

## WHOLE GENOME MULTI-LOCUS SEQUENCE TYPING (wgMLST)

The future of molecular typing

### MLST: a proven success

Multi-locus sequence typing (MLST) has proven its usefulness for molecular typing of bacteria. Classical MLST schemes typically define seven loci (housekeeping genes). Unique sequences for each locus are assigned allele numbers and bacterial strains are identified based on their allelic profiles, which is the combination of the seven allele numbers.

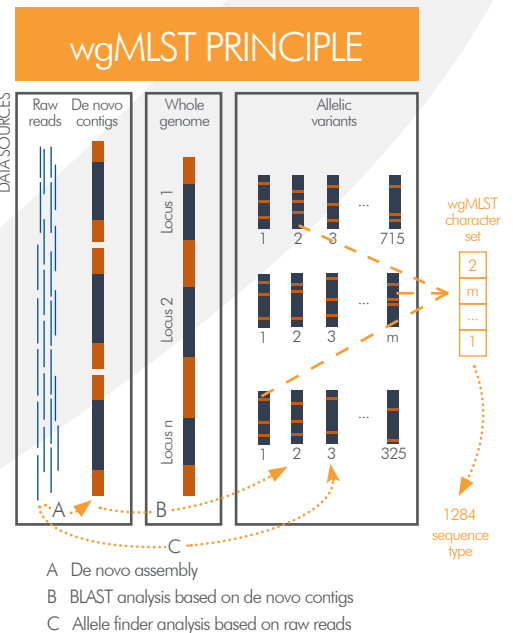
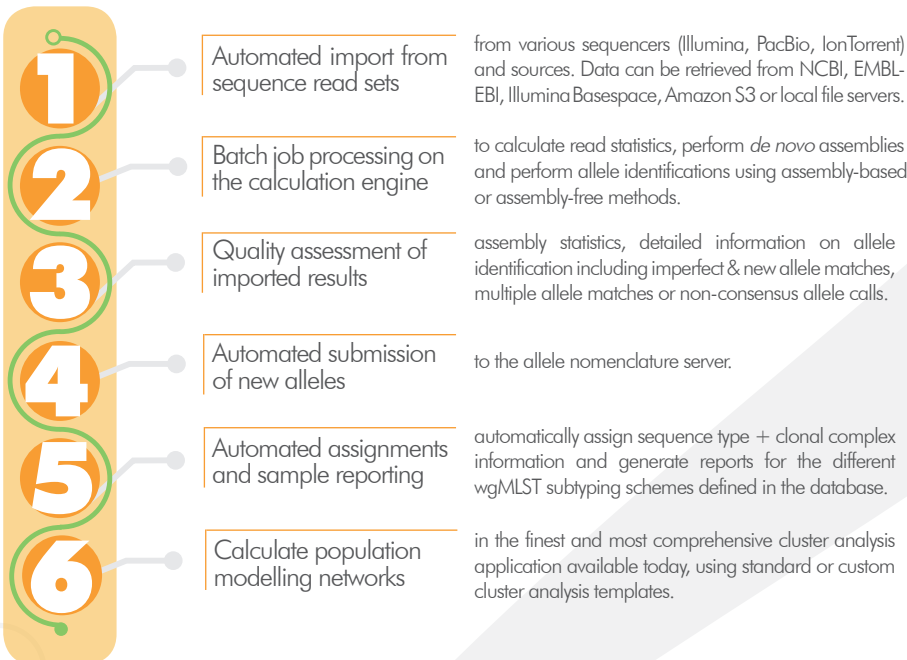
### MLST to wgMLST

Today, MLST can be extended to whole genome MLST (wgMLST). Since a much larger number of loci are taken into account, a much higher typing resolution can be obtained. NGS-based wgMLST therefore offers a fast and cost-effective way to analyze bacterial genomes and is rapidly replacing Sanger sequencing.

### wgMLST vs. wgSNP

In contrast to wgSNP analysis, wgMLST is based on the concept of allelic variation, meaning that recombinations and deletions or insertions of multiple positions are counted as single evolutionary events. This approach might be biologically more relevant than ones that consider only point mutations.

### whole genome MLST analysis in BioNumerics



## YOUR ADVANTAGES



WHY USE **BioNumerics** FOR YOUR wgMLST ANALYSIS?

- ✓ A lightweight database
- ✓ Integrated calculation engines
- ✓ Keep control of confidential data
- ✓ Flexible loci selection



## A lightweight database



Only the links to the sequence read sets, the wgMLST allelic profiles and their qualities are stored in the BioNumerics database, resulting in a light and responsive strain database. This also means that hardware requirements for your computer can be kept low!

## Keep control of confidential data



All metadata remains local & within the software.

Storage of the data and wgMLST analysis is very user-friendly and results are easily accessible. BioNumerics will link to batches of sequence read sets from NCBI, EMBL-EBI, Amazon S3, Illumina BaseSpace or local file servers. From the software, jobs can be posted directly on the calculation engine.

Using BioNumerics' impressive set of analysis tools, results stored in the database are available for statistical and population analysis, clustering and calculation of minimum spanning trees, partitioning, and identification.

### NOTE:

The wgMLST functionality is part of the free "WGS Tools plugin". The minimal configuration for wgMLST consists of the "Sequence Data", "Character Data" and "Tree and Network Interference" modules. Additionally, a calculation engine project is needed.

Please contact us for more information.

## Integrated calculation engines



Demanding calculations such as *de novo* assemblies can be performed on an external calculation engine. Choose between a virtually setup-free, pay-per-use cloud solution or a local deployment e.g. on a computer cluster (requires custom services).

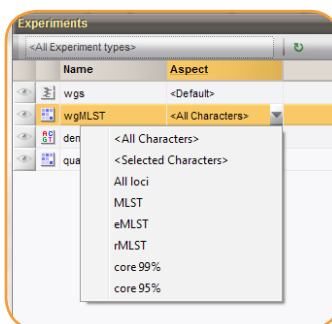
The Amazon calculation engine, which is seamlessly integrated in BioNumerics, is specifically designed to process hundreds of isolates within the hour and provides extremely fast turnaround times for the primary analysis.

## Flexible loci selection

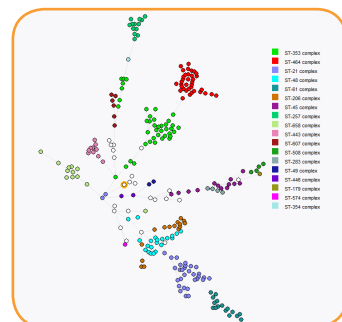


Based on the loci included in the wgMLST scheme, additional typing schemes can be defined on different levels, e.g. core genome MLST (cgMLST), ribosomal MLST (rMLST), etc.

The character views in BioNumerics offer a flexible tool to select the set of loci used for typing, cluster analysis (e.g. minimum spanning trees) or statistical tests present in the software.



Different typing schemes are defined from the wgMLST loci



Minimum spanning tree based on wgMLST data



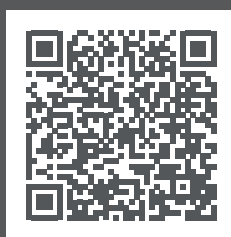
## CONVINCED? INTRIGUED? TRY IT FOR YOURSELF!

[www.bionumerics.com](http://www.bionumerics.com)

Scan the QR codes to access each step



1. Make sure you have a **BioNumerics** license (also see note above).



2. Request a calculation engine project to perform whole genome analyses.



3. Watch tutorial movies or download sample data for use in **BioNumerics**.

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