wgMLST SCHEMA

BIONUMERICS®
MICROBIAL DATA ANALYSIS SOFTWARE

Mycobacterium leprae

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 LEPRAE* wgMLST SCHEMA?

Mycobacterium leprae is mostly found in warm tropical countries and is the causative agent of leprosy which damages peripheral nerves and can affect the skin, eyes, nose and muscles, resulting in severe disabling formities. Although leprosy is often thought of as a disease of ancient times, the World Health Organization recorded 3.8 million new cases of leprosy from 105 different countries in the last decade. A wgMLST schema can help in the fast detection, characterization and mitigation of leprosy outbreaks.

| *Mycobacterium leprae* subschemes |
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| 2,237 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
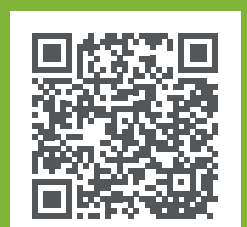
TRY IT ON YOUR OWN DATA TODAY!

1. Make sure you have a BIONUMERICS license
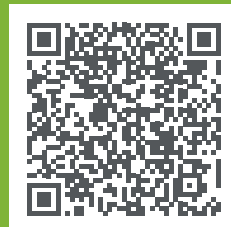
2. Request a Calculation Engine project

3. Learn from our wgMLST tutorial movies