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► To cite this version:

Oshma Chakoory, Sophie Marre, Pierre Peyret. RiboTaxa: Combined approaches for taxonomic resolution down to the species level from metagenomics data revealing novelties. JOBIM, Jul 2022, Rennes, France. . <hal-03898473>

HAL Id: hal-03898473

<https://hal.science/hal-03898473v1>

Submitted on 14 Dec 2022

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RiboTaxa: Combined approaches for taxonomic resolution down to the species level from metagenomics data revealing novelties

Oshma CHAKOORY^{1*}, Sophie MARRE¹, Pierre PEYRET^{1*}

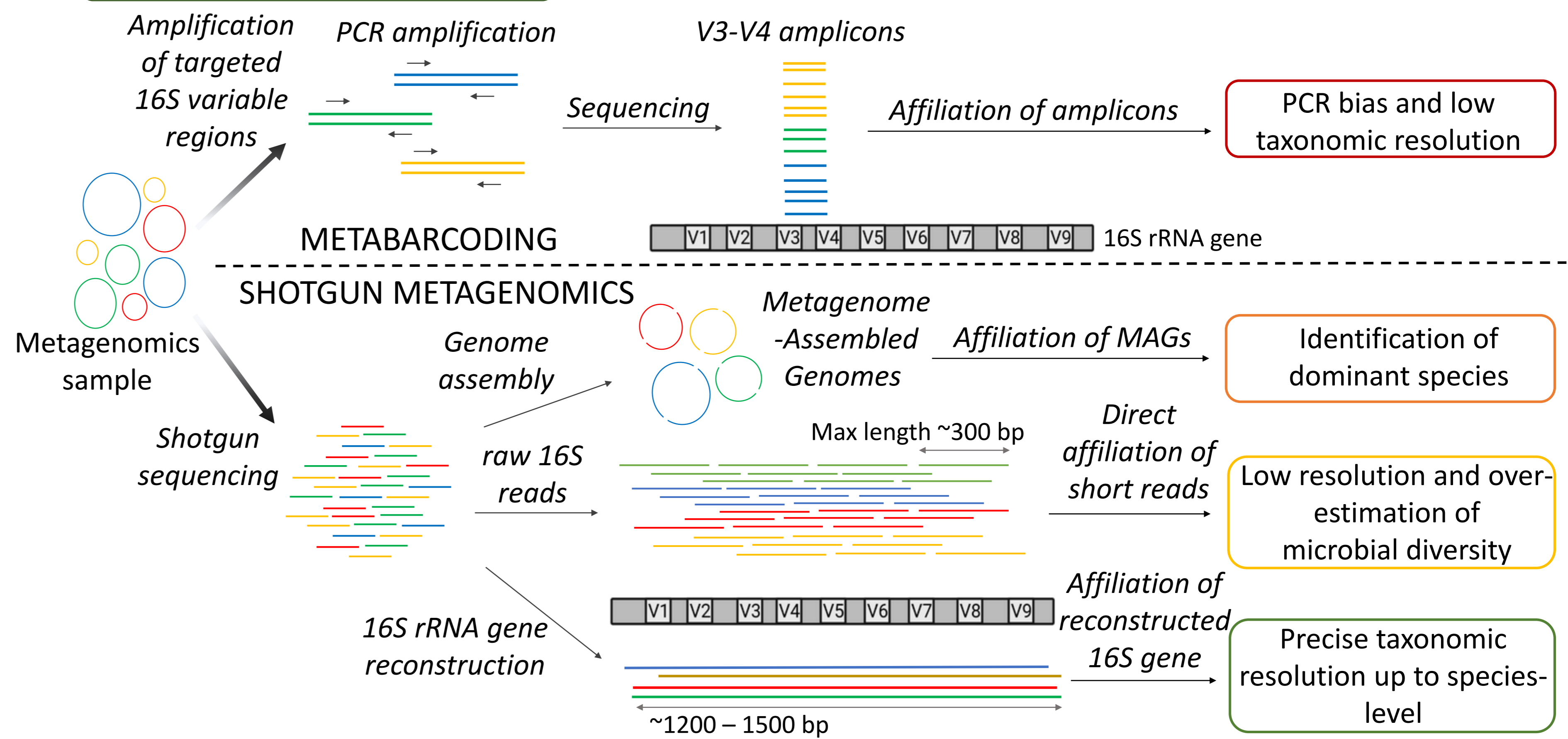
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Introduction

The microbiota contributes to the health of the hosts and the ecosystems. Altered microbial composition (dysbiosis) can be associated with pathologies and disrupt the functioning of the ecosystem.

There are two techniques to characterize the diversity of microbial communities:

- Metabarcoding
- Shotgun Metagenomics



Objectives

- Achieve species level identification of microorganisms using metagenomics data
- Identify dominant, subdominant/rare microorganisms
- Calculate relative abundance close to reality

Results

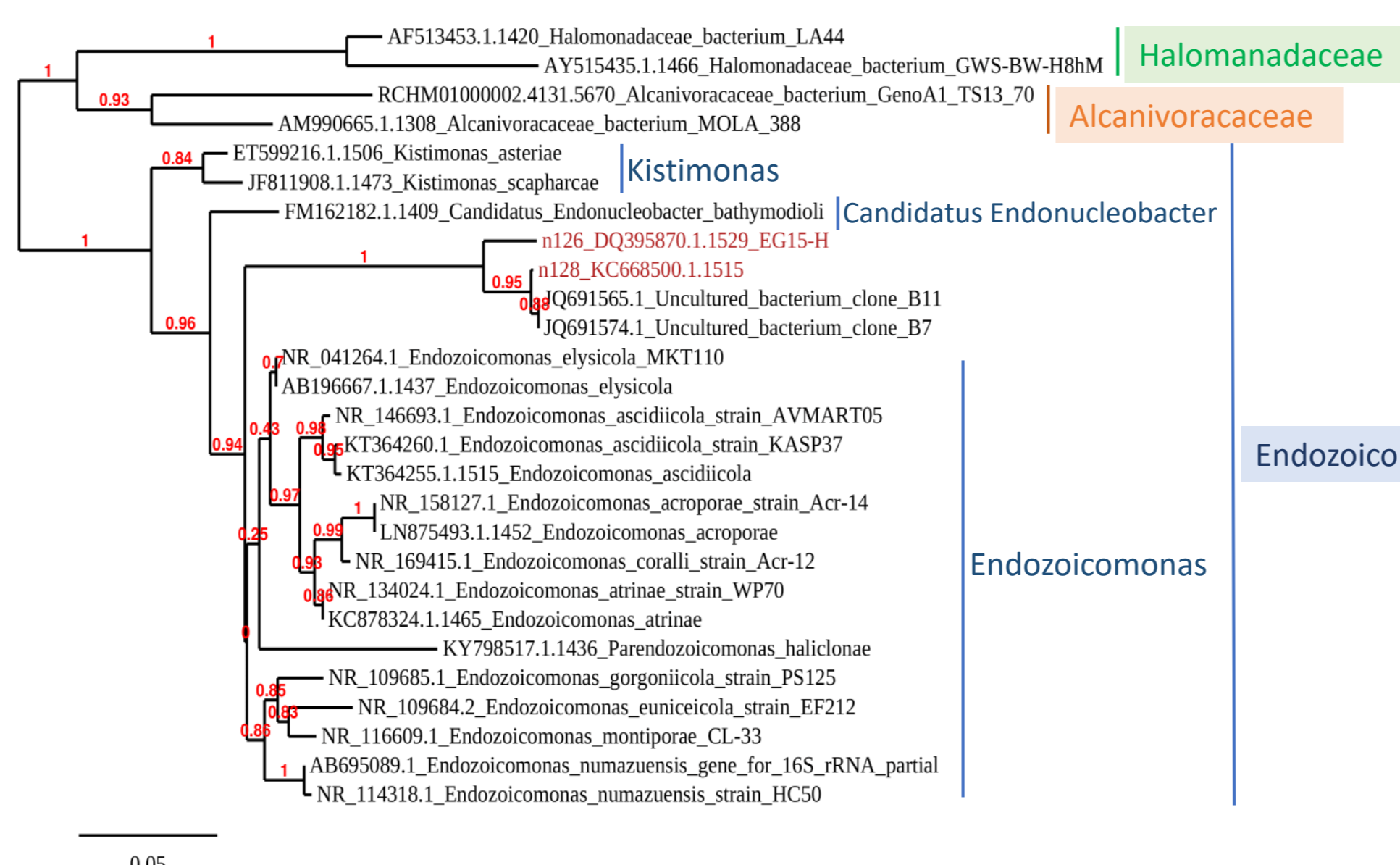
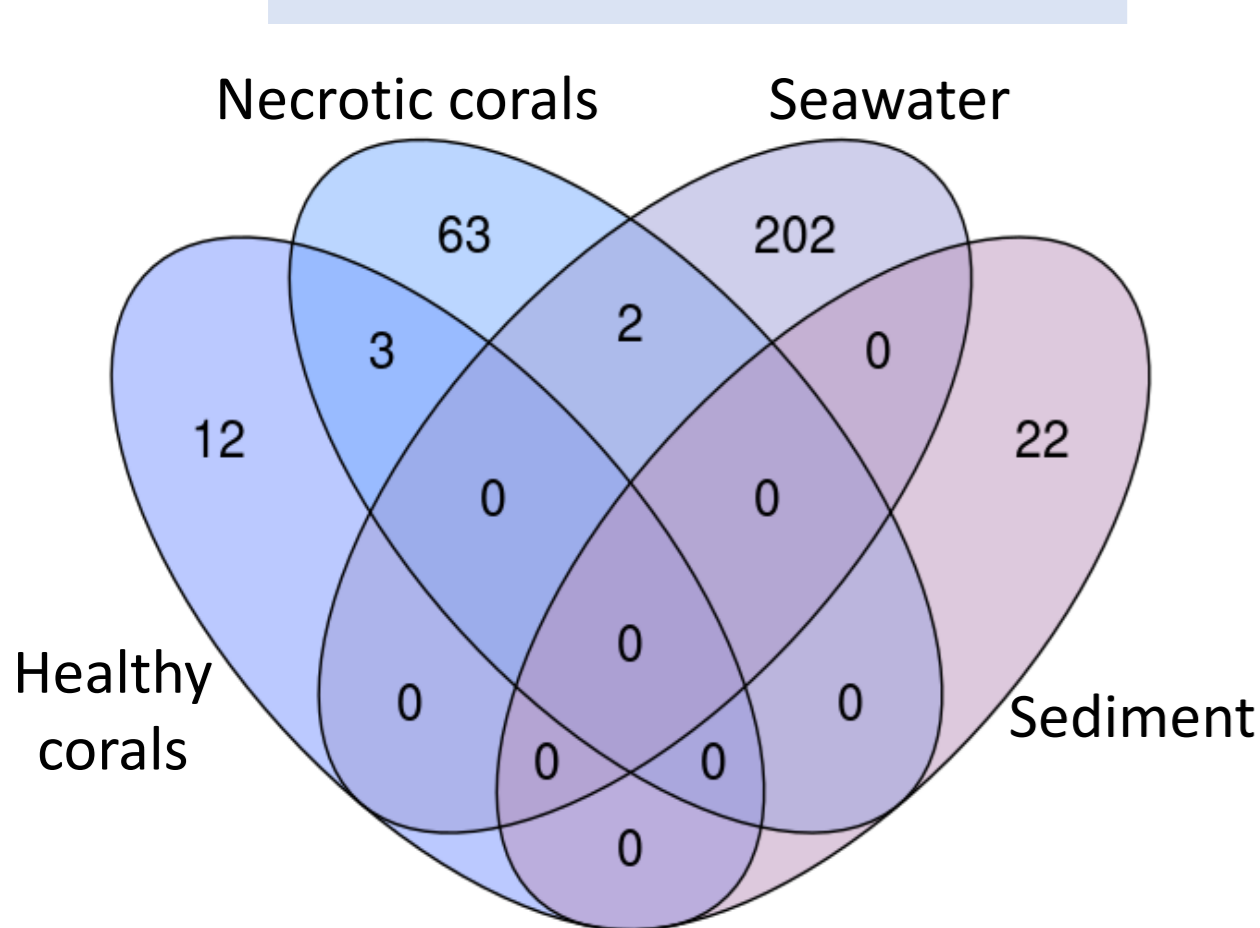
1. Microbial mock of 100 species (45 genera) from the human gut

	RiboTaxa	Precision	Recall	F-measure
Number of Genus detected	45	100%	100%	100%
Number of Species detected	72	100%	72%	83.72%

No false positives classification using RiboTaxa. Detection of subdominant/rare microorganisms.

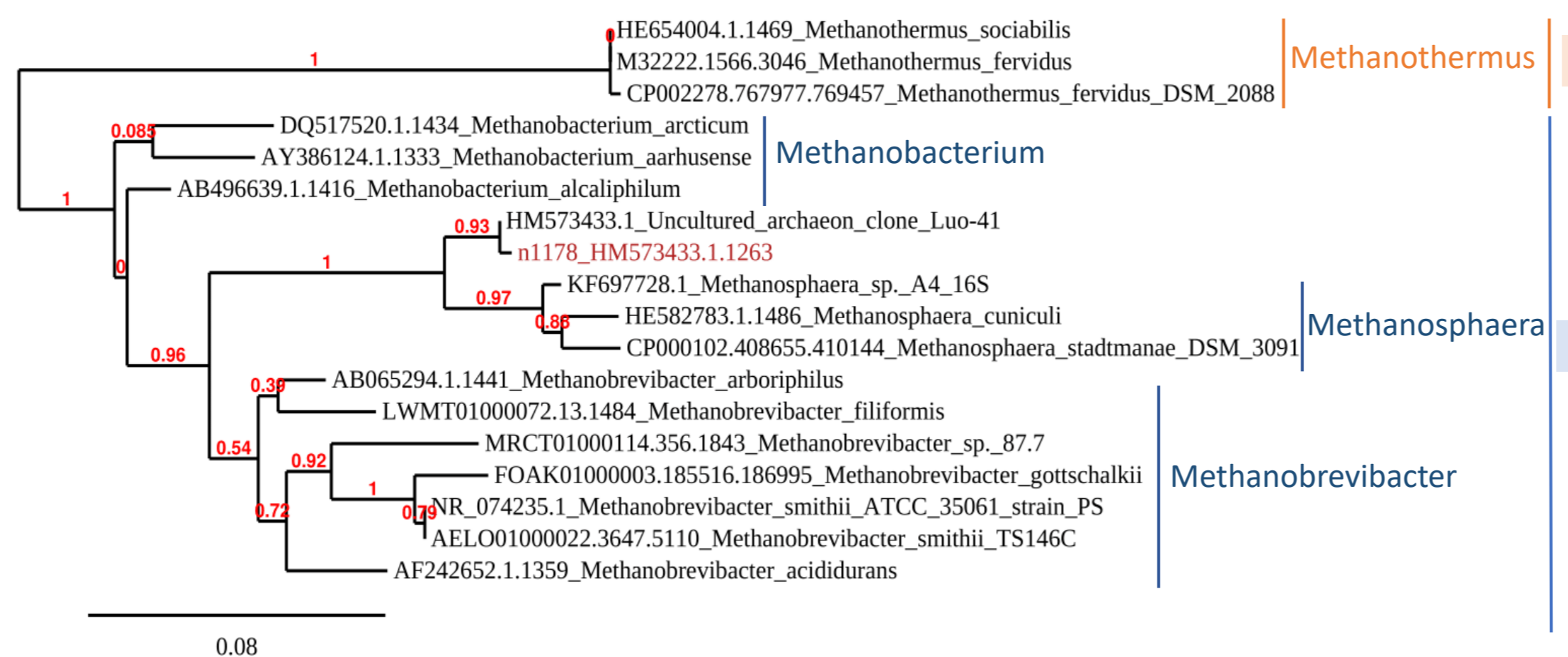
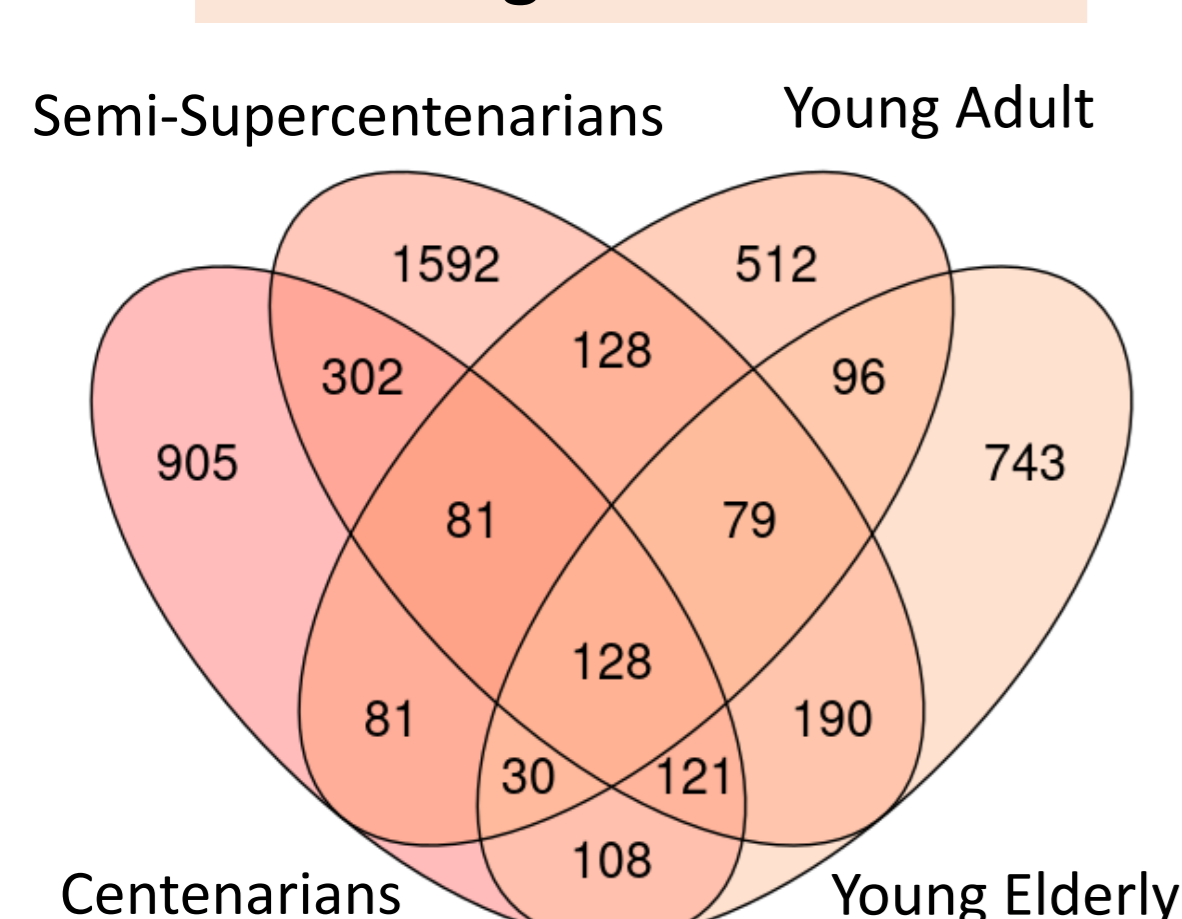
2. Real datasets from public database (NCBI/ENA)

Octocorals microbiome



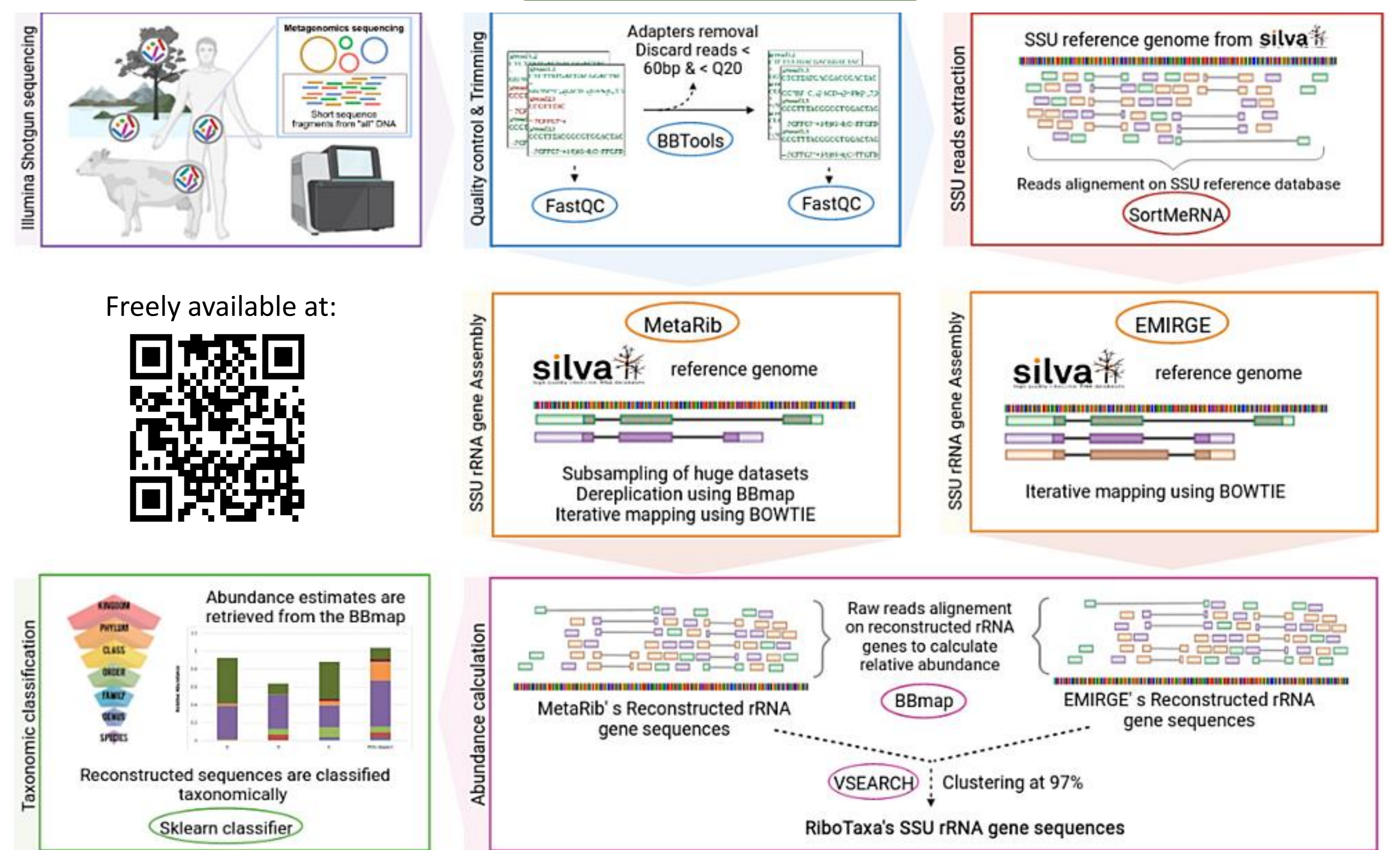
In a study focused on corals' health¹, RiboTaxa highlighted 2 species of uncultured *Endozoicomonas* which were dominant in the healthy tissue. Both species belonged to new genus opening new research perspectives on corals' health.

Human gut microbiome



In a study on human gut and extreme longevity², RiboTaxa detected the presence of an uncultured archaeon in semi-supercentenarians (aged 105 to 109 years) highlighting a new archaeal genus not yet described that could be species of interest participating in the longevity process.

Methodology



Freely available at:



Conclusion

- ✓ User-friendly metagenomics classifier
- ✓ High specificity without false positive detection
- ✓ Species relative abundance close to reality
- ✓ Reveals microbial novelties not detected by current approaches
- ✓ Can be applied to other phylogenetic markers

Acknowledgements

We are grateful to the Mésocentre Clermont Auvergne University and AuBi platform for providing help and computing and storage resources. Computations have been performed on the supercomputer facilities of the Mésocentre Clermont Auvergne University.

References

1. Keller-Costa, T., et al. (2021) Metagenomic insights into the taxonomy, function, and dysbiosis of prokaryotic communities in octocorals. *Microbiome*, 9, 72.
2. Rampelli, S., et al. (2020) Shotgun Metagenomics of Gut Microbiota in Humans with up to Extreme Longevity and the Increasing Role of Xenobiotic Degradation. *mSystems*, 5, e00124-20.