

SERRATIA MARCESCENS

for whole genome sequence typing

We are delighted to announce a schema for true whole-genome multi-locus sequence typing (wgMLST) of Serratia marcescens in BioNumerics. The schema brings easy and highly discriminatory detection of subtype- or outbreak-specific markers from whole genome sequencing data to your fingertips.

What is the schema exactly?

Using a selection of 299 annotated, publically available reference genomes capturing the known diversity within *S. marcescens*, a pangenomic schema with high discriminatory power was developed. Starting from the 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 pan-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 9,377 loci were added to the schema.

How will it help you?

The schema has high discriminatory power and allows for the detection of markers specific for subtypes or outbreaks, thus enabling more powerful classification and outbreak definition tools. Together with BioNumerics and our powerful cloud based Calculation Engine, it completes a high-throughput environment that enables a faster and more straightforward analysis of whole genome sequencing data for *S. marcescens*. The Calculation Engine's quality-controlled de

novo assembly possibilities allow you to easily assemble whole genome sequencing data without the need of local computing power. Moreover, 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 whole-genome multi-locus sequence typing schema for *S. marcescens* has been tested, validated and approved by our microbiologists. They took great care 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 simultaneously processing of many samples, the power of high-performance computing is brought to your desktop with only a few clicks.

Interested?

Request a calculation engine project today to get started:

