BioNumerics®

RELEASE NOTE

ENTEROCOCCUS FAECALIS

for whole genome sequence typing

We are delighted to announce a schema for true whole-genome multi-locus sequence typing (wgMLST) of Enterococcus faecalis. 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?

Starting from 493 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. The accessory schema consisting of 5,285 loci is then complemented with the classical MLST loci[1] to obtain maximal consistency with classical and novel multi-locus sequence typing initiatives for *Enterococcus faecalis*. The schema has been tested on a large dataset published by Raven et al.[2] and could reproduce the conclusions of this article in fewer analyses as well as provide additional insights.

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 more straightforward analysis of whole genome sequencing data for *E. faecalis*. 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 *E. faecalis* has been tested, validated and approved by our microbiologists. 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) Ruiz-Garbajosa P, Bonten MJ, Robinson DA, Top J, Nallapareddy SR, Torres C, Coque TM, Cantón R, Baquero F, Murray BE, del Campo R, Willems RJ. (2006) Multilocus sequence typing scheme for Enterococcus faecalis reveals hospital-adapted genetic complexes in a background of high rates of recombination. J Clin Microbiol. 2006 Jun, 44(6):2220-8.

(2) Raven KE, Reuter S, Gouliouris T, Reynolds R, Russell JE, Brown NM, Török E, Parkhill J, Peacock SJ (2016) Genome-based characterization of hospital-adapted Enterococcus faecalis lineages. Nat Microbiol 2016 Feb, (1):15033.

APPLIED MATHS

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