



A core-microbiome approach to identify key microbes and interactions in bioanode microbial communities

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Elie Desmond-Le Quéméner, Jean-Clément Flayac, Eric Trably, Nicolas Bernet. A core-microbiome approach to identify key microbes and interactions in bioanode microbial communities. EU-ISMET 2018, 4. European Meeting of International Society for Microbial Electrochemistry and Technology, International Society for Microbial Electrochemistry and Technology (ISMET). INT., Sep 2018, Newcastle, United Kingdom. hal-02737302

HAL Id: hal-02737302

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Submitted on 2 Jun 2020

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A core-microbiome approach to identify key microbes and interactions in mixed microbial bioanodes

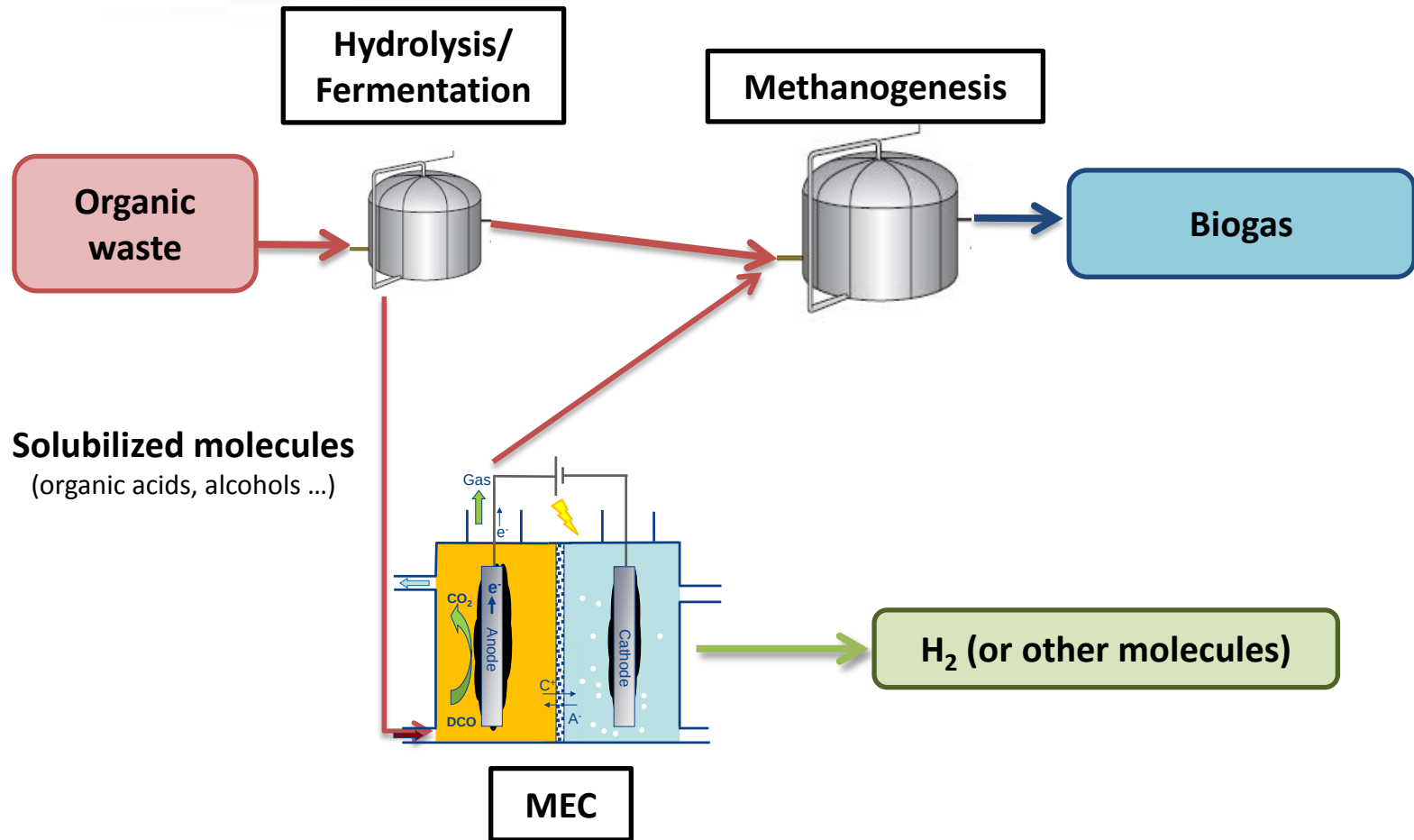
Elie Desmond-Le Quéméner, Clément Flayac, Eric Trably,
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Context: BES for waste treatment?

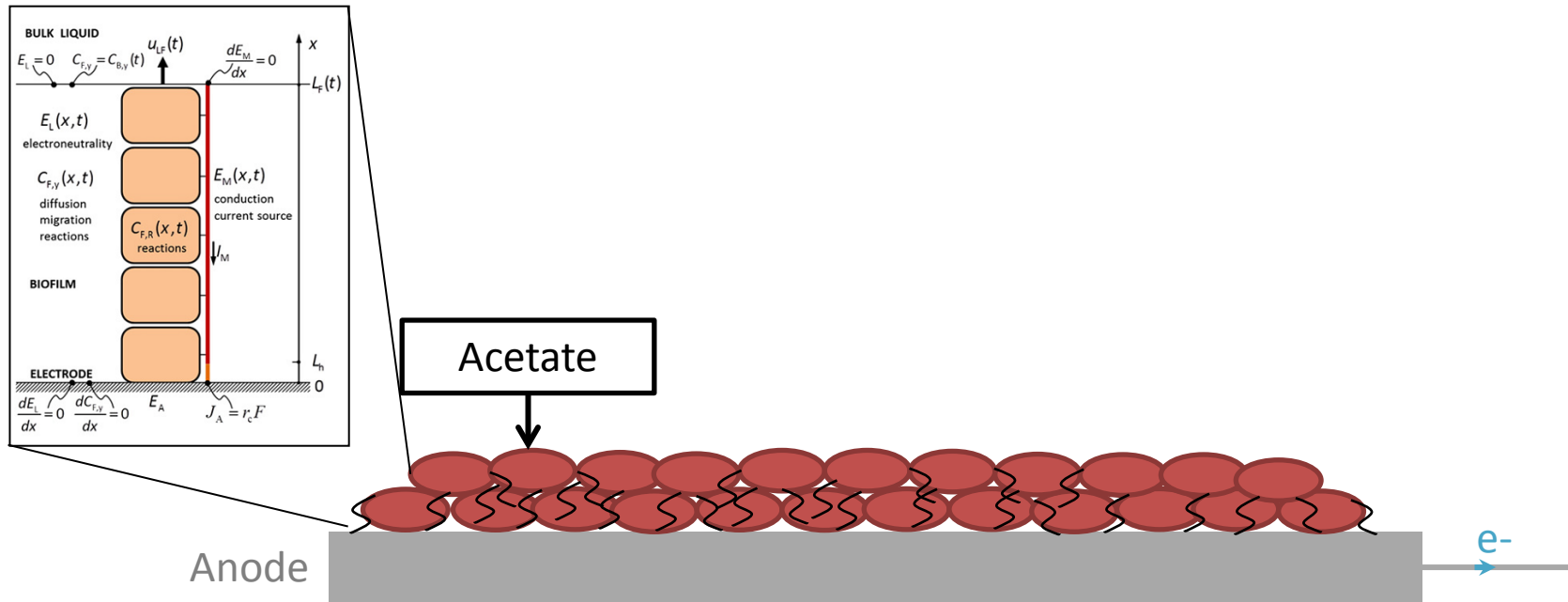
Feeding MEC with organic acids



Context: behavior of a BES fed with various organic acids?

Geobacter biofilms fed with acetate

B. Korth et al.,
Bioelectrochemistry 106
(2015) 194–206

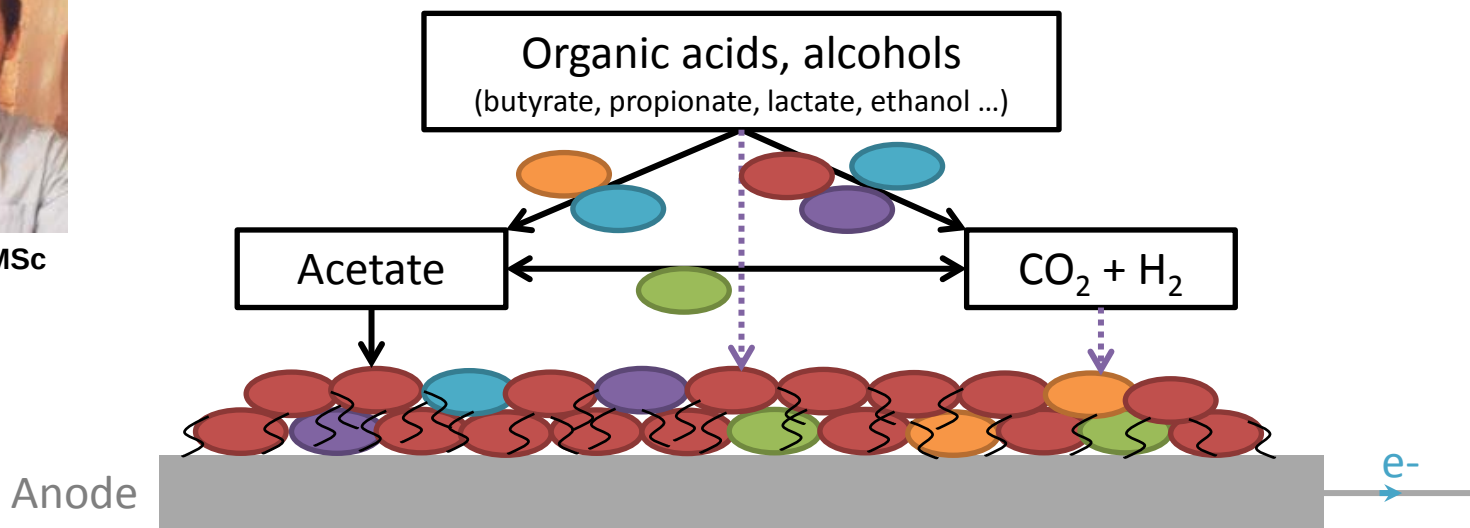


Context: behavior of a BES fed with various organic acids?

Performances and microbial community



C. Flayac, MSc

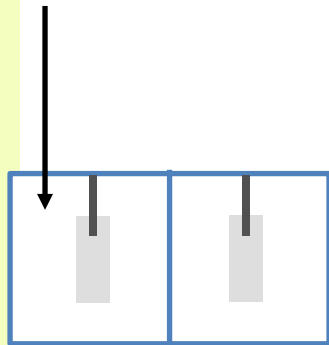


Material and methods

4 substrates with reactors in quadruplicates

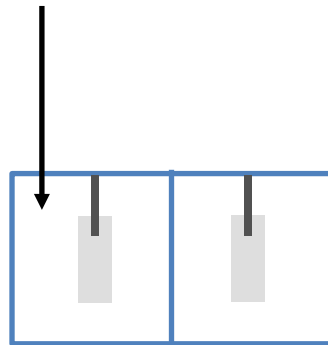
Version print

Acetate



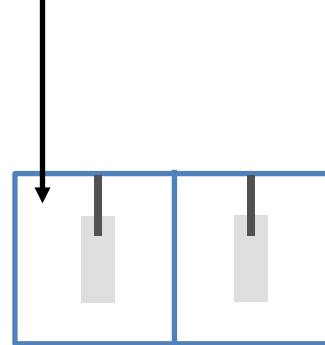
(x 4)

Lactate



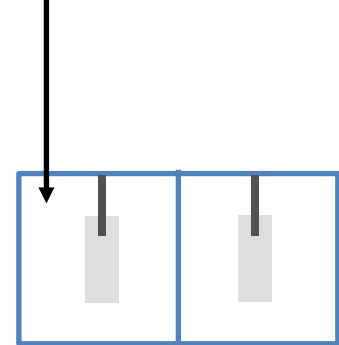
(x 4)

Propionate



(x 4)

Butyrate

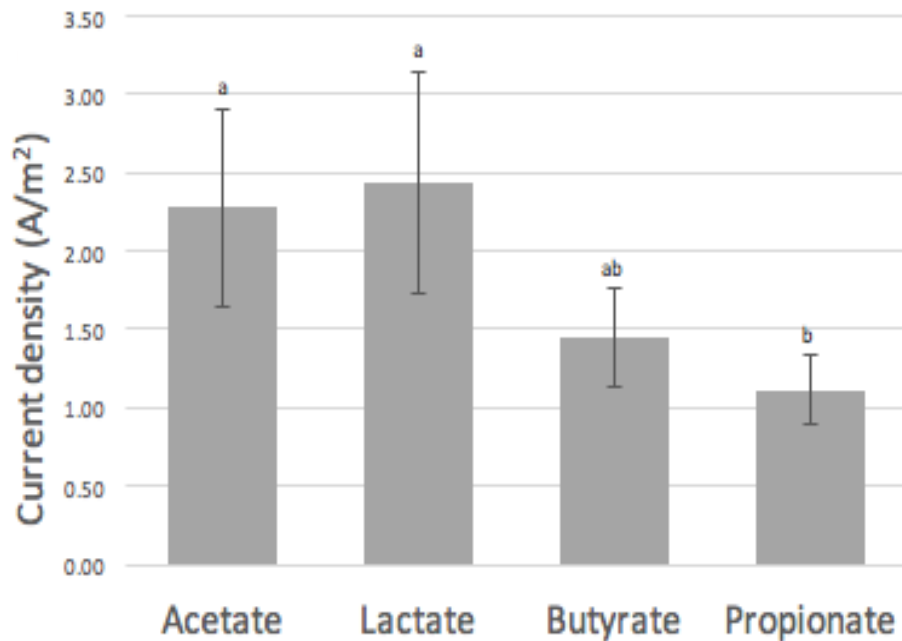


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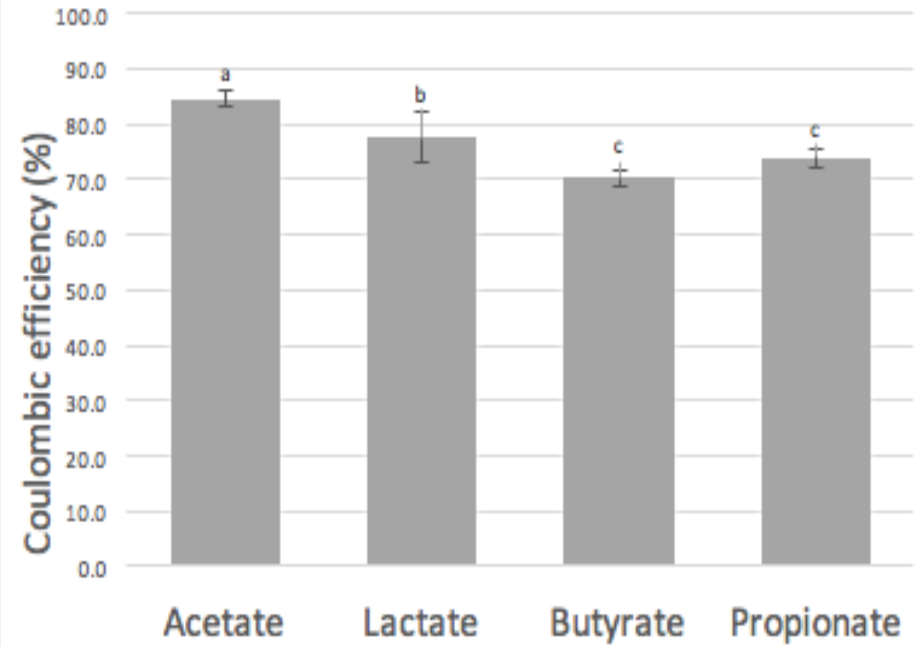
- Electrode: carbon plate
- Three-electrode setup with $E_{\text{anode}} = +450$ vs HNE
- pH=7
- Inoculum = Aerobic sludge
- [Metabolite]: 80 mM eq e-

Performances

Current densities (A/m²)

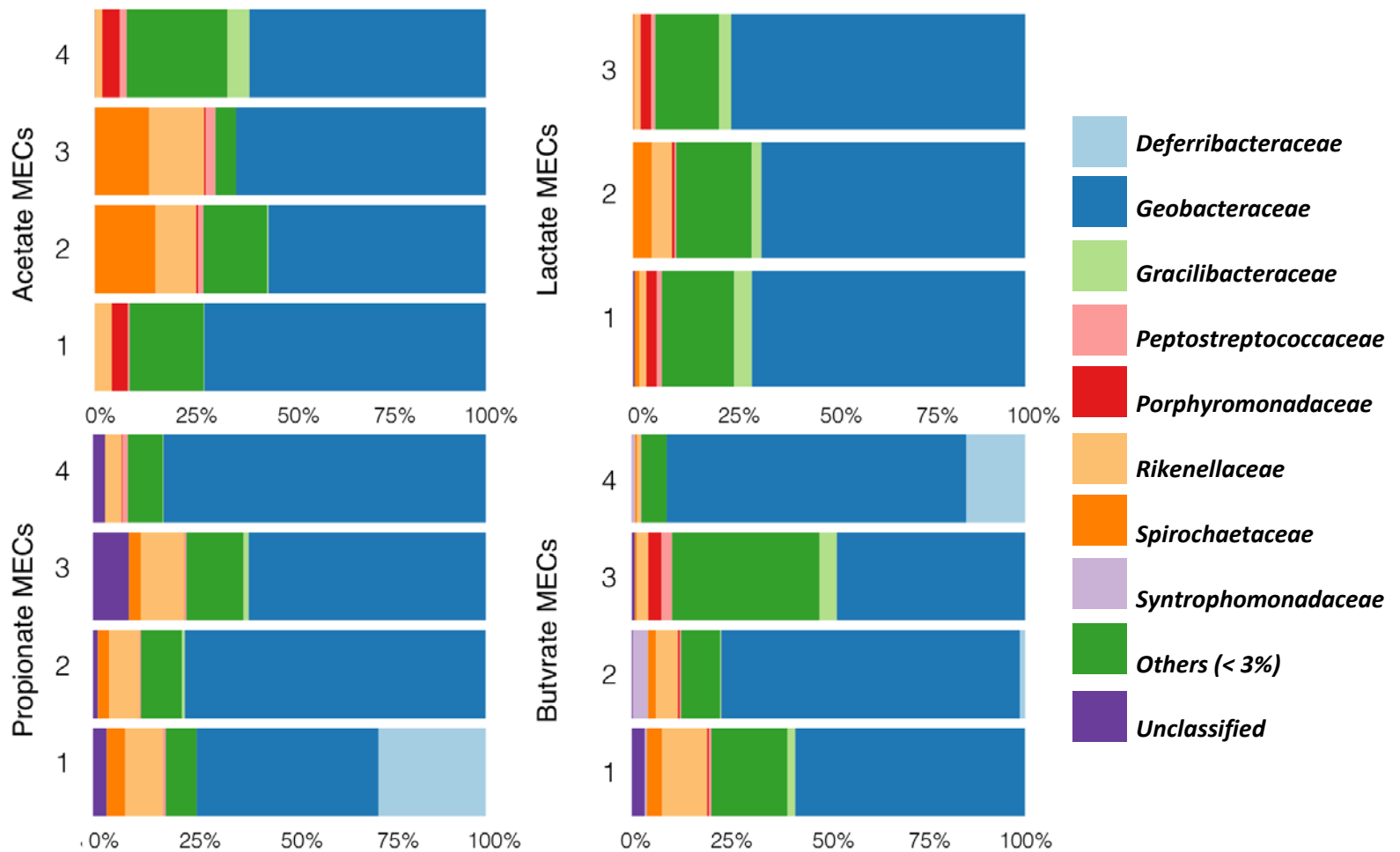


Coulombic efficiencies (%)



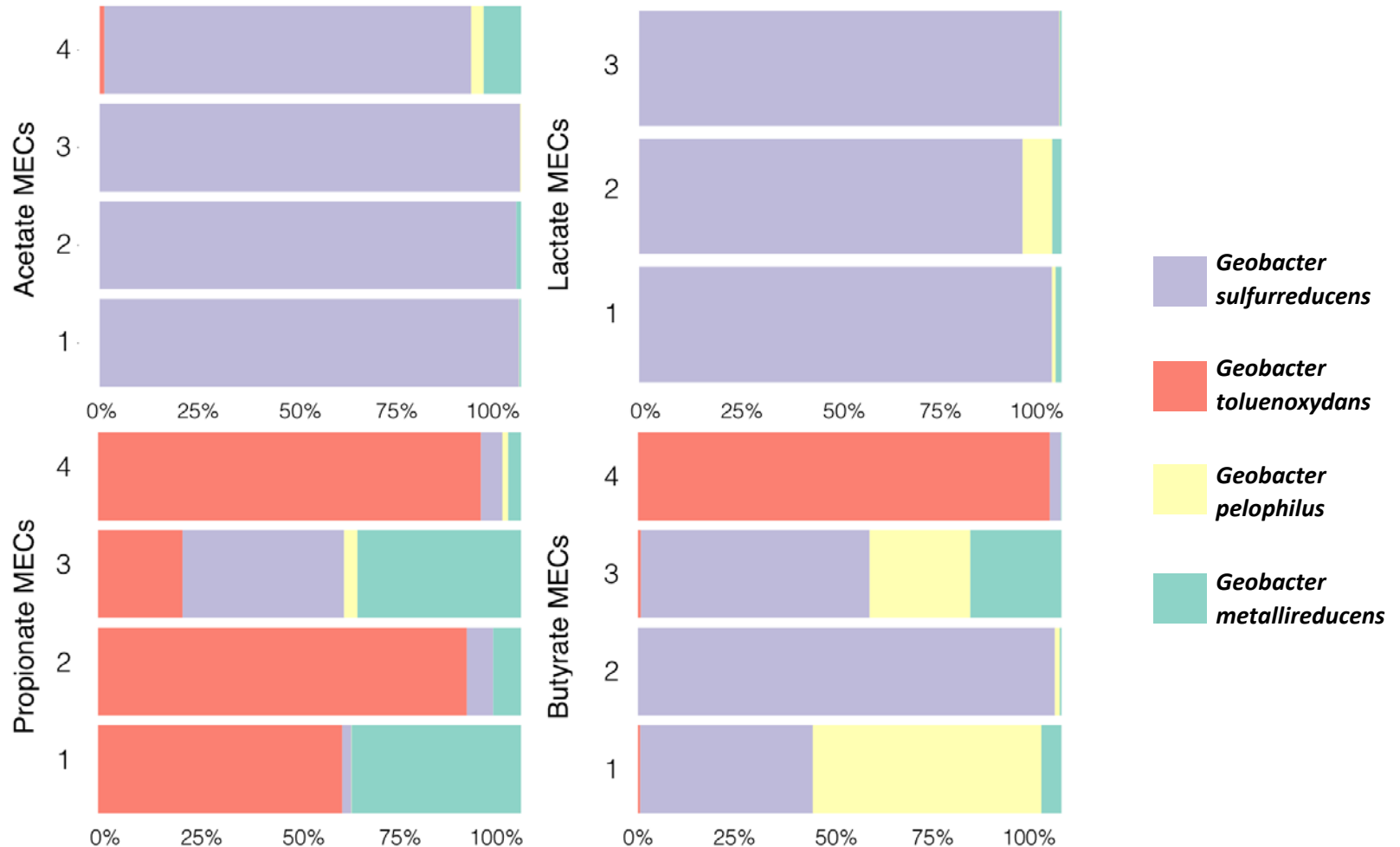
- Lactate- and Acetate-MECs had best performances

Microbial diversity in biofilms



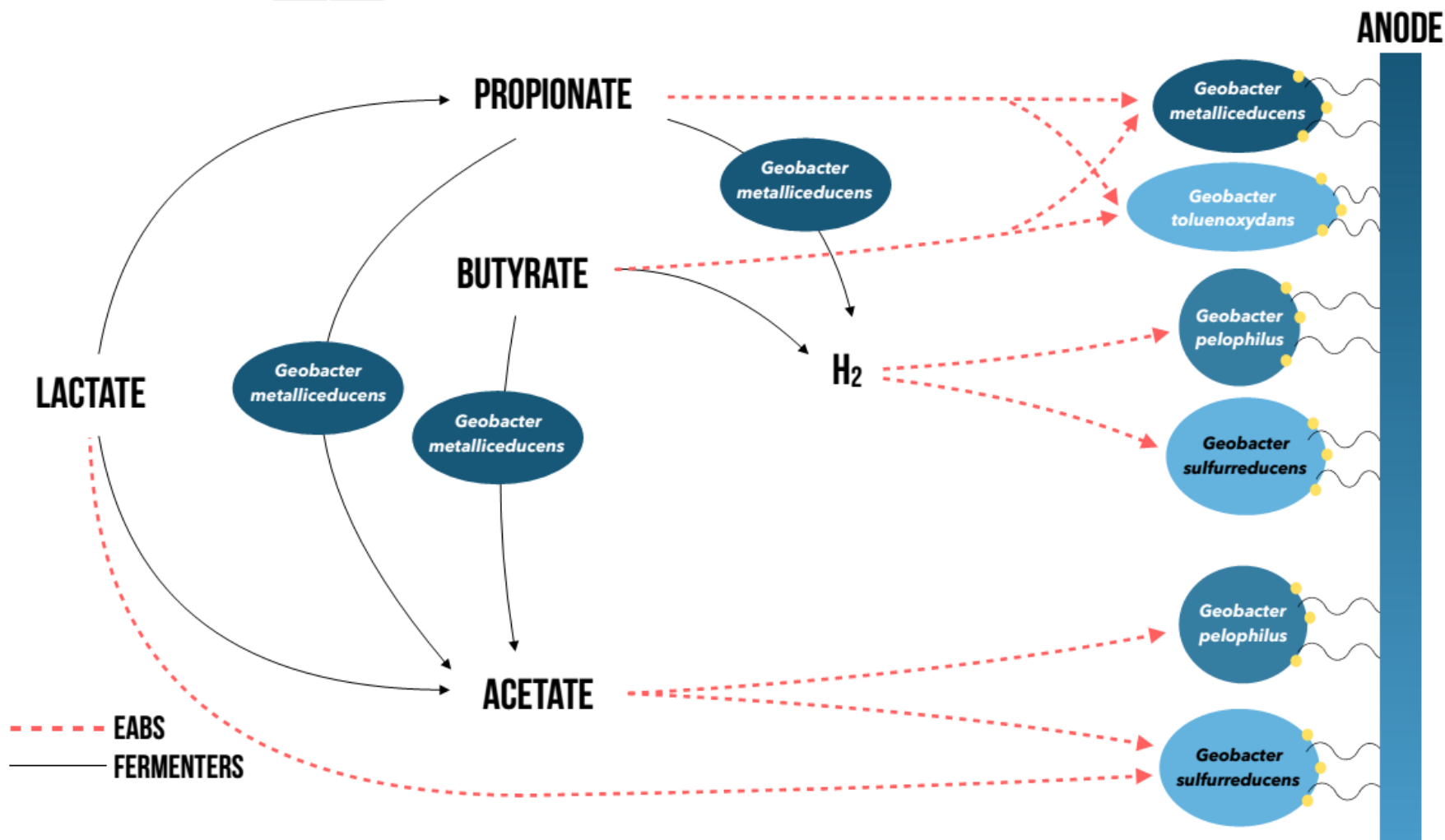
Dominance of the *Geobacteraceae* family

Diversity in the Geobacteraceae family



- **Acetate-MECs:** *G.sulfurreducens*
- **Lactate-MECs:** *G.sulfurreducens*
- **Propionate- & Butyrate-MECs:** Species mix

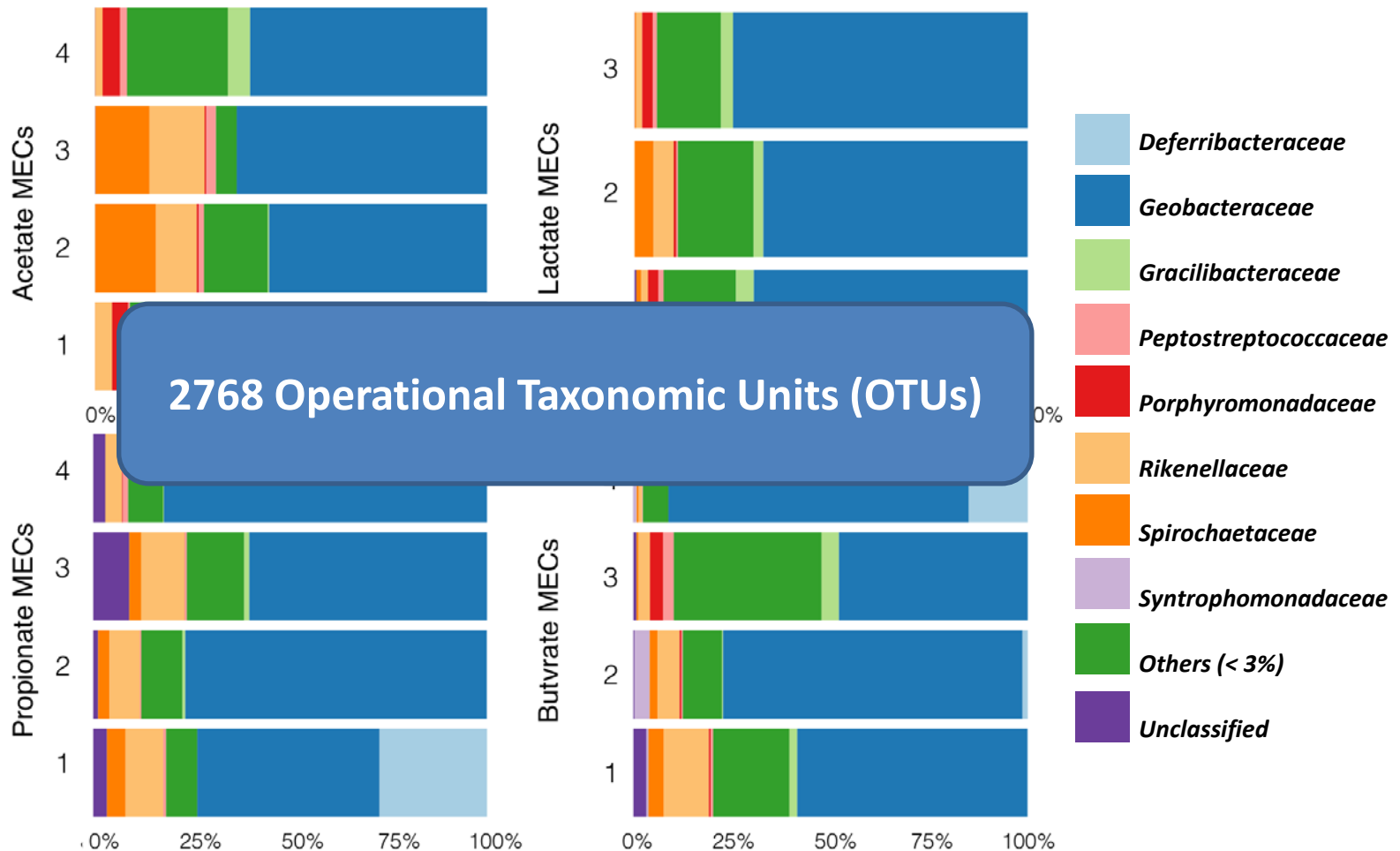
Possible pathways for organic acids oxidation



C. Flayac et al., Bioelectrochemistry 123 (2018) 219–226

Microbial diversity in biofilms

Interaction network beyond the Geobacteraceae family?



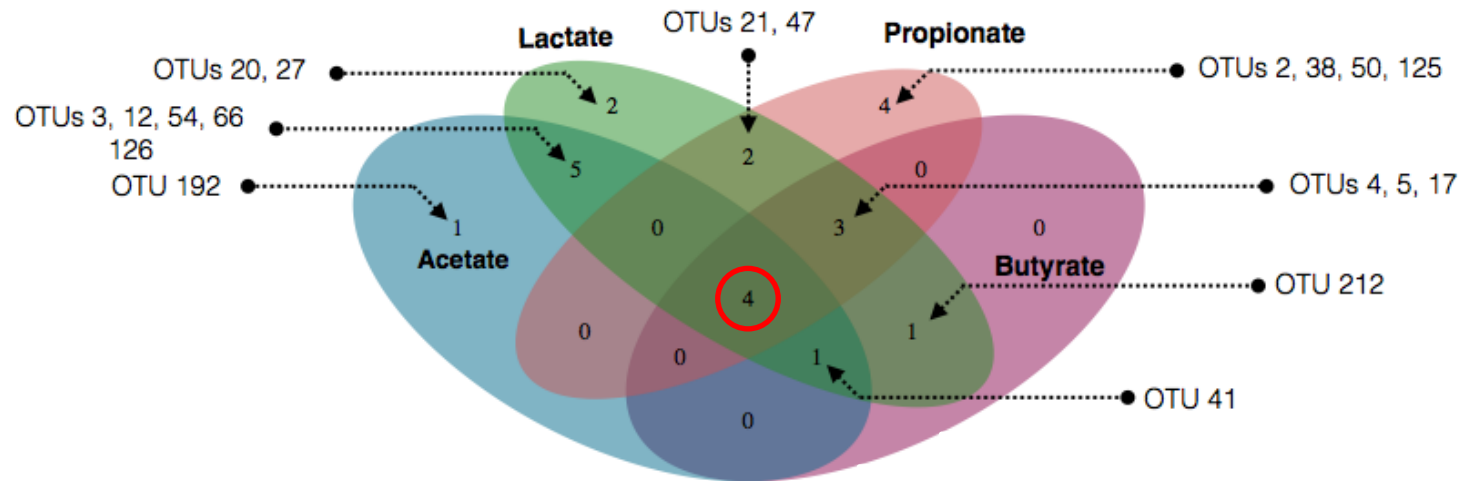
Anode Butyrate

Anode Propionate

**Core
microbio
me**

Anode Acetate

Anode Lactate

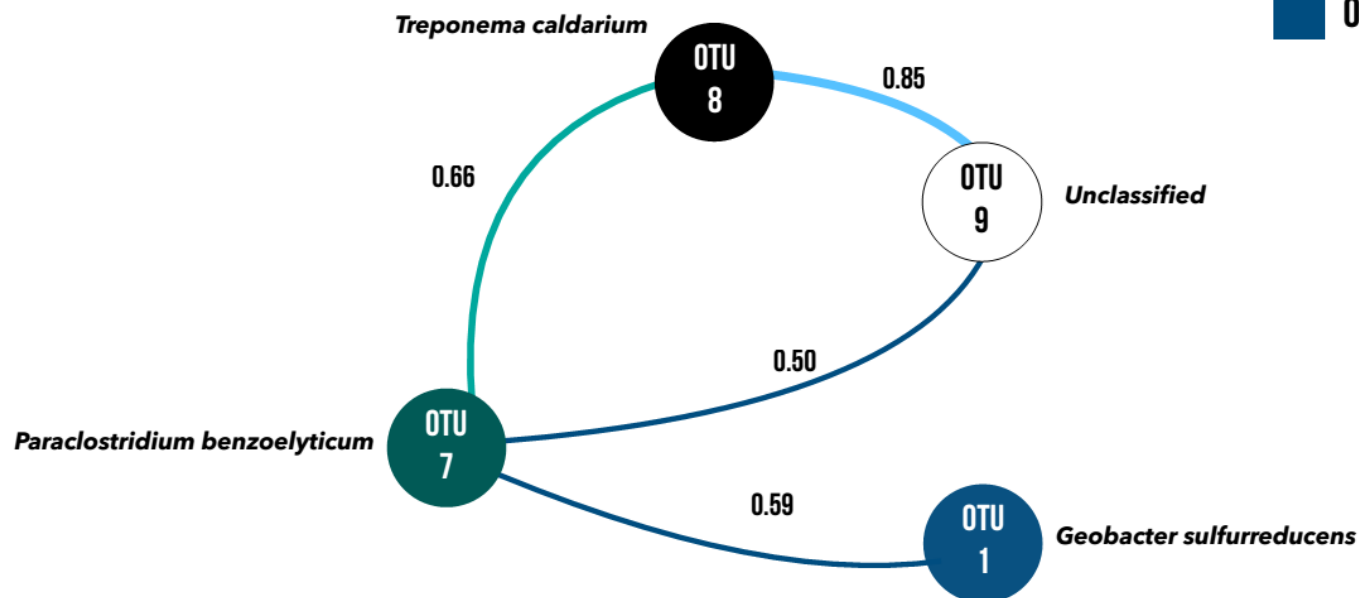
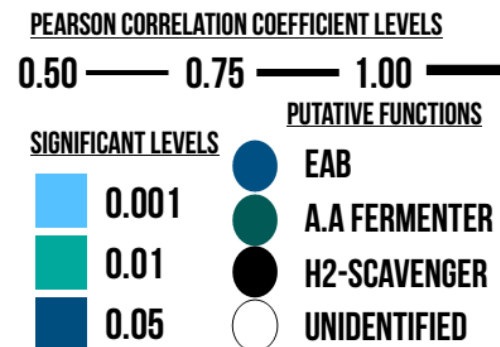


Biofilm core-OTUs

Possible functions

Taxa	OTU n° [%id]	Probable role	Substrat(s)	Product(s)	Ref.
<i>Geobacter sulfurreducens</i>	1 [100]	Anode respiration	Acetate, Formate, Lactate, H ₂	e ⁻ , H ₂ ?, CO ₂	(Bond and Lovley, 2003)
<i>Paraclostridium benzoelyticum</i>	7 [100]	Fermentation	Amino acids	H ₂ , CO ₂	(Sasi Jyothsna et al., 2016)
<i>Treponema caldarium</i>	8 [99]	Fermentation H ₂ -scavenger?	Glucose H ₂ , CO ₂ ?	H ₂ , CO ₂ , Acetate, Lactate	(Pohlschroeder et al., 1994)
unclassified Rikenellaceae	9	?	?	?	-

OTUs correlation network



Correlations with performances

Performances indices	OTU 1	OTU 7	OTU 8	OTU 9
Current density (A.m ⁻²)	-.32	-.74**	-.95***	-.79***
Coulombic efficiency (%)	.67**	.57*	.49	.19

Abundances of OTUs 8 (*Treponema caldarium*) and 9 (unclassified Rikenellaceae) are anti-correlated with current densities

- Slow oxidation mechanisms ?
- Mechanical disturbance of the biofilm ?
- Interactions ?

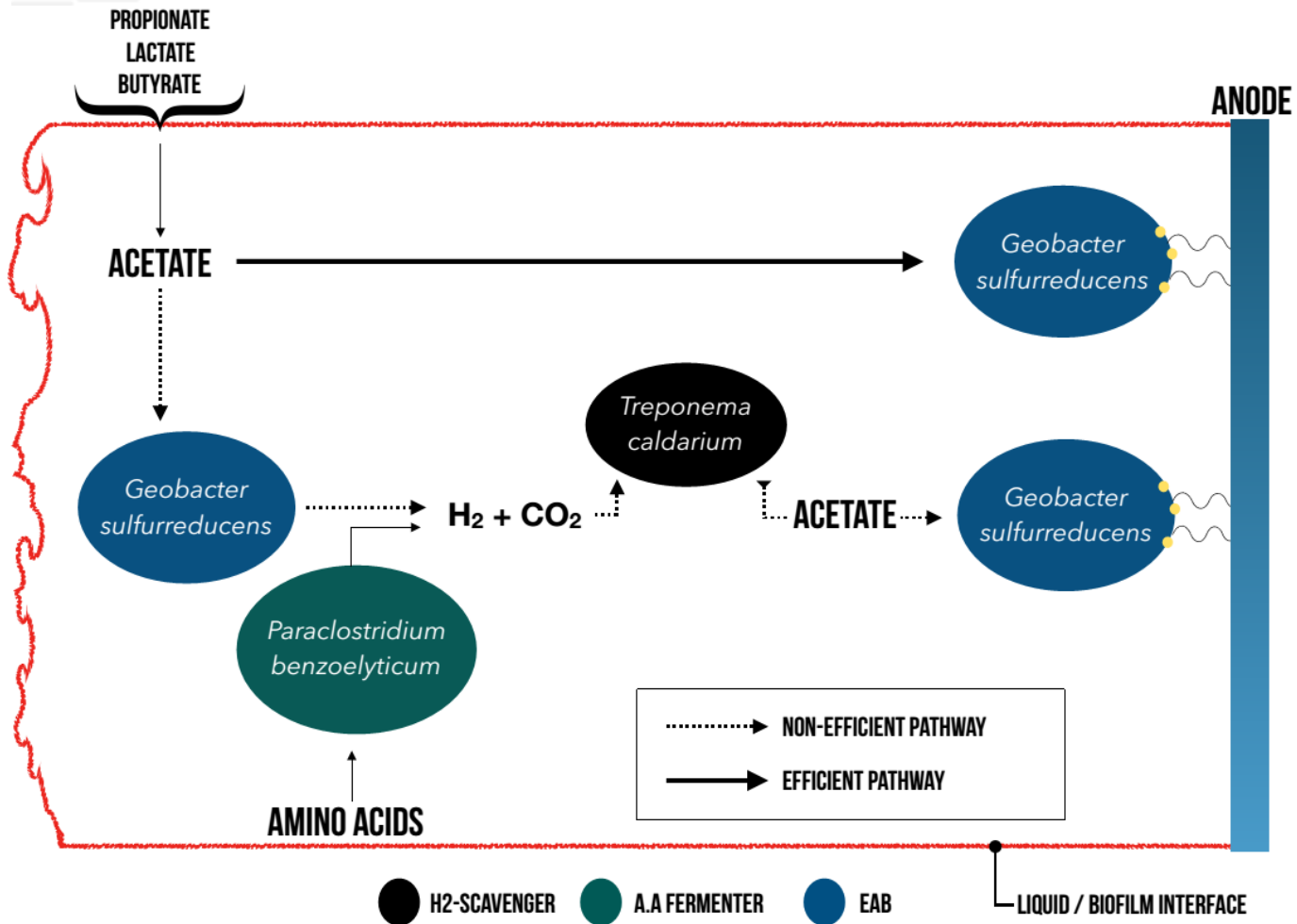


Treponema caldarium

Pohlschroeder et al., Arch Microbiol (1994) 161:17-2

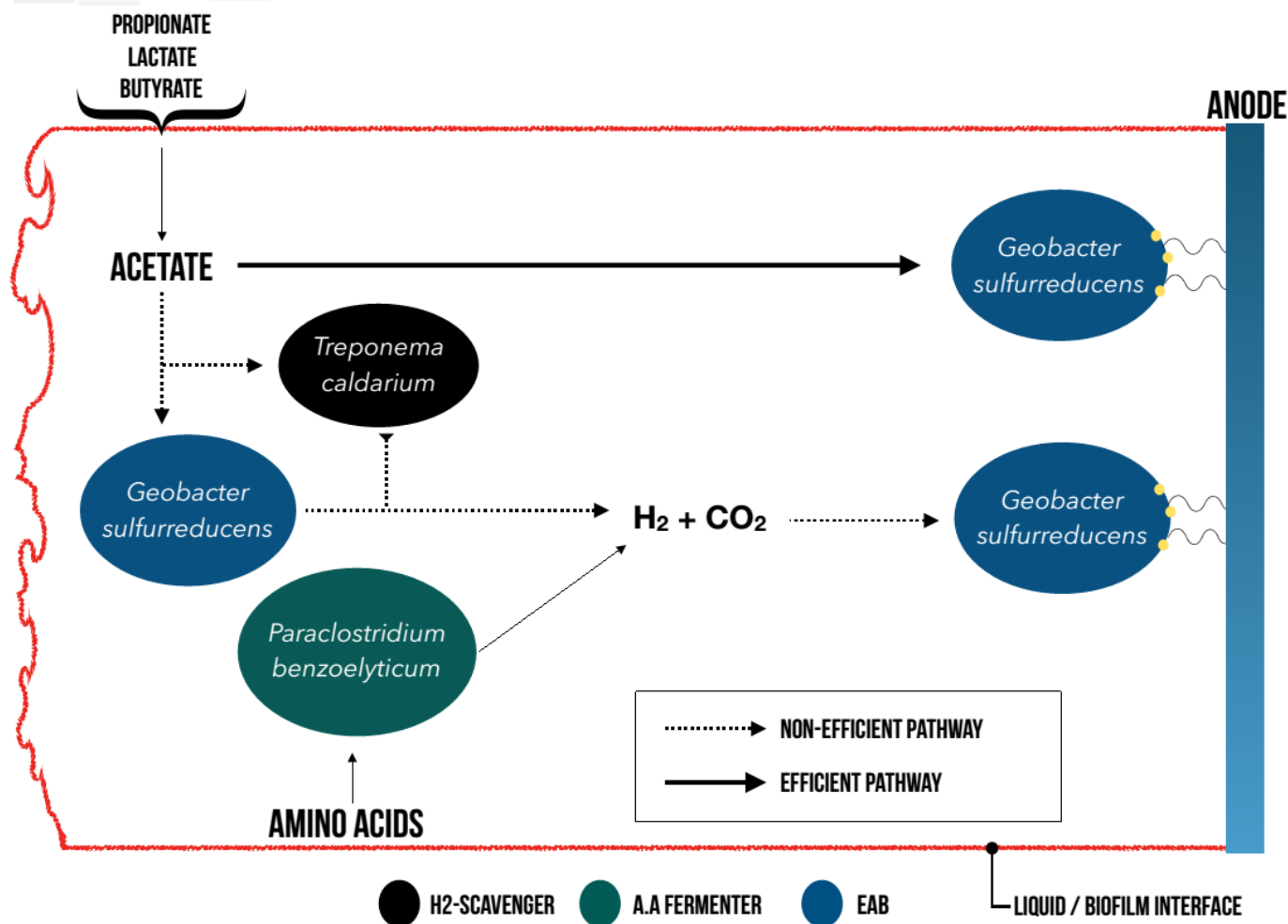
Putative biofilm pathways

Hydrogenotrophic acetogenesis by Spirochaetes?



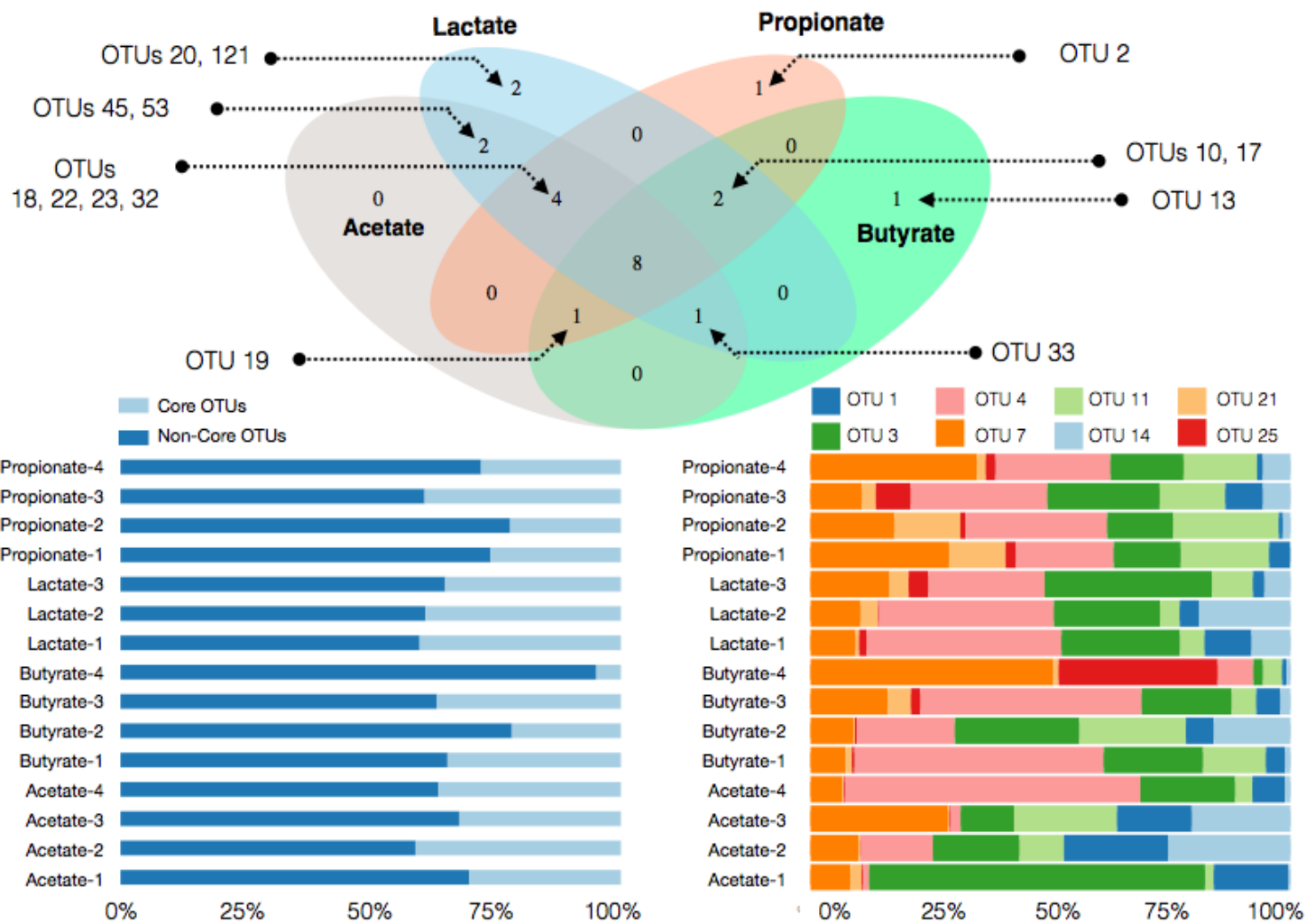
Putative biofilm pathways

Acetate oxidation by Spirochaetes?



S.-H. Lee et al. (2018) « Evidence of syntrophic acetate oxidation by Spirochaetes during anaerobic methane production ». *Bioresource Technology* 190 (2015) 543–549

Planktonic core-OTUs





Conclusions/perspectives

- **Statistics with replicated experiments are a power full tool** for exploring microbial diversity in bioprocesses
- **Core OTUs found in bioanodes** fed with various organic acids were: **electroactive bacteria**, **H₂ scavengers**, **acetate oxidizers** and **AA fermenters**
- **Spirochaetes may be a bioindicator of a loss of biofilm electroactivity**
 - Metabolism?
 - Mechanical disturbance of the biofilm?
- Perspective: in depth study of interactions between electroactive bacteria and other bacteria



Treponema caldarium

Pohlschroeder et al., Arch Microbiol (1994) 161:17-2

