



Bruker MBioSEQ™ Ridom Typer

Microbial Genomics For ID, Clonal and Plasmid Transmission Real-time Surveillance, and AMR Profiling Studies

Combining the best – Comparability of MLST and discriminatory power of PFGE

MBioSEQ Ridom Typer software - formerly known as SeqSphere - is designed for distributed work-groups (client/server model) and allows processing and analyzing of NGS (e.g., **Illumina**, **Ion Torrent**, **Pacific Biosciences** [PacBio], or **Oxford Nanopore Technologies** [ONT]) and Sanger sequence data. MBioSEQ Ridom Typer is the single solution for easy and automated whole genome microbial typing that empowers your laboratory for smarter decisions (*Nat Biotechnol.* **31**: 294, 2013).

Bacterial typing generates isolate-specific geno- or phenotypic characters that can be used to elucidate the sources and routes of spread of bacteria. Typing may also be used to identify emerging pathogenic strains or clones within a species (*Clin Microbiol Infect.* **13** [Suppl. 3]: 1, 2007). A variety of methods have been developed to generate isolate-specific fingerprints for genotyping. However, until recently there was no single typing method available to address all bacterial species, different population structures (monomorphic vs. panmictic), and all study types (e.g., evolutionary/phylogenetic, population genetics, or transmission chain/outbreak). For decades, the common typing method was based on multi locus sequence typing (**MLST**) of 5-7 housekeeping genes or pulse field gel electrophoresis (**PFGE**). However, these methods either lack discriminatory power or are labor intensive and difficult to standardize.

Now, microbiologists everywhere can experience the genomic revolution that benchtop next generation sequencing (**NGS**) provides. With fast and affordable microbial whole genome sequencing (**WGS**) and automated software analysis (**Fig. 1**), microbiologists can use genome-wide gene-by-gene allele calling of hundreds/thousands of genes (core genome MLST [**cgMLST**]) for genotyping (**Fig. 2**). cgMLST schemes consist of a fixed set of conserved genome-wide genes. Alleles are used instead of single nucleotide polymorphisms (**SNP**) or concatenated sequences to mitigate the effects of recombination and to enable for a global and public nomenclature. The high discriminatory power of cgMLST, coupled with rapid and simple WGS workflow, makes this complete solution ideal for everyday usage in a laboratory, e.g., for prospective surveillance of multi-drug-resistant bacteria in a hospital (*JCM* **54**: 2874, 2016 [Illumina] and *JCM* **63**: e0012125, 2025 [PacBio]). That is, **one disruptive, accurate, and highly reproducible genomic technology** (*JCM* **55**: 908, 2017) that fits any bacteria or virus (SARS-CoV-2), any research topic, and any lab is finally within reach for every microbiologist. MBioSEQ Ridom Typer is proven to work for many laboratories around the world by **thousands of publications** in peer reviewed journals ([Google Scholar](#)).

User friendly

Graphical user interface with no scripting or bioinformatics skills needed to process your data. Epidemiologic and DNA sequence data are stored in an **integrated database** that can trigger automatically clonal and plasmid transmission alerts.

Highly automated workflow

Download pre-defined typing schemes or quickly create your own scheme based on a reference genome or allele libraries. Setup a processing pipeline to analyze hundreds of your samples without any further user intervention.

Global nomenclature

Contribute to a 'Molecular Typing Esperanto' derived from WGS data by submitting new alleles to [cgMLST.org](#).

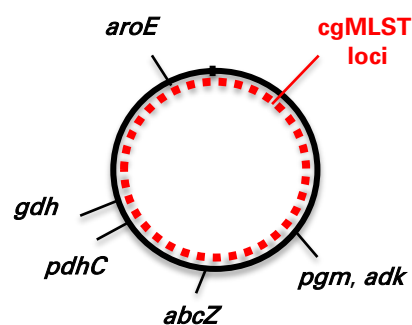


Figure 2. MLST of 6 genes versus genome-wide cgMLST. Shown are the 6 MLST targets for *Neisseria meningitidis* and red dots across the genome that represent symbolically the cgMLST loci/targets.

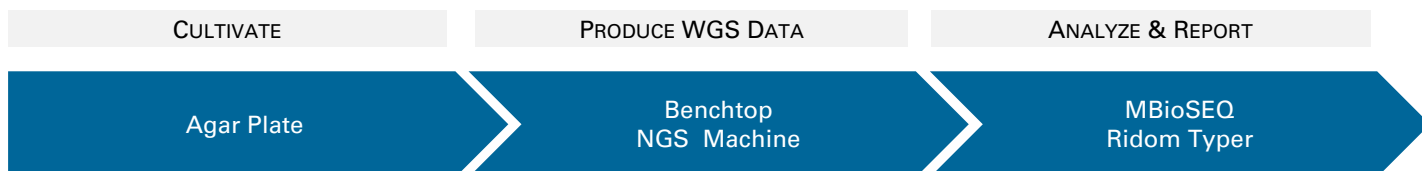


Figure 1. Microbial WGS next generation sequencing and genome-wide gene by gene (cgMLST) analysis workflow.

MBioSEQ Ridom Typer Key Features

DNA re-sequencing editor

Assemble **NGS** raw reads (**FASTQ**) with integrated VELVET, SKESA, SPADES, or BWA for short and FLYE or RAVEN for long read data. ONT data are polished in addition with MEDAKA v2 and our proprietary ONT-cgMLST-POLISHER (*JCM* **63**: e0036925, 2025). Import, process, and edit assembly files (ACE, BAM, FASTA). Import, process, and edit **Sanger** DNA sequence data too.

Pipeline for automated sequence data processing with QC

Define and start a pipeline to trim, down-sample, assemble, analyze, and type hundreds of NGS or Sanger data at once automatically. Define quality criteria (**QC**) for sample success. Intra- and inter-species contamination check with CHECKM2 and MASH SCREEN.

Characterize bacteria

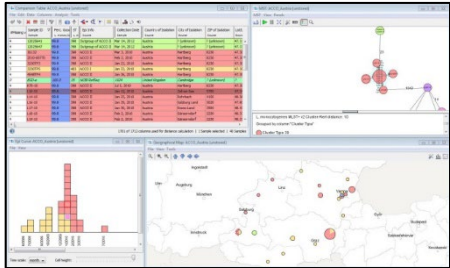
Species identification (**ID**) of bacteria by using GAMBIT and FASTANI. Type bacteria automatically by genome-wide allele or SNP calling from WGS data either on core genome and/or accessory genome level. Use public schemes for genotyping or define them by using the incorporated cgMLST TARGET DEFINER. Use TB-PROFILER or NCBI AMRFINDERPLUS for antimicrobial resistance (AMR) profiling. Apply *Salmonella* (SISTR), *E. coli*, and *L. monocytogenes* genoserotyping. MOB-SUITE and CGE MOBILEELEMENTFINDER plasmid reconstruction and characterization.

Database

Store, search, retrieve, export, and create reports from experiment, epi-data, and DNA sequence data stored in a local and integrated database. Data fields are compliant with the meta-data requirements of the EBI European Nucleotide Archive (**ENA**). Compare new sequence entries against stored data. Get automatically **clonal** and/or **plasmid transmission alerts** of clusters (*Microbiol Spectr.* **12**: e0210024, 2024). Manage and backup all data (sequence and epi-data). Download from NCBI GENOME complete/draft genomes or NCBI SRA reads. Submit with just one click raw read- and epi-data to EBI ENA.

Analytical tools

Visualize place, time, 'person', and type dimensions in a comparison table with built-in GIS, epi-curve, and phylogenetic tree (among others the minimum spanning tree algorithm is supported) functionality (**Fig. 3**). All dimension views are interactively-linked and exportable in publication quality format (SVG and EMF). Store tree coloring, topology, and selection of samples in a comparison table snapshot. Visualize and compare plasmids with PYGENOMEVIZ. **Search for group-specific SNPs**, e.g., for designing a cluster specific PCR screening assay (*Microbiol Spectr.* **10**: e0303622, 2022).



Community

- Download published typing schemes.
- Rapidly create and easily share typing schemes with others.
- Contribute optional to the world-wide expanding publicly available cgMLST.org server of allele nomenclature.
- **Consortium Server** functionality allows several MBioSEQ Ridom Typer users each with their own installation to share a minimum agreed upon amount of data. The shared data can be used for automatically triggered cross-institutional clonal matching alert emails.

Security/Privacy

- All your data stay **local** and **secure**.
- Various configurable user roles, user groups, and access controls.
- **Audit trail** functionality (who did, what and when) for accredited laboratories.
- Encryption (SSL) of all data in transmission.
- Configurable anonymization of meta-data like place and time before optionally submitting data to public repositories (e.g., ENA).

Figure 3. Place, time, 'person', and type dimensions visualized with MBioSeq Ridom Typer. Screenshots of a *Listeria monocytogenes* ready-to-consume food outbreak in Austria (*JCM* **53**: 2869, 2015).

Step-by-step TUTORIALS with demonstration data and fully-functional FREE TRIAL version are available via www.ridom.de

Minimum requirements for TRIAL: Microsoft Windows 64-bit, 8 GB RAM, 50 GB free disk space on C: partition, and Internet connection.

Computer Specifications	
Client	Microsoft Windows 10 (64-bit), WIN 11, or Linux 64-bit, quad-core processor , 16-32 GB RAM (Flye usage requires at least 32 GB RAM), and 1-2 TB hard disk. Internet connection required for license activation, to use the public cgMLST Nomenclature Server, and to download Task Templates (e.g., cgMLST schemes).
Server	Microsoft Windows 10 (64-bit), WIN 11, or Linux 64-bit, quad-core processor, 16 GB RAM, and 1-2 TB internal HD (with default settings 200,000 samples require about 1 TB; preferably SSD). For database backups a second 2-4 TB HD and optional a network attached storage (NAS) are highly desirable.

Please note that most computation is done on the Client computer (e.g., assembling). Therefore, computational power and amount of RAM are more important on the client than on the Server computer. Client and Server communicate by default via port 8064 (configurable) over the Intra-/Internet. Client and Server software can be installed on the same computer. – Multiple Client computers can use the same pipeline script for **speeding-up** the analysis for example of a sequencing run. Therefore, for **scaling-up** simply employ an additional Client computer. To use the power of a **Linux-Cluster** the MBioSEQ Ridom Typer Client pipeline can be started in command-line mode. SKESA, SPAdes, Flye, Raven, CheckM2, Mash, GAMBIT, SISTR, MOB-suite, MobileElementFinder, AMRFinder, TB-Profiler, and plasmid transmission detection with pyGenomeViz plasmid visualization are only supported by Linux- or Windows 10/11-Clients **with** installed **Windows Subsystem for Linux** (WSL). For **Illumina** raw read data (FASTQ) the in MBioSEQ Ridom Typer integrated SKESA, Velvet, or SPAdes *de novo* assemblers are recommended. For **Ion Torrent** data the usage of the SPAdes assembler is recommended. For **ONT** data the Flye or Raven assemblers with polishing are the options of choice, respectively. **PacBio** data should be assembled with Flye.

The license is limited to a period and a certain number of named user accounts on the Server. During the license period an **unlimited number of samples can be analyzed**. Each **named user account** allows to login interactively once at the same time. If somebody else logs in with the same account, a read-only mode is activated for this session. The Pipeline Mode also runs on behalf of a named user account but can run concurrently multiple times, i.e., for a 2 named user license in total 5, for 5 users in total 12, and for 30 users in total 75 **concurrent pipelines** are possible, respectively. The Client software can be installed on an unlimited number of computers. The license period starts with the activation of the license by the user. The license will expire after the defined period, and the software runs with read-only access unless a new license is ordered. Read-only access still allows to view and export all data stored in the database. Licenses include **updates** of Bruker MBioSEQ Ridom Typer and **free technical support** for installation and troubleshooting of the software within the licensing period.

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