

## Upcoming Events

EVBC does not endorse any of the listings and is only involved in events marked as **EVBC Events**.

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### International Hepatitis E Symposium 2020

28–30 May 2020, Berlin, Germany

*Multidisciplinary efforts are needed to characterize in detail the impact of HEV on Global Health, One Health, Personalized Health/Clinics and Virology.*

Abstract submission deadline **20 March 2020**

### 25th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME)

19–24 July 2020, Rio de Janeiro, Brazil

*The VEME workshop will provide both theoretical and practical training in phylogenetic inference and evolutionary hypothesis testing as applied in virology and molecular epidemiology.*

Abstract and application deadline **23 March 2020**

## Recent Selected Publications by EVBC Members

**Please also see the Newsletter Special Issue on SARS-CoV-2.**

LAMPA, LARge Multidomain Protein Annotator, and its application to RNA virus polyproteins. *Bioinformatics* [10.1093/bioinformatics/btaa065](#)

A microbiome silver bullet for honey bees. *Science* [10.1126/science.aba6135](#)

In Search of Covariates of HIV-1 Subtype B Spread in the United States-A Cautionary Tale of Large-Scale Bayesian Phylogeography. *Viruses* [10.3390/v12020182](#)

Phylogeographic reconstruction using air transportation data and its application to the 2009 H1N1 influenza A pandemic. *PLoS Comput Biol* [10.1371/journal.pcbi.1007101](#)

ICTV Virus Taxonomy Profile: Herelleviridae. *J Gen Virol* [10.1099/jgv.0.001392](#)

Accelerated viral dynamics in bat cell lines, with implications for zoonotic emergence. *eLife* [10.7554/eLife.48401](#)

Bacteriophages Isolated from Stunted Children Can Regulate Gut Bacterial Communities in an Age-Specific Manner. *Cell Host Microbe* [10.1016/j.chom.2020.01.004](#)

Host factor prioritization for pan-viral genetic perturbation screens using random intercept models and network propagation. *PLoS Comput Biol* [10.1371/journal.pcbi.1007587](#)

How to recognise and deal with dubious virus sequences? *Infect Genet Evol* [10.1016/j.meegid.2020.104242](#)

A case for a negative-strand coding sequence in a group of positive-sense RNA viruses. *Virus Evol* [10.1093/ve/veaa007](#)

Genomic monitoring to understand the emergence and spread of Usutu virus in the Netherlands, 2016-2018. *Sci Rep* [10.1038/s41598-020-59692-y](#)

Comparison of sequencing methods and data processing pipelines for whole genome sequencing and minority single nucleotide variant (mSNV) analysis during an influenza A/H5N8 outbreak. *PLoS One* [10.1371/journal.pone.0229326](#)

### Preprints

Metagenomics workflow for hybrid assembly, differential coverage binning, transcriptomics and pathway analysis (MUFFIN). *bioRxiv* [10.1101/2020.02.08.939843](#)

AncesTree: an interactive immunoglobulin lineage tree visualizer *bioRxiv* [10.1101/2020.02.17.952465](#)

Improved reference genome of the arboviral vector *Aedes albopictus* *bioRxiv* [10.1101/2020.02.28.969527](#)

## News and Announcements

**Special Issue Virus Sequencing and Functional Viral Metagenomics in Genes (MDPI).** The special issue is guest edited by EVBC member Klaus Jung. You may send your manuscript at any time up until the deadline.

Deadline for manuscript submissions: **31 August 2020**

**Happy 3rd Anniversary!** Three years ago, in the beautiful city of Jena, 55 scientists decided to found the EVBC to bring together the excellence of virology and bioinformatics in Europe.