BioNumerics®

RELEASE NOTE

CAMPYLOBACTER COLI/JEJUNI SCHEMA

for whole genome sequence typing

We are proud to present a schema for true whole genome multi-locus sequence typing (wgMLST) of C. coli and C. jejuni in BioNumerics. When used in combination with our cloud-based Calculation Engine, typing C. coli/jejuni isolates up to strain level using whole genome sequencing data is now easily accessible to everyone.

What is the schema exactly?

Based on the recent developments on the core genome MLST by *Cody et al., 2013*[1] and using the same set of 96 publicly available reference sequences that capture the known diversity of *C. coli/jejuni*[2], a pan-genomic schema has been defined in collaboration with international coworkers. By also capturing the accessory loci, they increased the discriminatory power of the schema. At the same time, the extended schema also allows for the detection of subtype- or outbreak-specific markers, thus enabling more powerful classification and outbreak definition tools.

Which loci are present?

Starting from the 96 annotated reference genomes, our 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, including 2186 loci, is then complemented with the 1343 core loci and 7 MLST loci to obtain maximal consistency with classical and novel multi-locus sequence typing initiatives for *C. coli/jejuni*.

How will it help you?

By using BioNumerics and the integrated powerful calculation infrastructure, analyzing whole genome sequencing data for *C. coli/jejuni* has become a lot more straightforward. Our cloud-based Calculation Engine offers a high-throughput environment for all your sample processing needs. Its quality-controlled de novo assembly possibilities allow you to easily assemble whole genome sequencing data without the need of local computing power. 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 BioNumerics wgMLST schema for *C. coli/jejuni* has been tested, validated and approved by our microbiologists.

Great care has been taken to create an analysis procedure that minimizes sample artifacts, while maintaining an enormous discriminatory power that supersedes the core genome schema.

With turnaround times of less than 30 minutes per sample and the ability to process many samples simultaneously, the power of high-performance computing will be brought to your desktop with few clicks.

Interested?

Click on this link to request a calculation engine project or scan the QR code:

References:

(1) Cody A.J., McCarthy N.D., Jansen van Rensburg M., Isinkaye T., Bentley S. D., Parkhill J, Dingle K.E., Bowler I.C., Jolley K. A. and Maiden M.C. (2013) Real-time genomic epidemiological evaluation of human Campylobacter isolates by use of whole-genome multilocus sequence typing. J Clin Microbiol. 2013 Aug; 51(8):2526-34.

(2) Lefébure T., Pavinski Bitar P.D., Suzuki H. and Stanhope M.J. (2010) Evolutionary Dynamics of Complete Campylobacter Pan-Genomes and the Bacterial Species Concept. Genome Biol Evol. 2010 Aug;2:646-655.

APPLIED MATHS

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