

## ENTEROCOCCUS RAFFINOSUS

schema for whole genome typing

We are proud to present a schema for true whole genome multi-locus sequence typing (wgMLST) of *E. raffinosus* in BioNumerics. When used in combination with our Calculation Engine, typing *E. raffinosus* isolates up to strain level using whole genome sequencing is now easily accessible to everyone.

### What is the schema exactly?

Based on the known diversity within *E. raffinosus*, a pan-genomic schema was developed. This schema has high discriminatory power allowing for the detection of subtype- or outbreak-specific markers, enabling more powerful classification and outbreak definition tools.

### Which loci are present?

Starting from the four publicly available and annotated reference genomes, our in-house developed schema creation procedure uses a sampling-based multi-reciprocal BLAST procedure to determine those sets of alleles that make up the stable loci in the accessory genome. A per-locus allele assessment procedure then determines the central prototype allele, and thus the definition of the locus. In this way, a total of 4,470 loci were added to the schema.

### How will it help you?

By using BioNumerics and the integrated powerful calculation infrastructure, analyzing whole genome sequencing data for *E. raffinosus* has become a lot more straightforward. Our cloudbased Calculation Engine offers a high-throughput environment for all your sample processing needs. Its quality-controlled de novo assembly possibilities allow you to easily assemble whole genome sequencing data without the need of local computing power. The two allele detection procedures (assembly-based and assembly free) allow you to perform fast and reliable allele calling for e.g. cluster detection which can be combined with whole genome SNP analysis to obtain the utmost resolution within your sample comparisons.

**The BioNumerics wgMLST schema for *E. raffinosus* has been tested, validated and approved by our microbiologists.**

**Great care has been taken to create an analysis procedure that minimizes sample artifacts, while maintaining an enormous discriminatory power.**

**With turnaround times of less than 30 minutes per sample and the ability to process multiple samples simultaneously, the power of high-performance computing will be brought to your desktop with a few clicks.**

### We are looking for you!

To further extend and elaborate our wgMLST schema definition for *E. raffinosus*, we are continuously looking for new collaborations.

If you are interested in a joint publication on wgMLST typing or other collaboration on *E. raffinosus* to assist you in your research or further extend our allele database capturing the diversity within the species, please contact us at [info@applied-maths.com](mailto:info@applied-maths.com).

### Interested?

Simply request a calculation engine project to get started:

