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Poster - D15

Using genomic signature to detect cases of coevolution in viral/host systems - The Poxviridae Family

Francisco Lobo, Empresa Brasileira de Pesquisa Agropecuária, Embrapa Informática Agropecuária, Brazil

Tarcísio Coutinho, Universidade Federal de Minas Gerais, Brazil

Short Abstract: Poxviridae viruses infect vertebrate or invertebrate hosts and, therefore, represent an interesting long-term evolution scenario to study coevolutionary patterns of viruses to their hosts. We generated dinucleotide odds ratio for poxviruses and their hosts coding sequences and detected potential coevolutionary trends in CpG usage when comparing Orthoptera and its virus.

Poster - D16
KOMODO2 – Large-scale genomic inference

Francisco Lobo, Empresa Brasileira de Pesquisa Agropecuária, Embrapa Informática Agropecuária, Brazil

Jorge Hongo, Universidade Estadual de Campinas, instituto de computação, Brazil

Short Abstract: We propose and validate a first-principled methodology to perform comparative genomics analyses and identify biologically meaningful biases in the distribution of annotation terms in groups of genomes classified according categorical variables (groups). Our approach can be used to understand and link biological mechanisms to genomes characteristics, niches and phenotypes.

Posters

Poster Presentation List & Schedule

Odd numbers:
Poster set up: Day 1 - all day long
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I) Genetic Variation Analysis

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