

LEGIONELLA PNEUMOPHILA SCHEMA

for whole genome sequence typing

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

What is the schema exactly?

Based on the core genome MLST definition published by Moran-Gilad *et al.*⁽¹⁾, the Applied Maths scientists extended the existing core genome MLST schema to a pan-genomic schema, echoing the known diversity of *L. pneumophila*, based on a set of 32 publicly available reference sequences. By also capturing the accessory loci, they increased the discriminatory power of the schema. At the same time, the extended schema also allows for the detection of subtype- or outbreak-specific markers, enabling more powerful classification and outbreak definition tools.

How will it help you?

By using BioNumerics and the integrated powerful calculation infrastructure, analyzing whole genome sequencing data for *L. pneumophila* has become a lot more straightforward. Our cloud-based Calculation Engine offers a high-throughput environment for all your sample processing needs. Its quality-controlled de novo assembly algorithms allow you to

Which loci are present?

Starting from the 32 annotated reference genomes, our in-house developed schema uses a sampling-based multi-reciprocal BLAST procedure to determine the allele sets that make up the stable loci in the accessory genome. A per-locus allele assessment procedure then determines the central prototype allele, simultaneously defining the locus. The accessory schema, including 4249 loci, is then complemented with the 1521 core loci and the 7 SBT⁽²⁾ loci to obtain maximal consistency with classical and novel multi-locus sequence typing initiatives for *L. pneumophila*.

easily assemble whole-genome sequencing data without the need for 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 *L. pneumophila* 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 that supersedes the core genome schema.

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.

Interested?

Click on [this link](#) to request a calculation engine project or scan the QR code:



References:

- (1) Moran-Gilad J *et al.* 2015. Design and application of a core genome multilocus sequence typing scheme for investigation of Legionnaires' disease incidents. *Euro Surveill*; 20(28). <http://dx.doi.org/10.2807/1560-7917.ES2015.20.28.21186>
- (2) Gaia V *et al.* 2005. A consensus sequence-based epidemiological typing scheme for clinical and environmental isolates of *Legionella pneumophila*. *J Clin Microbiol*;43:2047-52