



Genome Analysis

Quality Control And Assessment
De-Novo Assembly
Repeat Masking
Gene Finding

The OmicsBox Genome Analysis module allows to characterize and analyze newly sequenced genomes, from raw reads to gene structures in an efficient and user-friendly way.

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.

De-Novo Assembly

The assembly feature based on ABySS allows to reconstruct whole genome sequences without a reference genome or specific hardware requirements.

Repeat Masking

Mask repeats and low complexity DNA sequences of your eukaryotic genome assemblies with RepeatMasker to improve downstream gene predictions.

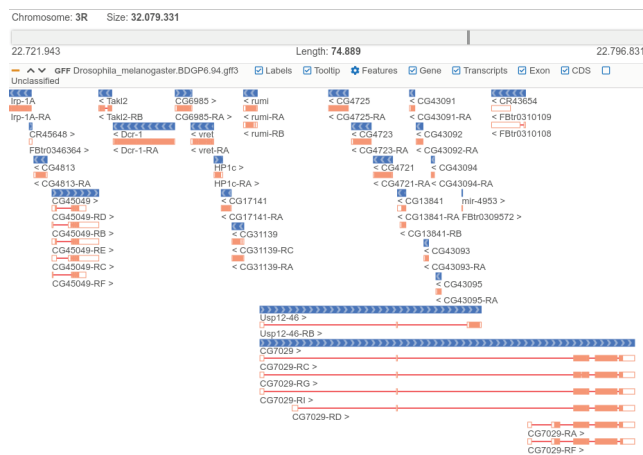
Gene Finding

Perform prokaryotic (Glimmer) and eukaryotic (Augustus) gene predictions to characterize genome structure. The eukaryotic gene prediction offers RNA-seq intron hint support.

About OmicsBox and BioBam

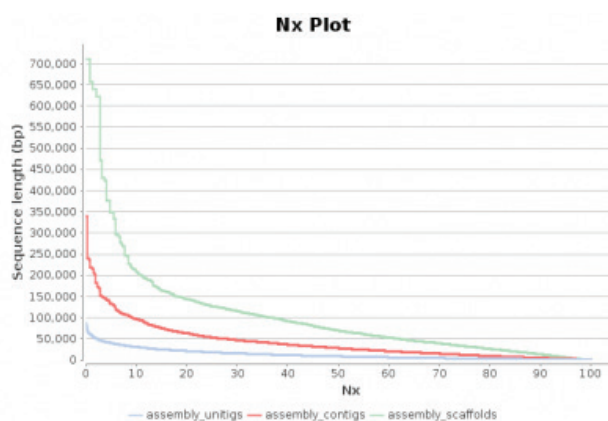
BioBam is a leading bioinformatics solution provider which accelerate research in disciplines such as agricultural genomics, microbiology or environmental NGS studies.

OmicsBox is a user-friendly bioinformatics desktop application for industry, academic and governmental research biologists from top private and public research institutions worldwide.



Genome Browser

Visualize your annotations in form of tracks to combine the genome sequences (.fasta) with alignments (.bam), intron-exon structure (.gff) and variant data (.vcf).



Statistics

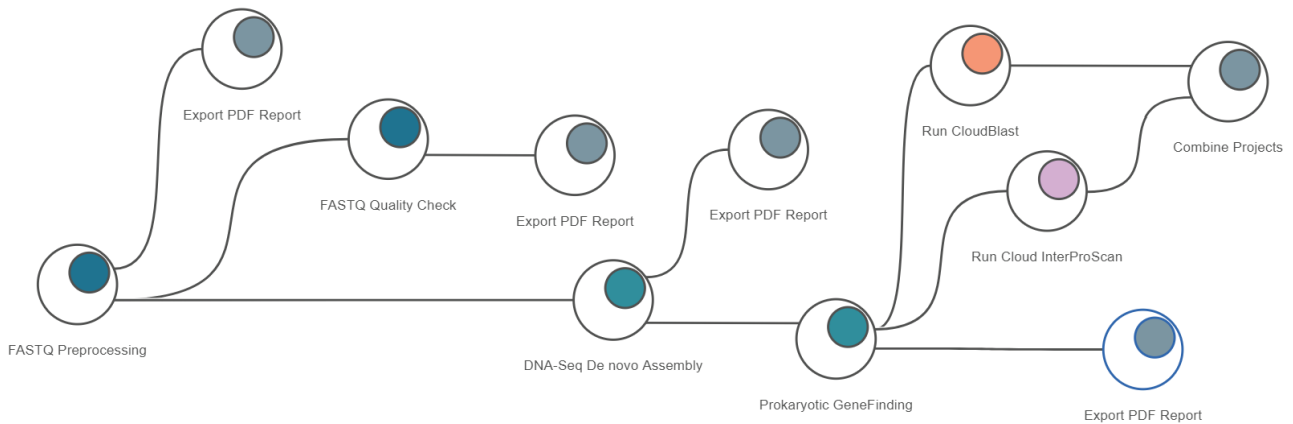
Different statistical charts and reports allow to evaluate the genome assembly and characterization processes and helps with the biological interpretation of the results.



OmicsBox

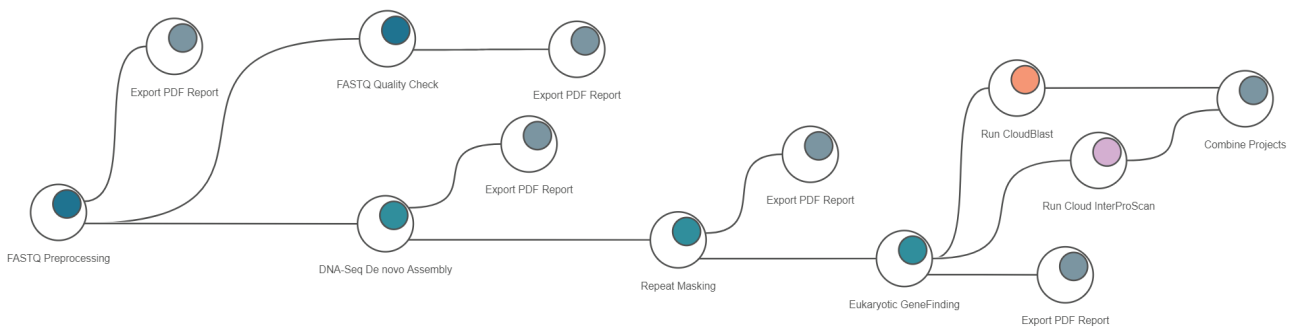
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Eukaryotic Genome Analysis

Generate a genome draft of eukaryotic species by assembling DNA-Seq reads without additional prior information. Detect and mask repetitive sequences and improve the gene prediction by providing RNA-Seq data.



Prokaryotic Genome Analysis

Genomes of bacteria and other prokaryotic organisms can be assembled and characterized in a fast and sensitive way. Proceed with the functional annotation of the resulting gene sequences.