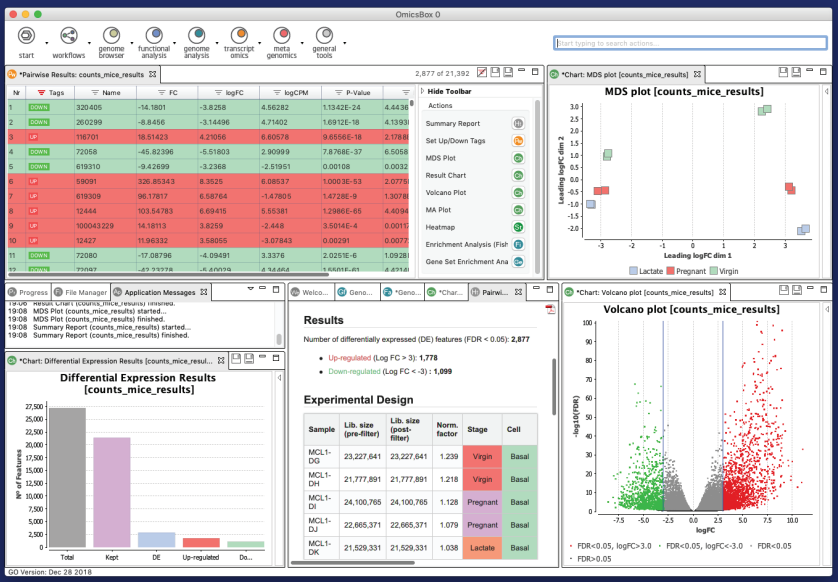
OmicsBox

BIOINFORMATICS MADE EASY

OmicsBox Overview

- Leading bioinformatics platform for the analysis of novel genomes.
- Internationally recognized as a leader in functional genomics, which is demonstrated by over 7000+ scientific research citations.
- User-friendly bioinformatics desktop application for industry, academic and governmental research biologists.
- Allows to gain biological insights fast and easy even for completely novel genomes.



Developed by BioBam

- OmicsBox is developed and maintained by BioBam Bioinformatics.
- BioBam is a bioinformatics solution provider based in Valencia, Spain.
- BioBam's solutions accelerate research in disciplines such as agricultural genomics, microbiology and environmental NGS studies; amongst others.

biobam
BIOINFORMATICS SOLUTIONS

OmicsBox Modules

Genome Analysis
De-Novo Assembly, Gene Finding, Repeat Masking, Coding Potential, Rfam

Transcriptomics
FastQC, Assembly, Quantification, Differential Expression (Pairwise, Time Series)

Functional Analysis
Blast2GO Annotation (GOs, COG, Enzymes, Domains), Enrichment Analysis, Visual Exploration

Metagenomics
Taxonomic and Functional Classification, MetaAssembly and GenePredictions, Comparative Analysis

OmicsBox
Workflows, Genome Browser (gff, vcf, fasta and bam), Projects, CloudComputation, Data Manipulation, Filtering, etc.

Subscription Options

1 Module
1 Year
1 User

Your Personal Plan

Multiple Modules, Years and Users

REQUEST YOUR FREE TRIAL

Genome Analysis

Quality Control	Use FastQC and Trimmomatic to perform the quality control of your sequencing data, to filter reads and to remove low quality bases.
De-Novo Assembly	The assembly features based on ABySS allows to reconstruct whole genome sequences without a reference and specific hardware requierments.
Repeat Masking	Mask repeats and low complexity DNA sequences of your eukaryotic genome assemblies to improve the downstream gene predictions.
Gene Finding	Perform prokaryotic (Glimmer) and eukaryotic (Agustus) gene predictions to gerenate GFF genome annotations. The eukaryotic gene predictions offers RNA-seq intron hint support.
Genome Browser	Visualize your annotations in form of tracks to combine the genome sequences (.fasta) with alignments (.bam), the intron-exon structure (.gff) as well as variant data (.vcf).

Functional Analysis

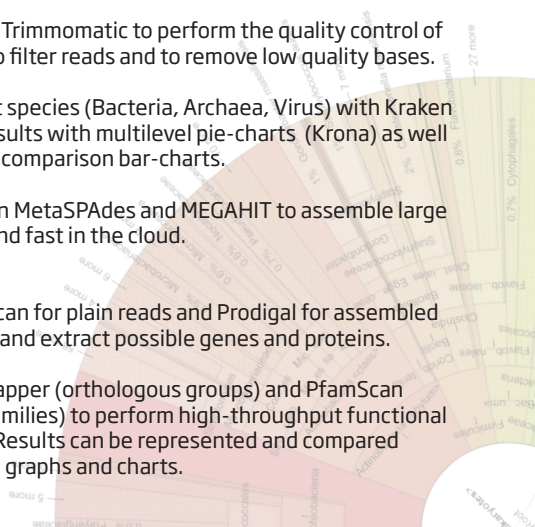
High-Throughput Blast and InterProScan	Use CloudBlast and CloudInterPro to perform fast sequence alignments and domain searches against a reference datasets of your choice.
Gene Ontology Mapping	Link potential homologs and domains with available functional information.
Blast2GO Annotation	The Blast2GO methodology allows to flexibly assign most reliable functional lables to novel sequence datasets, taking into account source quality and ontology hierarchies.
Enrichment Analysis	Use different enrichment analysis approaches to identify over and under represented molecular functions.
Functional Interpretation	Many different visualizations allow to evaluate the annotation process as well as help with the biological interpretation of experimental and functional analysis results.

Transcriptomics

De-Novo Assembly	Assemble short reads with Trinity to create a de-novo transcriptome without a reference genome.
RNA-Seq Alignment	Alignment of RNA-seq data to your reference genome making use of STAR, an ultrafast universal RNA-seq aligner via the OmicsBox Cloud.
Quantify Expression	Quantify expression at gene or transcript level via HTSeq or RSEM and with or without a reference genome.
Differencial Expression Analysis	Detect differencial expressed genes between experimental conditions or over time. All used frameworks, NOISeq, edgeR and maSigPro, are well-known and versatile statistical packages used for these types of analysis. Rich visualizations help to interpret results.
Enrichment Analysis	By combining differencial expression results with functional annotations, enrichment analysis allows to identify over- and under-represented biological functions.

Metagenomics

Quality Control	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 Interpretation	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.



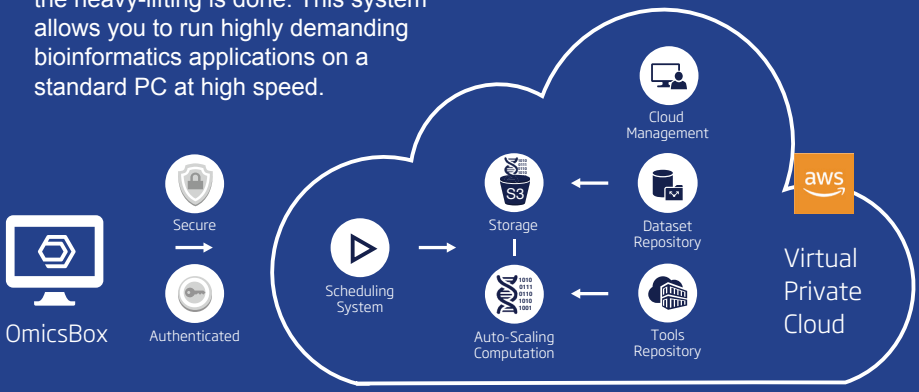
Examples, Tutorials, Videos

In our blog you can find many video tutorials, example analysis and datasets as well as information about the latest developments.
The BioBam blog is also a great resource to learn about all the different analysis steps and to stay up to date.

OmicsCloud

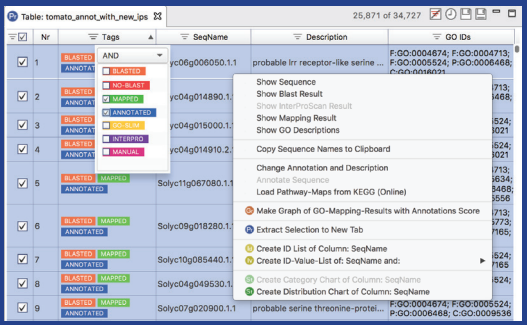
aws partner network
Standard
Technology Partner

Our cloud platform provides a secure, robust and auto-scalable backend to OmicsBox where most of the heavy-lifting is done. This system allows you to run highly demanding bioinformatics applications on a standard PC at high speed.



* The Cloud Cloud Platform is also available as dedicated solution. Please ask us for details.

One Box - One Solution

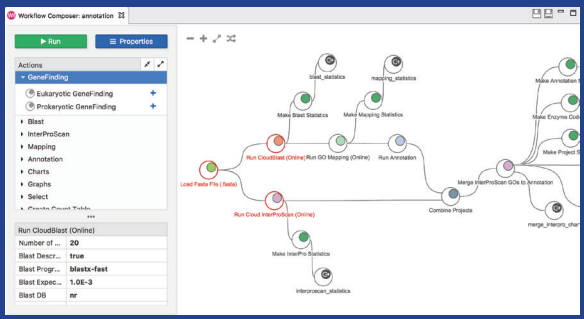


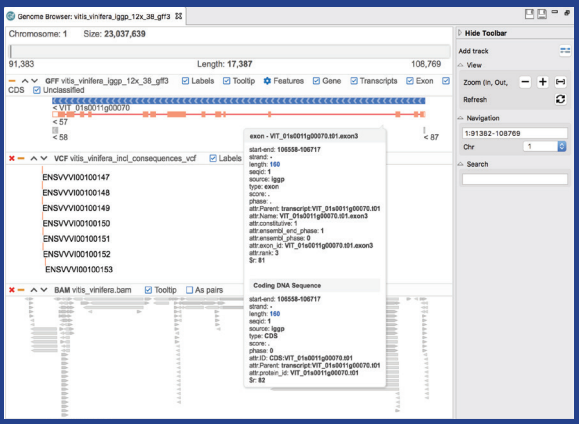
Powerful Tables

The rich user interface allows to process large datasets with ease. All tables can be filtered, sorted and, most importantly, combined with other result sets. It is easy to create and extract subsets for subsequent analysis steps.

Workflows

The Workflow Manager allows to create, run and save bioinformatics workflows. Create a workflow by dragging and dropping the analysis steps of your choice and configure and review all parameters in one place.



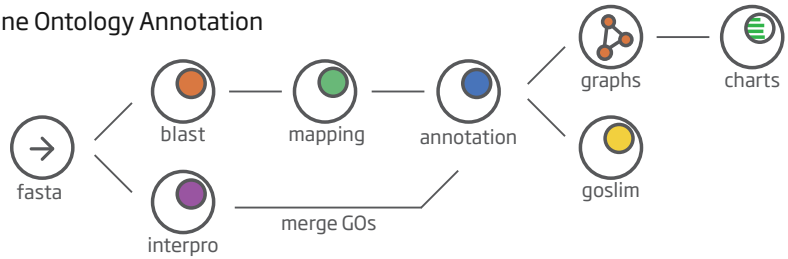


Genome Browser

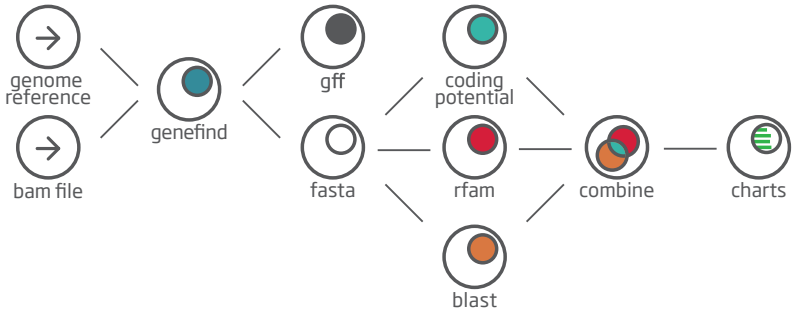
The Genome Browser offers the possibility to combine alignments (.bam) with gene annotations (.gff) and variant information (.vcf) via multiple tracks. Navigtion, filter and search options allow to review results in an easy and explorative way.

Example Workflows

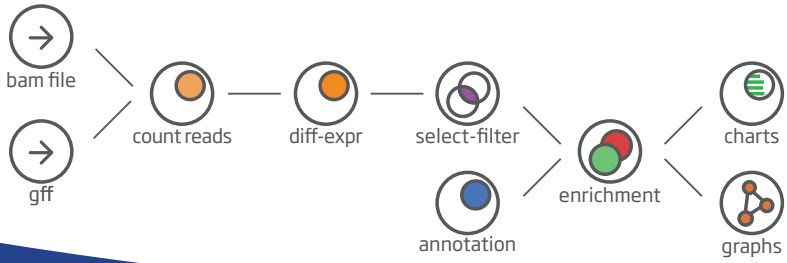
Gene Ontology Annotation



Genome Characterization



Differential Expression with Enrichment



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