BioNumerics®

RELEASE NOTE

CRONOBACTER SPP.

schema for whole genome typing

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

What is the schema exactly?

Based on the known diversity within the 7 species of the genus *Cronobacter* spp. and the cogMLST schema published by Forsythe et al.[1], a pan-genomic schema was developed. By also capturing the accessory loci, the discriminatory power was increased. 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 78 annotated reference genomes, capturing the whole genus' diversity, our inhouse 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. For maximal consistency with classical and novel multi-locus sequence typing initiatives the wgMLST schema consisting of the 1,865 cogMLST loci and the 13,862 identified accessory loci, is complemented with the loci for the classical and extended MLST schemas[1,2], the Gcog loci and the O-serotype loci as described in the pubMLST public database[3]. See figure for more information.

How will it help you?

By using BioNumerics and the integrated powerful calculation infrastructure, analyzing whole genome sequencing data for *Cronobacter* spp. 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.

Cronobacter spp. subschemas			
15,727	wgMLST loci	7	MLST loci
1,865	cogMLST loci	10	Ext-MLST loci
222	Gcog loci	9	Tax-MLST loci
2	O-serotype loci		

Great care has been taken by our microbiologists 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 the ability to process multiple samples simultaneously, the power of high-power computing will be brought to your desktop with a few clicks.

Interested?

Simply request a calculation engine project to get started:

References:

(1) Forsythe SJ, Dickins B, Jolley KA. 2014. Cronobacter, the emergent bacterial pathogen Enterobacter sakazakii comes of age; MLST and whole genome sequence analysis. BMC Genomics 15.1: 1.

(2) Baldwin A, Loughlin M, Caubilla-Barron J et al. 2009. Multilocus sequence typing of Cronobacter sakazakii and Cronobacter malonaticus reveals stable clonal structures with clinical significance which do not correlate with biotypes. BMC Microbiology 9.1: 223.

(3) https://pubmlst.org/bigsdb?db=pubmlst_cronobacter_seqdef&page=downloadAlleles (version May 2017)

APPLIED MATHS

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