



Metagenomics and Microbial Genomics

- Identify species, genes, transcripts and metabolic networks simultaneously from one dataset*
- Fastest, most specific analysis going from raw data (900M reads) to visualized results in 3 days*
- Investigate complex microbial communities without the need for culturing and design them in silico*

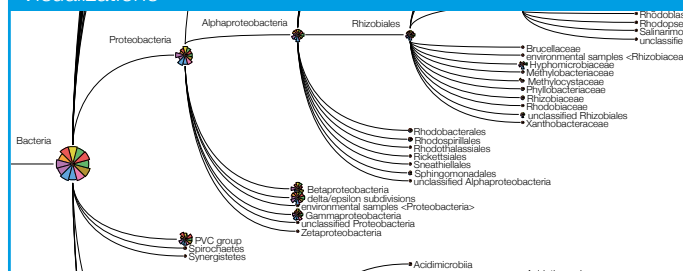
Computomics helps investigate the genetic repertoire of complex microbial communities and individual cultures. We identify species, genes, and pathways simultaneously. Our co-founder Daniel Huson and his team developed an ultrafast alignment algorithm, winner of the \$1 million DTRA Metagenomics Challenge.

Our key deliverable is enabling you to derive value from the results we obtain. Insightful, interpretable visualizations are an integral part of our work. With the help of our metagenomics analysis tool MEGAN, we help you investigate differences between individual organisms, communities and entire microbiomes.

Case Study

We compared dozens of microbial samples, considering gene content, metabolic pathways, and taxonomy. The speed of our award-winning alignment tool allowed annotations using multiple reference databases. We delivered results in several formats to ensure future accessibility.

Visualizations



Contact Our Expert Scientist

Ted is our expert on microbial genomics and visualization of metagenomics datasets. Contact Ted at tg@computomics.com for a free consultation about your microbial genomics project.



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