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4th International Conference on

APPLIED MICROBIOLOGY, ANTIBIOTICS, ANTIMICROBIALS AND BENEFICIAL MICROBES

May 20-21, 2019 Tokyo, Japan

Phage host exploration-sequence based classification of bacteriophages

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Bacteriophages are viral particles that infect and replicate inside bacterial organisms. Since they are specific to a particular strain of bacteria, advances in their research could lead to novel means of targeted treatment without adverse effects on natural microbiome in patient's body. Moreover, this treatment could be effective against bacterial strains with antibiotic resistance. One of the main bottlenecks of bacteriophage research is inability to cultivate some of the phages due to missing information about their hosts. A bioinformatics pipeline, called Phage Host Exploration (Pheri) was designed to predict bacteriophage hosts from its genomic sequence. The decision is supported by a set of genes that should correspond to the specificity of the phage. We evaluated the pipeline on a set of 6277 phage sequences downloaded from several publicly available databases. Our pipeline has a potential to assist in discovery and characterization of novel phages and underlying mechanisms behind their behavior.

Biography

Jaroslav Budis has pursued his Graduation from the Faculty of Mathematics, Physics and Informatics from the Comenius University in Bratislava, Slovakia. He is the main author and co-author of several publications in genomics, metagenomics and bioinformatics and four patent applications in non-invasive chromosomal detection, fetal disorders and the protection of genomic data, one of which has already been approved. He leads a team of eight bioinformatics scientists in the Geneton company.

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