BioNumerics®

RELEASE NOTE

BURKHOLDERIA CEPACIA COMPLEX

for whole genome sequence typing

We are delighted to announce a schema for true whole-genome multi-locus sequence typing (wgMLST) of Burkholderia cepacia complex 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 set of 336 publically available *B. cepacia* complex genomes all coding sequences in these genomes were captured. By also capturing the accessory loci, our microbiologists increased the discriminatory power of the schema. At the same time, the schema also allows for the detection of subtype- or outbreak-specific markers, thus enabling more powerful classification and outbreak definition tools. Starting from 336 annotated reference genomes, an 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 accessory genome. A per-locus allele assessment procedure then determines the central prototype allele, and thus the definition of the locus. As *B. cepacia* complex comprises several species, this is the largest schema developed up to now, with 45472 loci included. The accessory schema is then complemented with the classical MLST loci to obtain maximal consistency with classical and novel multi-locus sequence typing initiatives for *B. cepacia* complex.

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 *B. cepacia* complex. 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 *B. cepacia* complex has been tested, validated and approved by our microbiologists on several public datasets[1],[2].

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:

References:

[1] Miller RR, Hird TJ, Tang P, Zlosnik JEA (2015) Whole-genome sequencing of three clonal clinical isolates of *B. cenocepacia* from a patient with a cystic fibrosis. PLoS ONE 10(11) 2015, e0143472

[2] Sommerstein R, Führer U, Lo Priore E, Casanova C, Meinel DM, Seth-Smith HMB, Kronenberg A, Koch D, Senn L, Widmer AF, Egli A, Marschall J (2017) *Burkholderia stabilis* outbreak associated with contaminated commercially-available washing gloves, Switzerland, May 2015 to August 2016, Eurosurveillance 2017: 22(49): pii=17-00213

APPLIED MATHS

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