

EVOLUTION OF MICROBIAL COMMUNITIES AND NUTRIENT REMOVAL PERFORMANCES IN AEROBIC GRANULAR SLUDGE SEQUENCING BATCH REACTOR DURING CHANGE OF SUBSTRATE

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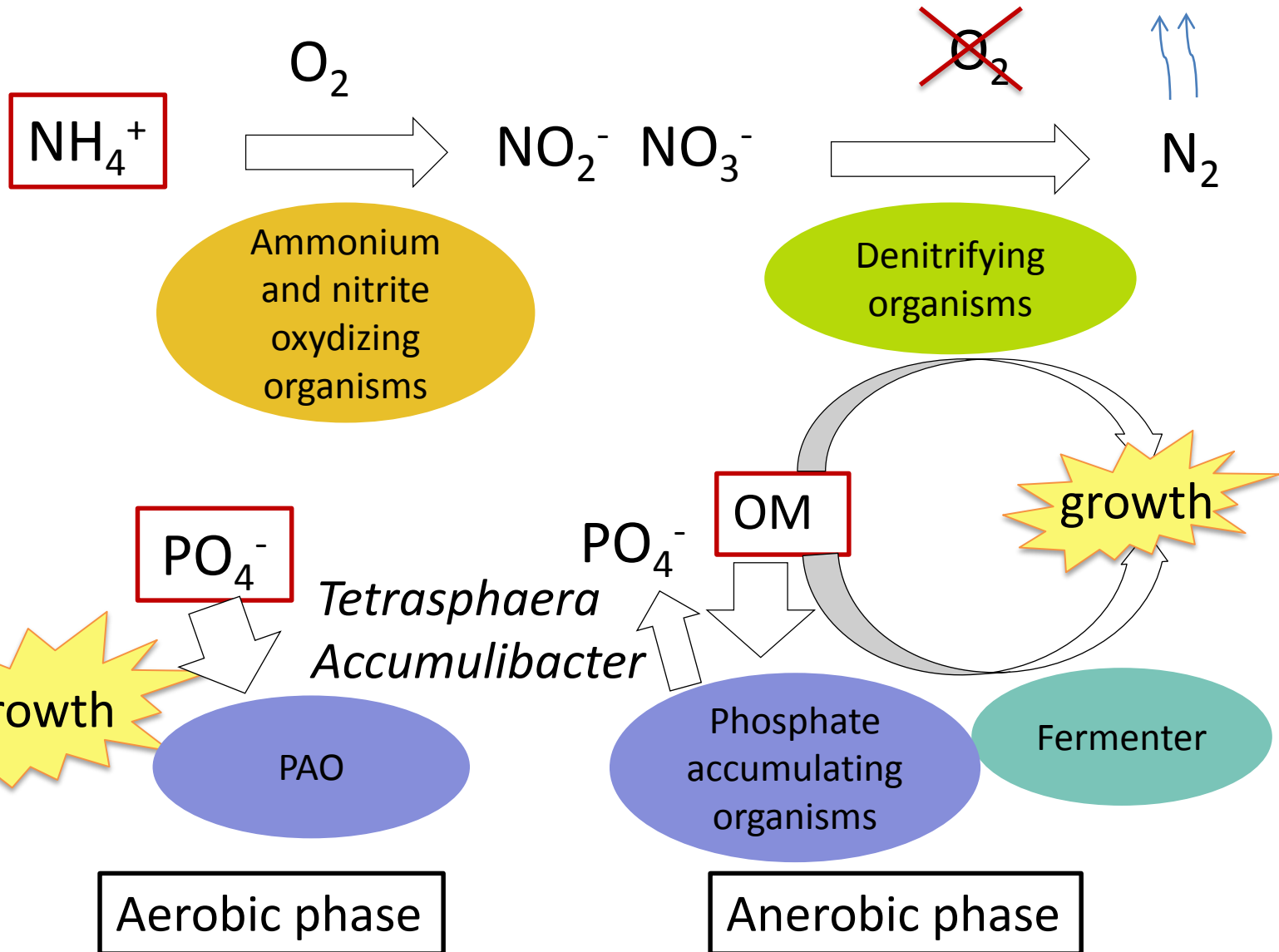
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Macropollutant removal from the wastewater

Introduction
Objectives
Method
Results
Conclusion



Activated sludge :

- aggregates of microbial origin
- Flocular structures, settle slowly

Aerobic granular sludge :

- settles significantly faster
 - Offers different red-ox conditions
 - Suited for biological phosphorus removal
 - > chemicals saving
- Space and time saving



After 1 min.
settling



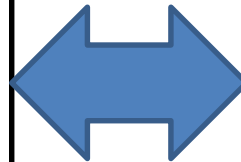
Make a step toward real conditions

Full-scale AGS fed with real wastewater

- Not easy to study
- Variable performances



<http://www.dutchwatersector.com/>



Lab scale AGS fed with acetate and propionate

- Easy to study
- Show stable performances



LBE reactor

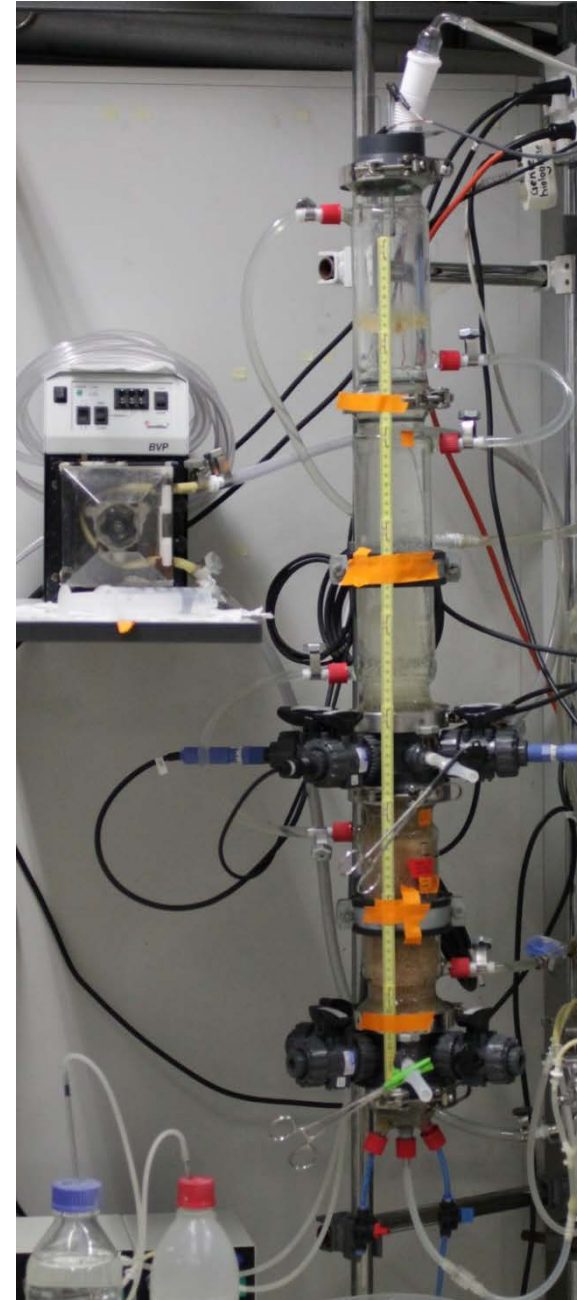
Aim of the experiment

- Maintain nutrient removal performances and granulation despite the substrate complexification
- Identify the taxa implicated in :
 - N-removal
 - P-removal
 - Granule cohesion



Experimental procedure

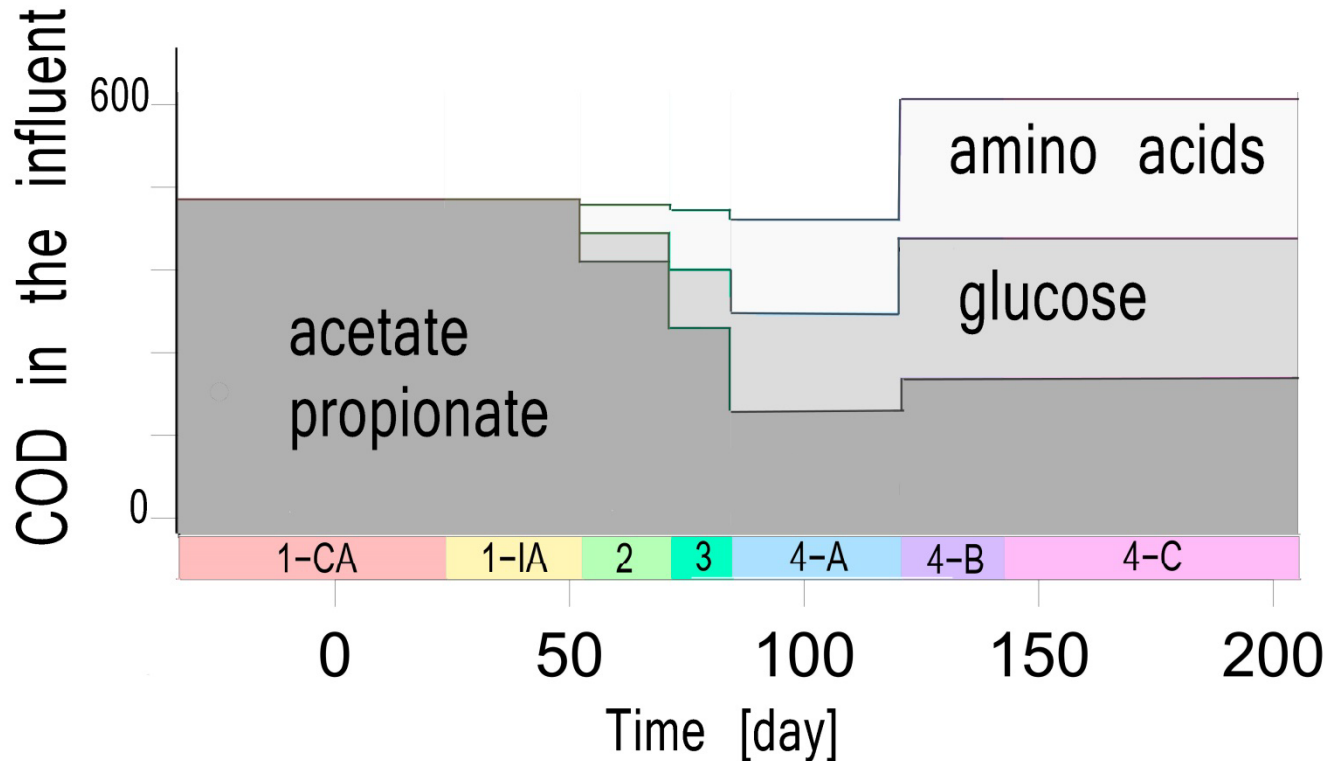
- Run an AGS sequencing batch reactor
- Progressively change the wastewater composition
- Monitor , COD, P and N-removal
- Take biomass samples, extract and sequence DNA (16rRNA gene)



Synthetic wastewater composition

PO_4^- : 22mg/L

NH_4^+ : 56 mg/L; 23 mg/L in 4-C



Experimental periods

Introduction

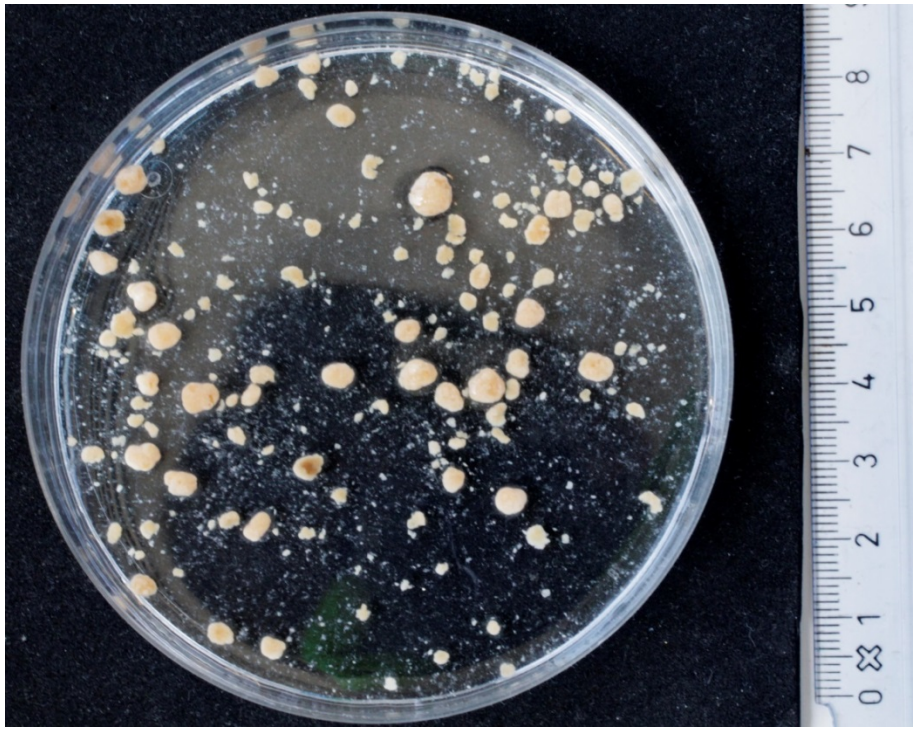
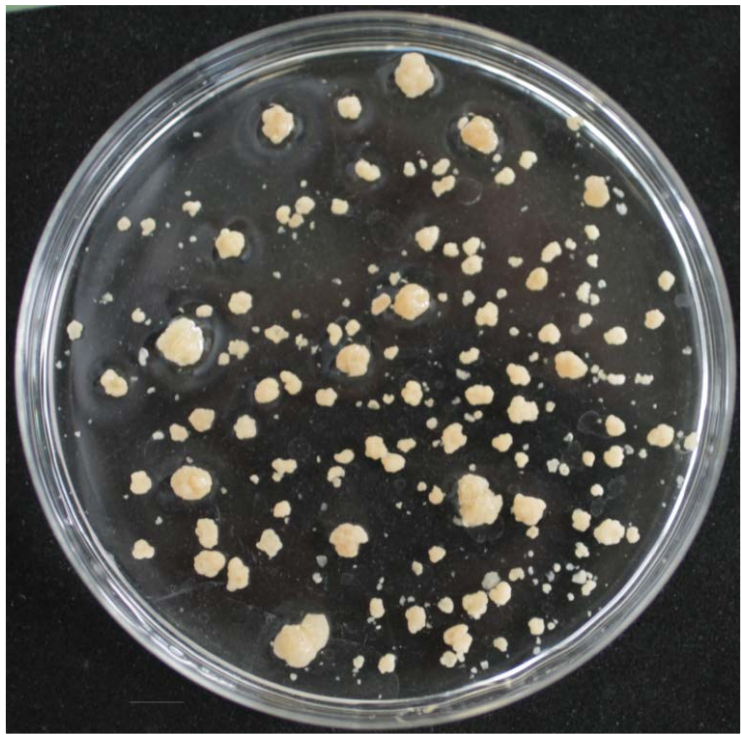
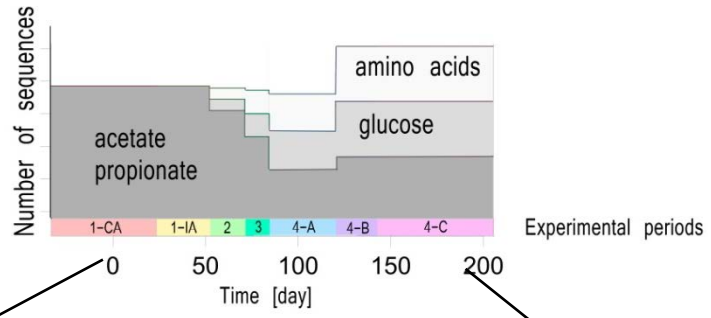
Objectives

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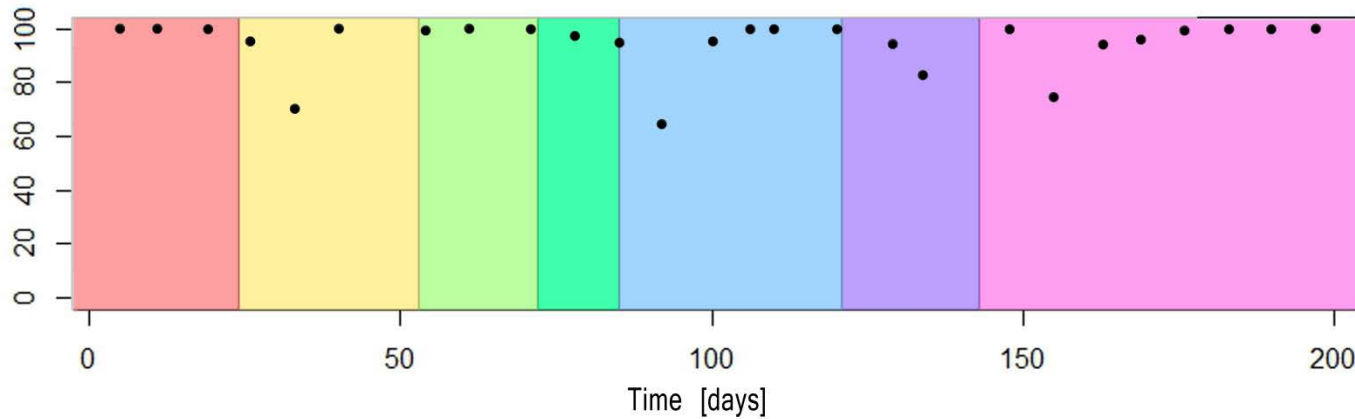
Conclusion

The substrat changes did not change the granule size distribution

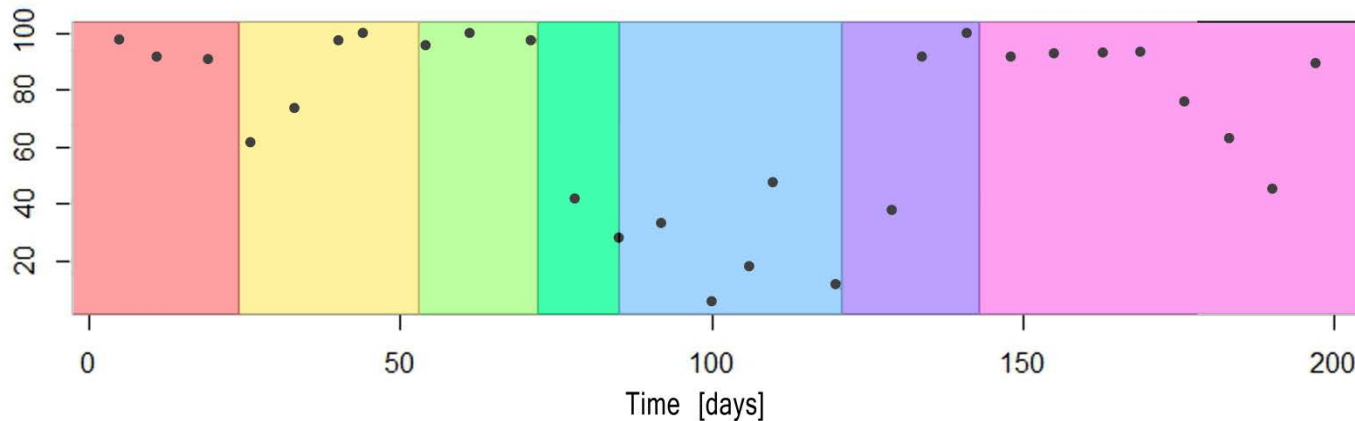


Nutrient removal efficiency during the substrate transition

Ammonium removal efficiency [%]

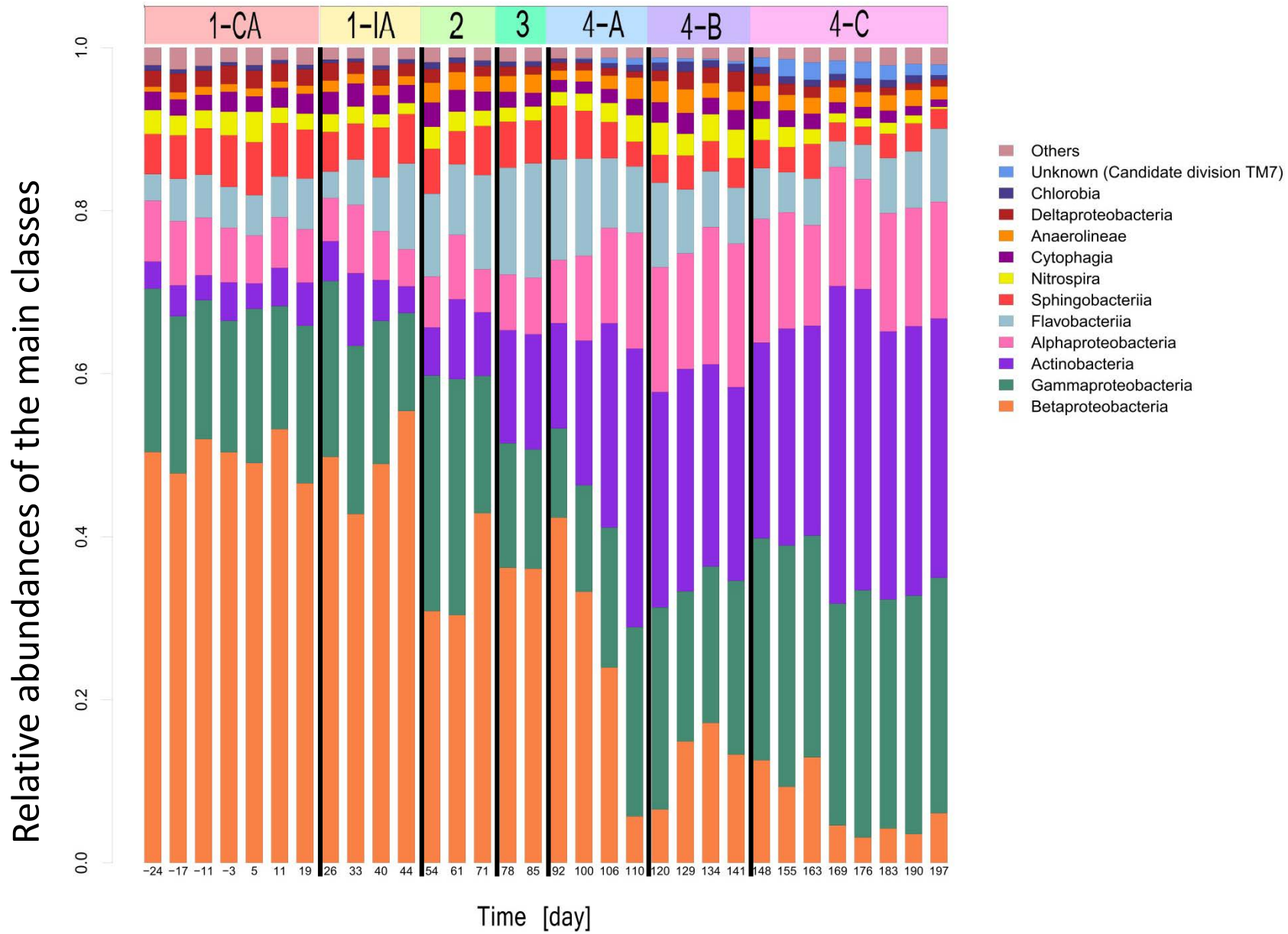


Phosphate removal efficiency [%]



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The abundances of main bacterial classes changed during the substrate change



Introduction

Objectives

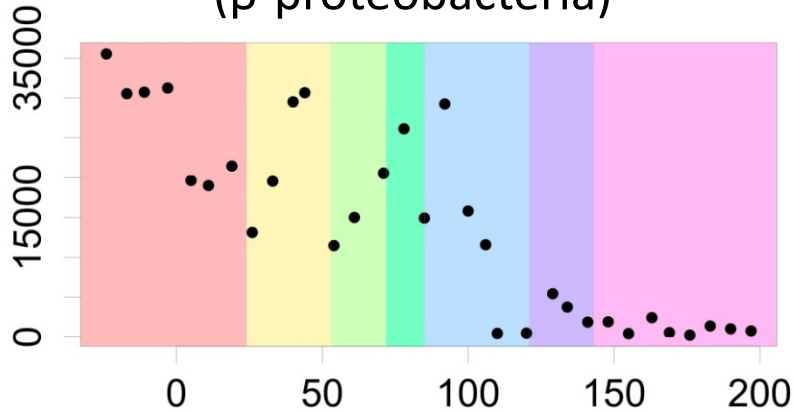
Method

Results

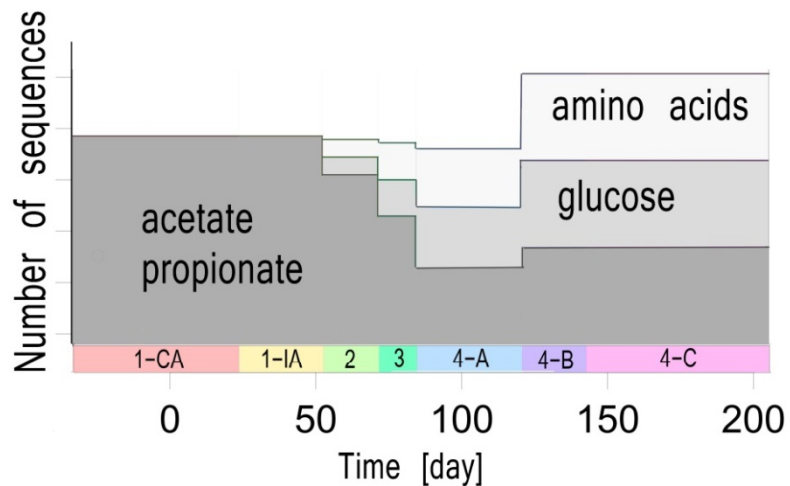
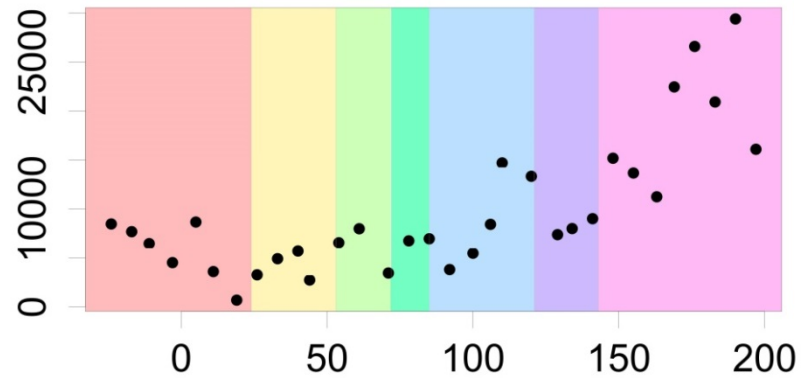
Conclusion

P-removal related bacteria

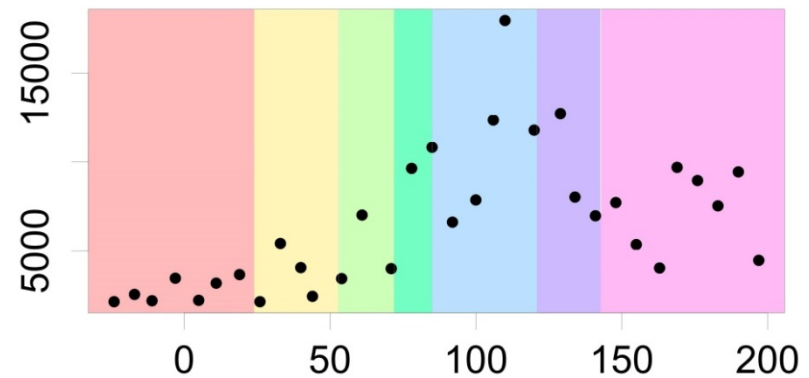
Accumulibacter
(β -proteobacteria)



Competibacter
(γ -proteobacteria)



Tetrasphaera
(Actinobacteria)



Introduction

Objectives

Method

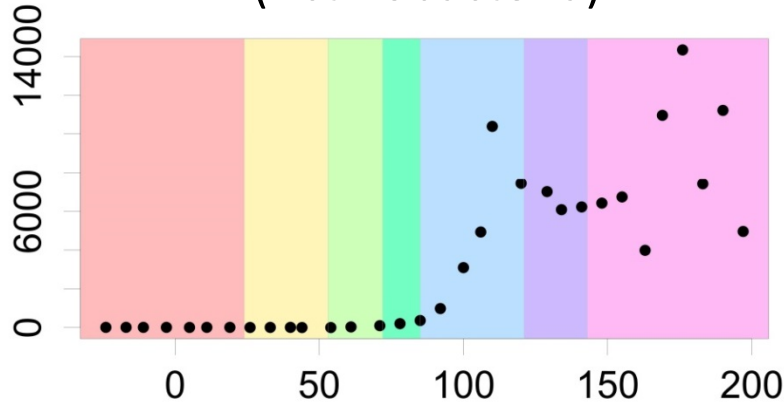
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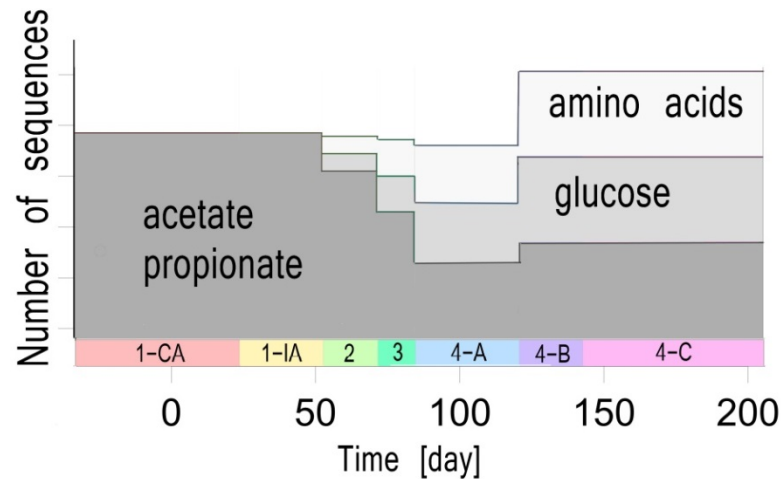
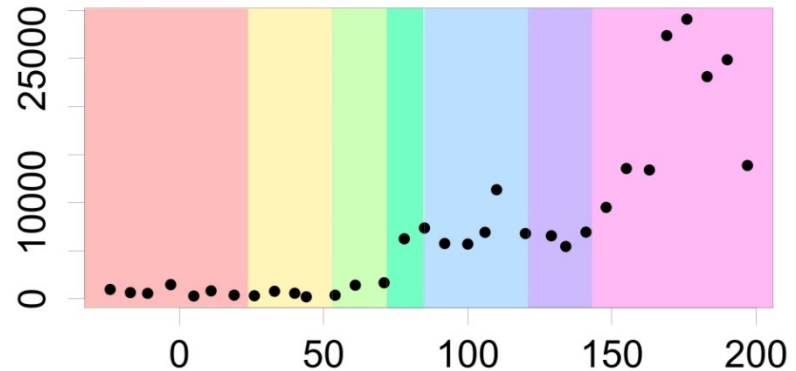


Fermenting bacteria

Propionicimonas
(Actinobacteria)



Propionicyclava
(Actinobacteria)



Introduction

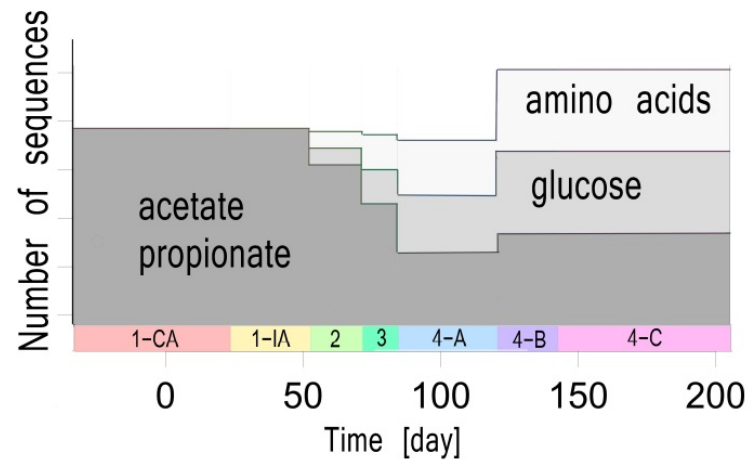
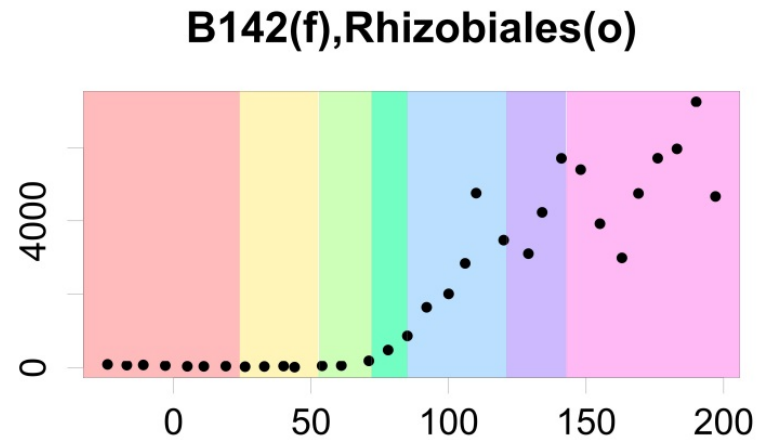
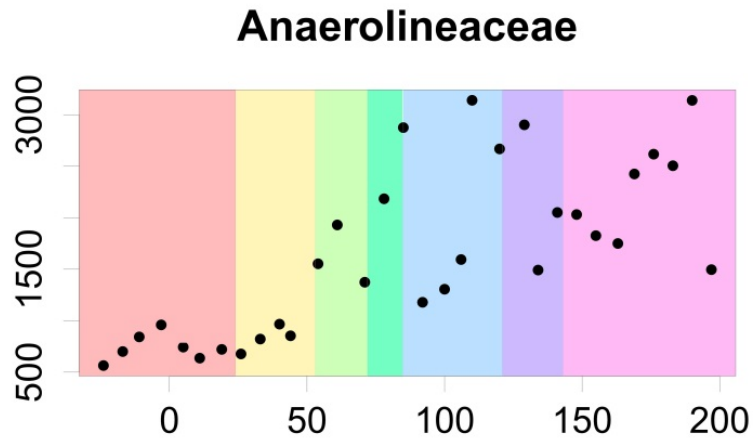
Objectives

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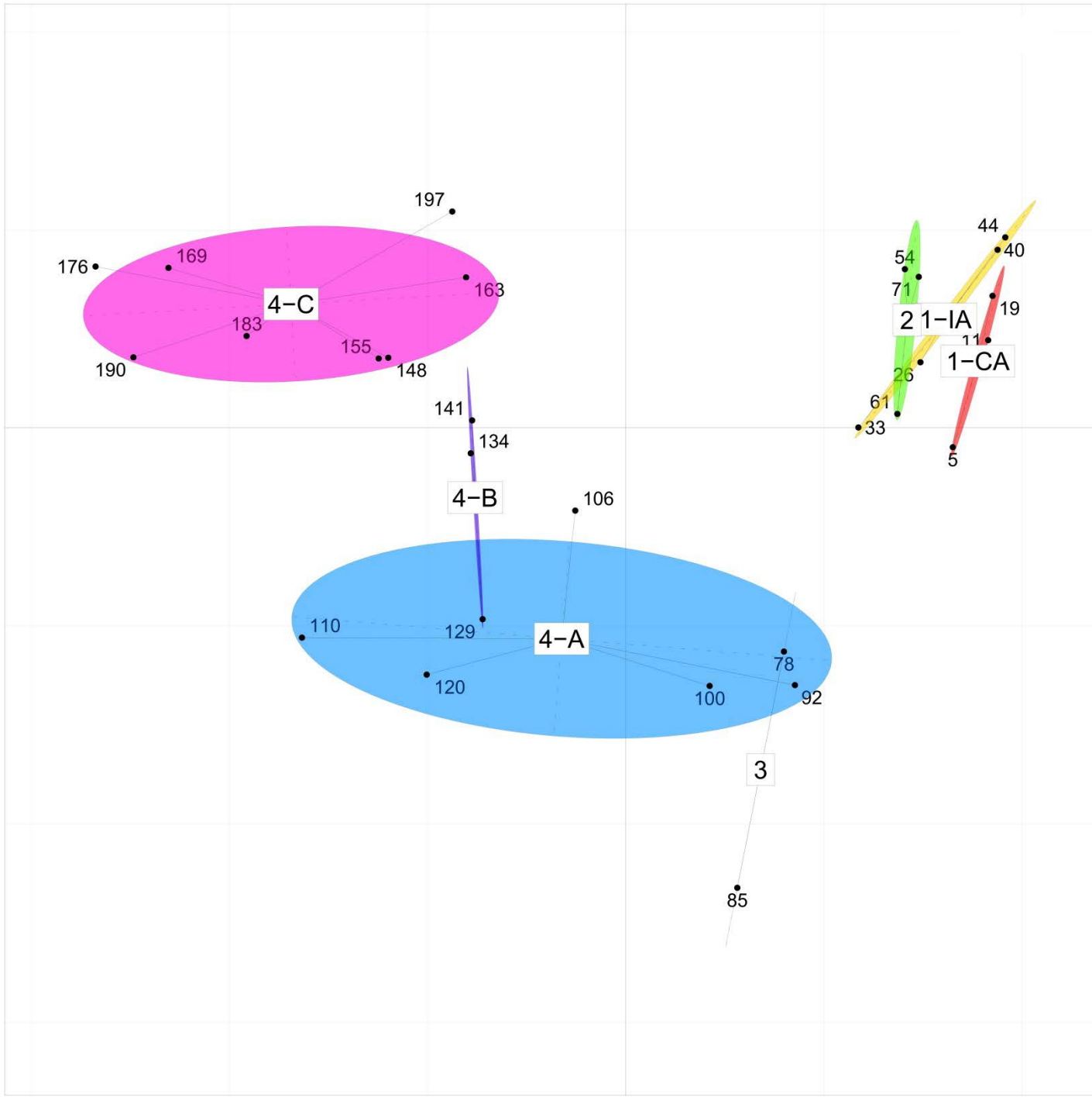
Results

Conclusion

Increasing population with undefined function



The sample characteristics clustered by process conditions





Conclusion and outlook

- The reactor performances remained high despite the change of substrat
 - A clear shift in the bacterial community structure was observed
 - *Accumulibacter* abundance decreased, seem to be partially replaced by *Tetrasphaera*
 - Populations (affiliated to Rhizobiales and Anaerolineaceae) were detected in high abundance with the mixed substrate, their role is not defined
 - Link function to taxa
- > whole metagenomic and metatranscriptomic analysis

Acknowledgments

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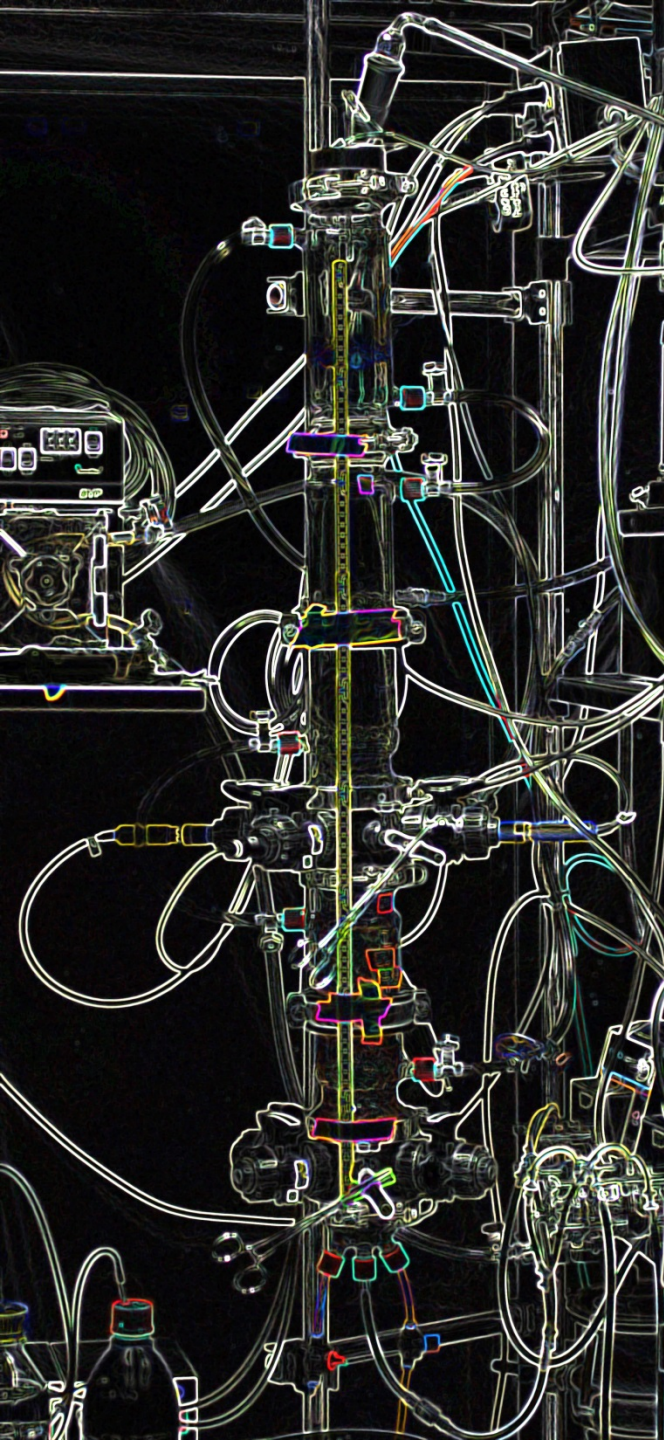
Christof Holliger



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attention !