



# Metagenomics

Taxonomic and Functional Classification, MetaAssembly and GenePredictions, Comparative Analysis

The OmicsBox Metagenomics Module allows to combine and integrate all necessary steps for a complete metagenome analysis in a flexible, and intuitive way. Main analysis steps are:

## Quality Control And Assessment

Use FastQC and Trimmomatic to perform the quality control of your samples, to filter reads and to remove low quality bases.

## Taxonomic Classification

Identify present species (Bacteria, Archaea, Virus) with Kraken and visualize results with multilevel pie-charts (Krona) as well as inter-sample comparison bar-charts.

## Metagenomic Assembly

Choose between MetaSPAdes and MEGAHIT to assemble large datasets easy and fast in the cloud.

## Gene Prediction

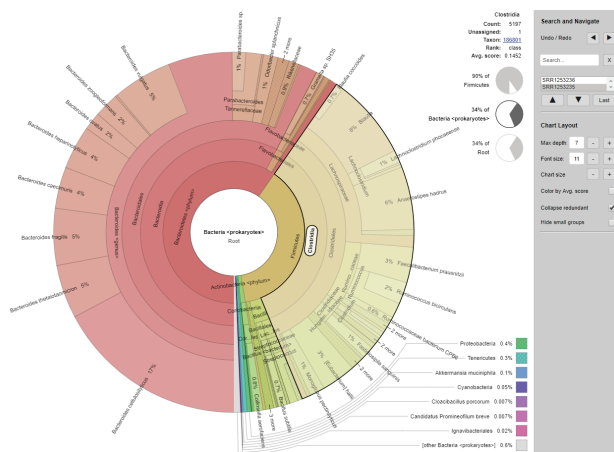
Use FragGeneScan for plain reads and Prodigal for assembled data to identify and extract possible genes and proteins.

## Functional Annotation

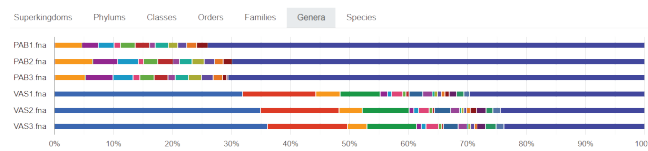
Use EggNOG-Mapper (orthologous groups) and PfamScan (domains and families) to perform high-throughput functional classifications. Results can be represented and compared visually with GO graphs and charts.

Rank	TaxID	Scientific Name	PAB1	PAB2	PAB3
superkingdom	2	Bacteria <prokaryotes>	11404	8852	10183
phylum	201174	Actinobacteria <phylum>	1421	998	1180
family	80864	Comamonadaceae			1604
class	1760	Actinobacteria <class>			1012
order	356	Rhizobiales			850
family	119060	Burkholderiaceae			553
order	976	Bacteroidetes <phylum>			377
family	1239	Firmicutes			458
order	72274	Pseudomonadales			444
family	135621	Pseudomonadaceae			430
order	204457	Sphingomonadales			285
genus	286	Pseudomonas			408
class	28221	Deltaproteobacteria	405	272	293

Sort and filter the taxonomic classification results, and extract all reads that belong to selected taxonomic units. Refine your reports with customized distribution charts in various styles.



Colorful and interactive charts help you to intuitively explore your data. Explore all samples with their relative species abundances and confidence scores within the complex hierarchies of metagenomic classifications.



Interactive bar charts help understanding inter-sample relations at for example the genus or species level.

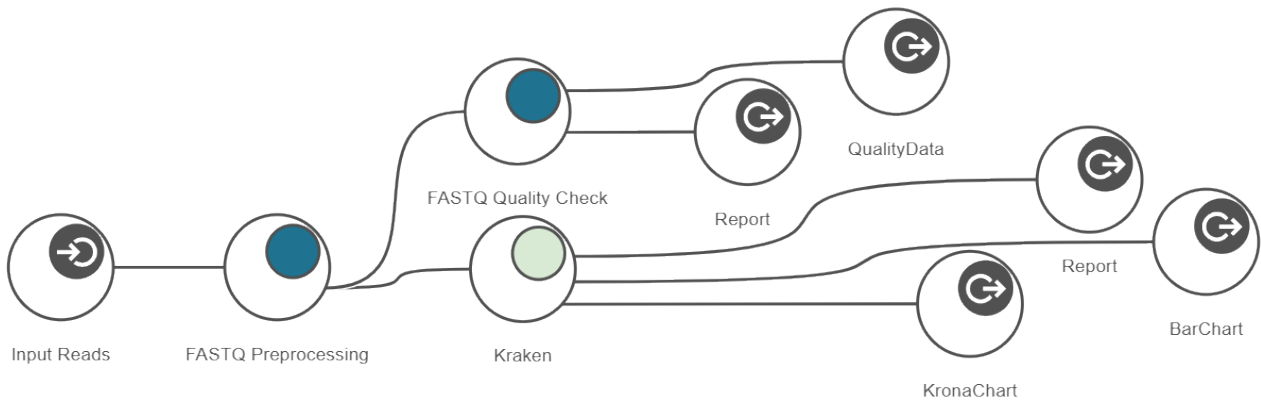
It shows you a quick overview of taxonomic abundance compositions between different samples.



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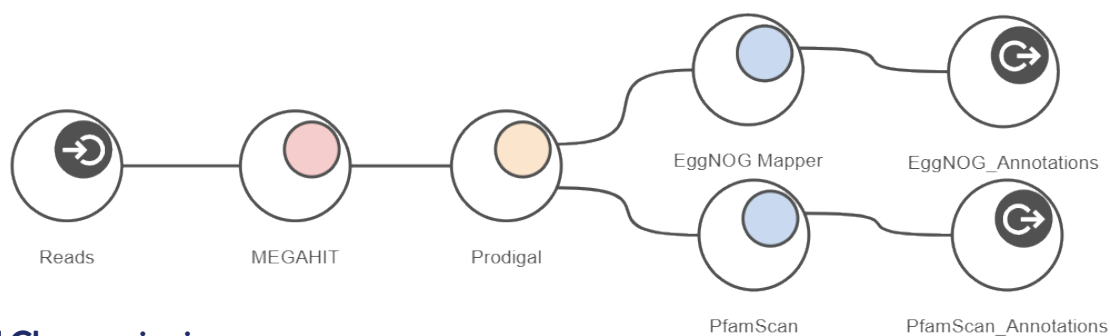


### Taxonomic Classification

This example workflow shows a basic taxonomic classification of metagenomics data with OmicsBox. The reads are preprocessed (Trimmomatic) and a report is generated (FastQC).

Kraken is used to identify and count all different operational taxonomic units (OTUs) for further interpretation.

The spreadsheet-like result can be filtered and organized. The PDF report gives a clean overview of most abundant OTUs at different levels for each sample. Results also include intra- and inter-sample comparison charts. The whole workflow can be started within a few clicks and computationally intensive parts run transparently on the cloud.



### Functional Characterization

Functional characterization of metagenomics data is a complex task. The OmicsBox Metagenomics Module allows you to design streamlined workflows to easily combine the typically resource-demanding assembly step with gene predictions, as well as high-throughput functional annotation for large metagenomics data-sets.

This example workflow shows the combination of MEGAHIT with Prodigal. Fast and comprehensive functional annotation is achieved with the integration of EggNOG- Mapper and PfamScan.

Results are presented in form of spreadsheets and can be filtered and visualized with hierarchical bar- and graph charts.