

Upcoming Events

- ❑ **The Second Annual Meeting of the European Virus Bioinformatics Center**
9th-10th April 2018 in Utrecht, Netherlands.

The conference will broadly focus on computational approaches in virology, and we welcome any contributions within this cross-disciplinary field. Sub-topics include (but are not limited to): virus discovery, diagnostics, (meta-)genomics, modelling, molecular structure, evolution, and viral ecology.

Registration is free of charge, and works on a first-come, first-serve basis.
details at <http://evbc.uni-jena.de/2nd-evbc-meeting>

- ❑ **23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)**
26th- 31st August 2018 in Berlin, Germany.
Organised by the University of Leuven, EVBC, and Robert Koch Institut

VEME2018 Comprises three main modules: The **Phylogenetic Inference** module offers a theoretical background and hands-on experience in phylogenetic analysis for those who have little or no prior expertise. An **Evolutionary Hypothesis Testing** is targeting participants who are well familiar with alignments and phylogenetic trees, and would like to extend their expertise to likelihood and Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylodynamics'). A **Next Generation Sequencing (NGS)** module will cover the more complex analysis of Next Generation Sequencing data. In addition, 6 dedicated **half day modules** cover topics such as Large Phylogenies, Transmission Clusters, Molecular Adaptation, Visualizing large phylogenies, Recombination and networks, and Virus Analysis Pipelines.

Abstract and application deadline is 31st of March 2018.
details at <https://rega.kuleuven.be/cev/veme-workshop/2018>

Collaboration opportunity via EVBC

- ❑ **ViMiFi** is a powerful new tool dedicated for **virologists** that detects potential **precursor microRNAs** within viral genome sequences and multiple sequence alignments. If you either have **small RNA-Seq** virus data, or you are specifically looking for **viral miRNAs**, Kevin would be happy to analyze your data (kevin.lamkiewicz@uni-jena.de).

Recent publications by EVBC members (you may send us your recent publications to appear here)

- Development and preliminary evaluation of a multiplexed amplification and next generation sequencing method for viral hemorrhagic fever diagnostics. **PMID: 29155823**
- In Silico Vaccine Strain Prediction for Human Influenza Viruses. **PMID: 29032900**
- Accurate quantification of within- and between-host HBV evolutionary rates requires explicit transmission chain modelling. **PMID: 29026650**
- Critical Assessment of Metagenome Interpretation-a benchmark of metagenomics software. **PMID: 28967888**
- Conserved RNA structures in the intergenic regions of ambisense viruses. **PMID: 29192224**
- Predicting cancer type from tumour DNA signatures. **PMID: 29183400**
- A phylogenomic analysis of Marek's disease virus reveals independent paths to virulence in Eurasia and North America. **PMID: 29151863**
- Complete genome sequences of two insect-specific flaviviruses. **PMID: 28918473**
- Phage Genome Annotation Using the RAST Pipeline. **PMID: 29134599**