmental data:  
topography, climate,  
soil, etc.



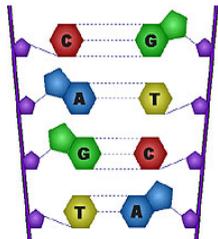
Geographic coordinates  
X, Y



GIS

Sampling  
Genetic data

Questionnaires  
Husbandry practices



# FAnGR monitoring

- FAO Global plan (2007) requires countries to monitor their FAnGR
- Countries like Austria, Germany, Great Britain have developed a monitoring system
- **GenMon** prototype under development in Switzerland (Duruz 2014)
- The system uses geographic information to assess endangerment
- And to communicate information by means of thematic maps



# GenMon-CH

## Welcome

Welcome on GenMon-CH, an open Web-GIS application for the monitoring of Farm Animal Genetic Resources (FAnGR).

This application is designed to rank breeds according to four criteria: Genetic diversity (estimated from pedigree data), Introgression, Geographical concentration and Agriculture sustainability (from Socio

The ranking of the breed is shown in the following table, while more information for each breeds (table, graphs, maps) are available if you click on more info.

Please refer to the [tutorial](#) for more information and for test data to try the application.

## Summary table

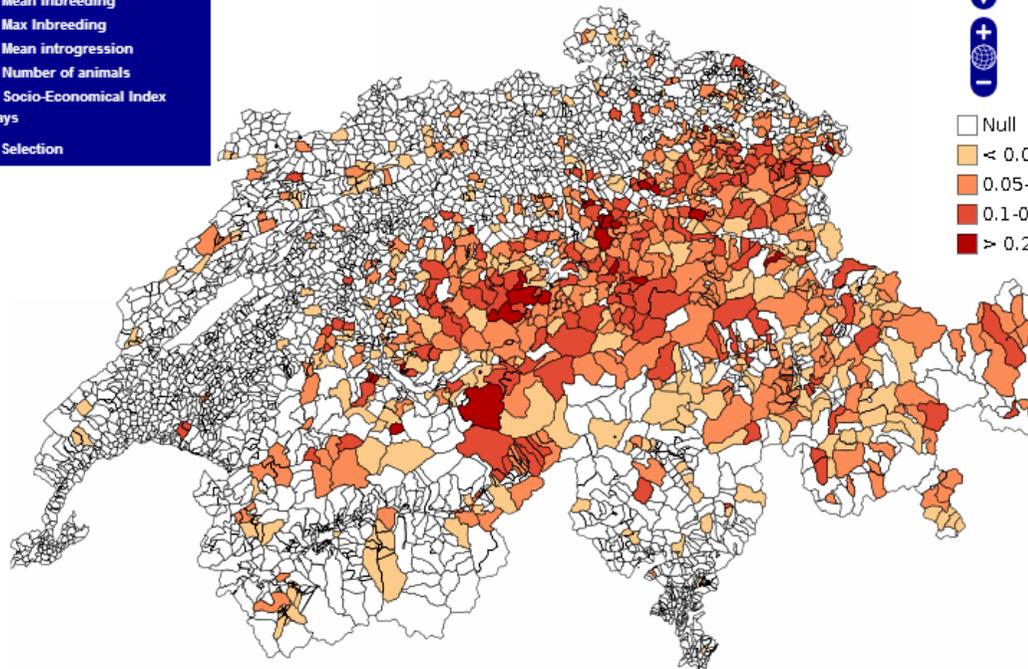
Breed name	Last year of data	Number individuals last GI	Average inbreeding last GI	Effective pop size range	Pedig Index (0-1)	Introg Index	Geog index (km)	BAS Index (0-1)	Global Index (0-1)	More Info
SN	2012	33306	0.103 <span style="color:red">■</span>	50-100 <span style="color:red">■</span>	0.008 <span style="color:red">■</span>	0 <span style="color:green">■</span>	13.02 <span style="color:red">■</span>	0.78 <span style="color:green">■</span>	0.393	<a href="#">more</a>
FM	2013	26877	0.0571 <span style="color:green">■</span>	50-100 <span style="color:red">■</span>	0.383 <span style="color:orange">■</span>	0.114 <span style="color:red">■</span>	57.66 <span style="color:green">■</span>	0.75 <span style="color:green">■</span>	0.454	<a href="#">more</a>
BFS	2012	43341	0.0467 <span style="color:green">■</span>	50-100 <span style="color:red">■</span>	0.474 <span style="color:orange">■</span>	0 <span style="color:green">■</span>	51.58 <span style="color:green">■</span>	0.707 <span style="color:green">■</span>	0.703	<a href="#">more</a>
SBS	2012	37712	0.0411 <span style="color:green">■</span>	50-100 <span style="color:red">■</span>	0.523 <span style="color:green">■</span>	0 <span style="color:green">■</span>	59.53 <span style="color:green">■</span>	0.719 <span style="color:green">■</span>	0.746	<a href="#">more</a>
BVO	2014	30469	0.033 <span style="color:green">■</span>	<span style="color:red">■</span>	0.594 <span style="color:green">■</span>	0.013 <span style="color:green">■</span>	58.52 <span style="color:green">■</span>	0.74 <span style="color:green">■</span>	0.812	<a href="#">more</a>
WAS			<span style="color:green">■</span>	<span style="color:red">■</span>	<span style="color:red">■</span>	<span style="color:green">■</span>	<span style="color:red">■</span>	<span style="color:red">■</span>		<a href="#">more</a>
Test			<span style="color:green">■</span>	<span style="color:red">■</span>	<span style="color:red">■</span>	<span style="color:green">■</span>	<span style="color:red">■</span>	<span style="color:red">■</span>		<a href="#">more</a>

**Base Layer**

- Mean Inbreeding
- Max Inbreeding
- Mean introgression
- Number of animals
- Socio-Economical Index

**Overlays**

- Selection



- Null
- < 0.05
- 0.05-0.1
- 0.1-0.2
- > 0.2

Add data for this breed (BVO):  No file chosen

See the format in the [tutorial](#).

Or go to the assisted upload section

See spatial distribution (BVO):

[PDF: PopRep Population Report BVO](#)

[PDF: PopRep Inbreeding Report](#)

## Effective population size

Table: Effective population size according to different computations

Method	Ne
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Figure: Effective population size ( $N_{e,FP}$ ) and pedigree completeness

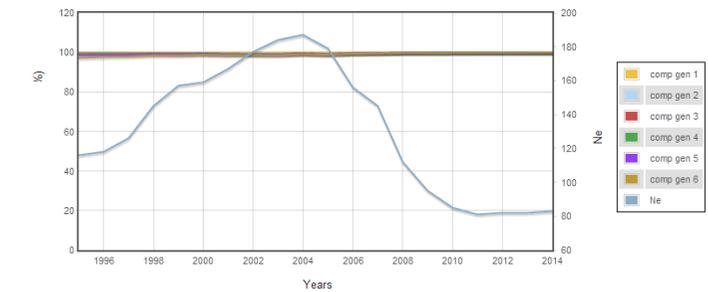
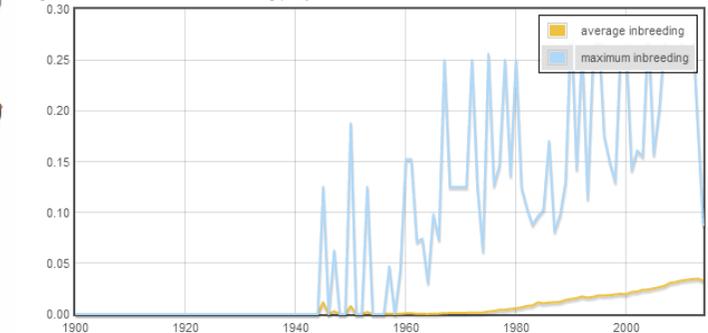


Figure: Maximum and mean inbreeding per year



# Geointelligence

- Breed, demography, **biology**, population genetics
- Geodata (sampling design, **geo**coordinates)
- Communication skills, thematic **mapping**
- Database, spatial database, **web** protocols, web design
- **GIS** software, programming languages, data processing
- **Computer science**

**Understanding of  
mechanisms controlling the  
evolution of species**

# PERSPECTIVES

Science, 2010

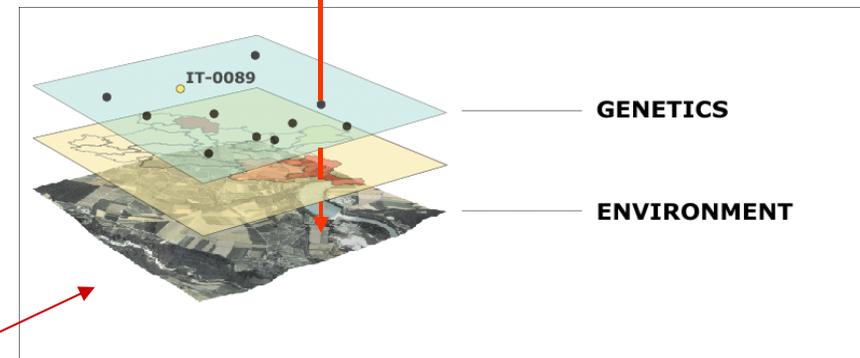
ECOLOGY

## Time to Tap Africa's Livestock Genomes

Olivier Hanotte,<sup>1</sup> Tadelle Dessie,<sup>2</sup> Steve Kemp<sup>3</sup>

Fortunately, the fields of genetics and genomics (3–5) offer a new start for the sustainable improvement of African livestock productivity. Landscape genomics links genome-wide information to geo-environmental resource analysis to identify potentially valuable genetic material. Typically, researchers will perform a genome-wide scan on a number of animals from populations living in different habitats or across an ecological cline (from dry to wet areas, for instance).

### Landscape genomics

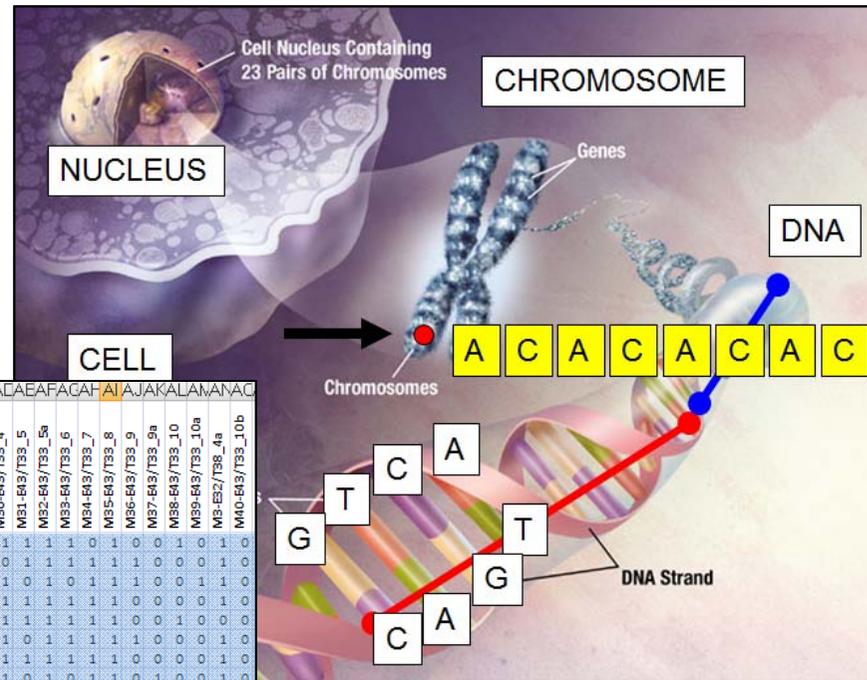
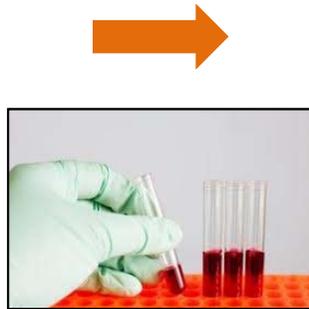


- Correlative approaches and spatial statistics

### Genome-wide information

- Paradigm shift and transition phase

# Genetic data



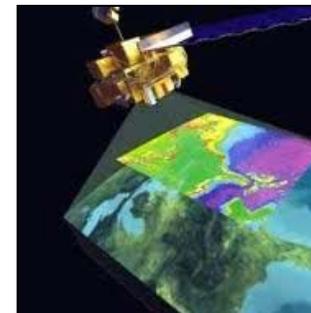
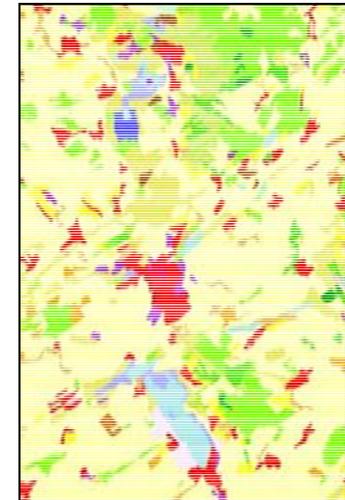
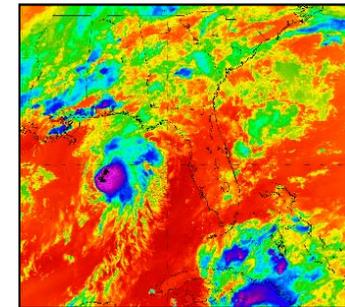
	A	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AE	AC	AL	AE	AF	AG	AI	AJ	AK	AL	AM	AN	AO										
1	farmid	longitude	latitude	ANIMALID	M100-E45/T32_37	M101-E45/T32_38	M102-E45/T32_39	M10-E32/T38_9	M11-E32/T38_10	M12-E32/T38_11	M13-E32/T38_11a	M14-E32/T38_11b	M15-E32/T38_12	M16-E32/T38_13	M17-E32/T38_14	M18-E32/T38_15	M19-E32/T38_17	M1-E32/T38_3a	M20-E32/T38_17a	M21-E32/T38_19	M22-E32/T38_20a	M23-E32/T38_21	M24-E32/T38_21b	M25-E32/T38_22	M26-E32/T38_22a	M27-E43/T33_1	M28-E43/T33_2	M29-E43/T33_3a	M2-E32/T38_4	M30-E43/T33_4	M31-E43/T33_5	M32-E43/T33_5a	M33-E43/T33_6	M34-E43/T33_7	M35-E43/T33_8	M36-E43/T33_9	M37-E43/T33_9a	M38-E43/T33_10	M39-E43/T33_10a	M3-E32/T38_4a	M40-E43/T33_10b							
2	PT-0015	-8.2676	41.6848	CHPOBRA3	1	1	1	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	1	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0		
3	PT-0022	-7.9273	41.5847	CHPOBRA26	1	1	1	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	1	0	0	0	0	1	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0		
4	PT-0023	-7.9273	41.5847	CHPOBRA28	1	1	1	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	1	0	0	0	1	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0		
5	PT-0023	-7.9273	41.5847	CHPOBRA29	1	1	1	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0	1	0	1	0	1	0		
6	PT-0021	-7.8426	41.395	CHPOBRA23	0	0	0	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	1	0	
7	PT-0021	-7.8426	41.395	CHPOBRA25	1	1	1	1	1	1	0	0	0	1	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
8	PT-0017	-7.8269	41.4732	CHPOBRA10	1	1	1	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	1	0
9	PT-0017	-7.8269	41.4732	CHPOBRA11	1	1	0	0	1	1	0	0	0	1	0	1	1	0	1	0	1	0	0	0	0	0	1	0	0	0	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	1	0
10	PT-0017	-7.8269	41.4732	CHPOBRA12	1	0	0	Na	1	1	0	0	0	1	0	1	0	1	0	1	0	1	0	0	0	0	1	1	0	0	0	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	1	0
11	PT-0020	-7.8215	41.4235	CHPOBRA21	0	1	0	1	1	1	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	1	0
12	PT-0020	-7.8215	41.4235	CHPOBRA22	1	1	0	1	1	1	0	0	0	1	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
13	PT-0019	-7.7811	41.439	CHPOBRA18	1	1	1	1	1	1	0	0	0	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
14	PT-0019	-7.7811	41.439	CHPOBRA19	1	1	1	1	1	1	0	0	0	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
15	PT-0018	-7.78	41.4379	CHPOBRA13	1	1	1	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
16	PT-0018	-7.78	41.4379	CHPOBRA14	1	1	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
17	PT-0018	-7.78	41.4379	CHPOBRA15	1	1	1	0	1	1	0	0	0	1	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
18	PT-0016	-7.7291	41.4752	CHPOBRA5	1	1	1	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
19	PT-0016	-7.7291	41.4752	CHPOBRA6	1	0	0	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
20	PT-0016	-7.7291	41.4752	CHPOBRA8	1	0	0	1	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
21	ES-0060	-6.00263	37.7014	CHSPFLR35	1	0	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
22	ES-0060	-6.00263	37.7014	CHSPFLR37	1	0	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
23	ES-0060	-6.00263	37.7014	CHSPFLR38	1	1	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
24	ES-0060	-6.00263	37.7014	CHSPFLR39	1	1	1	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	
25	ES-0060	-6.00263	37.7014	CHSPFLR40	1	1	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
26	ES-0059	-5.79995	37.9703	CHSPFLR27	1	1	0	0	1	1	1	0	0	1	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
27	ES-0059	-5.79995	37.9703	CHSPFLR28	1	1	0	1	1	1	1	0	0	1	1	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0
28	ES-0059	-5.79995	37.9703	CHSPFLR29	1	1	1	1	1	1	1	Na	Na	1	1	0	1	Na	Na	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	1	0	1	0	1	0	

GENETICS



# Environmental data characterizing sampling locations

GEO			GENETICS													ENVIRONMENT							
1	farmid	animalid	DARJMP29_allele2_137	DARJMP29_allele2_139	DARJMP29_allele2_141	DARJMP29_allele2_143	DARJMP29_allele2_145	DARJMP29_allele2_147	DARJMP29_allele2_149	DARJMP29_allele2_151	DARJMP29_allele2_153	DARJMP29_allele2_155	DARJMP29_allele2_157	DARJMP29_allele2_159	DARJMP29_allele2_161	DARJMP29_allele2_163	DARJMP29_allele2_165	DARJMP29_allele2_167	wndjan	altitude	wndfeb	wndmar	wndapr
1044	PL-4005	OAPLPOM25	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.1	22	4.6	5	4.4
1045	PL-4005	OAPLPOM26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.1	22	4.6	5	4.4
1046	PL-4006	OAPLPOM01	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	5.3	153	4.8	4.9	4.3
1047	PL-4006	OAPLPOM15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	153	4.8	4.9	4.3
1048	PL-4006	OAPLPOM24	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	5.3	153	4.8	4.9	4.3
1049	PL-4007	OAPLPOM05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	250	4.8	5	4.5
1050	PL-4007	OAPLPOM16	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	5.3	250	4.8	5	4.5
1051	PL-4008	OAPLPOM09	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1052	PL-4008	OAPLPOM19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1053	PL-4008	OAPLPOM20	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1054	PL-4009	OAPLPOM10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.5	87	5	5.2	4.6
1055	PL-4009	OAPLPOM21	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.5	87	5	5.2	4.6
1056	PL-4010	OAPLPOM08	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	5.4	208	4.9	5.1	4.5





# Logistic regression

Individuals			Genetic markers													Environmental variables																		
1	farmid	animalid	DARJMP29_allele2_137	DARJMP29_allele2_138	DARJMP29_allele2_140	DARJMP29_allele2_141	DARJMP29_allele2_142	DARJMP29_allele2_143	DARJMP29_allele2_144	DARJMP29_allele2_145	DARJMP29_allele2_146	DARJMP29_allele2_147	DARJMP29_allele2_148	DARJMP29_allele2_149	DARJMP29_allele2_150	DARJMP29_allele2_151	DARJMP29_allele2_152	DARJMP29_allele2_153	DARJMP29_allele2_154	DARJMP29_allele2_155	DARJMP29_allele2_156	DARJMP29_allele2_157	wndjan	altitude	wndfeb	wndmar	wndapr							
1044	PL-4005	QAPLPOM25	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.1	22	4.6	5	4.4
1045	PL-4005	QAPLPOM26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.1	22	4.6	5	4.4
1046	PL-4006	QAPLPOM01	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	153	4.8	4.9	4.3
1047	PL-4006	QAPLPOM15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	153	4.8	4.9	4.3
1048	PL-4006	QAPLPOM24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	153	4.8	4.9	4.3
1049	PL-4007	QAPLPOM05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	250	4.8	5	4.5
1050	PL-4007	QAPLPOM16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.3	250	4.8	5	4.5
1051	PL-4008	QAPLPOM09	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1052	PL-4008	QAPLPOM19	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1053	PL-4008	QAPLPOM20	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.2	166	4.8	5	4.4
1054	PL-4009	QAPLPOM10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.5	87	5	5.2	4.6
1055	PL-4009	QAPLPOM21	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.5	87	5	5.2	4.6
1056	PL-4010	QAPLPOM08	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.4	208	4.9	5.1	4.5

Multiple parallel logistic regressions

# High performance computation of landscape genomic models integrating local indices of spatial association

Sylvie Stucki<sup>1,\*</sup>, Pablo Orozco-terWengel<sup>2</sup>, Michael W. Bruford<sup>2</sup>, Licia Colli<sup>3</sup>, Charles Masembe<sup>4</sup>, Riccardo Negrini<sup>3,5</sup>, Pierre Taberlet<sup>6,7</sup>, Stéphane Joost<sup>1,\*</sup> and the NEXTGEN Consortium<sup>8</sup>

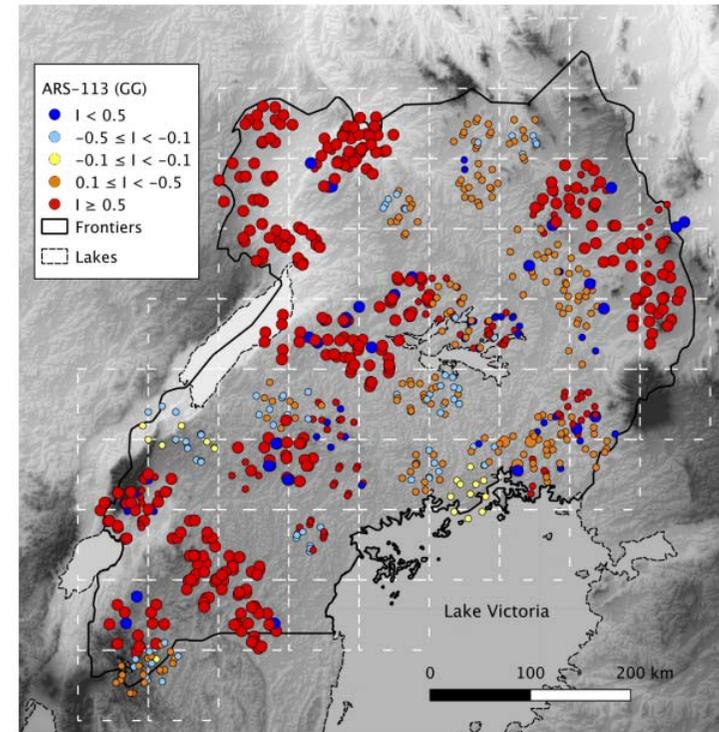
<http://lasig.epfl.ch/sambada>

**Computation time (in hours)**

**Spatial statistics**

	41,215 SNPs 804 samples	634,849 SNPs 102 samples
Samβada	1.2	2.9
Samβada biv.	8.7	18.4
BayEnv	41.3	62.,2
LFMM	3.2	16.0
LFMM (mono)	6.1	58.1

23 environmental variables



(a) ARS-113 (GG)

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# Adaptations to Climate-Mediated Selective Pressures in Sheep

Feng-Hua Lv,<sup>1</sup> Saif Agha,<sup>2,3</sup> Juha Kantanen,<sup>4,5</sup> Licia Colli,<sup>6,7</sup> Sylvie Stucki,<sup>2</sup> James W. Kijas,<sup>8</sup> Stéphane Joost,<sup>2</sup> Meng-Hua Li,<sup>\*1</sup> and Paolo Ajmone Marsan<sup>6,7</sup>

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animals likely underlying environmental adaptation in domestic animals.

## Impact of Climate on Energy Metabolism and Endocrine and Autoimmune Regulation

Our results suggest that the process of autochthonous sheep breeds adaptation to extreme climates is principally mediated by complex, integrated energy metabolic responses, as observed in rodents (Rezende et al. 2004). Climate is known to have an important impact on animal physiology and fit-

ness (McManus et al. 2011). Consequently, long-term thermal stress can result in energy metabolic adaptation, as well as heat and cold tolerance, in particular breeds. Meanwhile, variation in animal morphology, including body size (large vs. small) and shape (fat-tailed vs. thin-/short-tailed), also follows basic thermoregulatory principles to dissipate or conserve body energy in different climates. In addition, several breeds (e.g., Norwegian White Sheep) grow particularly large in cold regions that are dry/warm in early spring and warm/wet in late summer, where conditions favor continued grass growth (Nielsen et al. 2013); however, several breeds grow small in the

# Geointelligence

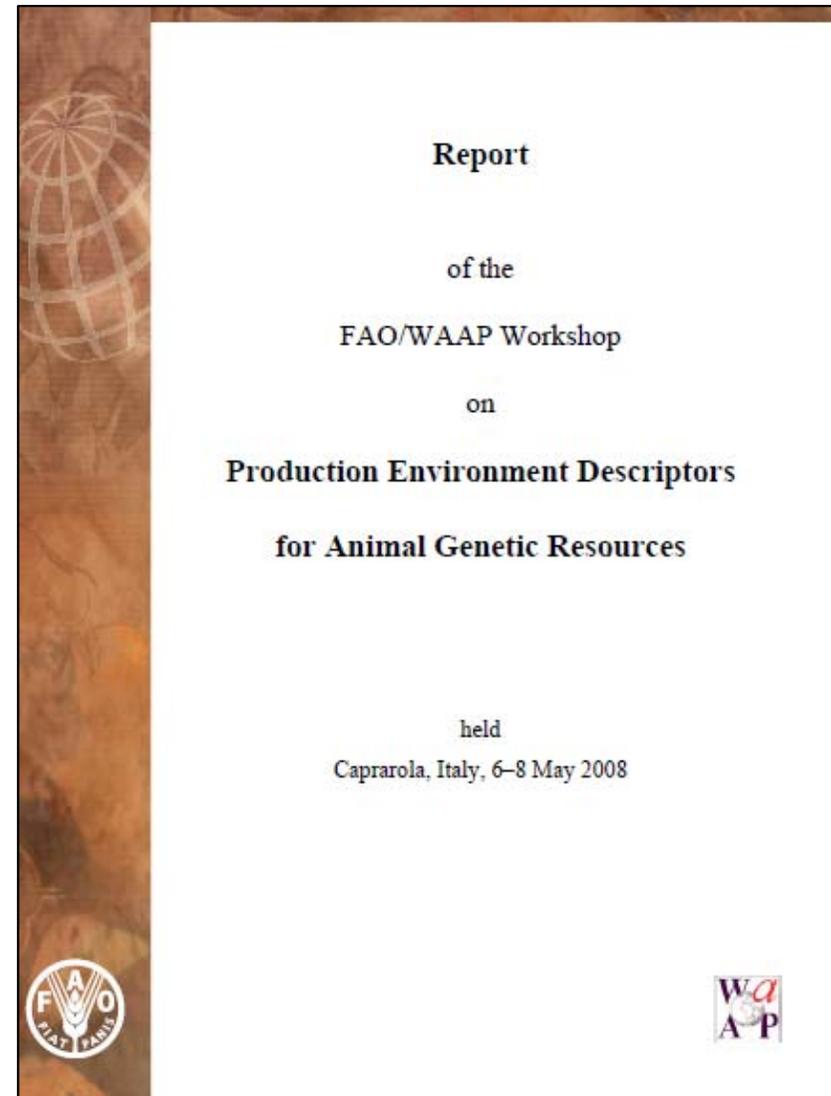
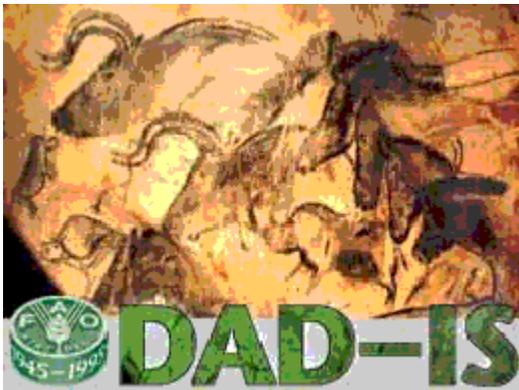
- Breed, **biology**, population genetics, genomics
- Geodata (sampling design, **geo**coordinates)
- Communication skills, thematic **mapping**
- **GIS** software, programming languages
- Spatial **statistics**, High Performance Computing (HPC) for data processing
- **Computer science**

# Limit

- An important problems we need to overcome for effective livestock genomic resources conservation
- to enforce the recording of geographical coordinates of any sampled animal as a **standard rule**
- so that we can fully benefit from the power of **bio**informatics

# Report on **PEDs** for FAnGR in 2008

- Edited by FAO & WAAP



# Recommendation

X,Y

## *Conclusions*

The analysis presented above leads to four main conclusions for the further development of PEDs:

1. The selection of criteria, indicators and variables to be included in the descriptive scheme should be guided by their relation to adaptive traits and the degree to which they affect animal performance.
2. Natural and management environment should be distinguished to account for the difference between external variables (not under the control of the livestock keeper) and internal factors (controlled by livestock keepers) affecting the adaptedness of species/breeds and animal performance. This distinction also facilitates the operationalization of data collection.
3. The georeferencing of breed locations in order to enable linkages to information available in other georeferenced databases should be initiated as soon as possible. This will decrease the required data collection and data entry by National Coordinators for the Management of Animal Genetic Resources and enable a continuous refinement of the description of production environments, as it is expected that an increasing number of datasets, with improving resolutions, will become available in the near future.

# Conclusion

- In both cases, an original combination of skills including molecular biology, computer science and geographic information science is necessary
- New knowledge will be extracted from the present data tsunami (large molecular, environmental, and socio-economic datasets)
- ... only if we train a new generation of students/scientists able to develop innovative **transdisciplinary** and efficient **geo**computing tools



Thank you for your attention !

