



Upcoming Events

- ❑ **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.

Reminder, details at <https://rega.kuleuven.be/cev/veme-workshop/2018>

- ❑ **The fourth Annual Training Course on Viral Genomics & Bioinformatics**
20th-24th August 2018 in Glasgow University, UK.

The 5-day course consists of a series of lectures and practical exercises that directly address bioinformatics challenges posed by the current surge of sequence data, with a focus on viral data sets and analyses. The course will enable participants to understand and deal with high-throughput sequence datasets and encourage the exchange of ideas among diagnosticians, virologists, bioinformaticians and evolutionary biologists.

Reminder, details at <https://www.gla.ac.uk/researchinstitutes/iii/cvr/events/oietraining>

Recent Selected Publications by EVBC Members

- A new era of virus bioinformatics, *Virus Res*, **PMID: 29751021**
- Ortervirales: New Virus Order Unifying Five Families of Reverse-Transcribing Viruses, *J Virol*, **PMID: 29618642**
- Tunneling Nanotubes as a Novel Route of Cell-to-Cell Spread of Herpesviruses, *J Virol*, **PMID: 29491165**
- Consistent prediction of mutation effect on drug binding in HIV-1 protease using alchemical calculations, *J Chem Theory Comput*, **PMID: 29847122**
- LiveKraken - Real-time metagenomic classification of Illumina data, *Bioinformatics*, **PMID: 29868852**

News and Announcements

- ❑ **PoreCamp course:** The EVBC will be organising a course that spans 5 days and will provide hands-on sessions on library preparation, loading and running the MinION Oxford Nanopore sequencer, as well as data analysis. As this is an introductory course, all researchers/ clinicians are welcome. Participants do not require both wet-lab and bioinformatics skills to benefit from the course -- training will be provided in both components. If you are interested please contact us (evbc@uni-jena.de). We will then coordinate to determine the best date. The registration fee is 1000 Euro. The cost includes one flow cell per participant as well as all reagents needed during sequencing. Participants are encouraged to bring their own sample DNA/ RNA. Participants do not need to bring a laptop or MinION sequencer. The fee does not include travel and accommodation.

