

Microbial Genomics and Metagenomics

From data to discovery

Bioinformatics in Microbiology

Microbiome profiling is used to detect microbes in metagenomic samples, and to explore links between taxonomic or functional profiles and external factors like patient health or plant yield.

Microbial typing of isolates at the whole genome level is useful to characterize pathogens, or to provide quality control for valuable strains.

Outbreak analysis leverages whole genome information for pathogen typing and epidemiological outbreak investigation.

Addressing common challenges

A lack of integrated analytics leaves organizations with the burden of integrating and maintaining all the bioinformatics-, statistics- and visualization tools required for their microbial research.

High sample volumes are common thanks to the throughput capacity of modern NGS instruments. But sample load introduces a computational burden and makes managing data and metadata challenging.

QIAGEN Microbial Genomics Pro Suite

Integrated analytics deliver research continuity
All analytics for microbial genomics and metagenomics come fully integrate into one scalable and enterprise-ready solution. Data and sample-metadata management is included.

Focus on what matters

We shift the focus from data to discovery. Preconfigured workflows streamline the processing of raw NGS data allowing researchers to focus on the interpretation of results.

High performance algorithms

Designed to save time and compute resources, and to be accessible to bioinformatics experts and non-bioinformaticians alike.

Features

Pathogen Typing and Outbreak Analysis

Infectious diseases impact public health globally and come with a personal burden for patients as well as with a high economic burden. Detecting and controlling pathogen outbreaks early is key to protecting public health. Whole genome analysis offers unique advantages when used for typing and characterizing microbial isolates.

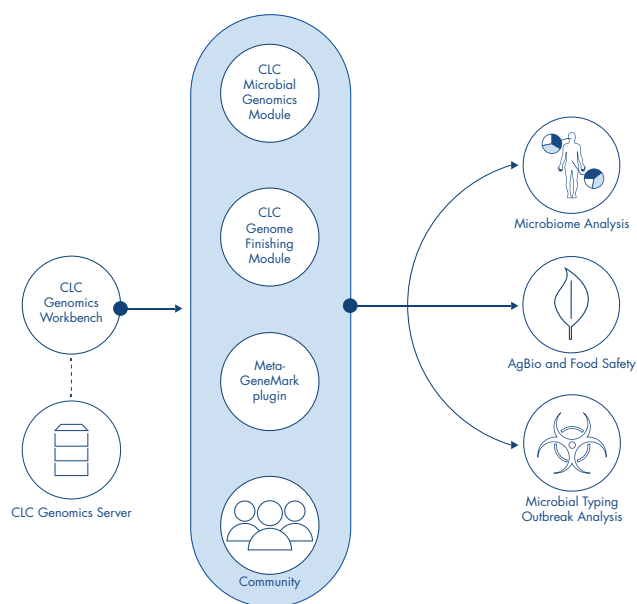
Isolate management – Samples, metadata and all typing results are collected in an Analysis Dashboard providing a powerful overview of outbreak isolates.

Typing – A single analysis Workflow for typing returns different types of information for any number of isolates:

- Perform automated NGS-MLST (Multi locus sequence typing).
- Report taxonomy.
- Report sample contamination.
- Find closest known reference genome.
- Find antimicrobial resistance genes.

Microbial genomics powered by quality components

QIAGEN Microbial Genomics Pro Suite is built on CLC Genomics Workbench, the industry standard platform for bioinformatics computing. Plugins and Modules add a layer of specialized tools and workflows to CLC Genomics Workbench, creating a comprehensive solution for microbial genomics and metagenomics data analysis. There is more: Experts in the field of microbial genomics are using the QIAGEN Microbial Genomics Pro Suite to bring additional tools and services to the user community.



Phylogenetic analysis

- K-mer based trees from raw NGS reads, assembled contigs, and closed genomes.
- Whole-genome SNP trees for accurate outbreak investigation and source tracking of pathogen isolates.
- Trees can be explored in the context of typing results, epidemiological data or other sample information.

Assembly of microbial reference genomes

- Short read and hybrid assembly.
- Scaffolding, contig joining and genome finishing.

PacBio *de novo* assembly made fast and easy

- Raw PacBio reads are error-corrected and *de novo* assembled using a novel approach that can quickly convert reads to high quality reference genomes.

Genome Annotation

- The MetaGeneMark plugin carries out gene finding.
- Annotate gene models with Pfam- and GO information, or with top BLAST hits.

Microbiome Profiling

All animals and plants live in close association with microbial communities. When investigating microbial communities, the main questions include which microorganisms are present, how abundant are they and what are they capable of? Explore the taxonomic and functional profiles of microbiomes, and associate microbiome profiles with disease state, diagnosis, diet, agricultural crop or livestock yield, or other.

Taxonomic Profiling of Microbiomes

Amplicon sequencing data

- De novo or reference based OTU-clustering of 16S-, 18S-, and ITS rRNA data.
- Support for common taxonomy databases Greengenes, Silva, and UNITE, as well as custom databases.

Shotgun metagenomic sequencing data

- Determine with high precision absolute and relative abundance of microbes in metagenomics samples.
- Filter out data contamination originating from host DNA.



- Users who wish to use CosmosID highly curated reference databases can use the CosmosID plugin for microbiome profiling.

Functional Profiling of Microbiomes

- Assemble and annotate whole metagenome data sets with class leading accuracy and performance.
- Functional profiling using PFAM, Gene Ontology and BLAST.

Visualization and Statistical Analysis in the context of metadata

- Stacked bar charts, area charts and zoomable sunburst diagrams can be used to explore and compare both, the taxonomic and functional composition of metagenomic samples.
- User-friendly Diversity Analysis tools for Alpha- and Beta diversity estimation for comparing diversity and compositional similarity between samples.
- Principal Coordinate Analysis (PCoA) plots in 2D and 3D and HeatMaps cluster samples based on microbiome composition.

- Run PERMANOVA analysis to assess statistical support for clustering.
- Merge abundance tables for direct comparison of diversity metrics across samples.
- Explore the taxa or gene function that vary most across sample categories. Use state of the art multifactorial differential abundance analysis to measure fold change, estimate statistical significance and explore correlations between sample categories.
- Graphing and statistical testing leverages sample metadata.



Genome Reference Database

- Direct import of Bacteria, Archaea, Virus, Fungi, and Protozoa reference genomes from NCBI's broad collection of microbial content.
- A table provides an overview of covered taxonomic range, assembly status and size of included genomes.
- With filters for taxonomy and assembly-quality, database contents can be optimised by the user. Remove low quality assemblies for higher confidence taxonomic assignments. Minimise computer resources and analysis time by reducing redundancy of database entries.

- Monitor predicted file size of database during the design, before the download begins.
- Download deep databases of pathogen specific reference genomes from NCBI RefSeq of the NCBI Pathogen Detection Project.

Workflows

Preconfigured, but customisable, Workflows streamline learning and running microbial bioinformatics analysis. Users are guided from raw NGS reads to fully interactive visual results in just a few steps.

Get your trial at www.qiagenbioinformatics.com

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