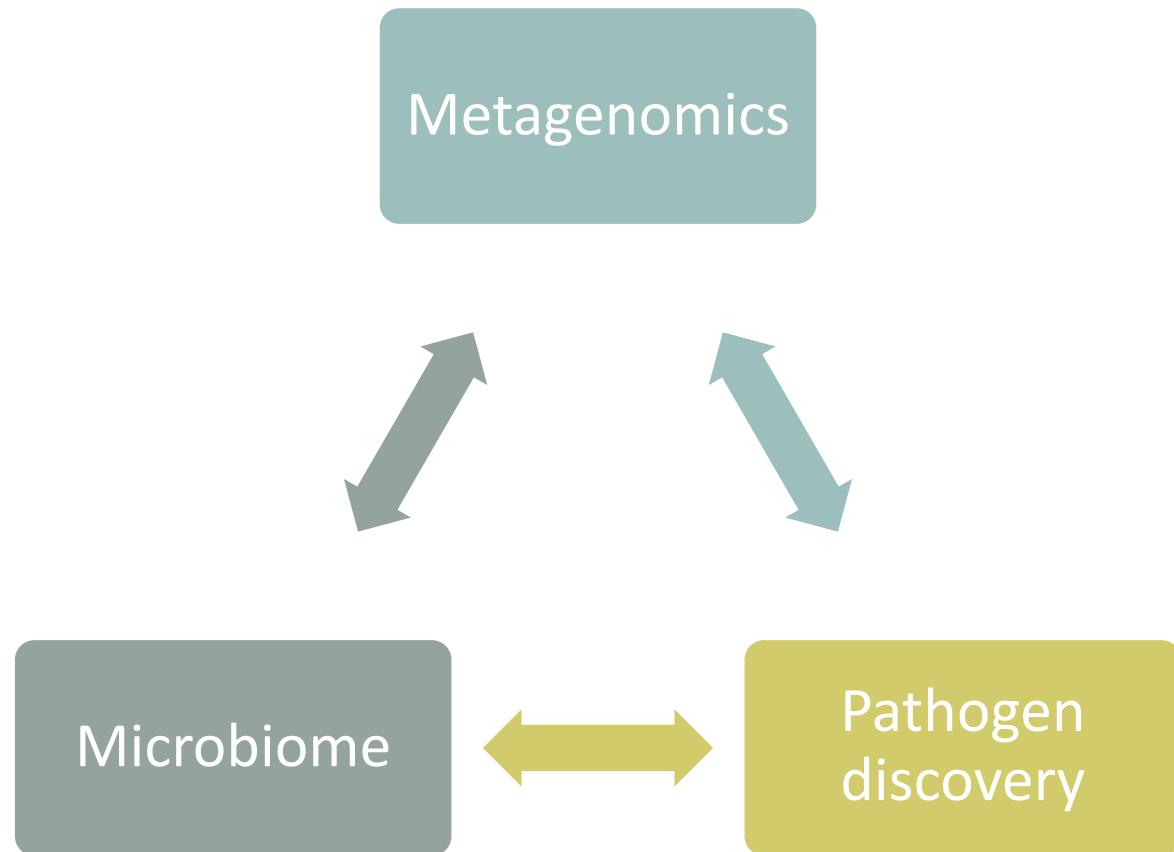




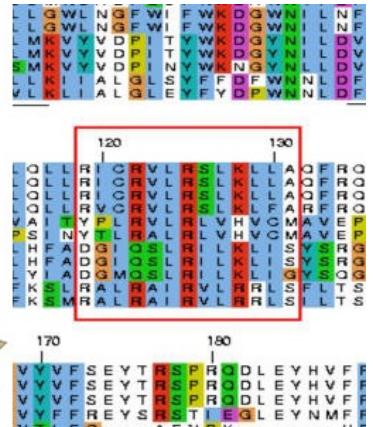
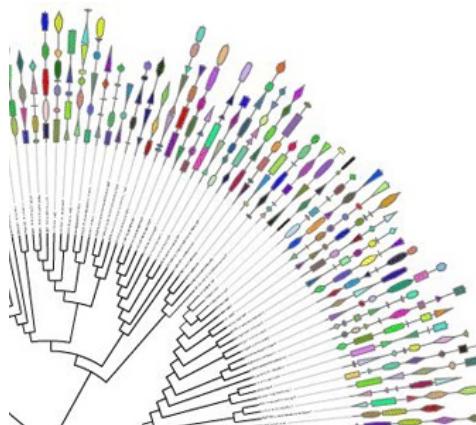
Metagenomics

Paúl Cárdenas A., MD, PhD

Why metagenomics?

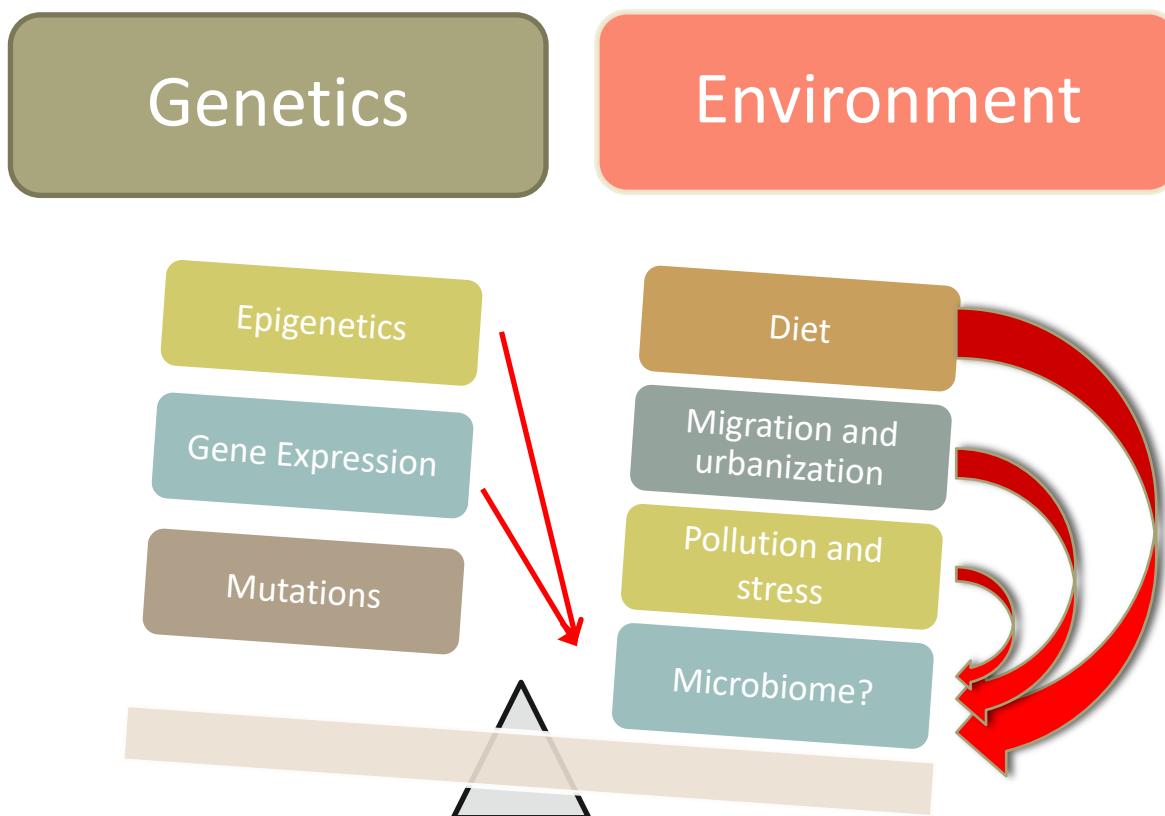


Why was it not possible before?



¿Why it is essential to study the microbiome?

Multifactorial Diseases

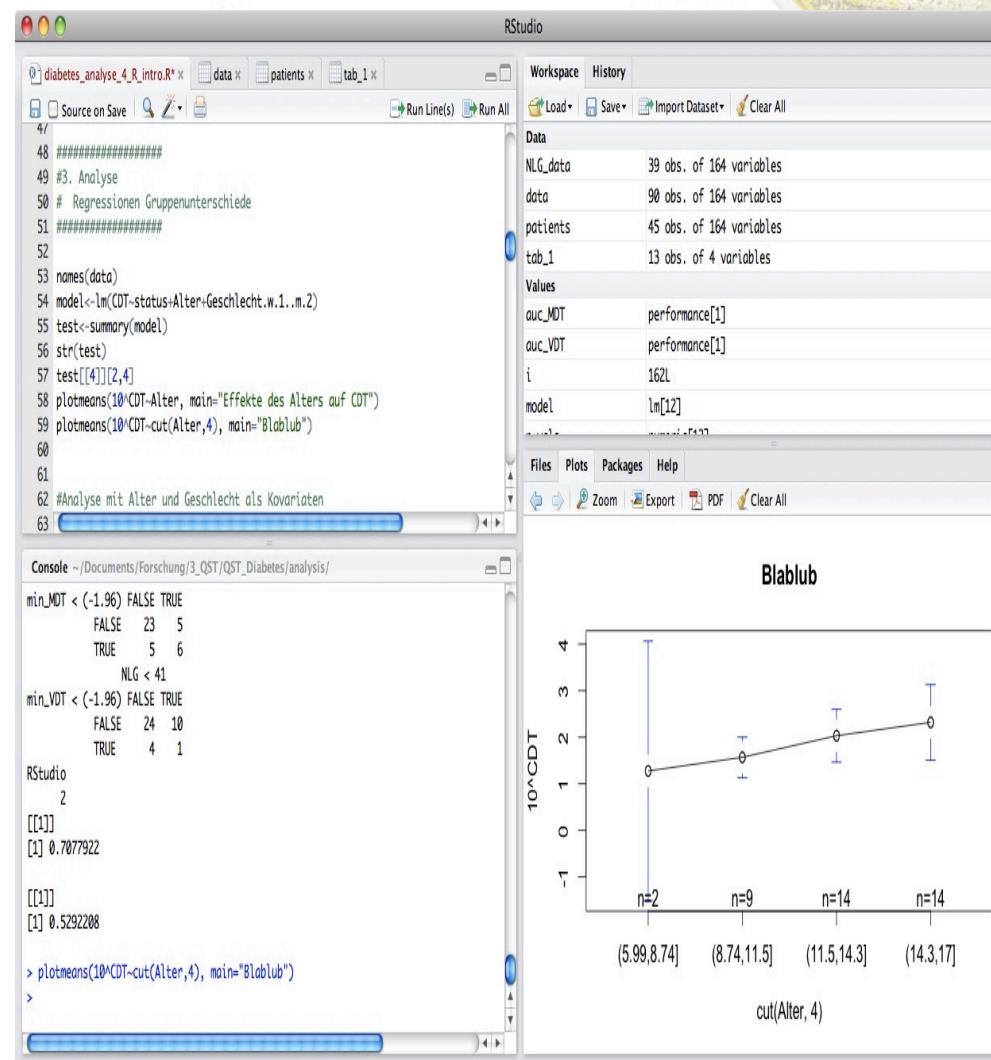


Next generation sequencing

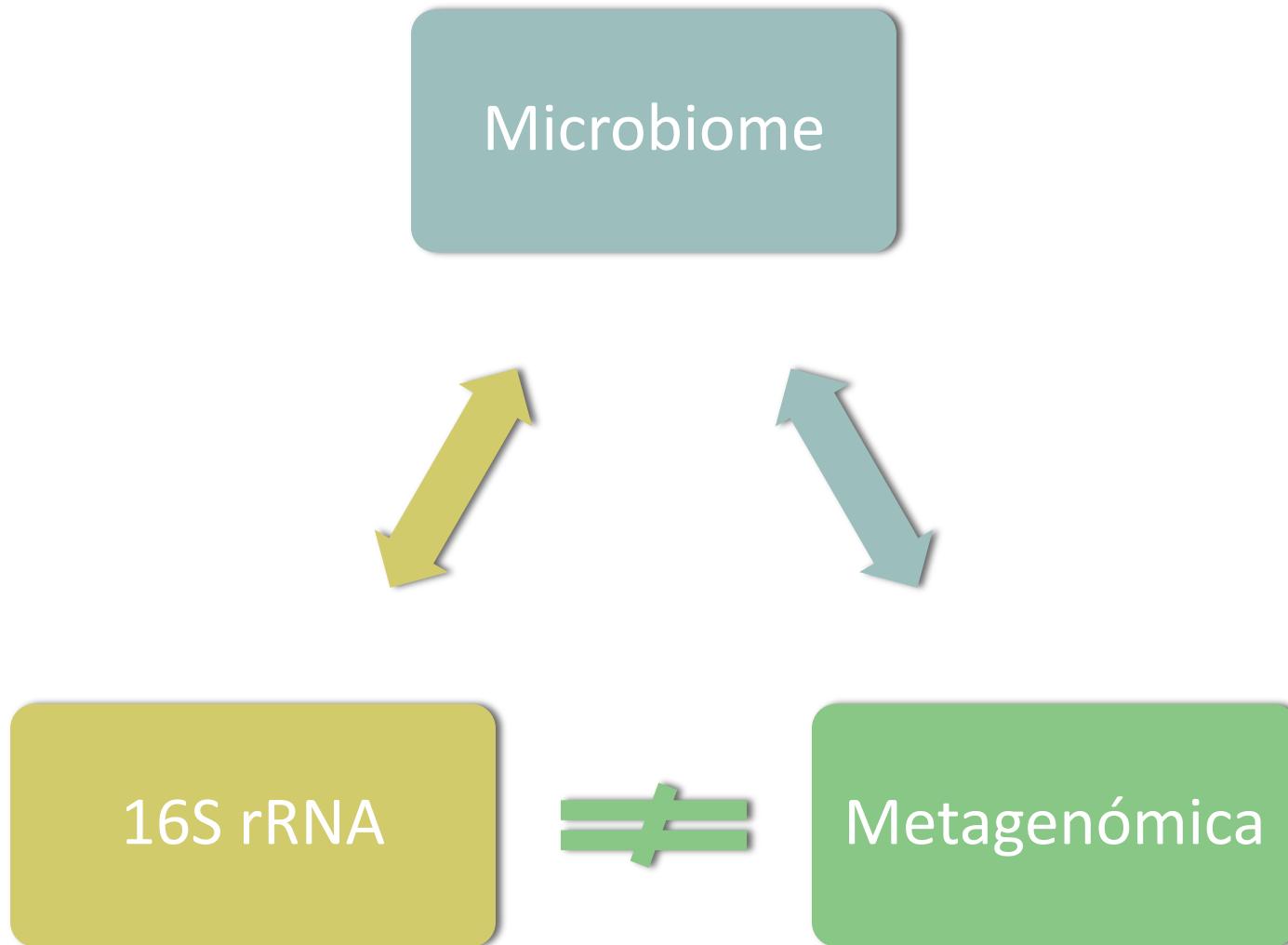


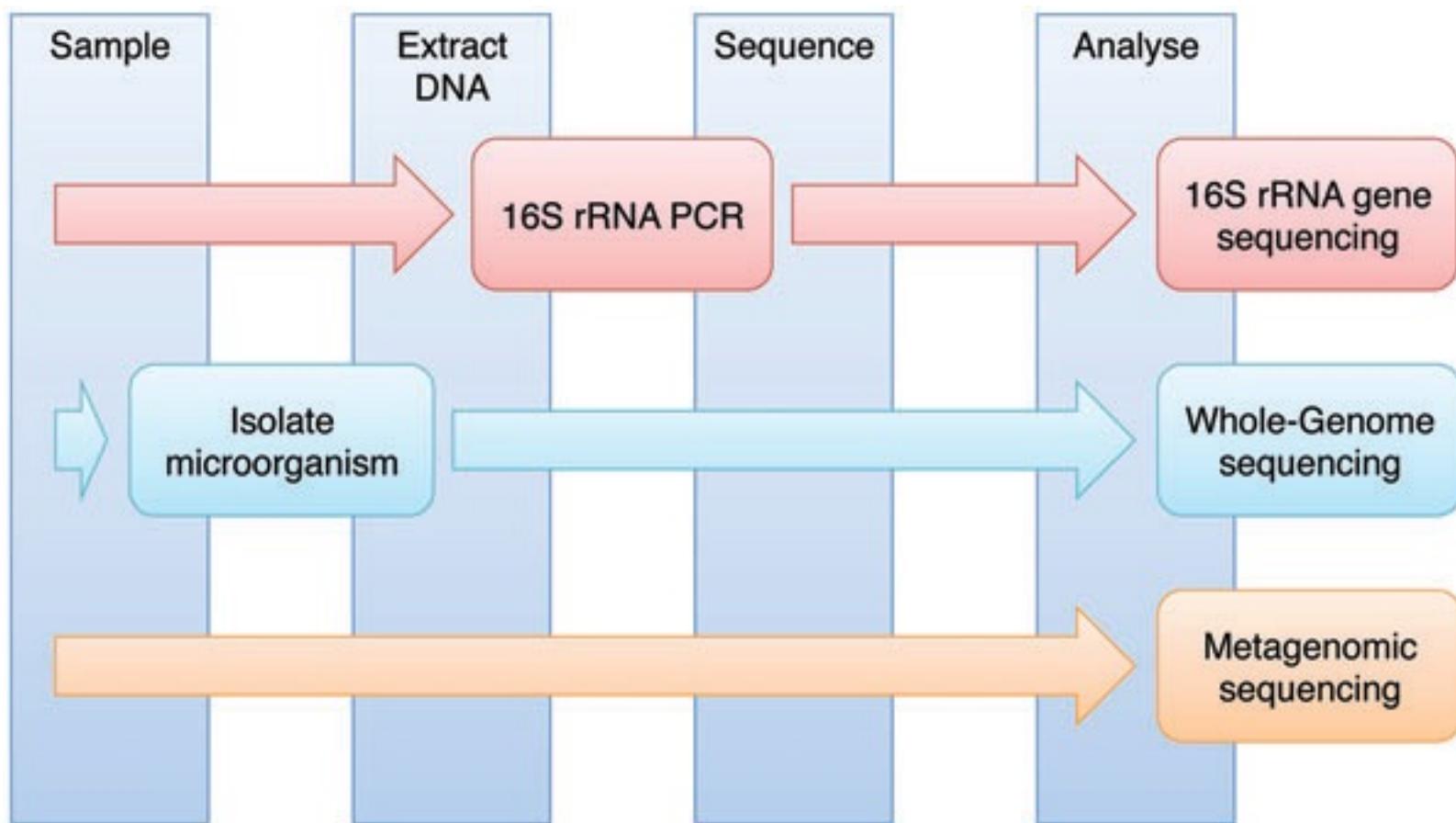
Qiime

R - Phyloseq

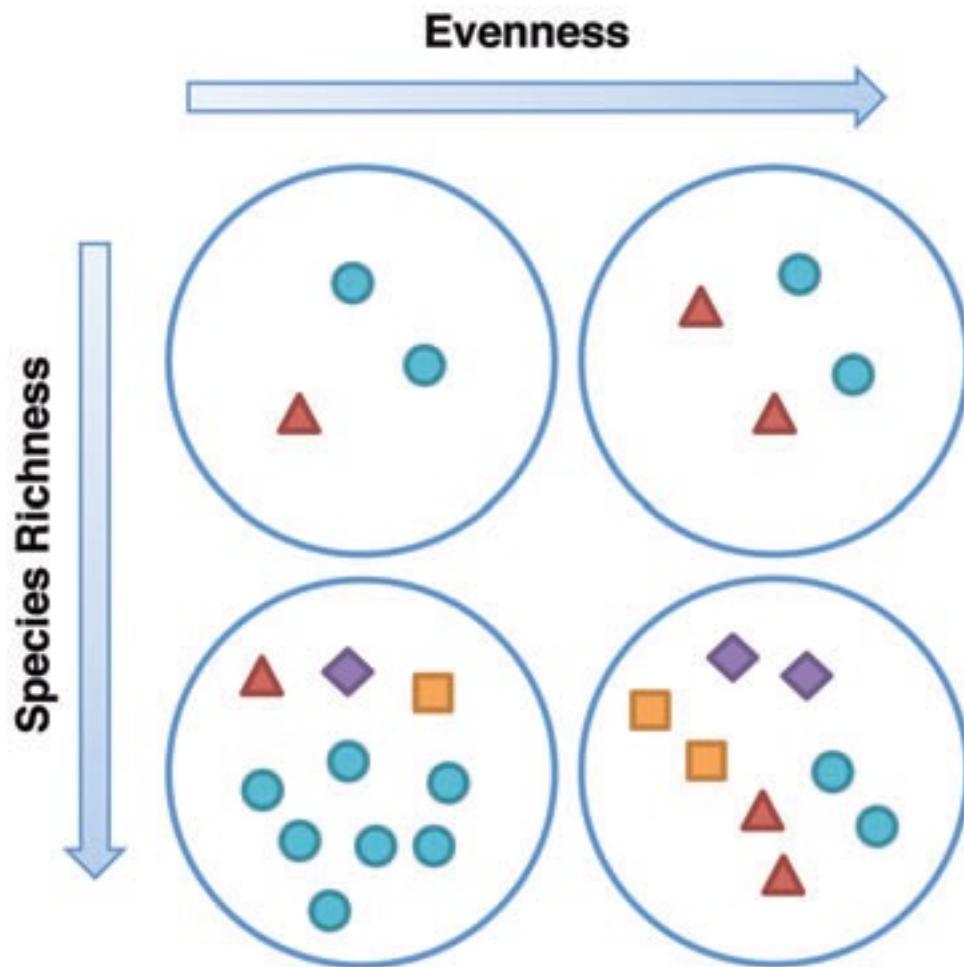


Types of microbiome analysis

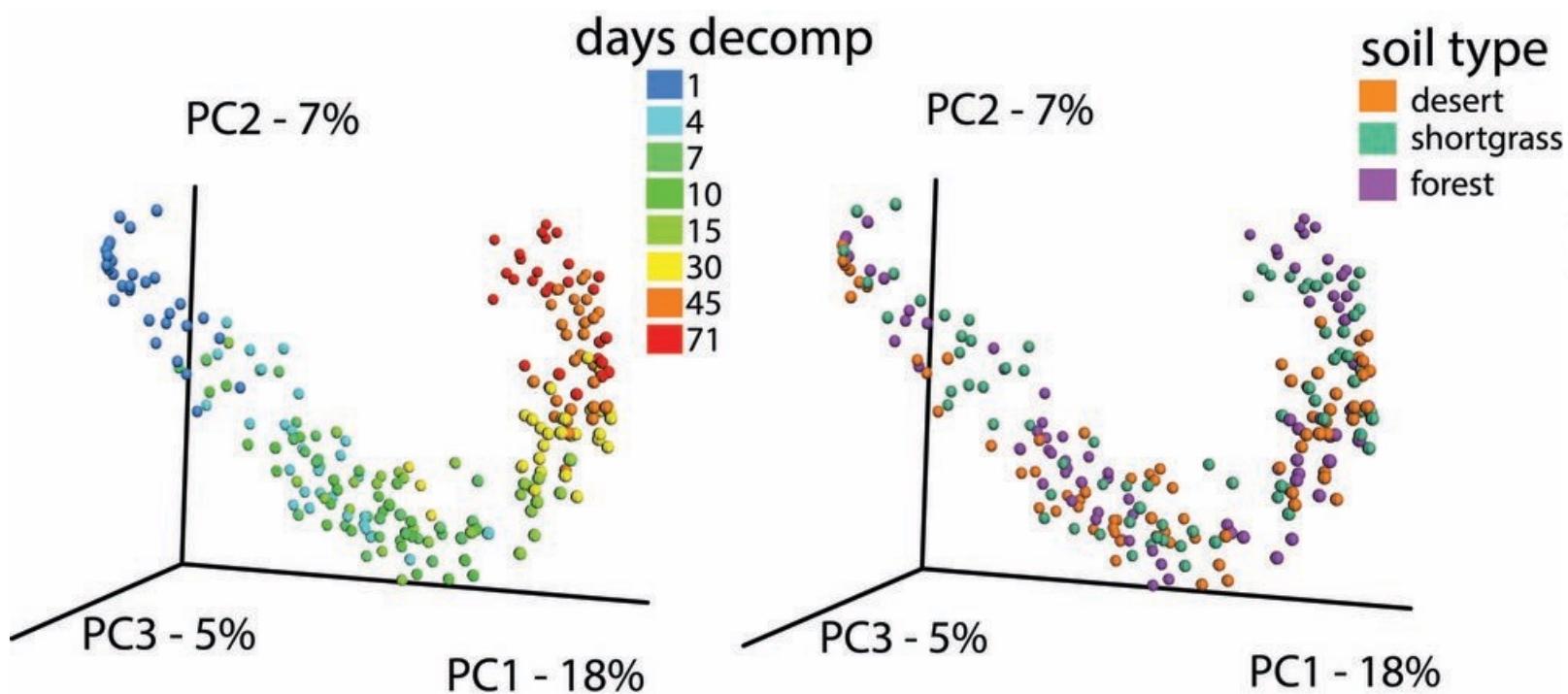




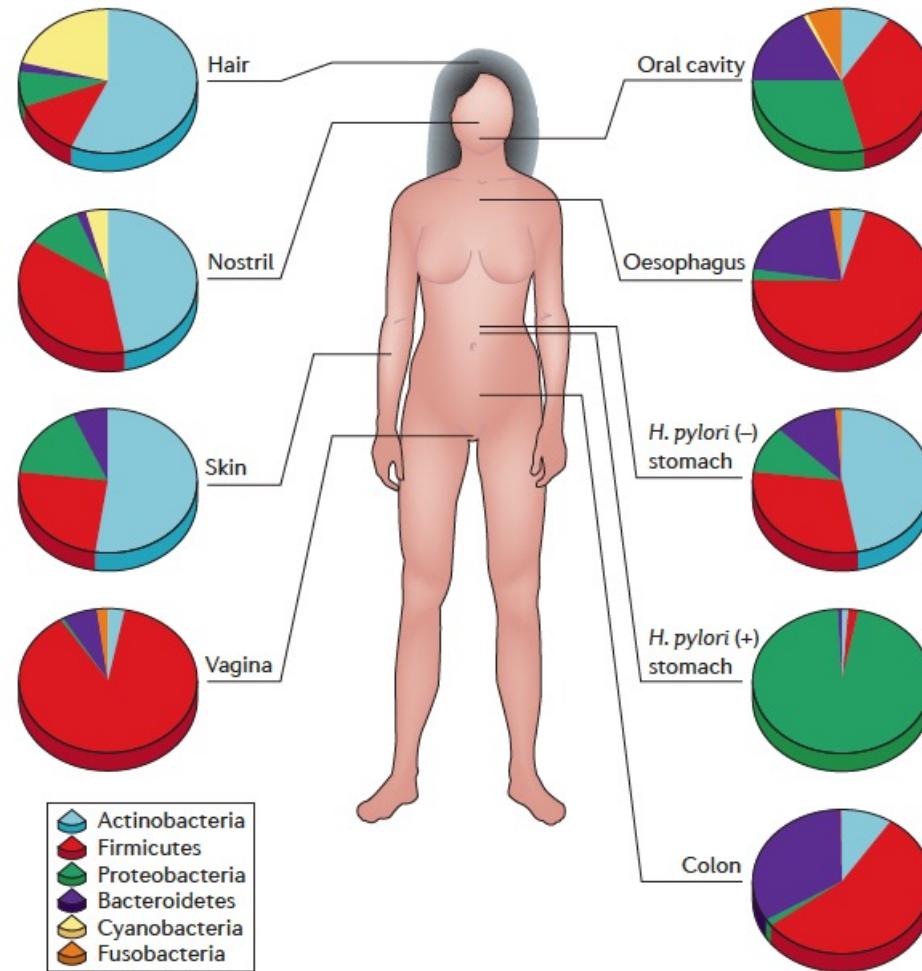
Alpha diversity

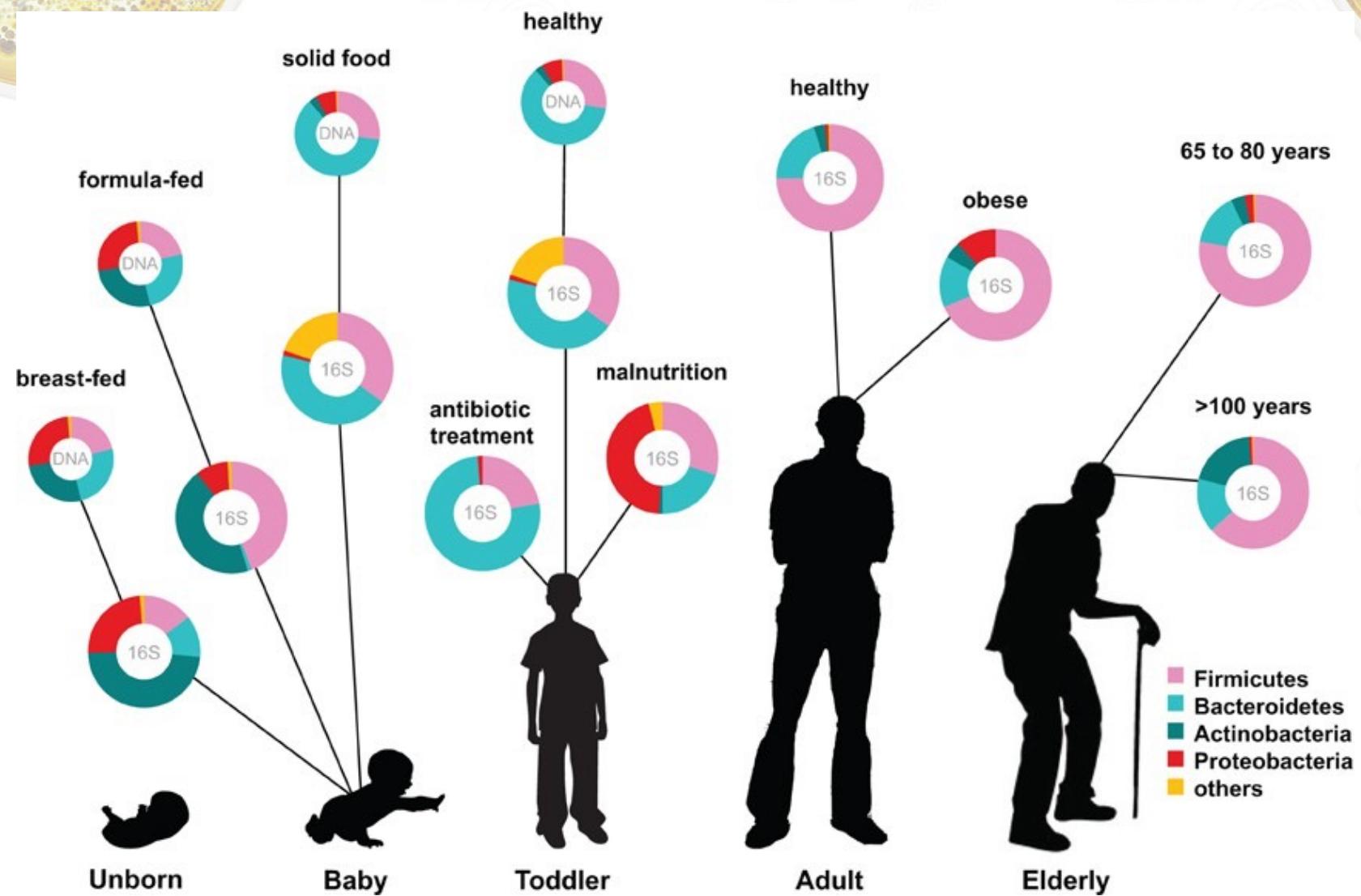


Beta diversity



Relative abundance





Zhang 2009

How does the microbiome contributes in health?

- Producing vitamins and cofactors: vitamin B12
- Protecting directly against the development of pathogens: *C. difficile* colitis
- Immune system development: allergies and asthma
- Immune system normal function: antibiotics produces diarrhoea
- Producing metabolites that regulate other systems like Central Nervous System

Methods for metagenomics

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← Platform Directory

q2Galaxy

Container:	q2galaxy
Scope:	Tool Publishing
Summary:	QIIME 2 Galaxy Docker image.



Comments

- Starting with the 2021.4 release of QIIME 2, this Docker image is automatically updated as QIIME 2 is updated. This container is maintained by the QIIME 2 team.
- QIIME 2 is a next-generation microbiome bioinformatics platform that is extensible, free, and open source.

User Support

- QIIME 2 has [extensive documentation](#), an [online and free workshop](#), and a [support forum](#).
- There is also a [video](#) describing how to launch the QIIME 2 Galaxy Docker image (on Windows!).

Quotas

- None

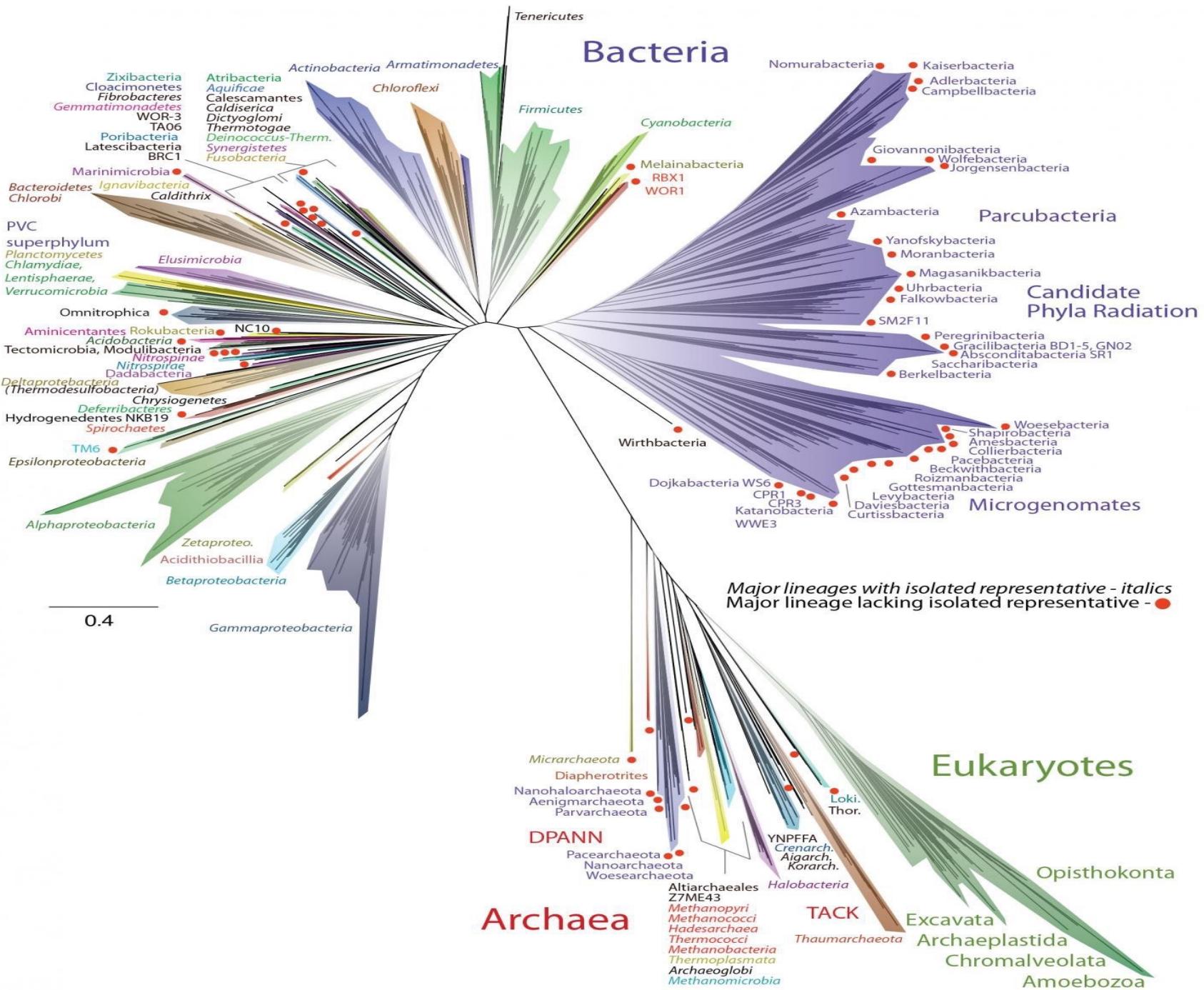
Citations

- Bolyen, E., Rideout, J.R., Dillon, M.R. et al. Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology* 37, 852–857 (2019). <https://doi.org/10.1038/s41587-019-0209-9>

Sponsors

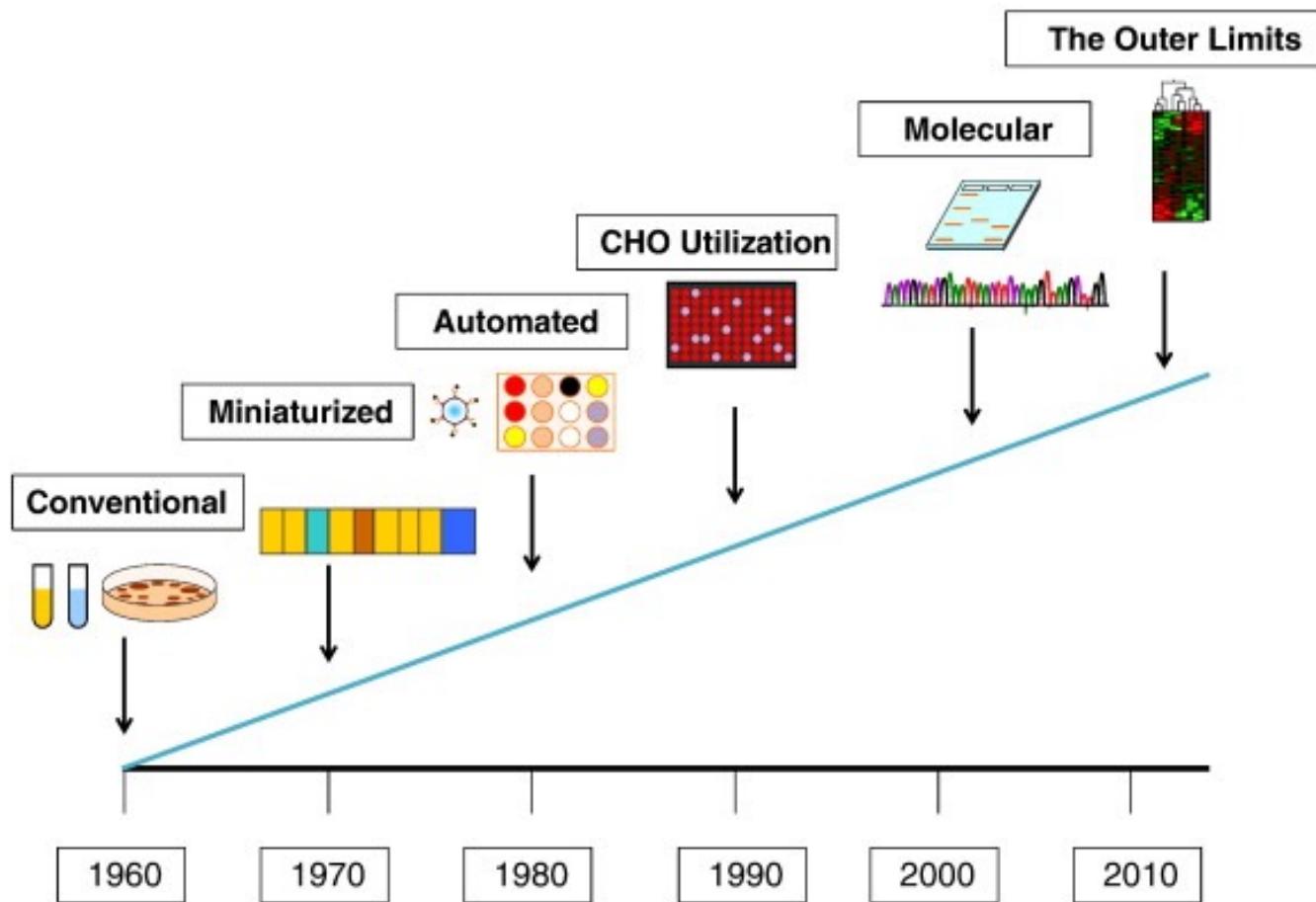
- The [QIIME 2 Project](#)

Pathogen discovery



- Those that are difficult or time-consuming to isolate
 - e.g., *Mycobacteria*
- Hazardous organisms
 - e.g., *Histoplasma*, *Coccidioides*
- Those without reliable testing methods
 - e.g., *HIV*, *HCV*
- High-volume tests
 - e.g., *S. pyogenes*, *N. gonorrhoeae*, *C. trachomatis*

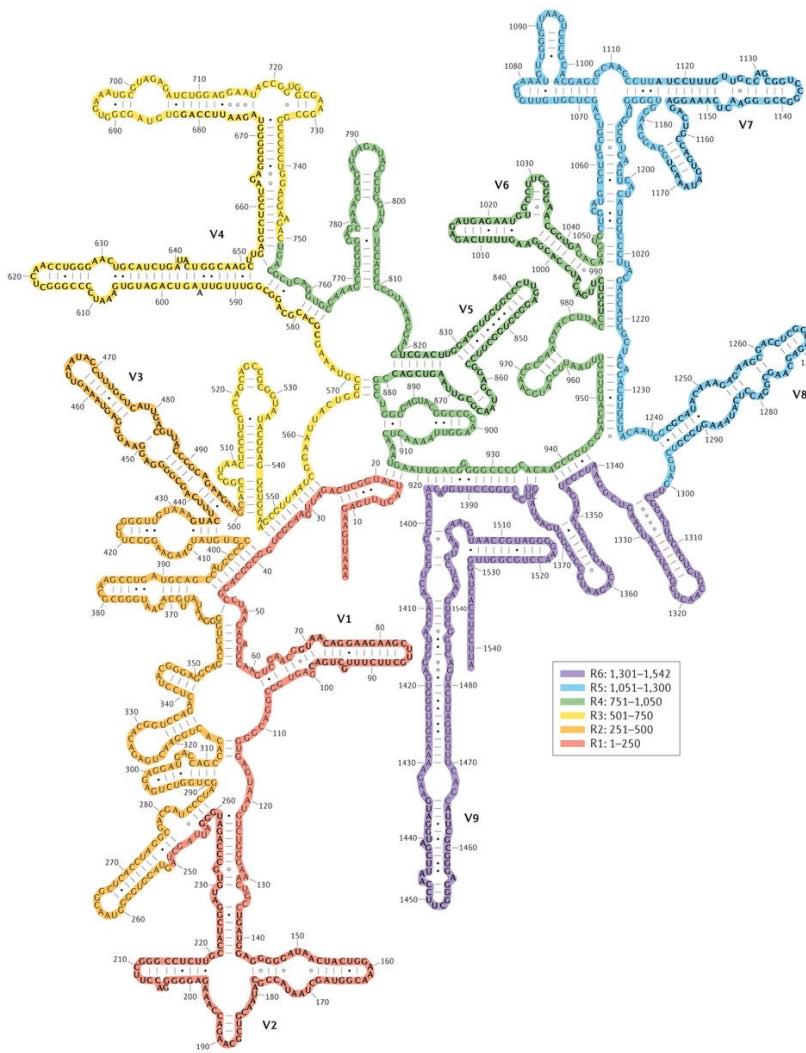
¿Cómo?



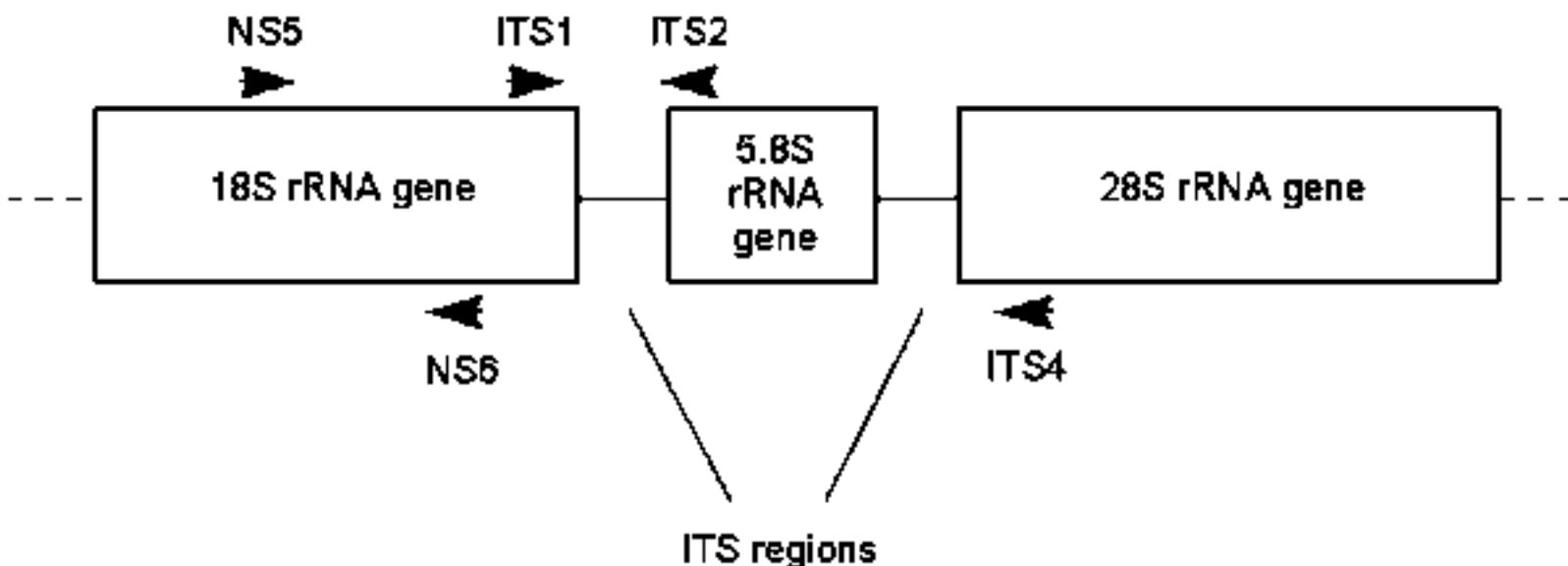
Specimen Collection

- Preserve viability/nucleic acid integrity of target microorganisms
- Avoid contamination
- Appropriate time and site of collection (blood, urine, other)
- Use proper equipment (coagulant, wood, or plastic swab shafts)
- Commercial collection kits are available
- The Clinical and Laboratory Standards Institute (CLSI) has guidelines for proper specimen handling

Selecciona el marcador apropiado



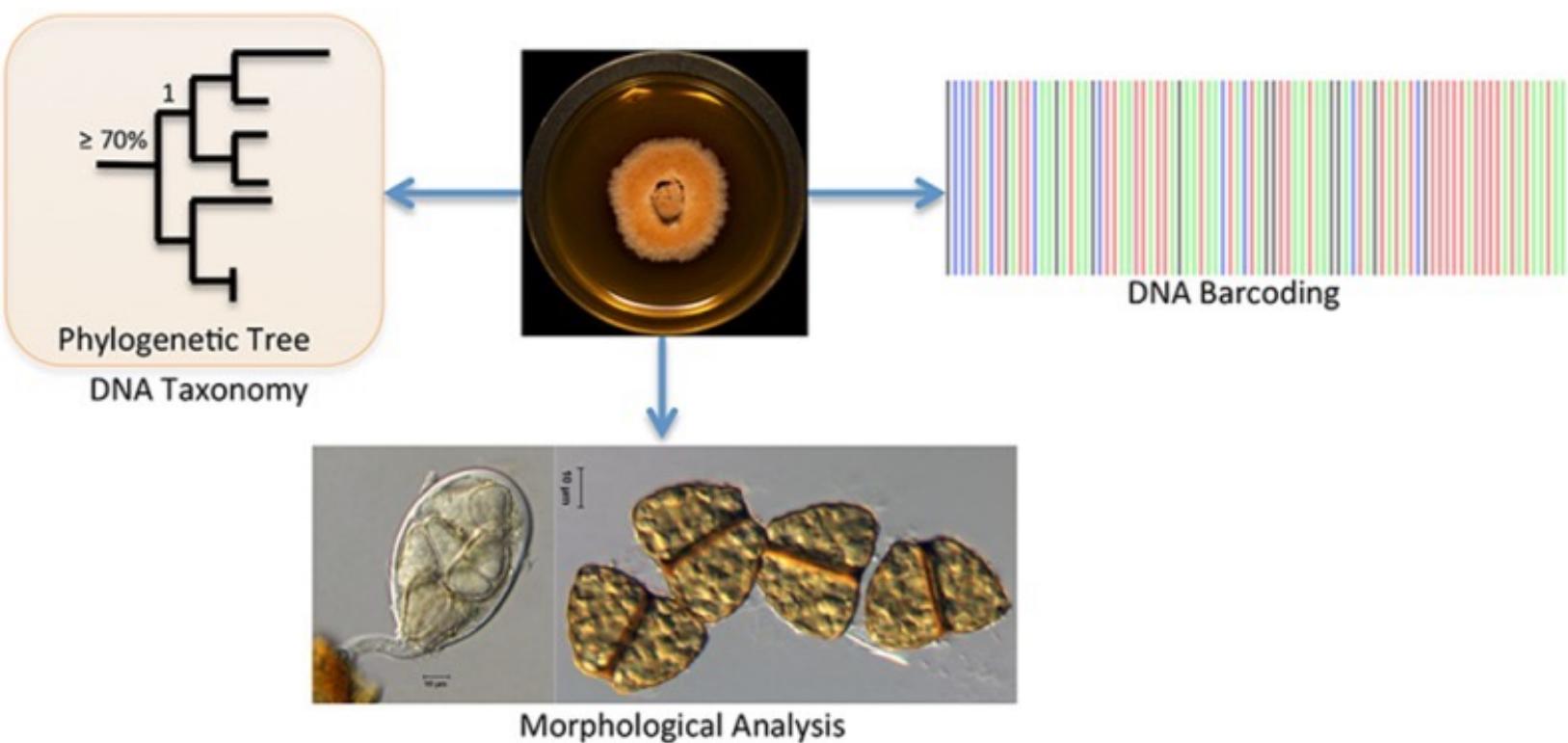
Molecular marker



Viruses

- “Classical methods” of detection include antibody detection, antigen detection, or culture.
- Molecular methods of detection include target, probe, and signal amplification.
- Tests are designed for identification of viruses, determination of **viral load** (number of viruses per ml of fluid), and genotyping by sequence analysis.

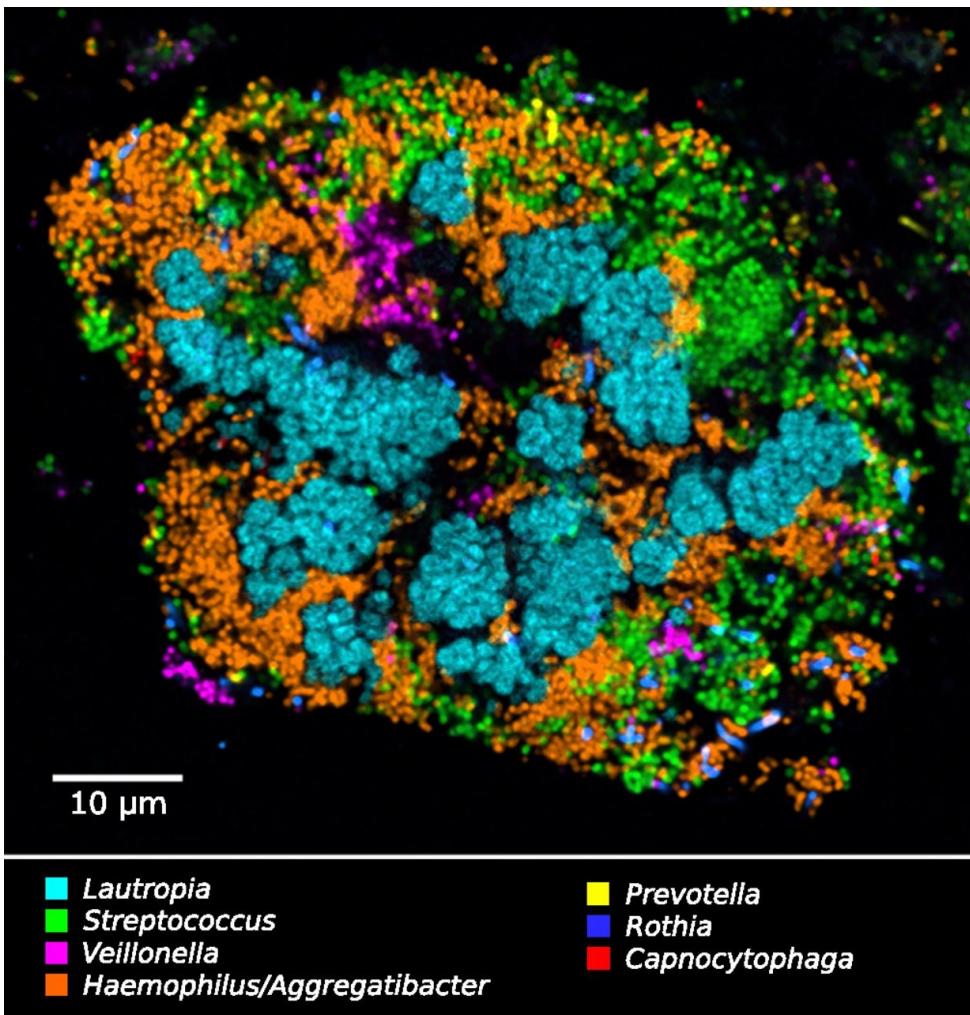
Fungi



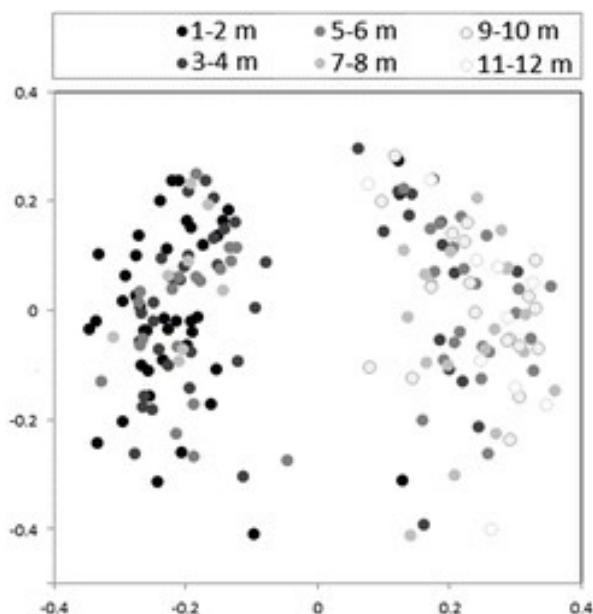
Protozoa



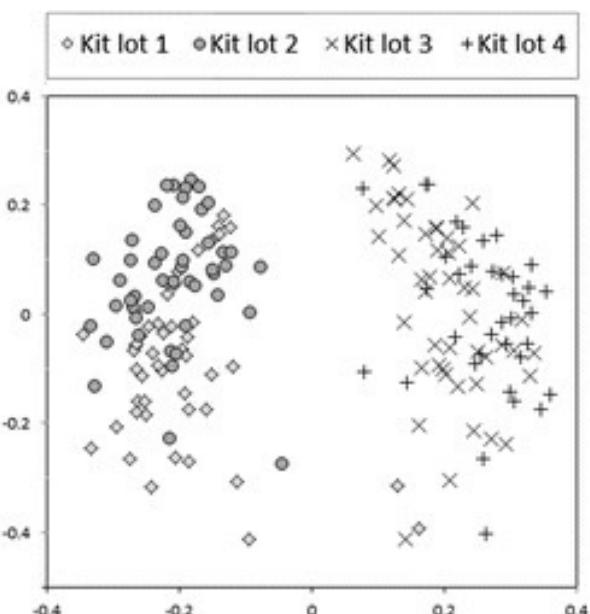
FISH



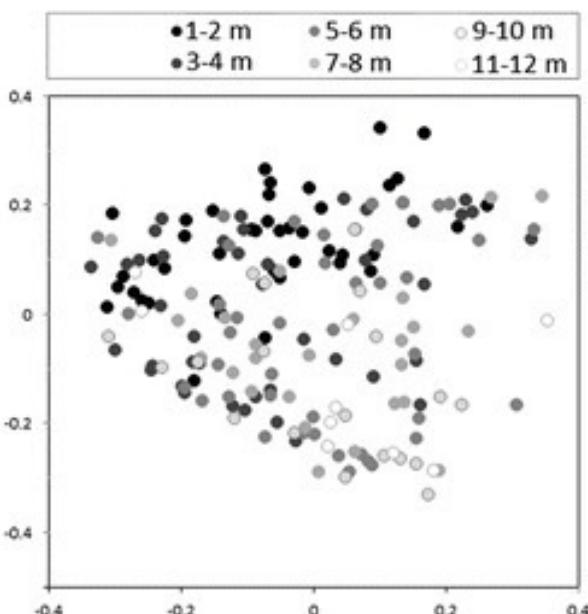
Contaminomics



a) Full data coloured by age (months)

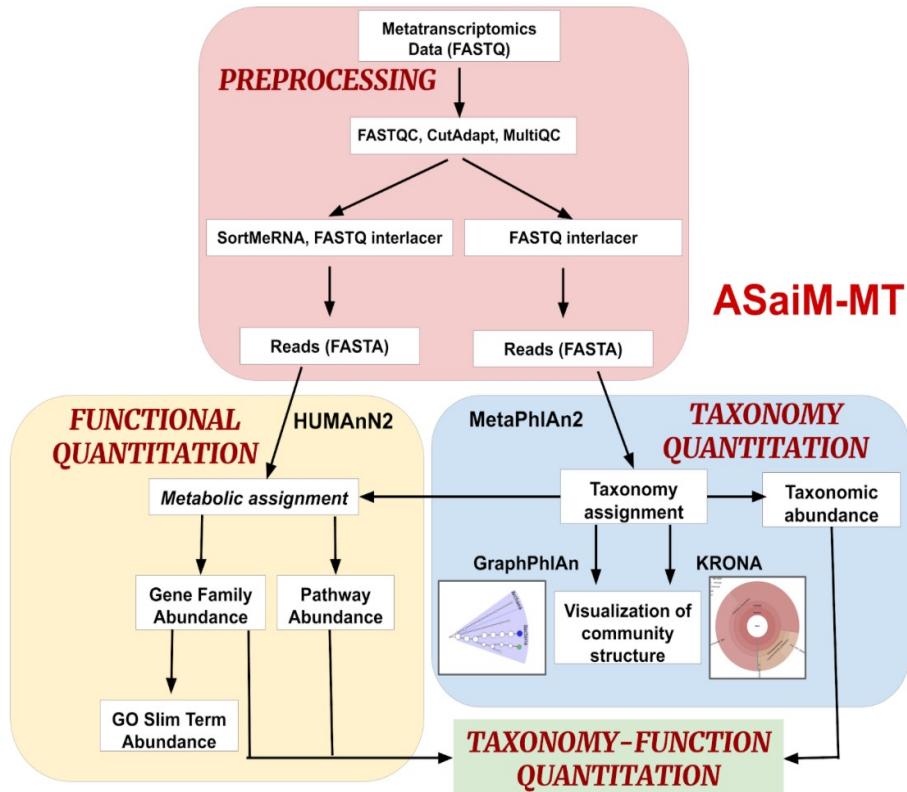


b) Full data coloured by extraction kit



c) Contaminant OTUs removed

Methods for pathogen discovery



The workflow is divided into 4 parts:

1. **Preprocessing** - Process raw metatranscriptomics data to perform further analysis.
2. **Taxonomy Quantitation** - Assignment of taxonomy along with abundance values and visualization.
3. **Functional Quantitation** - metabolic assignment of identified functions and gene and pathway abundance annotation.
4. **Taxonomy-Function Quantitation** - combine taxonomy and functional quantitation values into relative abundance values at different levels such as e.g. the abundance of a pathway between phyla.

Methods for pathogen discovery

[Home](#) [Web Server](#)  [Source](#) 



Fast and sensitive taxonomic classification for
metagenomics

Web server – Submit job

Use the form to upload fastq/fasta file(s) and choose options.

Once uploading is completed, press the Submit button at the bottom of the page.

Only upload one data set at a time.

Job Name

You can give a custom name to your submission.

e-mail

Receive a notification after your submission has been processed. [?]

File with sequencing reads *

Nucleotide sequences must be in compressed FASTA or FASTQ format [?]

Select file

File name:

Start upload

Progress:

Upload a second file for paired-end sequencing

Examples

- Bugseq
- <https://bugseq.com/demo/metagenomic>
- CZID (Free-register needed)
- <https://chanzuckerberg.zendesk.com/hc/en-us/articles/13756558532884-CZ-ID-Pipeline-Overviews>
- Epi2Me (Nanopore)
- <https://epi2me.nanoporetech.com/shared-report-395775?tokenv2=9e175ddb-df8f-4312-9e97-e85edeb11d38&tab=Reports>
- Kaiju
- <https://kaiju.binf.ku.dk/server>