

FRANCISELLA TULARENSIS SCHEMA

for whole genome sequence typing

We are delighted to announce a schema for true whole-genome multi-locus sequence typing (wgMLST) of *Francisella tularensis* 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?

Following the recent developments on the core genome MLST¹ and using a selection of 226 annotated, publically available reference genomes capturing the known diversity within *F. tularensis*, the scientists at Applied Maths extended the core genome MLST schema to a pan-genomic schema. By also capturing the accessory loci, they increased the discriminatory power of the schema.

Starting from the 226 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, 1,661 accessory loci were added to the 1,147 core loci, resulting in a total of 2,808 validated loci.

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 a lot more straightforward analysis of whole genome sequencing data

for *F. tularensis*. 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 *F. tularensis* has been tested, validated and approved by our microbiologists on several public datasets.

With turnaround times of less than 30 minutes per sample and simultaneous processing of multiple samples, the power of high-performance computing is brought to your desktop with only a few clicks.

Simply request a Calculation Engine project to get started. We have wgMLST tutorials available online.

Don't have a BioNumerics license yet? Try it for FREE for one month.

INTERESTED?

Request a calculation engine project today to get started:



Reference:

⁽¹⁾ Antwerpen MH, Prior K, Mellmann A, Höppner S, Splettstoesser WD, and Harmsen D. Rapid high resolution genotyping of *Francisella tularensis* by whole genome sequence comparison of annotated genes ("MLST+"). PLoS ONE. 2015, 10: e0123298; e0123298