



Using a combination of binning strategies and taxonomic approaches to unravel the anaerobic digestion microbiome

Campanaro, Stefano; Treu, Laura; Kougias, Panagiotis; Zhu, Xinyu; Bassani, Ilaria; Bazzega, Martina; Angelidaki, Irini

Publication date:
2016

Document Version
Peer reviewed version

[Link back to DTU Orbit](#)

Citation (APA):
Campanaro, S., Treu, L., Kougias, P., Zhu, X., Bassani, I., Bazzega, M., & Angelidaki, I. (2016). *Using a combination of binning strategies and taxonomic approaches to unravel the anaerobic digestion microbiome*. Abstract from 16th International Symposium on Microbial Ecology, Montreal, Canada.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Using a combination of binning strategies and taxonomic approaches to unravel the anaerobic digestion microbiome

Stefano Campanaro*¹, Laura Treu², Panagiotis Kougias², Xinyu Zhu², Ilaria Bassani², Martina Bazzega¹, Irini Angelidaki²

1 University of Padova, Italy, 2 Technical University of Denmark, Denmark

Metagenomic sequencing is a fundamental tool to identify the functional potential of the prokaryotic species present in microbial communities, particularly for the unculturable microbes. Recent advances in software dedicated to metagenomic assembly allow nowadays to generate collections of scaffolds comprehensive of thousands genome sequences, but the binning of these scaffolds into OTUs representative of microbial genomes is still challenging. In the attempt to obtain a deep characterization of the anaerobic digestion microbiome, different metagenomic binning approaches were integrated into a new tool. To facilitate the binning process, this tool integrates two strategies; the taxonomic assignment of scaffolds and the clustering based on coverage values. By applying this procedure, 373 high quality genomes involved in the anaerobic digestion process have been extracted and annotated using COG, KEGG, SEED and Pfam. These high throughput approaches pose nowadays other basic challenges related to the computational effort needed for the taxonomic assignment of hundreds new microbial genomes. It is also mandatory to verify if other DNA sequences deriving from the same species are already present in public databases. Metagenomics raise new fundamental questions regarding the definition of what a microbial species is and how it can be defined solely considering its genome. In order to address these issues we have developed a collection of scripts to check the presence of the same genome sequence not only in different assemblies, but also in public databases and, finally, to simplify its functional annotation.