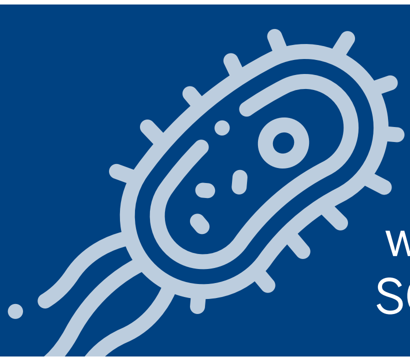

wgMLST
SCHEMA

BIONUMERICS®

MICROBIAL DATA ANALYSIS SOFTWARE

Mycobacterium bovis

WHAT IS wgMLST AND WHY DO YOU NEED A SCHEMA FOR IT?

Whole genome MLST (wgMLST) is an extension of the more traditional MLST, allowing a much higher typing resolution. It offers a fast and cost-effective way to analyze bacterial genomes. A schema is essential for the wgMLST technique to work as it defines the loci to which allele numbers are assigned. It represents the basis for a stable nomenclature that you can use to communicate about outbreaks, epidemics, evolution, etc...

WHY DID WE DEVELOP A *MYCOBACTERIUM BOVIS* wgMLST SCHEMA?

Mycobacterium bovis is the causative agent of tuberculosis, which if not treated correctly can be fatal, in cattle. It is as such related to *Mycobacterium tuberculosis*, the bacterium causing tuberculosis in humans. However, *M. bovis* can be zoonotic and infect humans. Especially in developing countries the number of human infections is rising. A well-defined wgMLST schema can help in typing and outbreak detection and mitigation.

Mycobacterium bovis subschemes
4,701 wgMLST loci

HOW WILL IT HELP YOU?

Turnaround time < 30 min

Simultaneous sample processing possible

- ✓ Defines a **robust set of loci**, validated and approved by our microbiologists
- ✓ Contains **minimal sample artifacts**, while keeping great discriminatory power
- ✓ Represents the known **diversity** of the species
- ✓ Allows **detection of markers** specific to a certain strain, enabling powerful classification and outbreak identification

TRY IT ON YOUR OWN DATA TODAY!

1. Make sure you have a BIONUMERICS license

2. Request a Calculation Engine project

3. Learn from our wgMLST tutorial movies