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Metagenomic analysis on hydrogen assisted carbon dioxide fixation for biomethane production

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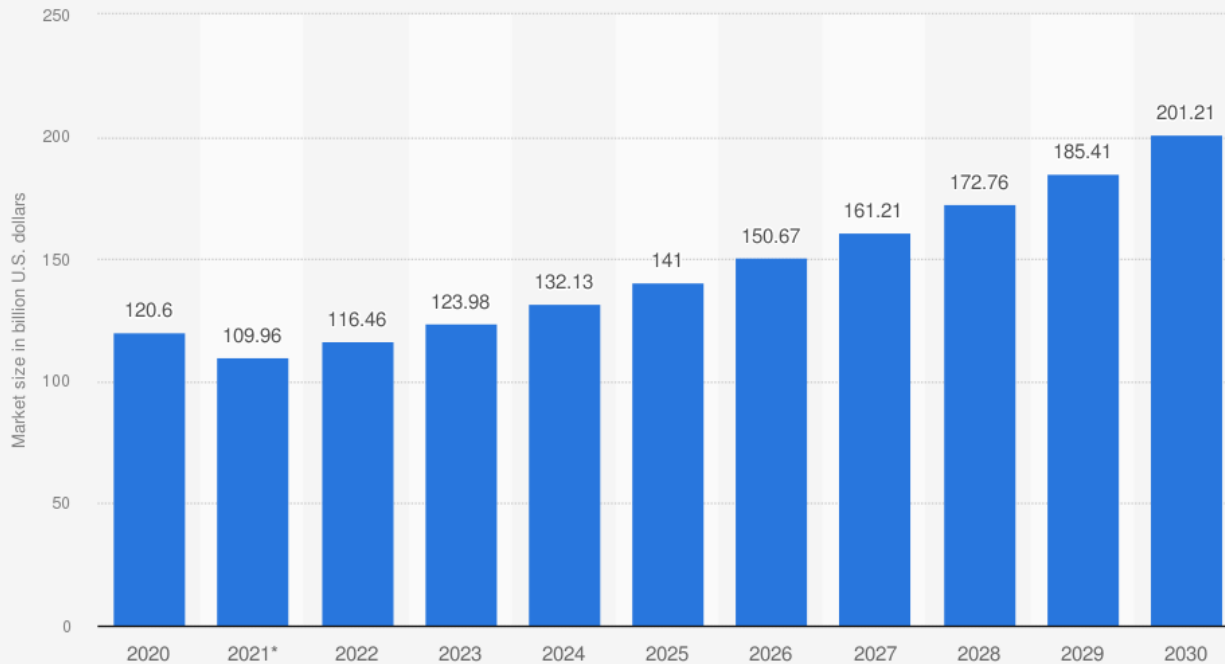
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Biofuels as a source of biogenic emissions

Market value of biofuels worldwide in 2020 and 2021, with a forecast until 2030 (in billion U.S. dollars)



Source
Precedence Research
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Additional Information:
Worldwide; 2020 and 2021

→ **Increased Biogenic Effluent Gases**

Main routes of biogenic effluent gases production

Anaerobic digestion

Anaerobic digestion is a complex biological process in which microorganisms break down organic matter in the absence of oxygen. This process leads to the production of biogas as an end product.

Main biogenic emissions: CH_4 , CO_2 and N_2O

Ethanol fermentation

Ethanol fermentation, also known as alcohol fermentation, is a metabolic process in which microorganisms, such as yeasts, convert sugars into ethanol (ethyl alcohol) and carbon dioxide in the absence of oxygen.

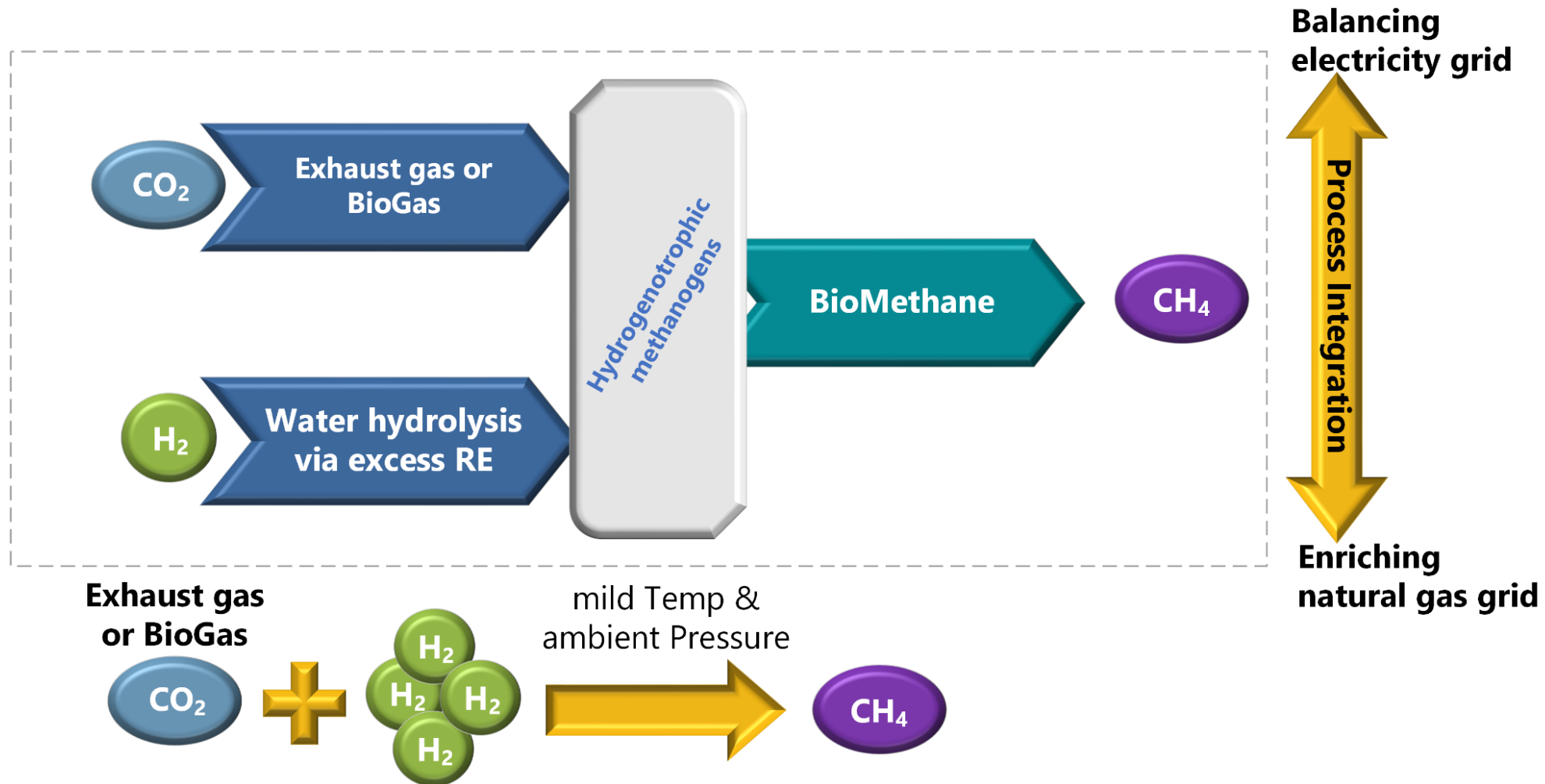
Main biogenic emissions: CO_2

Thermochemical processes

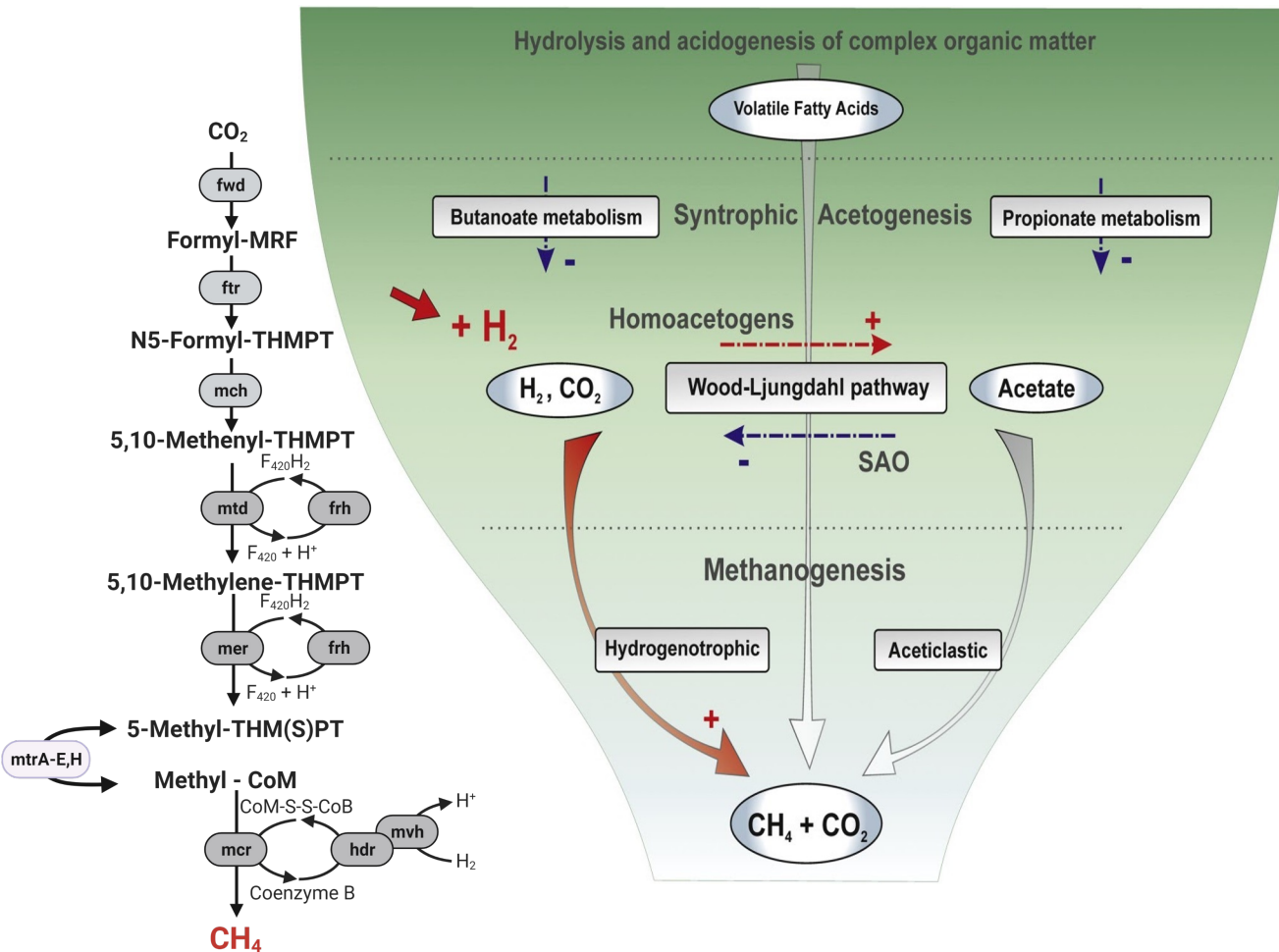
Thermochemical processes encompass various technologies, including pyrolysis, gasification, and liquefaction. The "bio" aspect in thermochemical processes comes from the use of biomass as the feedstock.

Main emissions: CO_2 and CO

H₂ assisted carbon dioxide fixation for biomethane



Important aspect for efficient biomethanation



Biological fixation of CO_2 with the use of external H_2 can follow different metabolic routes:

- **Hydrogenotrophic methanogenesis**
archaea directly convert CO_2 to CH_4
- **Homoacetogenic bacteria** convert CO_2 to acetate



if acetoclastic methanogenic archaea convert the acetate into CH_4

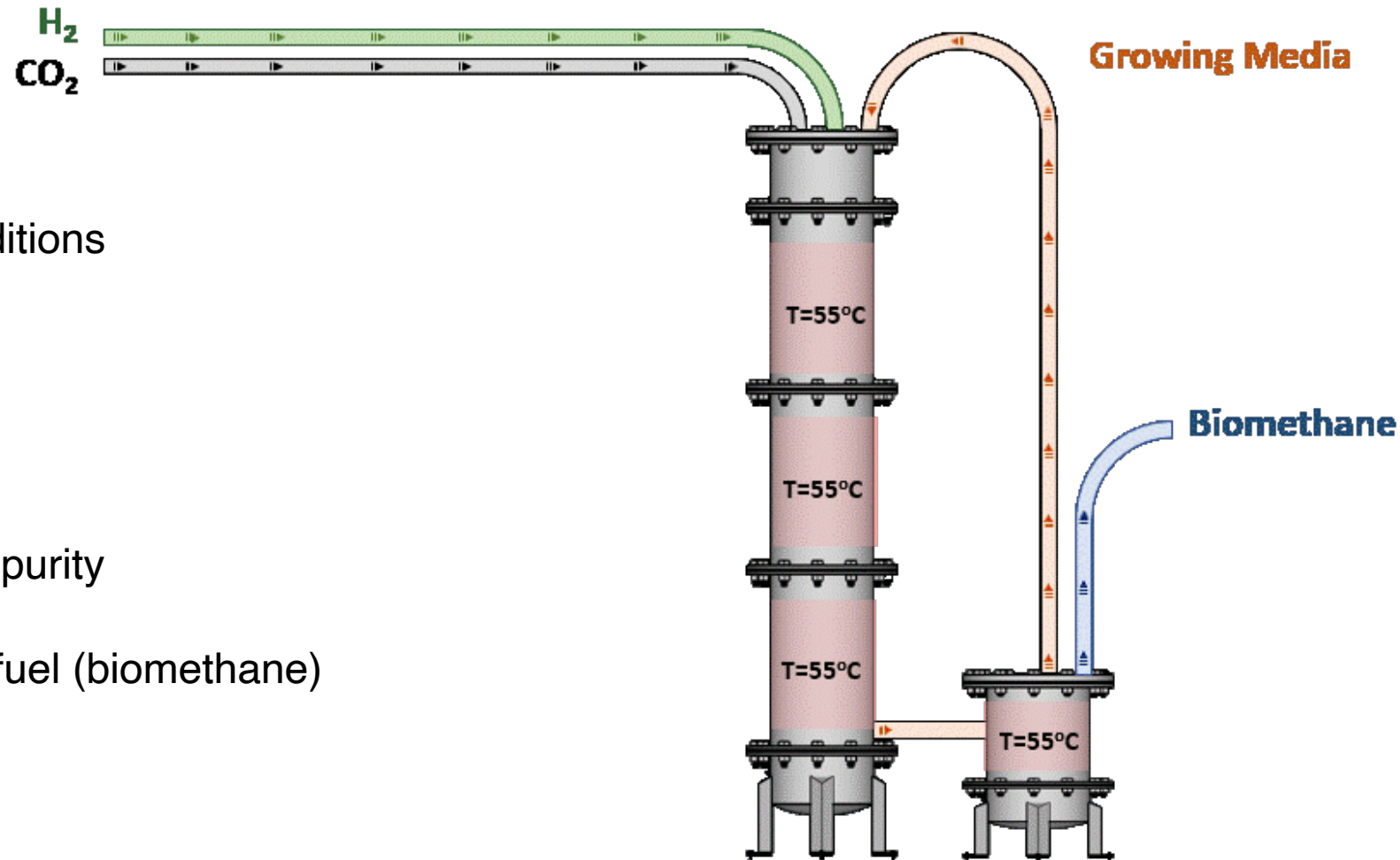


if acetate accumulates in the system

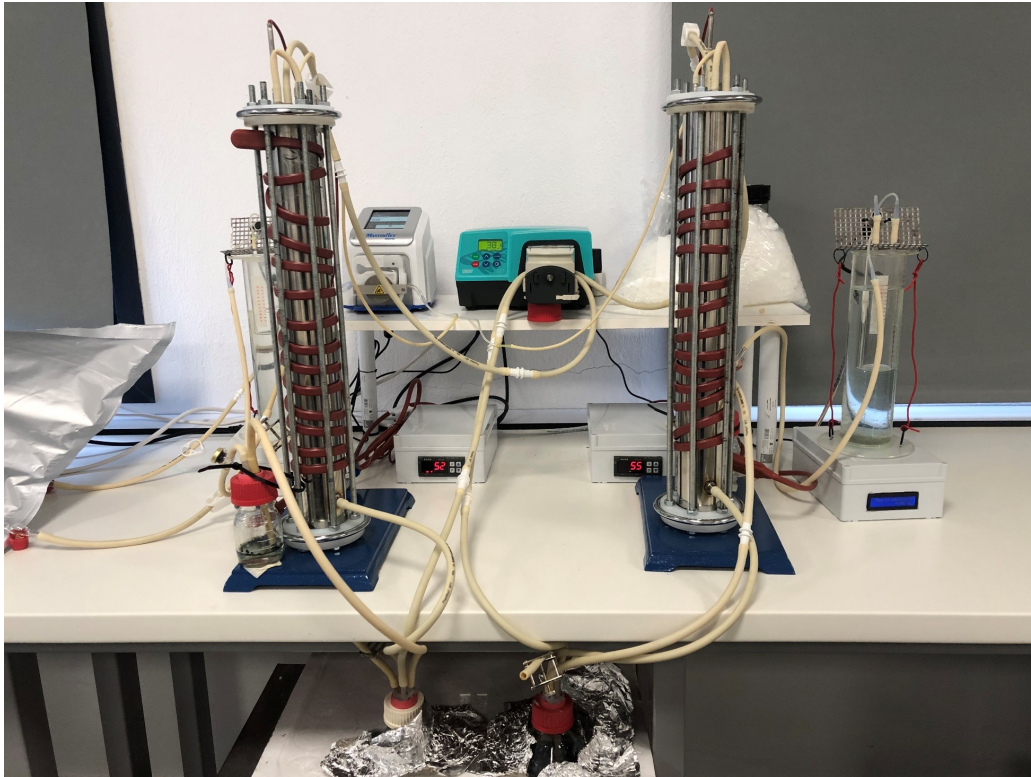
The concept of using TBR for biomethanation



- ✓ Operation in mild temperature conditions
- ✓ Operation in ambient pressure
- ✓ No need for pure microbial culture
- ✓ Process is not affected by the CO₂ purity
- ✓ Transformation of CO₂ to 3-gen biofuel (biomethane)



Aim and Objectives



Assess the **biomethanation efficiency** of Trickle Bed Reactors packed with **activated carbon** or with **Raschig rings**, in terms of:

- CH₄ concentration in the output gas
- pH and the volatile fatty acids (VFA) concentrations
- Microbial community structure

Operating conditions

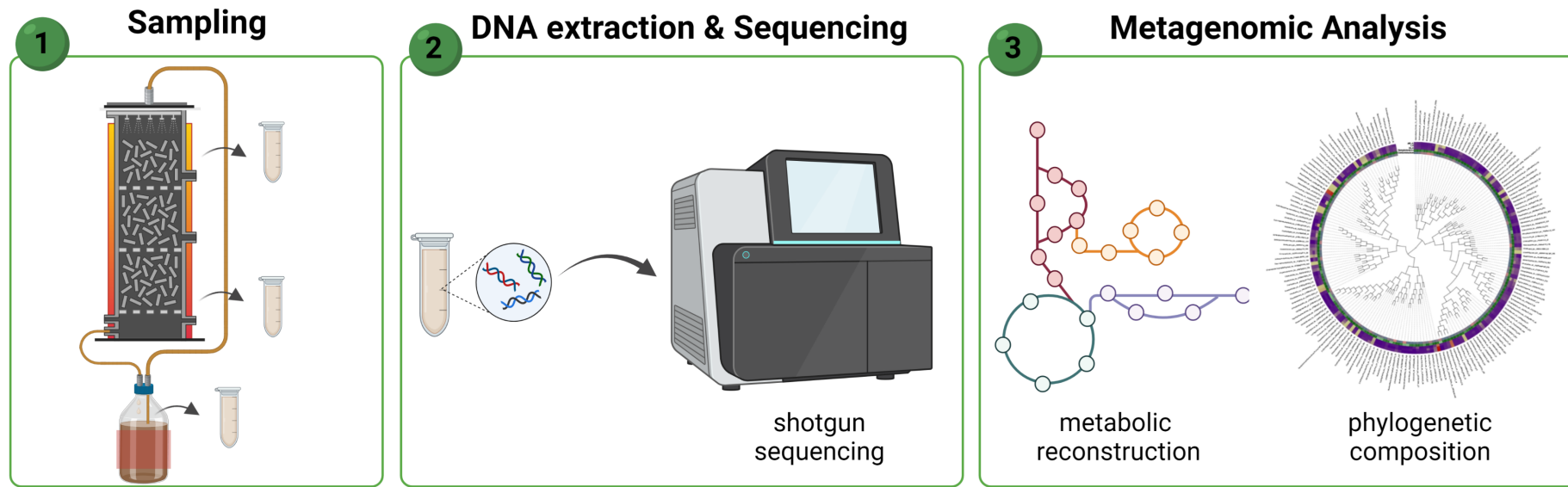
- Temp: 55°C
- GRT: 12-8-10-6-4-3-2-1 h
- Packing material
 - TBR1: activated carbon pellet
 - TBR2: raschig rings
- Metagenomic Microbial analyses

Materials and Methods

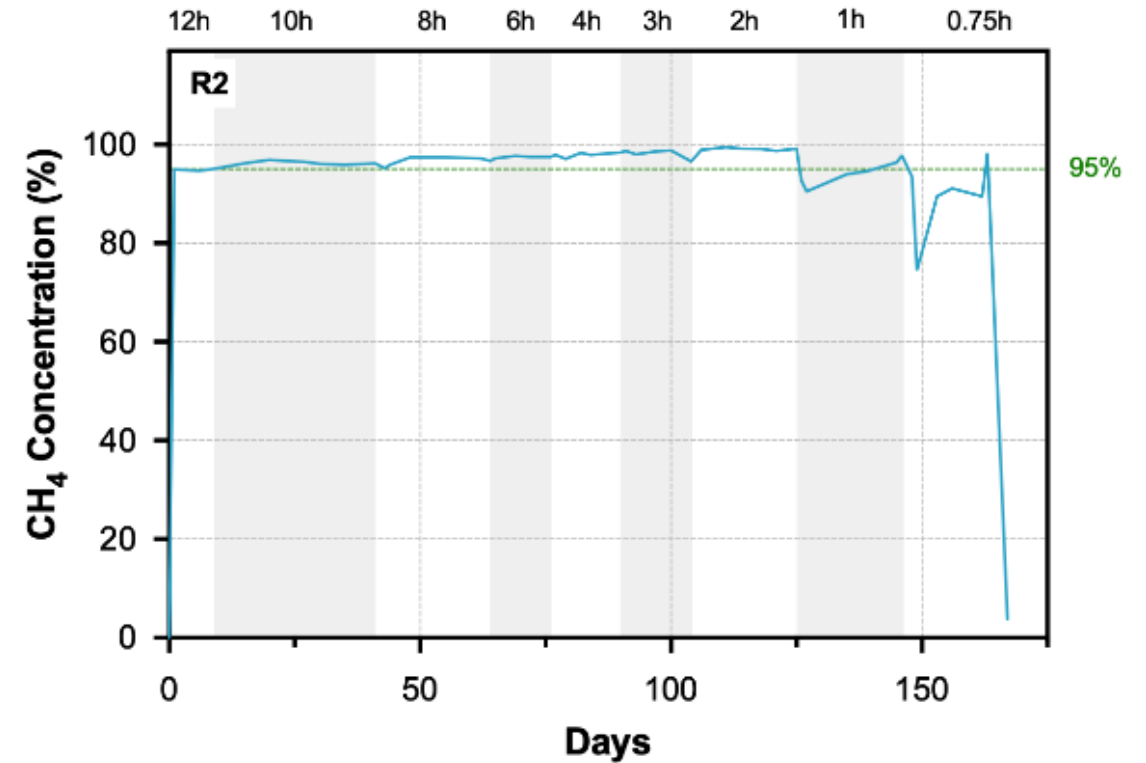
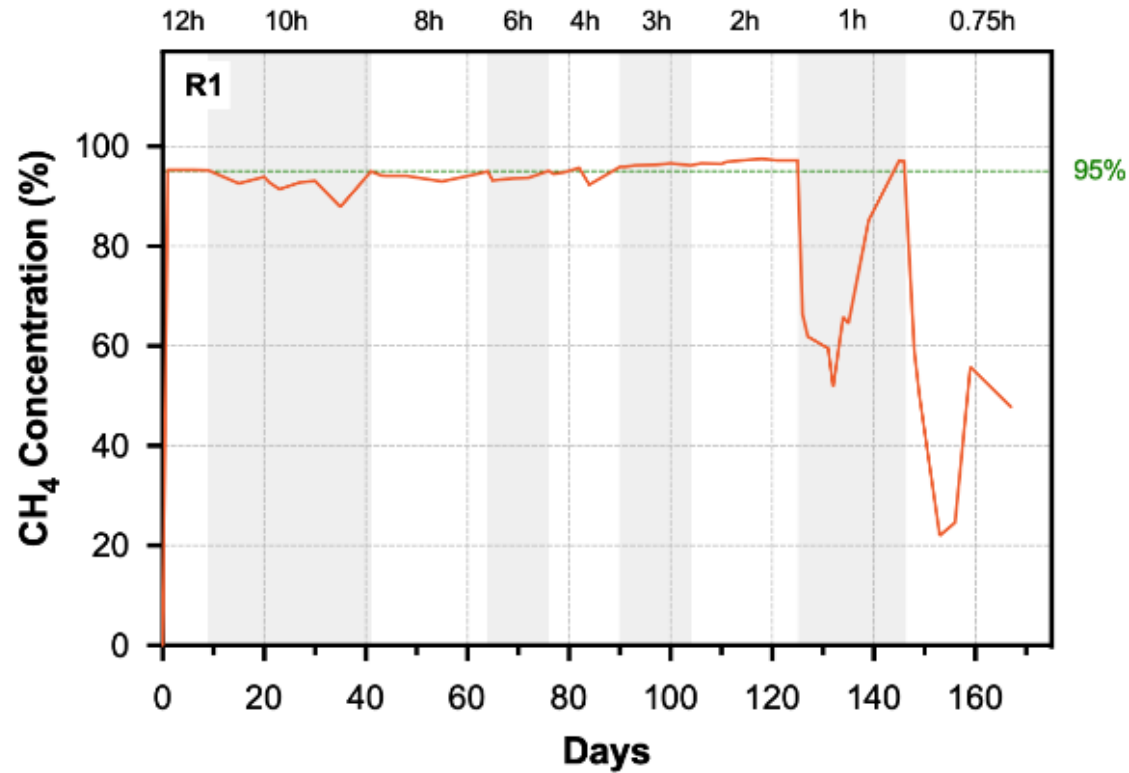
Genomic Samples:

- Initial inoculum
- Biofilm in the upper part of each TBR
- Biofilm in the lower part of each TBR
- Liquid (planktonic cells) of each TBR

Under steady state
conditions in the GRT of 1h

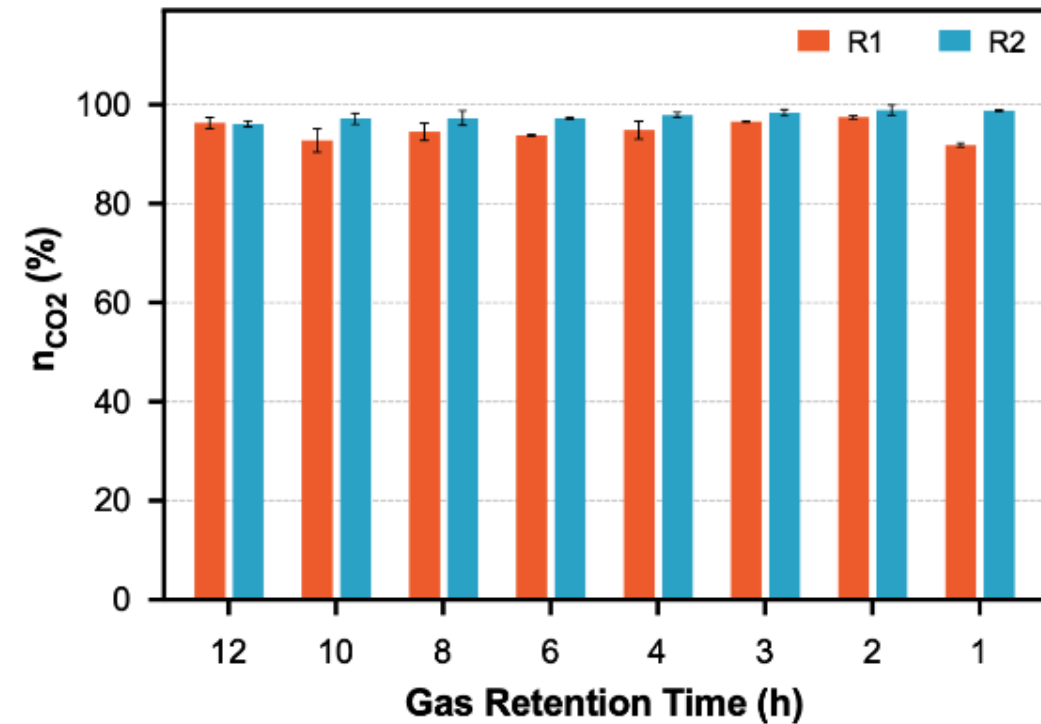
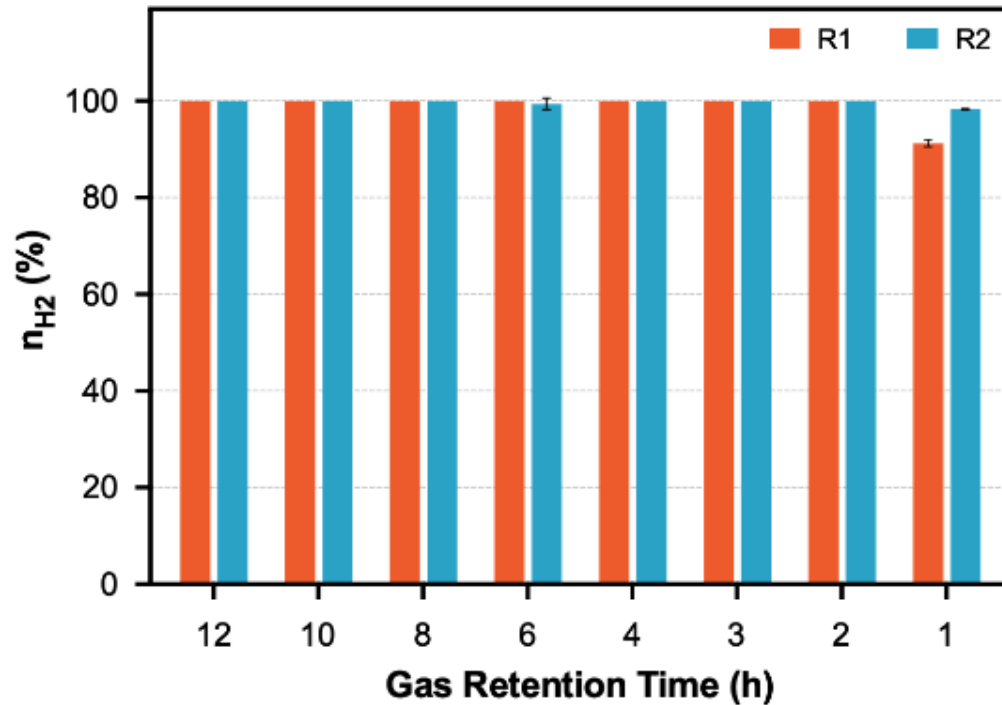


Biomethane production – CH₄ (%) in the output gas



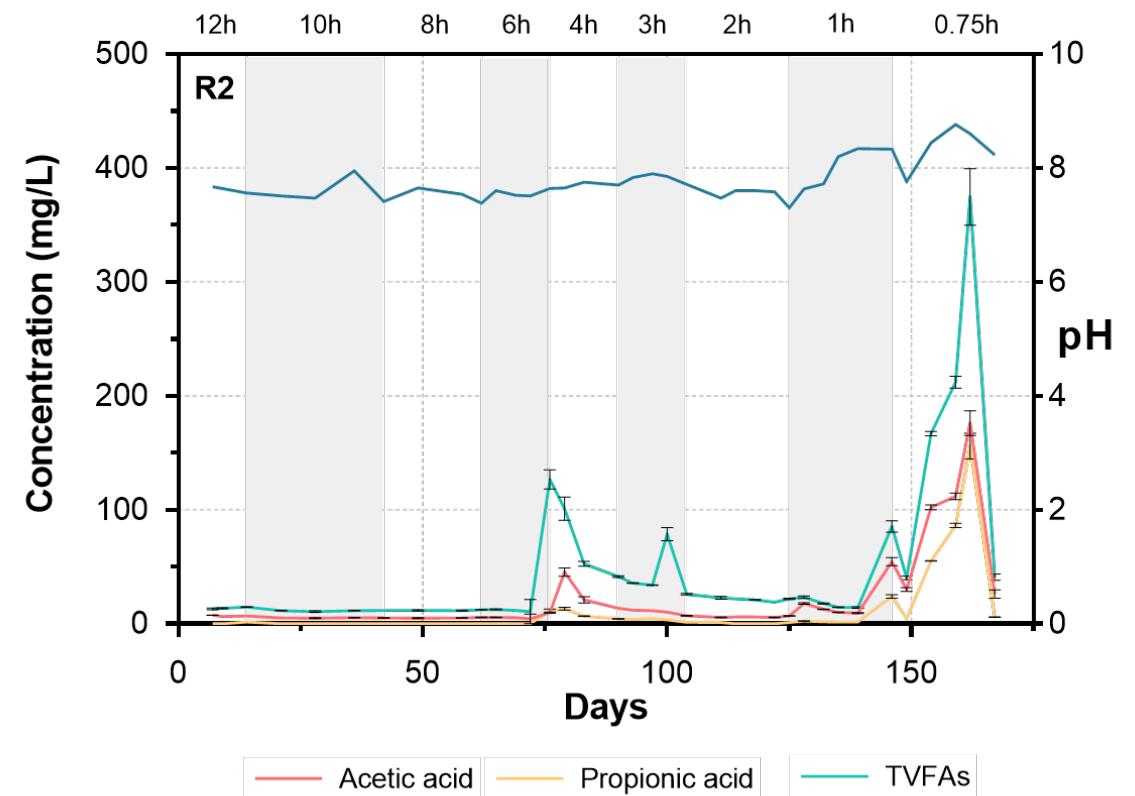
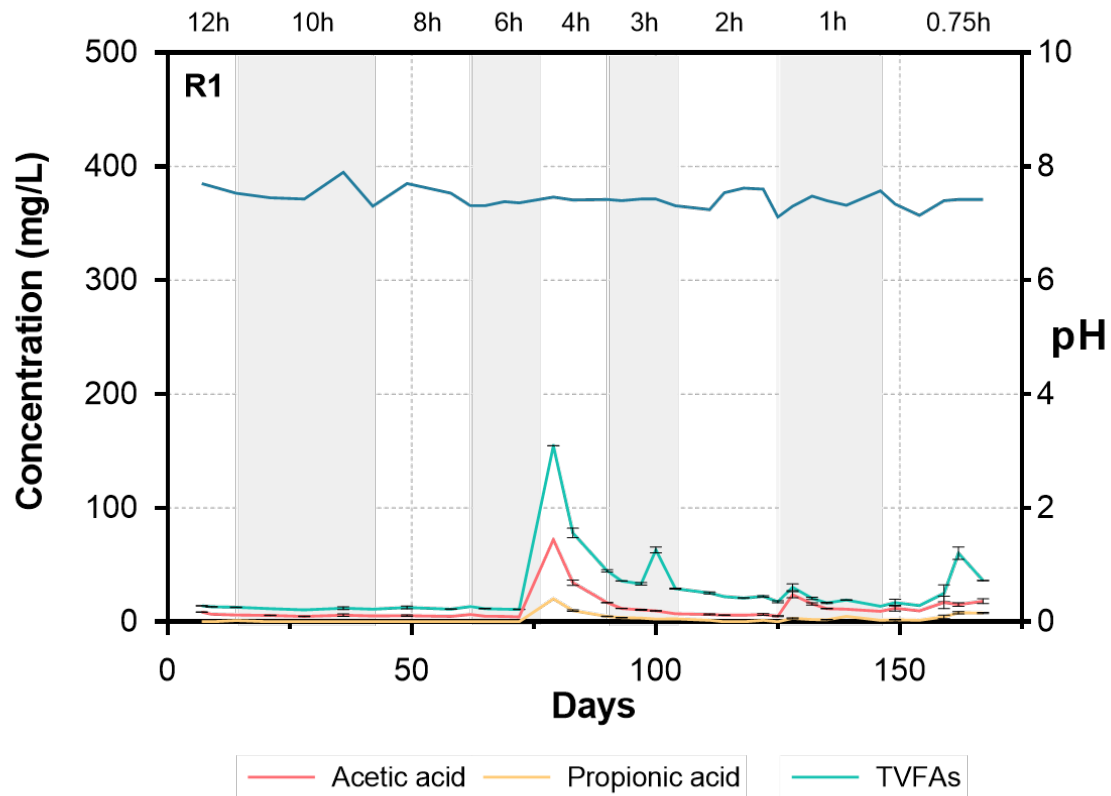
Concentration of methane at the output gas of TR1 (carbon pellets) and TR2 (raschig rings) during the different Gas Retention Times.

Biomethane production – CO₂ and H₂ efficiencies



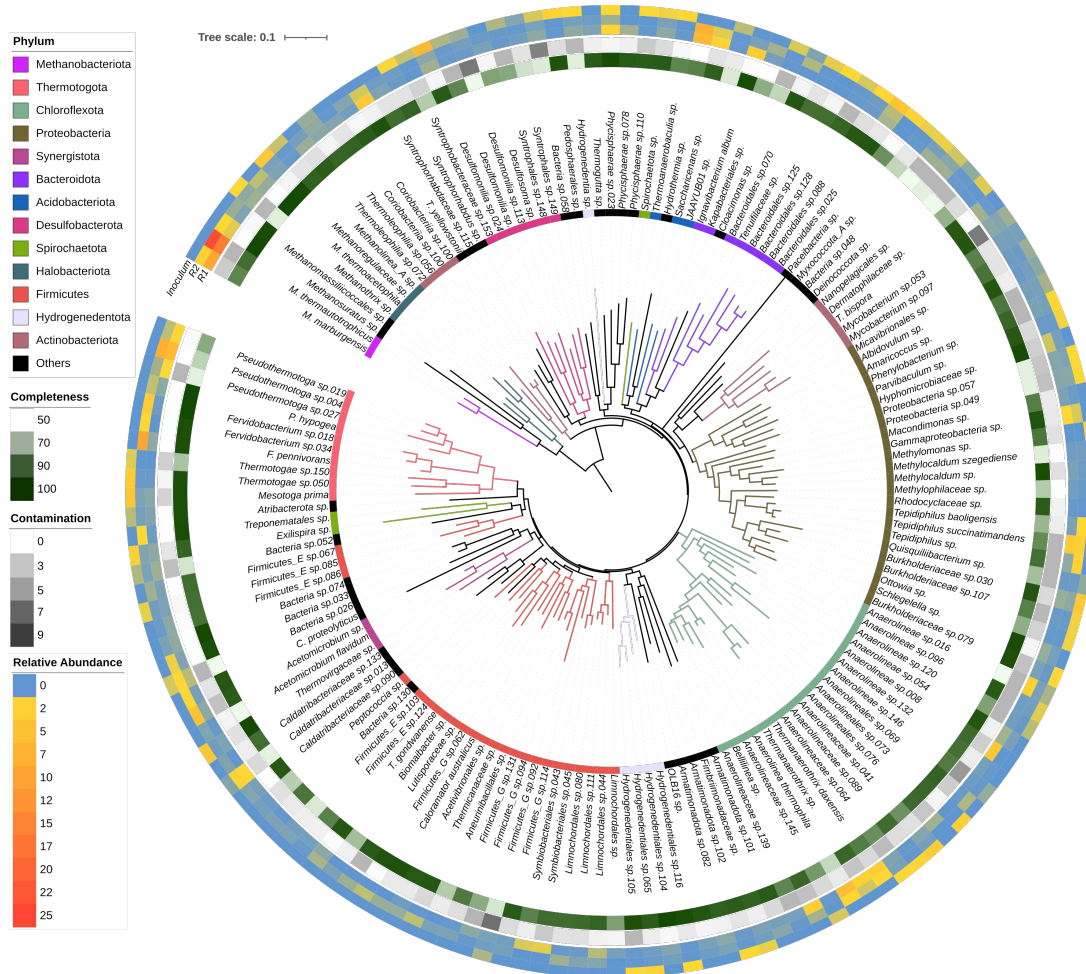
Efficiency of CO₂ capture and H₂ conversion rates in TR1 (carbon pellets) and TR2 (raschig rings) during the different Gas Retention Times.

Biomethanation performance – pH and VFA



pH and VFA concentrations of (carbon pellets) and TR2 (raschig rings) during the different Gas Retention Times.

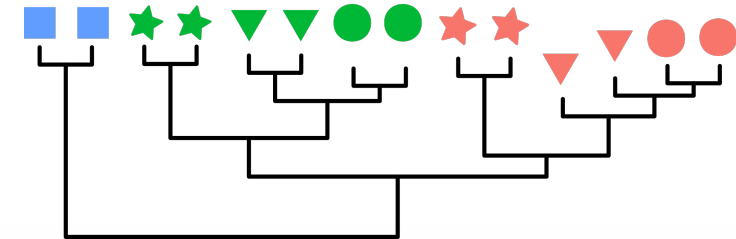
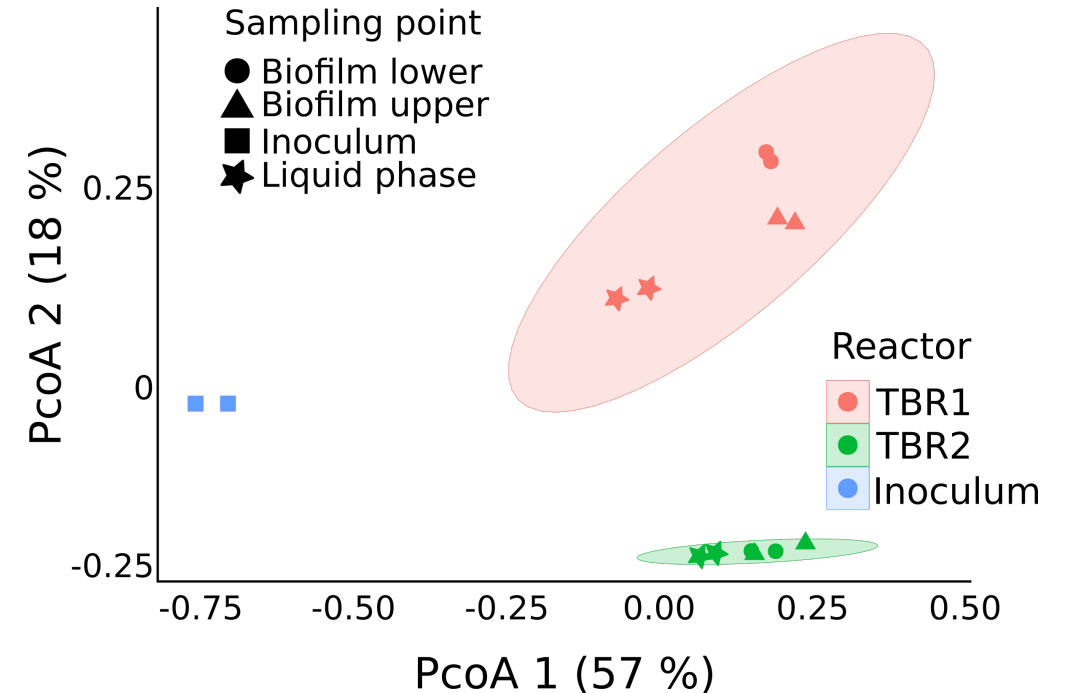
Overview of microbial community



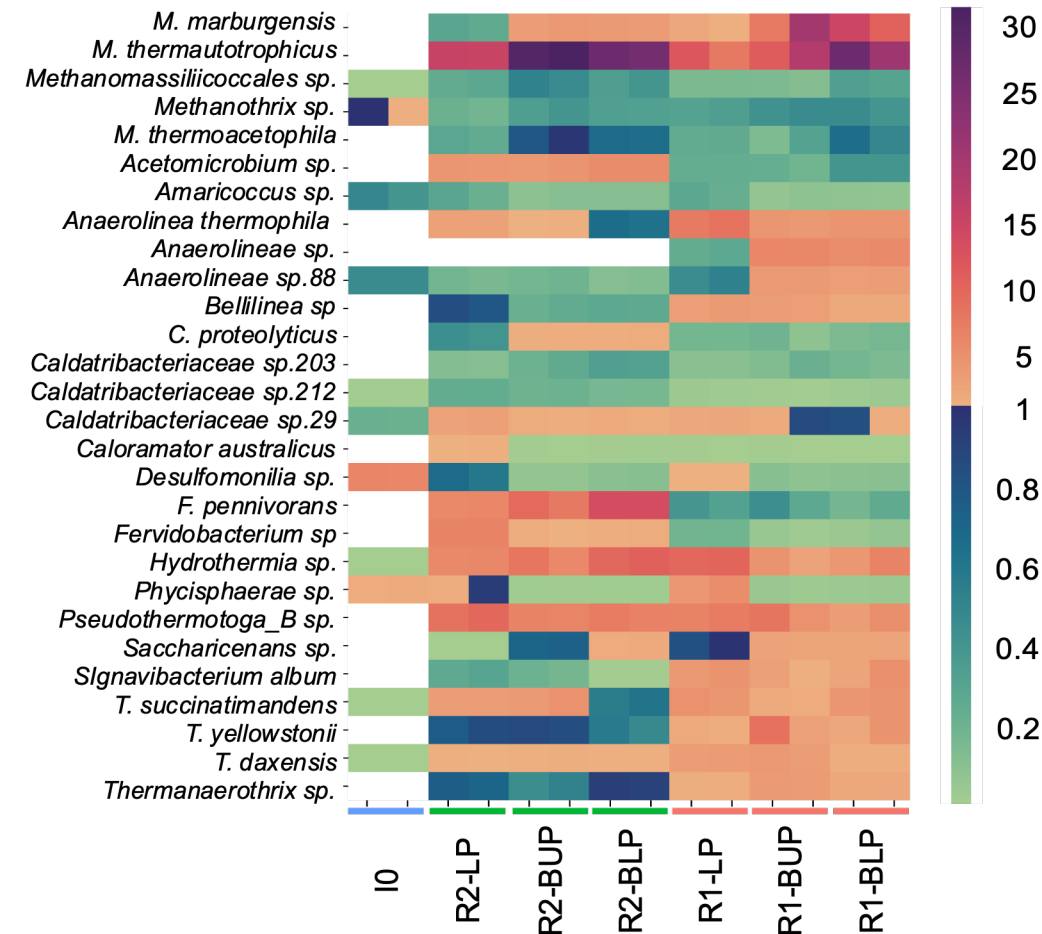
- 156 Metagenome Assembled Genomes
- 35 Phyla
- *Firmicutes* (16%) and *Proteobacteria* (15%) the dominant phyla
- Methanogenic representatives from 4 phyla
- Bacteria represented the majority of microbial community:
 - Inoculum: 95%
 - Liquid phase: 82-89%
 - Biofilm: 56-80%

Microbial community structure

- PCoA analysis showed **distinct behavior** between the samples from the inoculum and those from the reactors
- **Biofilms presented greater separation**, indicating higher diversity compared to liquid phase
- **TBR1 presented greater variation between the lower and the upper part** (dissimilarity bray curtis being between 0.19 and 0.3) compared to TBR2 (dissimilarity bray curtis being between 0.15 and 0.2)
- HCA suggested a **stronger separation between the lower and the upper part of biofilm in TBR1**, compared to TBR2

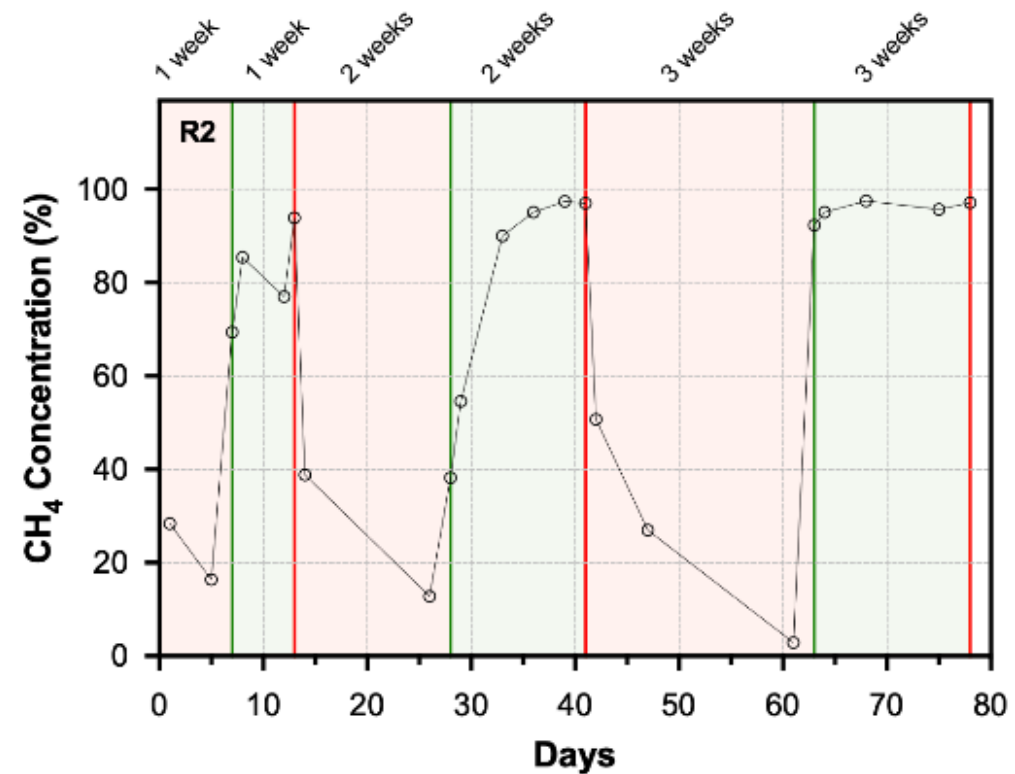
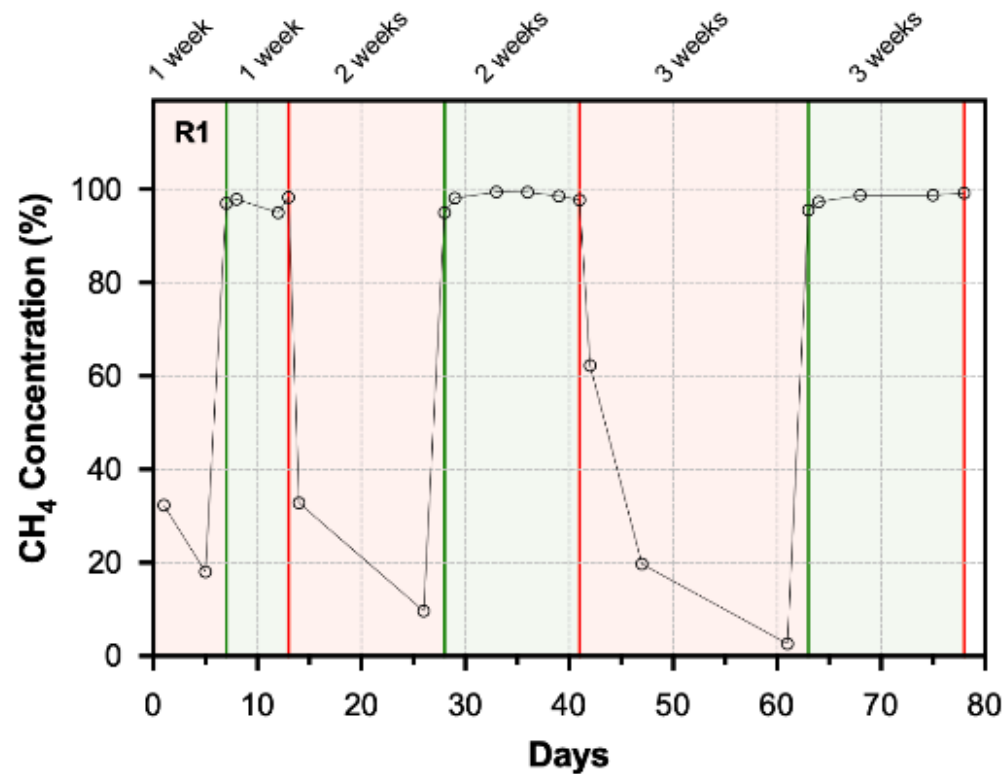


Microbial community synthesis



- *Methanothermobacter thermautotrophicus* dominance in both reactors
- *Methanothermobacter thermautotrophicus*, *Methanotherix_B thermoacetophila* and *Methanomassiliicoccales* sp. were more present in the upper part of the reactors
- Distinct preference of some microorganisms for one of the two materials
- A plethora of syntrophic bacteria were present in both reactors (e.g., *Caldatribacteriaceae* sp., *Coprothermobacter proteolyticus*, *Anaerolineaceae* sp. and *Symbiobacteriales* sp.)

Sneak peek on the current experimental work



Process performance of TR1 (carbon pellets) and TR2 (raschig rings) under intermittent provision of CO₂ and H₂.

Conclusions

- **Raschig rings** achieved higher biomethanation efficiency, resulting in **CH₄ purity of >95%** for GRTs 10-2h.
- GRT of 0.75h was the critical point for **process failure**.
- Biofilm formation can be significantly affected by **the flux of gasses from the top to the bottom** of the reactor.
- The biofilm communities in both reactors were predominantly dominated by the methanogen called ***Methanothermobacter thermautotrophicus***.
- Certain microorganisms displayed a **clear preference for one of the two materials**.

Acknowledgements



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Thank you for your attention!

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