OmicsBox

The OmicsBox Metagenomics Module allows to combine and integrate all necessary steps for a complete metageneome analysis in and 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.

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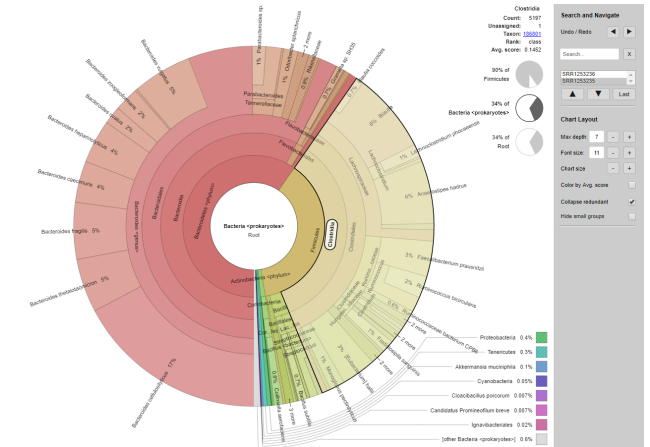
Colorful and interactive charts help you to intuitively explore your data. Explore all samples with their relative species abundances and confidence scores within the complex hierarchies of metagenomic classifications.
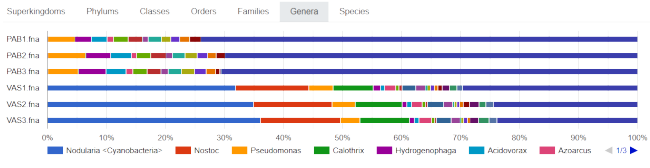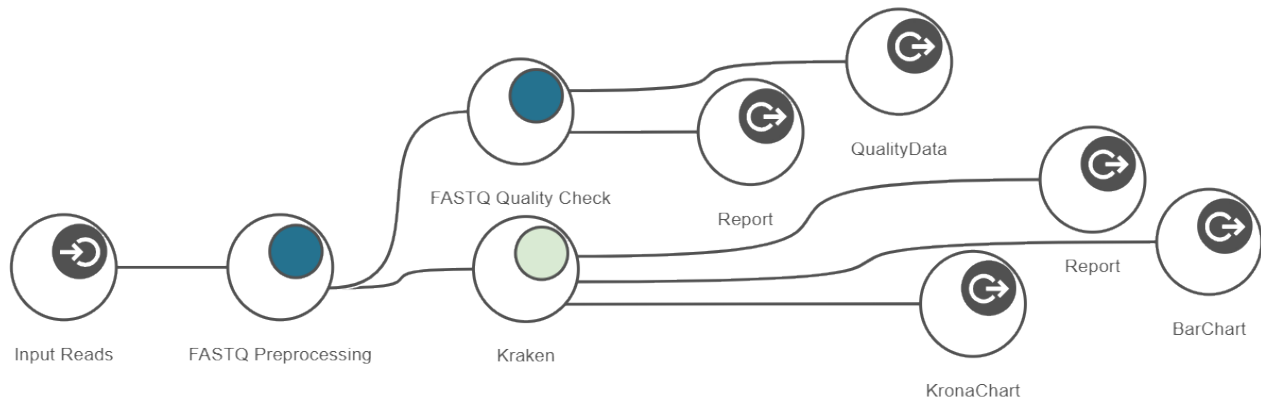

Interactive bar charts help understanding inter-sample relations at for example the genus or species level.

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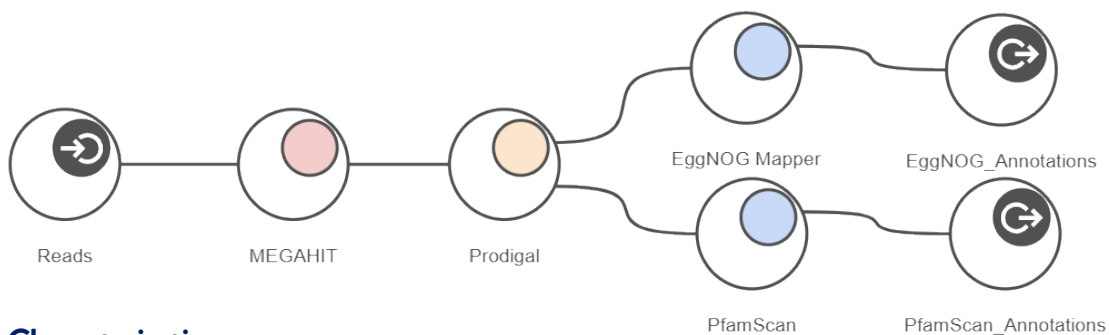
Metagenomics

Taxonomic and Functional Classification, MetaAssembly and GenePredictions, Comparative Analysis

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 datasets.

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 hierachical bar- and graph charts.