

MetaGenomic analysis of short and long reads



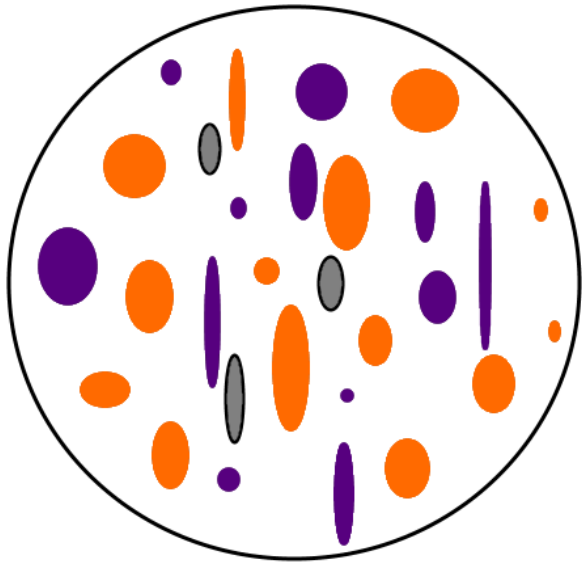
Felix Manske, Institute of Bioinformatics, Muenster (Germany)



Who?
What?

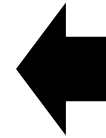


Who is in my sample?

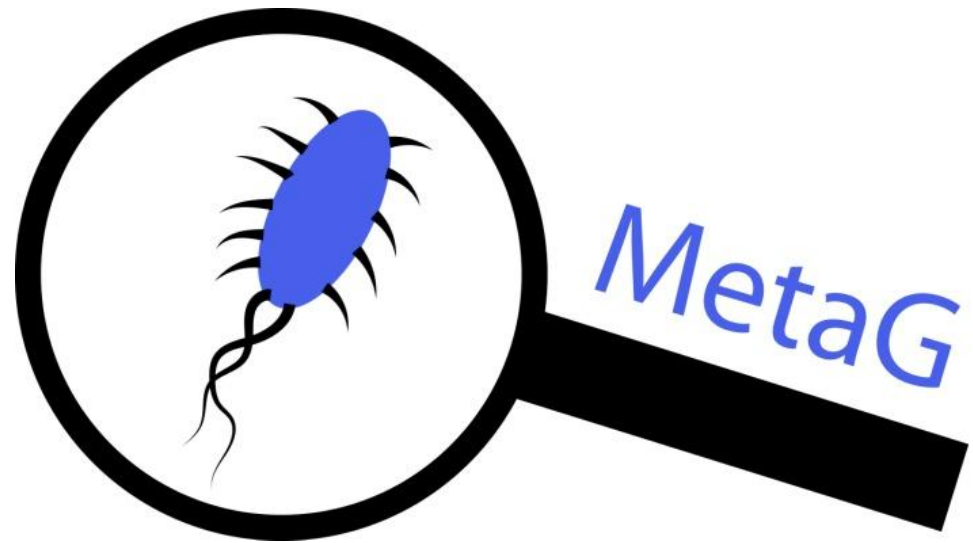


1 % culturable

Marker genes



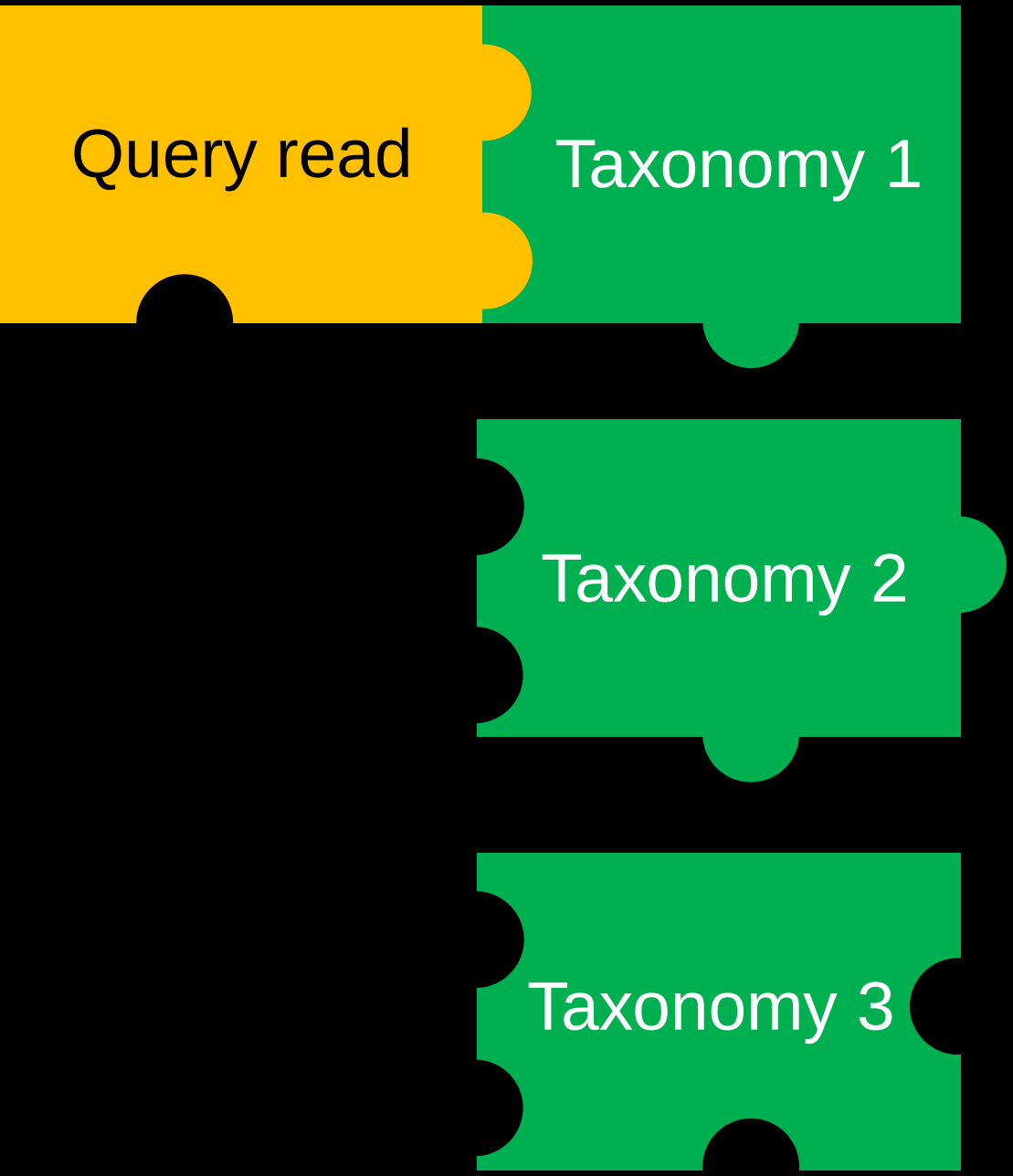
> 58 % missing from databases

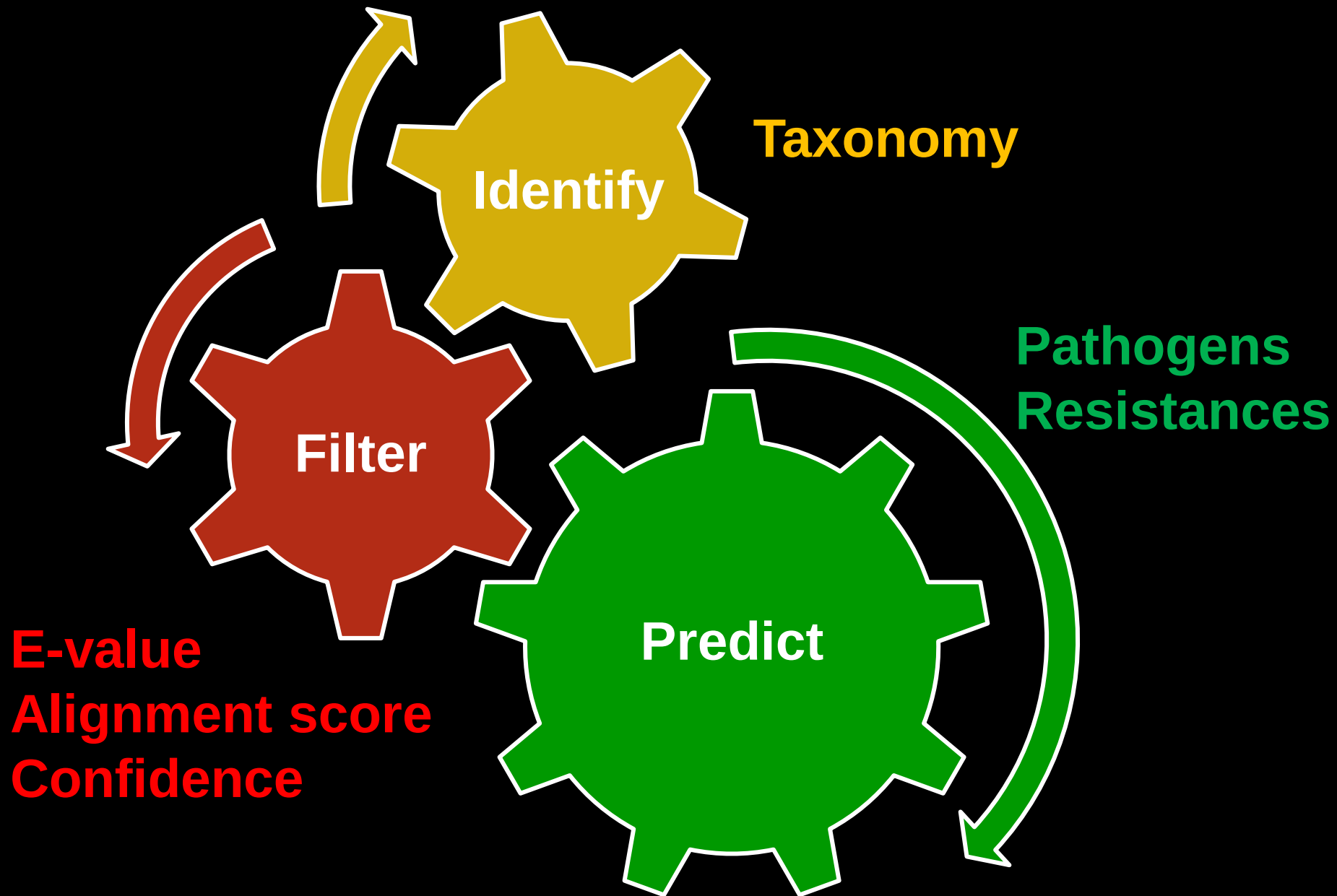


- Marker gene analysis
- Short, long reads
- Default settings

LAST aligner

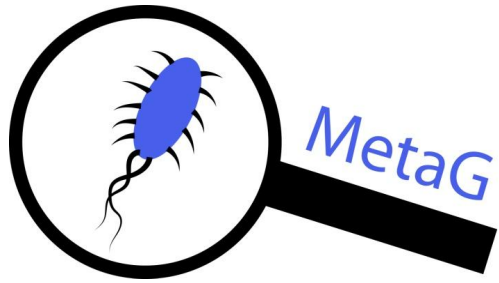
Kiełbasa et al. 2011

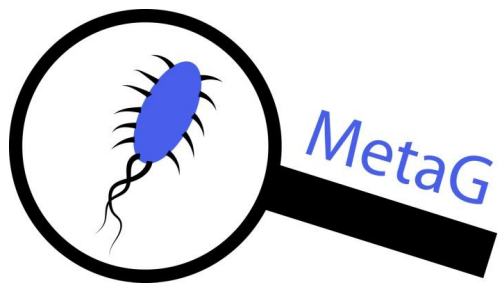


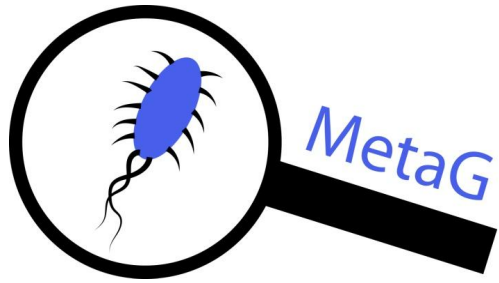


So what?

Access & Design

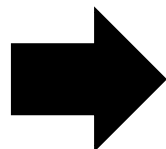
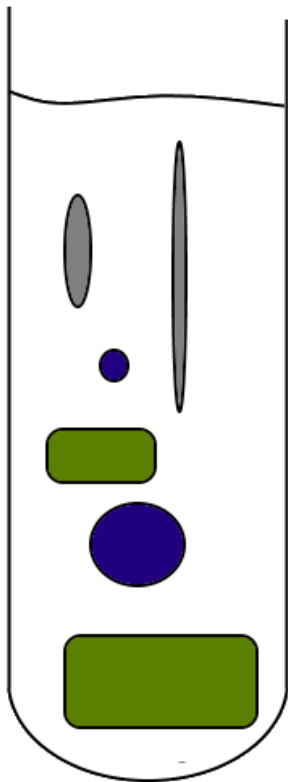




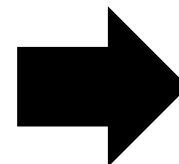


Performance

Using default settings



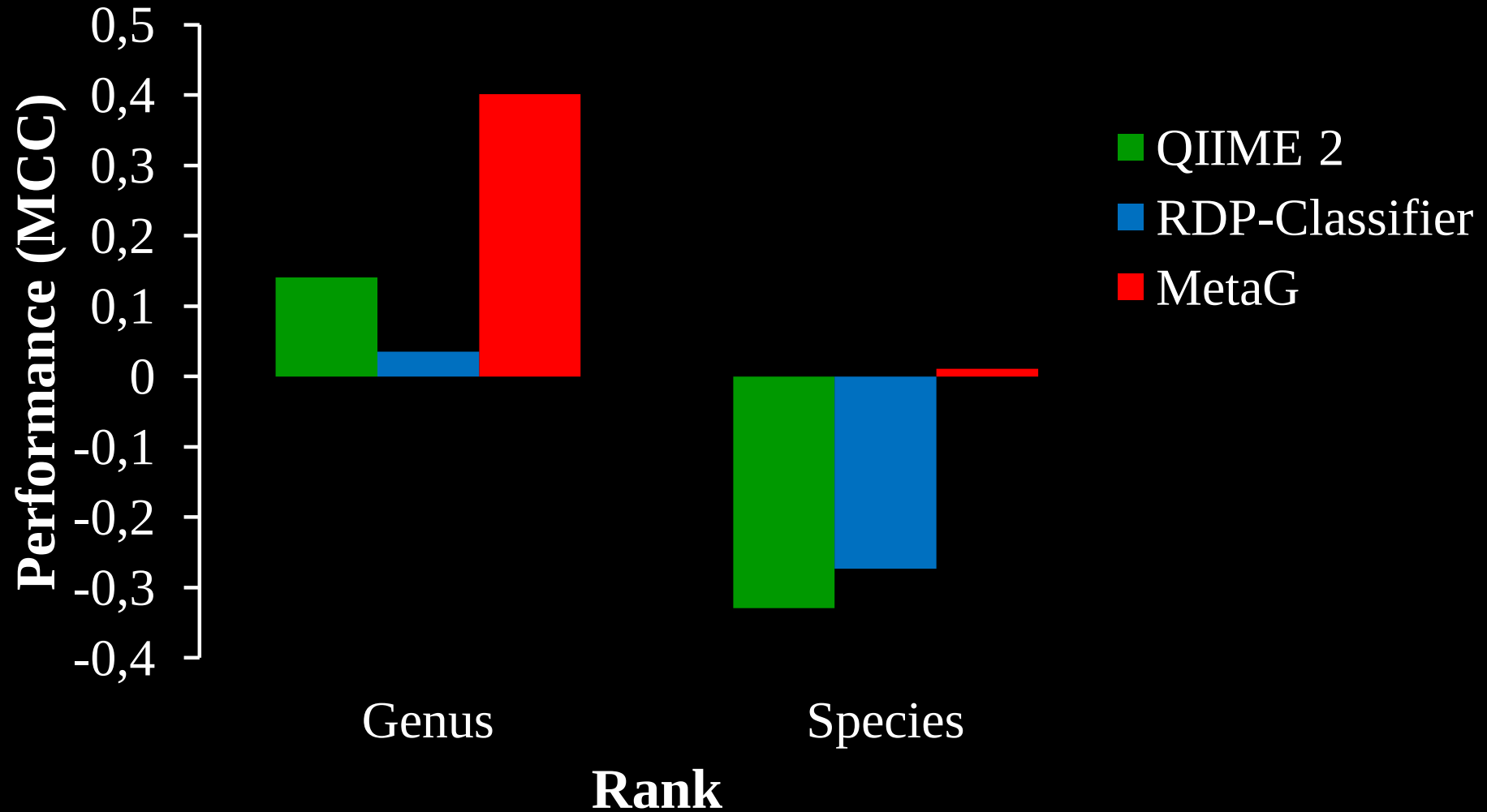
OR

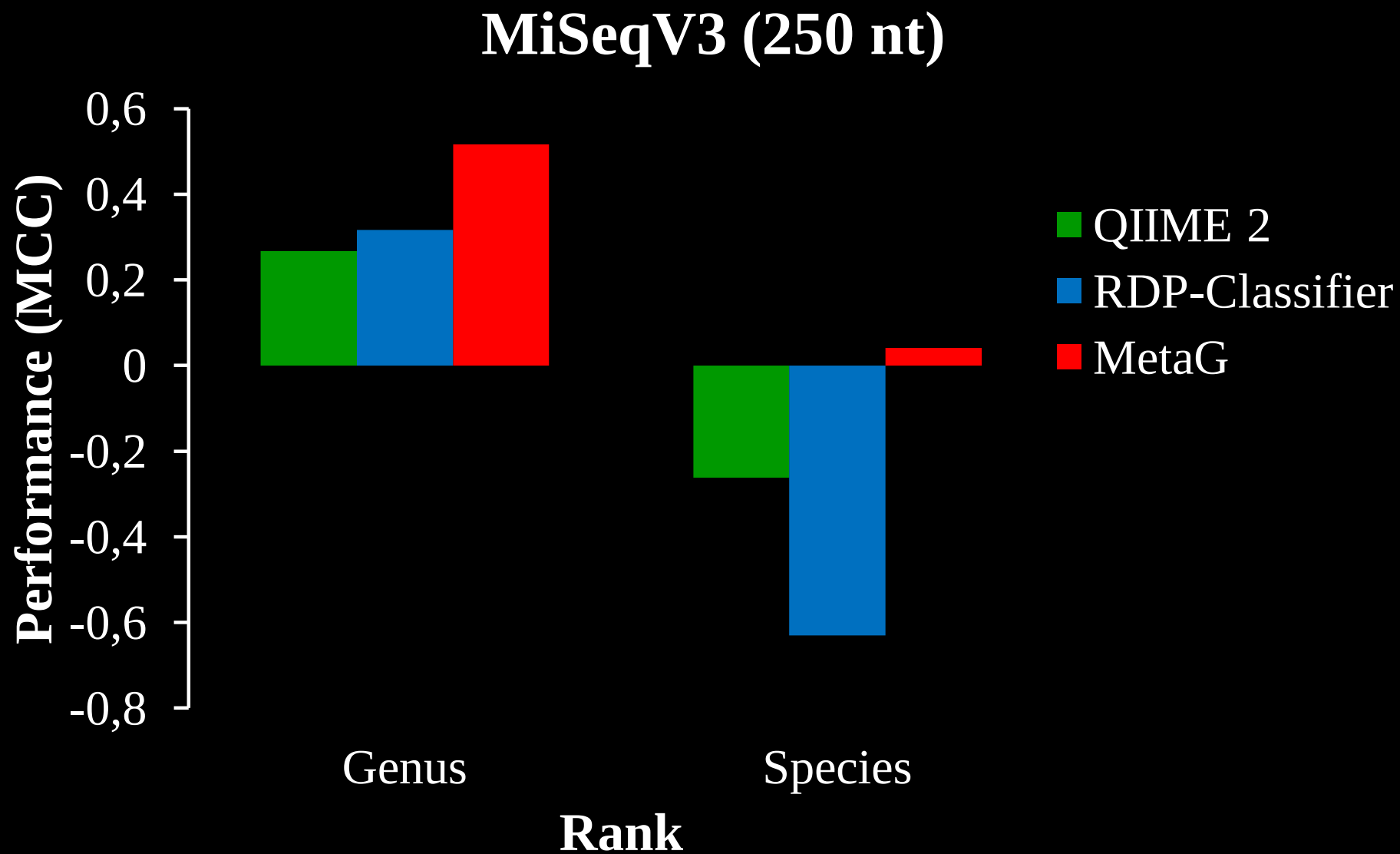


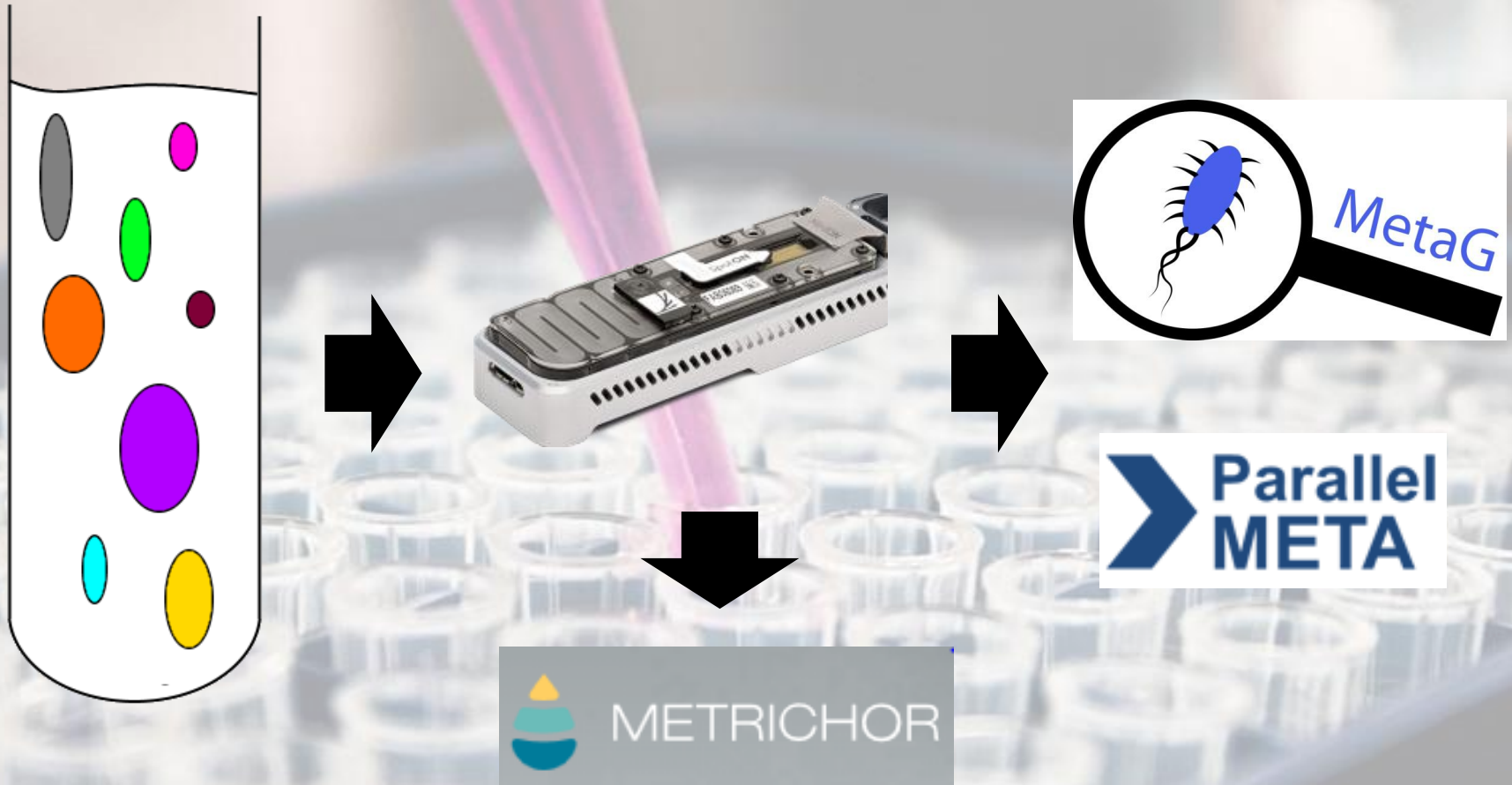
Matthew's
Correlation
Coefficient

+1 
-1 

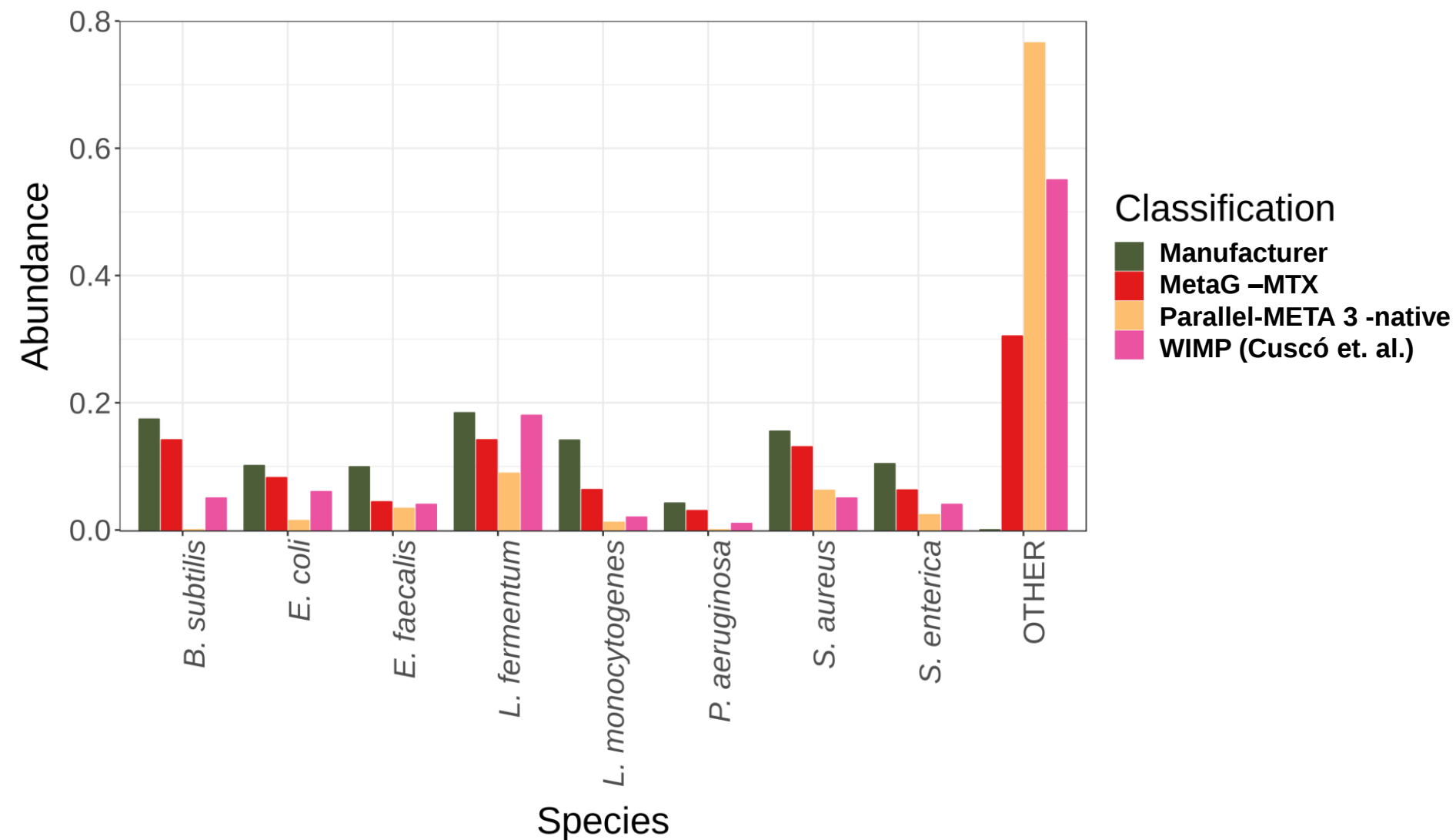
Nanopore R9, 2D (max. 1415 nt)





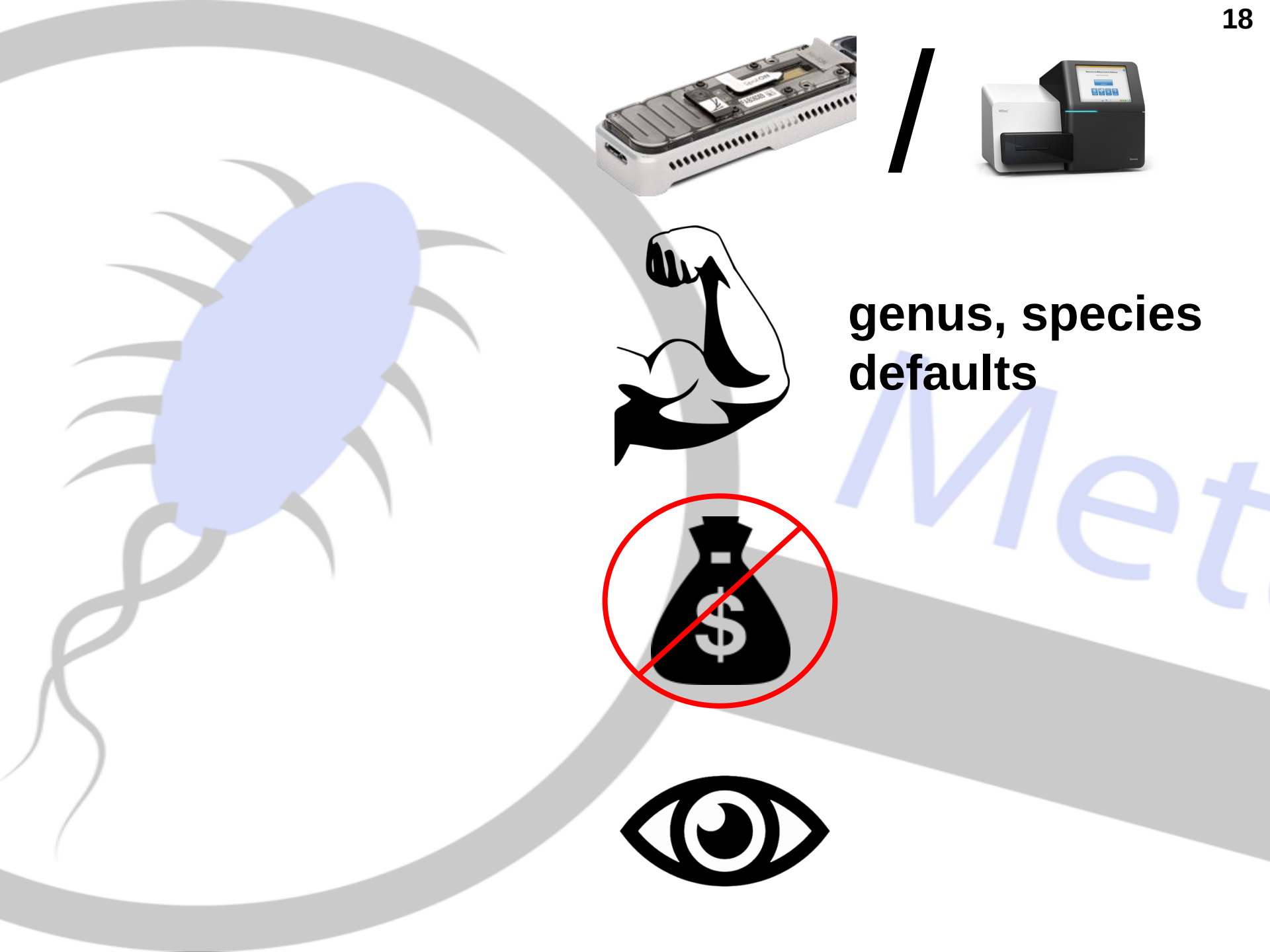


ZymoBIOMICS Cuscó et al. 2018

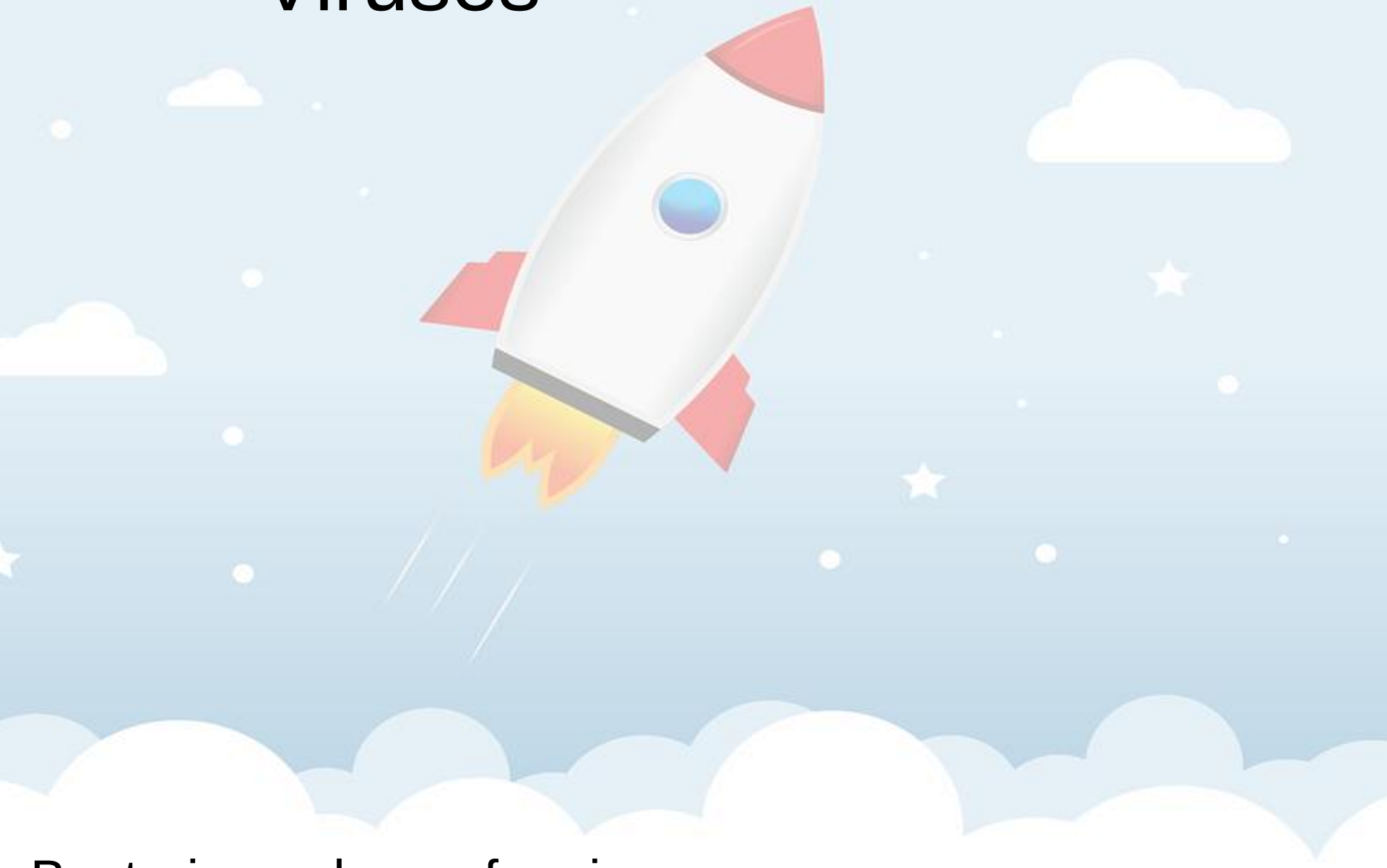




**genus, species
defaults**



Viruses



Bacteria, archaea, fungi

Viruses

Load file



Typing of variables



bioinformatics.uni-muenster.de/tools/metag/index.hbi?

Acknowledgements



Thank you!

Petri dish: Michael Schiffer (Unsplash)

Radioactive: Yves Alarie (Unsplash)

Factory: Victor Garcia (Unsplash)

Hospital: Martha Dominguez de Gouveia (Unsplash)

MetaG logo by Maciej Makalowski

Metrichor: <https://metrichor.com/technology.html#>; accessed 19.06.2019

Onecodex: https://dgivdslhqe3qo.cloudfront.net/careers/photos/28715/thumb_photo_1490652721.png; accessed 19.06.2019

Parallel-META: <http://bioinfo.single-cell.cn/images/PM3.png>; accessed 19.06.2019

QIIME 2: <https://qiime2.org/assets/img/qiime2.svg>; accessed 19.06.2019

RDP: <https://rdp.cme.msu.edu/images/rdpinsider108x81.png>; accessed 19.06.2019

Eye: mohamed_hassan (Pixabay)

MinION: <https://nanoporetech.com/sites/default/files/s3/minion-cutout.png>; accessed 19.06.2019

Money: OpenClipart-Vectors (Pixabay)

Miseq: <https://www.illumina.com/content/dam/illumina-marketing/images/systems/v2/systems-carousel/system-carousel-miseq-right.png>; accessed 23.06.2019

Lab: Louis Reed (Unsplash)

Muscle: OpenClipart-Vectors (Pixabay)

Rocket: Designer-kottayam (Pixabay)

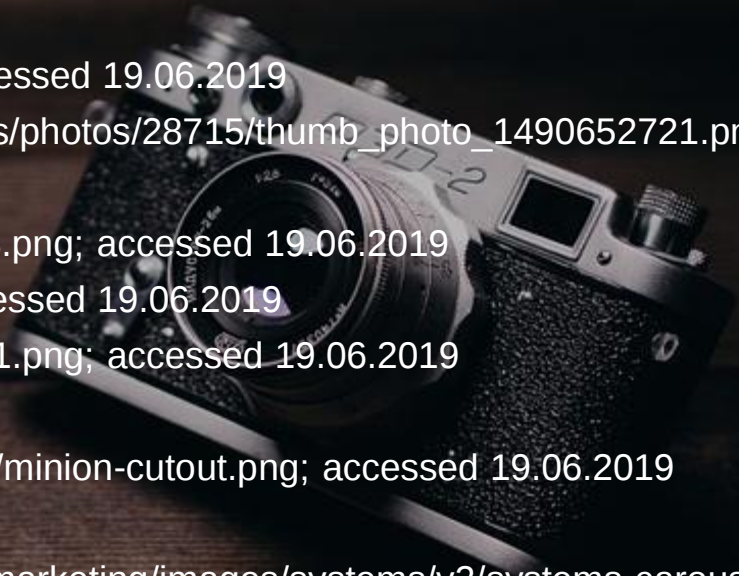
Francesco: https://www.uni-muenster.de/imperia/md/images/evolution/catania/fittosize_554_784_da25c3fa3809decfd4ce0dea3cf7e7ef_catania.jpeg; accessed 10.06.2019

Group picture by Jonas Bohn; August 2018

Tabea: <http://www.bioinformatics.uni-muenster.de/home/images/group-pic.jpg?lang=en>; accessed 11.06.2019

Wolfgang: <http://www.bioinformatics.uni-muenster.de/images/wolfgang.jpg>; accessed 10.06.2019

Camera: Republica (Pixabay)



References

- Cuscó, Anna, Carlotta Catozzi, Joaquim Viñes, Armand Sanchez, and Olga Francino. 2018. “Microbiota Profiling with Long Amplicons Using Nanopore Sequencing: Full-Length 16S rRNA Gene and Whole *Rrn* Operon [Version 1; Referees: 2 Approved, 3 Approved with Reservations].” *F1000Research* 7 (1755). <https://doi.org/10.12688/f1000research.16817.1>.
- Kielbasa, Szymon M., Raymond Wan, Kengo Sato, Paul Horton, and Martin C. Frith. 2011. “Adaptive Seeds Tame Genomic Sequence Comparison.” *Genome Research* 21: 487–93. <https://doi.org/10.1101/gr.113985.110>.
- Louca, Stilianos, Florent Mazel, Michael Doebeli, and Laura Wegener Parfrey. 2019. “A Census-Based Estimate of Earth’s Bacterial and Archaeal Diversity.” *PLOS Biology* 17 (2): e3000106. <https://doi.org/10.1371/journal.pbio.3000106>.
- Torsvik, V., R. Sørheim, and J. Goksøyr. 1996. “Total Bacterial Diversity in Soil and Sediment Communities—A Review.” *Journal of Industrial Microbiology* 17 (3–4): 170–78. <https://doi.org/10.1007/BF01574690>.