ESCHERICHIA COLI FUNCTIONAL GENOTYPING

## Conventional vs whole genome methods: the advantages

Foodborne bacteria such as enterohemorrhagic *E. coli* pose a major threat to public health. To detect outbreaks in an early stage and prevent widespread infections, being able to accurately identify and characterize these bacteria in a rapid manner is of key importance. Conventional methods for serotyping, virulence profiling, and antimicrobial susceptibility testing are time-consuming and often require complex workflows. Alternatively, whole genome sequence data provides highly detailed genotypic information and has the potential to replace some of these conventional methods.

E. coli genotyping in BioNumerics

Various *E. coli* genotyping tools have been bundled in one single BioNumerics application, making it a very user-friendly and easy-to-use typing tool. Screening for all or a subset of traits can be launched with one single click and the genotyping analysis results are summarized in an easy accessible and customizable report. The typing results are stored in the BioNumerics database and can be analyzed in combination with other data sets at any time.

Impressive list of genotyping tools

The *E. coli* genotyping application contains public databases for serotype, virulence and resistance prediction, as well as plasmid and prophage detection. The reference databases are based on the data sets available from Center for Genomic Epidemiology, DTU, combined with private knowledge. An in-silico PCR tool is also implemented, making it possible to detect e.g. Shiga toxin gene subtypes and virulence genes, mimicking the wet lab PCR.
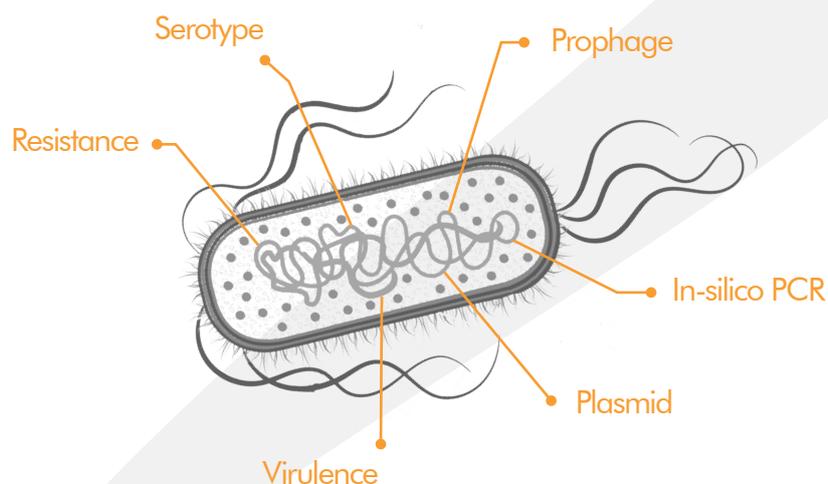
YOUR ADVANTAGES

WHY USE **Bio**Numerics FOR YOUR *E. COLI* TYPING?

- ✓ Impressive list of genotyping tools
- ✓ Fast BLAST screening
- ✓ Rich database environment
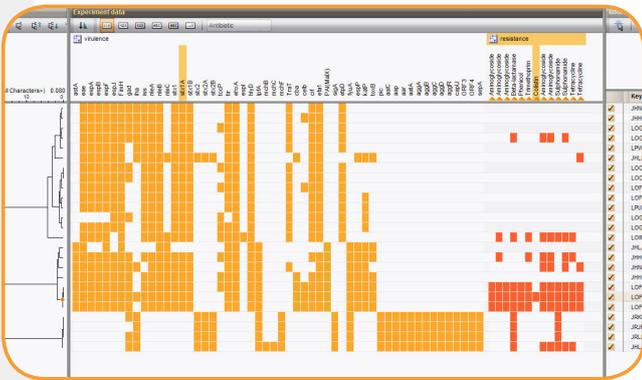- ✓ Detailed reporting

Fast BLAST screening

The various *E. coli* genotyping tools start from the assembled sequences stored in the BioNumerics database, and use a BLAST-based approach to detect and identify the genes of interest. A minimum sequence identity and minimum length coverage needs to be specified to detect the best matching target sequence in the genome.

Rich database environment

The typing results are recorded as information fields and/or character data in the BioNumerics database and can be clustered and analyzed together with other data sets leading to a more efficient interpretation of the data.

Detailed reporting

The genotyping results are combined with strain information and presented clearly in a customizable report. A summary of predicted serotype, virulence and resistance prediction, as well as plasmid and prophage detection is displayed.

Hyperlinks are present linking to the detailed BLAST results of the predicted traits. Detailed BLAST results include locus identifiers, BLAST similarity scores, and descriptive information on the detected genes.

NOTE:

The *E. coli* functional genotyping plugin is a free online add-on. The minimum configuration for installation of the plugin includes the "Character Data", "Sequence Data" and "Genome Analysis Tools" modules. Please contact us for more information.
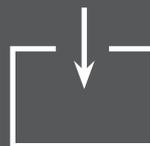

CONVINCED? INTRIGUED? TRY IT FOR YOURSELF!

www.bionumerics.com
Scan the QR codes to access each step

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

2. Download the free plugin directly from the software. No admin rights needed!

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