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Selected Publications by EVBC Members

Glacier ice archives nearly 15,000-year-old microbes and phages.

Microbiome [10.1186/s40168-021-01106-w](#)

Haploflow: strain-resolved de novo assembly of viral genomes. *Genome Biol* [10.1186/s13059-021-02426-8](#)

Deep learning-based real-time detection of novel pathogens during sequencing. Now published in *Brief Bioinf* [10.1093/bib/bbab269](#)

RaFAH: Host prediction for viruses of Bacteria and Archaea based on protein content. *Patterns* [10.1016/j.patter.2021.100274](#)

EpitopeVec: Linear Epitope Prediction Using Deep Protein Sequence Embeddings. Now published in *Bioinformatics* [10.1093/bioinformatics/btab467](#)

Ecogenomics of Groundwater Phages Suggests Niche Differentiation Linked to Specific Environmental Tolerance. *mSystems* [10.1128/mSystems.00537-21](#)

Molecular detection and genomic characterization of diverse hepaciviruses in African rodents. *Virus Evol* [10.1093/ve/veab036](#)

Investigation of Salmonella Phage-Bacteria Infection Profiles: Network Structure Reveals a Gradient of Target-Range from Generalist to Specialist Phage Clones in Nested Subsets. *Viruses* [10.3390/v13071261](#)

Comparative Pathogenesis, Genomics and Phylogeography of Mousepox. *Viruses* [10.3390/v13061146](#)

Modular Evolution of Coronavirus Genomes. *Viruses* [10.3390/v13071270](#)
Detection of Alpha- and Betacoronaviruses in *Miniopterus fuliginosus* and *Rousettus leschenaultii*, two species of Sri Lankan Bats. *Vaccines* [10.3390/vaccines9060650](#)

ICTV Virus Taxonomy Profile: Inoviridae. *J Gen Virol* [10.1099/jgv.0.001614](#)

Genetic lineage characterization and spatiotemporal dynamics of classical insect-specific flaviviruses: outcomes and limitations. *Virus Res* [10.1016/j.virusres.2021.198507](#)

Benchmark of thirteen bioinformatic pipelines for metagenomic virus diagnostics using datasets from clinical samples. Now published in *J Clin Virol* [10.1016/j.jcv.2021.104908](#)

Expanding standards in viromics: in silico evaluation of dsDNA viral genome identification, classification, and auxiliary metabolic gene curation. *PeerJ* [10.7717/peerj.11447](#)

Changes to virus taxonomy and to the International Code of Virus Classification and Nomenclature ratified by the International Committee on Taxonomy of Viruses (2021) *Arch Virol* [10.1007/s00705-021-05156-1](#)

Augur: a bioinformatics toolkit for phylogenetic analyses of human pathogens. *J Open Source Softw* [10.21105/joss.02906](#)

Reviews

The importance of enterovirus surveillance in a post-polio world. *Lancet Infect Dis* [10.1016/S1473-3099\(20\)30852-5](#)

Update on Potentially Zoonotic Viruses of European Bats. *Vaccines* [10.3390/vaccines9070690](#)

Fostering reproducibility, reusability, and technology transfer in health informatics. *iScience* [10.1016/j.isci.2021.102803](#)

Preprints

BERTax: taxonomic classification of DNA sequences with Deep Neural Networks. *bioRxiv* [10.1101/2021.07.09.451778](#)

Hundreds of viral families in the healthy infant gut. *bioRxiv* [10.1101/2021.07.02.450849](#)

 [EVBC publications website](#)

Tools and Resources

Augur: real-time phylodynamic analysis analyses of human pathogens.

BERTax: taxonomic classification of DNA sequences.

DeePac-Live: real-time detection of novel pathogens during sequencing.

EpitopeVec: Linear Epitope Prediction Using Deep Protein Sequence Embeddings.

Haploflow: strain-resolved de novo assembly of viral genomes.

RaFAH: Random Forest Assignment of Hosts for viruses of Bacteria and Archaea.

 [Virus tools website](#)

viruses in silico | EVBC Lectures

Machine Learning methods for Immune Repertoires

12. August 2021 | 04–05 pm CEST

[online](#)

Dr. Günter Klambauer, JKU, Austria

A central mechanism in machine learning is to identify, store, and recognize patterns. How to learn, access, and retrieve such patterns is crucial in Hopfield networks and the more recent transformer architectures. In this talk, Dr. Klambauer will exploit the high storage capacity of modern Hopfield networks to solve a challenging multiple instance learning (MIL) problem in computational biology: immune repertoire classification. Accurate and interpretable machine learning methods solving this problem could pave the way towards new vaccines and therapies. He will present DeepRC, a method that integrates modern Hopfield networks into deep learning architectures for massive MIL such as immune repertoire classification.

 [Register](#)

News and Announcements

The new Impact Factor for MDPI Viruses is **5.048**. Don't forget to submit to our [special issue "Virus Bioinformatics"](#).

ViBioM 2022 pre-registration for EVBC members opens on 1st September 2021.

Vacancies

Professorship W3 or W2/W3 Tenure Track for Bioinformatics at Center for Computational and Theoretical Biology (CCTB) in Würzburg.

Application deadline: **20 August 2021**

Postdoc position and 3 PhD positions at the AG Data Science in Biomedicine at University of Marburg.

Application deadline: **20 August 2021**

Professorship W2 Theoretical evolutionary biology at Center for Computational and Theoretical Biology (CCTB) in Würzburg.

Application deadline: **17 September 2021**

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