

Send us your news to evbc@uni-jena.de.

For more frequent updates, please follow us on Twitter [@EVirusBioinfC](#).

Recent Selected Publications by EVBC Members

Epidemiological hypothesis testing using a phylogeographic and phylodynamic framework. *Nat Commun* [10.1038/s41467-020-19122-z](https://doi.org/10.1038/s41467-020-19122-z)

Ensembl 2021. *Nucleic Acids Res* [10.1093/nar/gkaa942](https://doi.org/10.1093/nar/gkaa942)

Rfam 14: expanded coverage of metagenomic, viral and microRNA families. *Nucleic Acids Res* [10.1093/nar/gkaa1047](https://doi.org/10.1093/nar/gkaa1047)

Prophages are associated with extensive CRISPR-Cas auto-immunity. *Nucleic Acids Res* [10.1093/nar/gkaa1071](https://doi.org/10.1093/nar/gkaa1071)

Measuring reproducibility of virus Meta-Genomics analyses using bootstrap samples from FASTQ-Files. *Bioinformatics* [10.1093/bioinformatics/btaa926](https://doi.org/10.1093/bioinformatics/btaa926)

First isolation, *in-vivo* and genomic characterization of zoonotic variegated squirrel Bornavirus 1 (VSBV-1) isolates. *Emerg Microbes Infect* [10.1080/22221751.2020.1847604](https://doi.org/10.1080/22221751.2020.1847604)

Mathematical modeling of hepatitis C RNA replication, exosome secretion and virus release. *PLoS Comput Biol* [10.1371/journal.pcbi.1008421](https://doi.org/10.1371/journal.pcbi.1008421)

Virosaurus A Reference to Explore and Capture Virus Genetic Diversity. *Viruses* [10.3390/v12111248](https://doi.org/10.3390/v12111248)

HCV Genetic Diversity Can Be Used to Infer Infection Recency and Time since Infection. *Viruses* [10.3390/v12111241](https://doi.org/10.3390/v12111241)

Reviews and more

HBV evolution and genetic variability: impact on prevention, treatment and development of antivirals. *Antiviral Res* [10.1016/j.antiviral.2020.104973](https://doi.org/10.1016/j.antiviral.2020.104973)

Sustainable Microbiome: a symphony orchestrated by synthetic phages. *Microb Biotechnol* [10.1111/1751-7915.13697](https://doi.org/10.1111/1751-7915.13697)

Preprints

VirION2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature. *bioRxiv* [10.1101/2020.10.28.359364](https://doi.org/10.1101/2020.10.28.359364)

Ancient evolution of hepadnaviral paleoviruses and their impact on host genomes. *bioRxiv* [10.1101/2020.11.02.364562](https://doi.org/10.1101/2020.11.02.364562)

MetaPop: A pipeline for macro- and micro-diversity analyses and visualization of microbial and viral metagenome-derived populations. *bioRxiv* [10.1101/2020.11.01.363960](https://doi.org/10.1101/2020.11.01.363960)

EpitopeVec: Linear Epitope Prediction Using Deep Protein Sequence Embeddings. *bioRxiv* [10.1101/2020.11.26.395830](https://doi.org/10.1101/2020.11.26.395830)

 [EVBC publications website](#)

Upcoming Events

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

ISMB/ECCB 2021

25–29 July 2021, Lyon, France online

Tutorial proposals deadline: 14 December 2020

 [Subscribe to EVBC Event Calendar](#)

Tools and Resources

Archaeopteryx: visualization and analysis of highly annotated phylogenetic trees.

EpitopeVec: predicts linear B-cell epitopes.

Influenza Research Database: contains avian and non-human mammalian influenza surveillance data, human clinical data, phenotypic characteristics of viruses, and genomic / proteomic data; including **Influenza Swine H1** and **Highly Pathogenic H5N1 Clade Classification Tools** and **Metadata-driven Comparative Analysis Tool for Sequences**.

MetaPop: macro- and micro-diversity analyses and visualization of microbial and viral metagenome-derived populations.

metaviralSPAdes: tool for identifying viral genomes in metagenomic assembly graphs.

RESEQ: efficient generation of bootstrap reads from FASTQ-file to measure reproducibility of virus meta-genomics analyses.

Rfam: comprehensive annotation of viral RNA families starting with Flavivirus and Coronaviridae RNAs.


ViPR Genotyping/Subtyping Tools: **HCV**, **Dengue**, **Zika**

virarecon: assembly and intra-host/low-frequency variant calling for viral samples.

VirAnnot: automated identification of operational taxonomy units for virome sequencing data.

VirION2: integrated short- and long-read metagenomic wet-lab and informatics pipeline to study the genomic diversity of viruses.

Virosaurus (virus thesaurus): curated virus genome database, aimed at facilitating clinical metagenomics analysis.

 [Virus tools website](#)
(currently under maintenance)

New Members

We have invited outstanding scientists in virus bioinformatics for membership. We welcome:

- **Richard Neher**, University of Basel, Switzerland
- **Peter Simmonds**, University of Oxford, United Kingdom
- **Alexandra Zhernakova**, UMC Groningen, Netherlands

 [EVBC members website](#)

Vacancies

Bioinformatician for Molecular Immunology | Ruhr-University Bochum

The Dept. of Molecular Immunology is looking for a Bioinformatics PostDoc with an interest in regulation of gene expression influencing immune responses and development of immune cells. [Details](#).

Application deadline: **10 December 2020**

 [Find a job](#)

This is sure to be a holiday season of intensely mixed emotions, to cap off a year unlike any other.

The pandemic has made us even more aware of the importance of accelerating research in viral bioinformatics. Many thanks to all of you for your commitment to the

EVBC and for advancing the field. We wish you moments of peace and connections with family and friends even if they can't be in person.

We are looking forward to a new (and hopefully better) year.