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Meteor2: accurate taxonomic profiling of host-associated microbial communities for shotgun metagenomics

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INTRODUCTION

- Detection and quantification of microbial species is a fundamental task in metagenomics.
- Most metagenomic tools tend to focus on a single aspect: taxonomical, functional or strain analysis.
- Here, we introduce Meteor2, a versatile tool for taxonomic, functional, and strain-level profiling of metagenomic samples, relying on microbial gene catalogues.

CODE AVAILABILITY

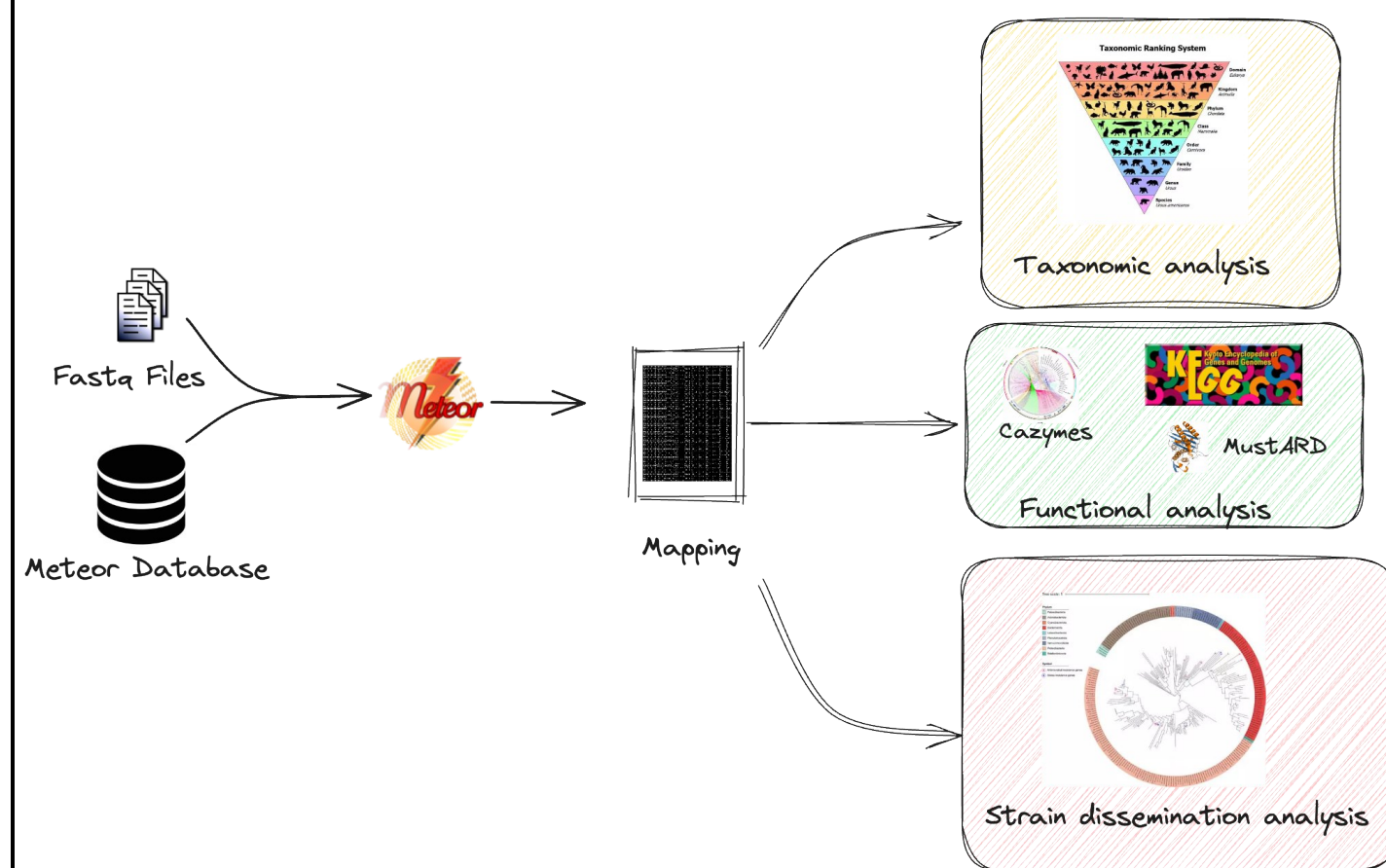
<https://github.com/metagenopolis/meteor>

Installation instructions:

- Docker:** `ghozlane/meteor`
- pip:** `pip install meteor`
- bioconda:** `bioconda/meteor`

METHODS

- Meteor2 aligns reads on non-redundant microbial gene catalogs covering a specific host-associated ecosystem. At this time, we provide 10 catalogs for pig, mouse, chicken, rat, rabbit, dog, cat and human microbiota (gut, skin and oral cavity).

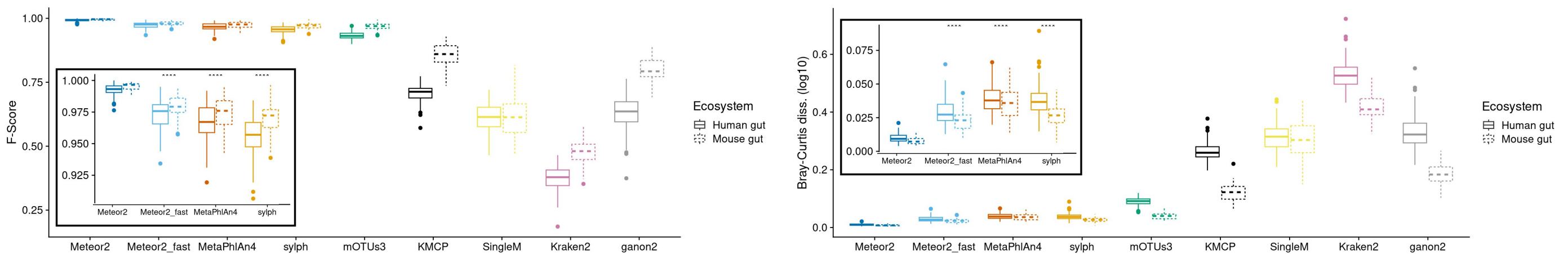


RESULTS

- To assess Meteor2 performance, we generated two simulated datasets mimicking respectively mouse (62 samples) or human fecal metagenomes (100 samples) using 5,114 high-quality genomes.

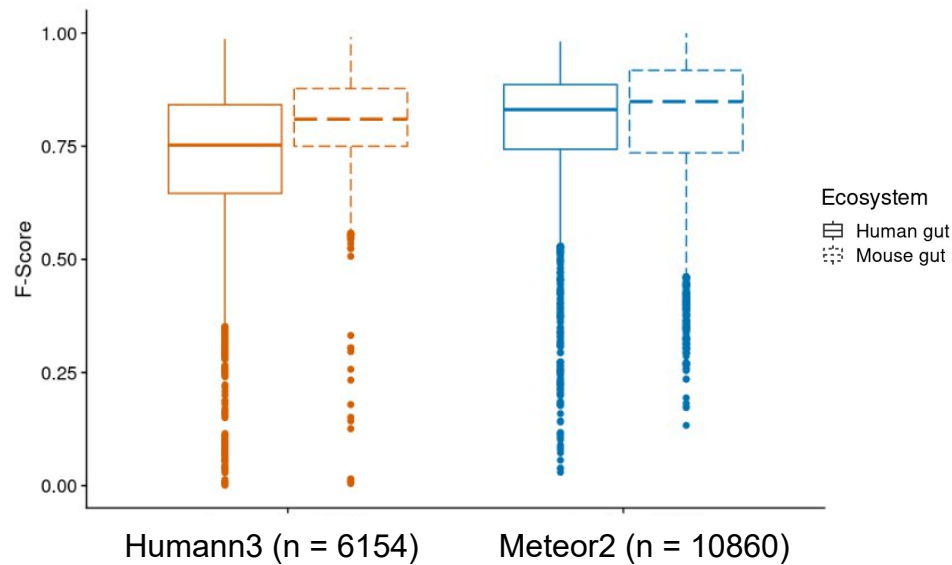
Taxonomic level:

Comparison with 7 existing tools



Functional level:

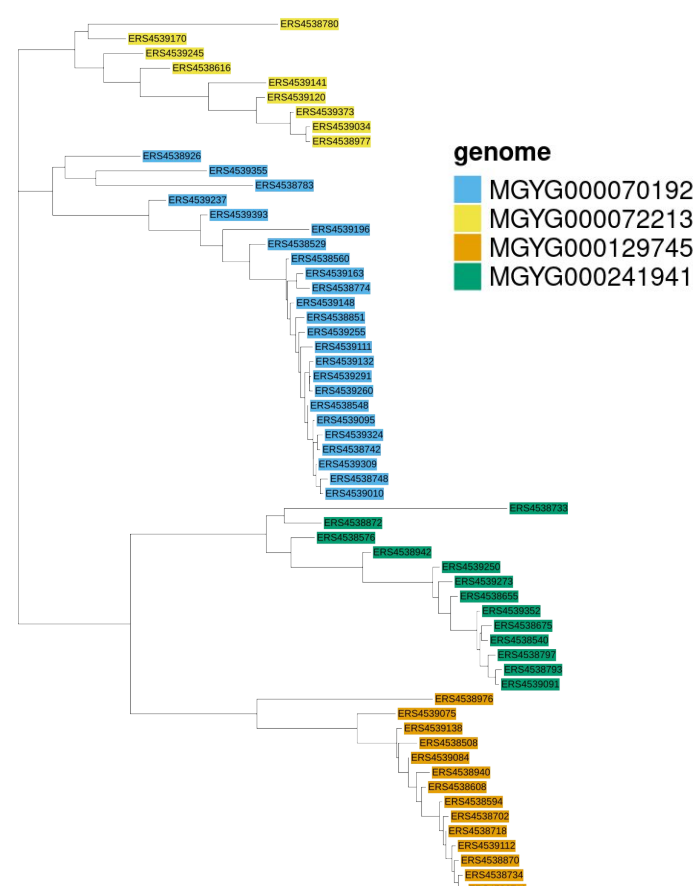
Comparison with Humann3 based on Uniref90 database



Ability of Meteor2 and Humann to accurately identify Uniref90 IDs carried by a species in a simulated sample, based on the Uniref90 IDs present in the associated genome.

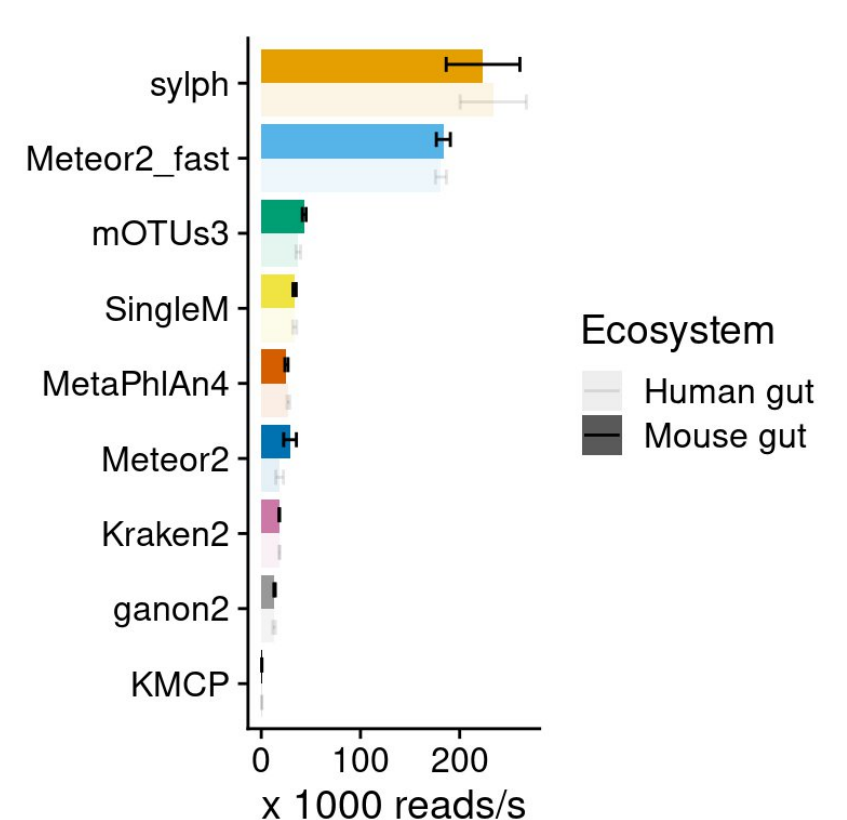
Strain level:

Tree of *Phocaeicola vulgatus*



Time performance:

Note: Meteor2 includes functional profiling.



CONCLUSION

- Overall, Meteor2 was the best at detecting and estimating abundance of (subdominant) species.
- Meteor2 is a comprehensive approach that not only enhances the accuracy and depth of microbial profiling but also simplifies metagenomic studies workflow.