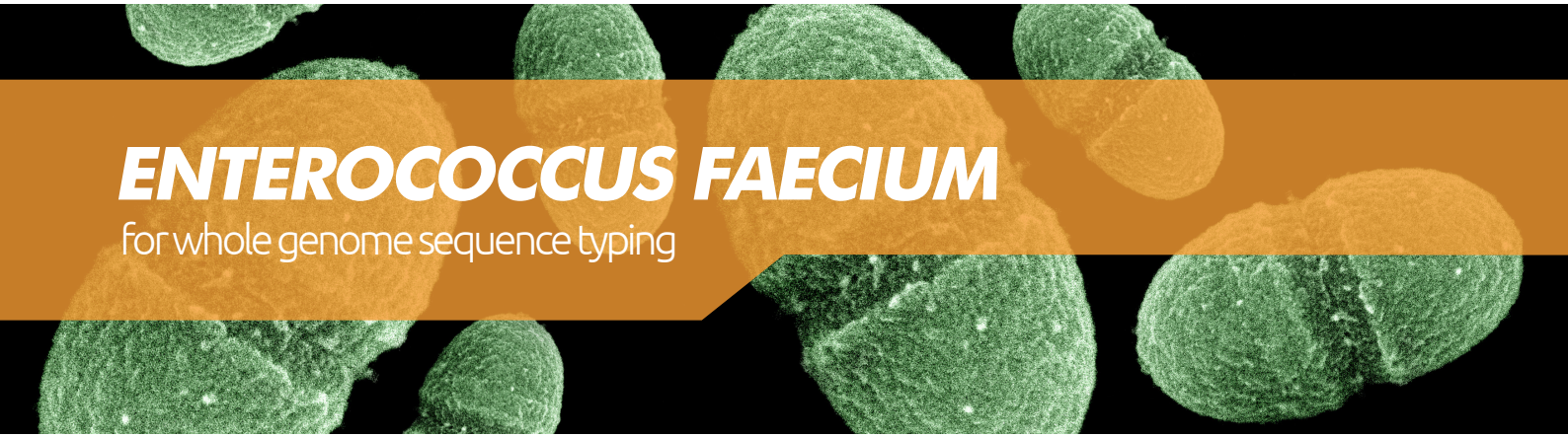
BioNumerics®

RELEASE NOTE



ENTEROCOCCUS FAECIUM

for whole genome sequence typing

We are delighted to announce a schema for true whole-genome multi-locus sequence typing (wgMLST) of Enterococcus faecium. 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 510 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 5,489 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 faecium*.

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. faecium*. 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.

Our microbiologists have, amongst others, tested this schema for E. faecium on several published datasets[2,3]. They have validated and approved the schema and 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) Homan WL, Tribe D, Poznanski S, Li M, Hogg G, Spalburg E, Van Embden JD, Willems RJ. (2002) Multilocus sequence typing scheme for Enterococcus faecium. J Clin Microbiol. 2002 Jun, 40(6):1963-71.

(2) De Been M, Pinholt M, Top J, Bletz S, Mellman A, van Schaik A, Brouwer E, Rogers M, Kraat Y, Bonten M, Corander J, Westh H, Harmsen D, Willem RJL (2015) Core Genome Multilocus Sequence Typing Scheme for High-Resolution Typing of Enterococcus faecium. J Clin Microbiol 2015 Dec, 53(12): 3788-3797.

(3) Sivertsen A, Pedersen T, Larssen KW, Bergh K, Rønning TG, Radtke A, Hegstad K (2016) A Silenced vanA Gene Cluster on a Transferable Plasmid Caused an Outbreak of Vancomycin-Variable Enterococci. Antimicrob Agents Chemother 2016 Jul 60(7): 4119-4127

APPLIED MATHS

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