

Award-winning Microbiome Analysis

UNRIVALLED ACCURACY AND PRECISION

Data analysis is the most common bottleneck in the metagenomics workflow, but what if you could have access to a user-friendly platform that generates microbiome profiles with industry-leading accuracy and precision?

The CosmosID Cloud Application is bioinformatics software that relies on validated^{1,2,3} databases and algorithms specifically designed for maximum sensitivity, precision and lowest false positive rates.^{1,4} Unlike other solutions, CosmosID delivers **strain-level results** – we understand that the biologically informative and actionable unit in microbiology is not a genus or species, but ultimately a strain and its unique genetic and metabolic properties.

With NGS analysis results in just a few minutes, you can focus on what really matters – the interpretation or publication of your results using robust visualization tools and export features.

BENEFITS

- > Industry-leading accuracy
- > Analysis in minutes
- > No bioinformatics skills required
- > Detailed, intuitive visualizations
- > Command line interface⁵ for bioinformatics experts
- > Supports data import from Illumina BaseSpace and SRA
- > Publication ready results

FEATURES

METAGENOMIC ANALYSIS

- 16S, ITS, shotgun
- Import from Illumina BaseSpace and SRA
- Microbiome profiling, microbial ID
- Machine learning-based filters reduce false-positives
- Antimicrobial Resistance (AMR) & Virulence
- Shotgun functional profiling with MetaCyc and GO Terms databases
- Export of raw results and graphics

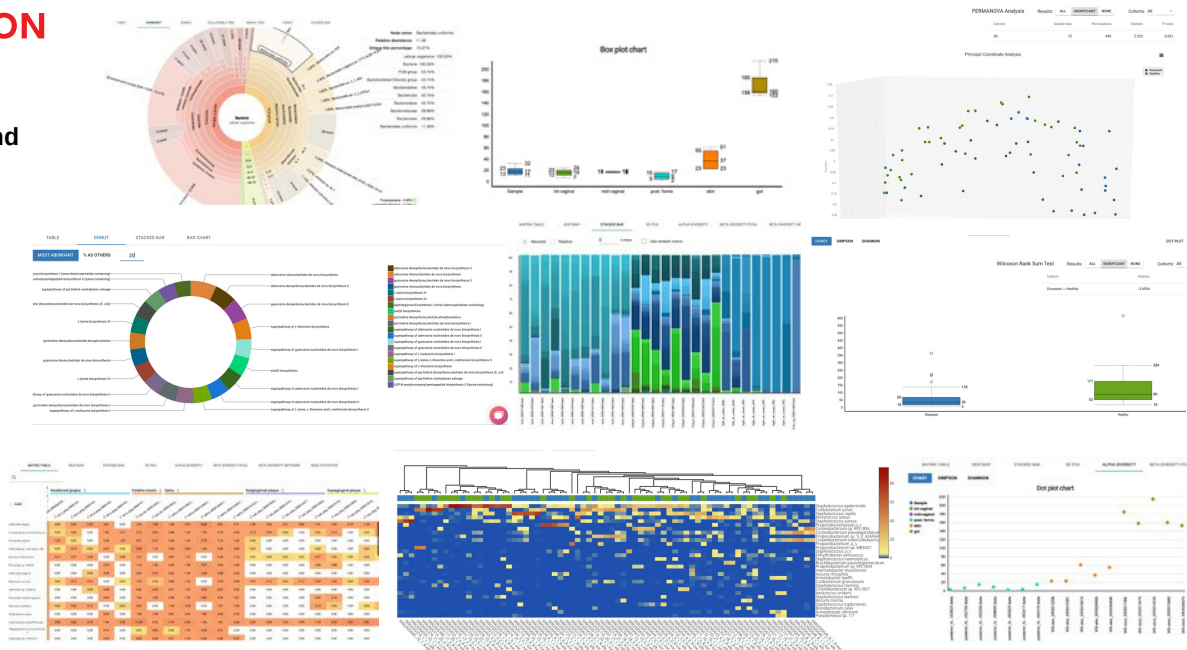
COMPARATIVE ANALYSIS

- Define cohorts and metadata
- Compare individual samples and cohorts
- Identify most / least abundant taxa and functional features per cohort
- Calculate alpha and beta diversity
- Wilcoxon rank sum and PERMANOVA statistical test of significance for alpha and beta diversity cohort wise comparison

DATA INTERPRETATION

Interactive visualizations for microbial strains, MetaCyc Pathways, GO Terms, AMR, and Virulence factors:

- Interactive abundance tables for samples and cohorts
- Sunburst plots
- Stacked bar charts
- Donut charts
- Dendrograms of identified strains
- Alpha diversity with Wilcoxon rank sum test
- Beta diversity with PERMANOVA test³
- PCA and PCoA
- Heatmaps with cohort and features clustering
- And more



COSMOSID DATABASES

CosmosID users have access to the world's largest and most comprehensive continuously curated database.

METAGENOME ANALYSIS BUILT ON KNOWLEDGE

Key characteristics:

- >1 decade of continuous curation of public and proprietary data
- 160,000+ genomes and gene sequences
- Commensals, pathogens, and environmental microbes
- Covers all microbial kingdoms
- AMR and Virulence Markers
- Customizable

How it works:

CosmosID uses a proprietary kmer based approach to identify genomic regions that are either unique and strain-specific, or shared among distinct lineages of microorganisms.

These kmers are stored in phylogenetically organized databases and mapped uniquely to nodes and leaves on the tree-like database ontology, allowing for highly accurate microbial identification as well as taxonomic classification at strain-level.

Using kmers from all regions of the genomes further contributes to the high confidence in microbial identification.

BENEFITS

- > **Sensitivity:** lower miss-rate through leading database volume and content
- > **Specificity:** fewer misidentifications and strain-level resolution due to phylogenetic database structure
- > **Precision:** machine learning based filters predict and reduce false positive signatures
- > **Less bias:** owed to unbiased inclusion of pathogens, commensals, and environmental microbes alike

IDENTIFY



Bacteria



Viruses



Fungi



Protists



Specialty
Databases

CHARACTERIZE



Antibiotic
Resistance



Virulence
Factors



Plasmids



Phages



AWARD WINNING PERFORMANCE TO POWER YOUR RESEARCH

CosmosID has been recognized as industry leader in multiple independent software validations.¹ Recent examples include:

MOSAIC Community Challenge Strain #1 *Host: Janssen Human Microbiome Institute, Janssen Pharmaceuticals*

- Highest score in strain-level microbial profiling
- 64% higher score than second best contender

PrecisionFDA CFSAN Pathogen Detection Challenge *Host: US Food and Drug Administration, CFSAN*

- Highest number of correctly identified samples
- Highest scores for correct taxonomic classification at strain-level
- Lowest number of false positives

References:

1. <https://www.prnewswire.com/news-releases/cosmosid-demonstrates-industry-leading-performance-for-strain-level-microbiome-analysis-in-mosaic-challenge-and-precisionfda-challenge-300669250.html>
2. Yan, Q, et al. (2018). Evaluation of the CosmosID Bioinformatics Platform for Prosthetic Joint-Associated Sonicate Fluid Shotgun Metagenomic Data Analysis. Journal of Clinical Microbiology. <http://doi.org/10.1128/JCM.01182-18>
3. Janes, V. A., Matamoros, S., Willemsse, N., Visser, C. E., de Wever, B., Jakobs, M. E., et al. (2017). Metagenomic sequencing to replace semi-quantitative urine culture for detection of urinary tract infections: a proof of concept. bioRxiv, 178178. <http://doi.org/10.1101/178178>
4. <https://www.cosmosid.com/blog-in/2019/3/20/extensive-academic-study-shows-cosmosids-best-in-class-accuracy-and-unrivaled-detection-resolution>
5. <https://github.com/CosmosID/cosmosid-cli>