



Issue June 2017

Events

There are some events which could be of interest for you:

- ❑ **The German Conference on Bioinformatics,**
18th – 21st September, 2017 in Tübingen.
GCB is meant as a platform for the German and European bioinformatics community.
For details have a look at <http://www.gcb2017.de/>
We are happy to announce that the GCB will have a session on virus bioinformatics.
- ❑ **Conference: Computational Intelligence methods for Bioinformatics and Biostatistics,**
7th -9th September, 2017 in Cagliari.
CIBB is meant as a multi-disciplinary forum for researchers interested in the application of computational intelligence, in a broad sense, to open problems in bioinformatics, biostatistics, systems and synthetic biology and medical informatics.
For details have a look at <http://cibb2017.unica.it/call.php>
We are happy to announce that Manja Marz is invited to this event to introduce the EVBC
- ❑ **International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology,**
27th August -1st September, 2017 in Lisboa.
VEME provides both theoretical and practical training in phylogenetic inference and evolutionary hypothesis testing as applied in virology and molecular epidemiology.
For details have a look at <https://rega.kuleuven.be/cev/veme-workshop/2017>
We are happy to announce that Manja Marz is invited to this event to introduce the EVBC

Tools

We have extended in our webpage the list of virus-bioinformatics tools and databases that could be of interest for you. We would be happy to link your tools as well. That can be for beta-testing, while submitting or after publication. The new tools added:

Antigenic Patches -- The graph-cut based algorithm clusters protein sites based on their antigenic weight into antigenic patches

DIGS -- a database-integrated genome-screening tool that provides a framework for implementing automated in silico screening of sequence databases using BLAST in combination with MySQL

DisCVR -- a Diagnostic tool for detecting known human viruses in clinical samples from NGS data

GLUE -- protocol for working with multiple sequence alignments (MSAs) and for generating standardized reports using MSAs and data. GLUE also provides tools for managing MSAs and data, and can be used in combination with the MySQL

Tanoti -- a BLAST guided reference based short read aligner. It is developed for maximising alignment in highly variable next generation sequence data

ViCTree -- a bioinformatic framework that automatically selects new candidate virus sequences from GenBank, generates multiple sequence alignments, calculates a maximum likelihood phylogeny and integrates the sequences into the existing phylogenetic trees.

For details, please have a look at <http://evbc.uni-jena.de/tools/>

Publications

New publications by our members:

Fuchs, Jonas, et al. "Evolution and antiviral specificity of interferon-induced Mx proteins of bats against Ebola-, Influenza-, and other RNA viruses." *Journal of Virology* (2017): JVI-00361.

Please help us to spread your news by sending us information and news which should be spread.

