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Selected Publications by EVBC Members

 [All publications on Pubmed](#)

geNomad is a classification and annotation framework that combines information from gene content and a deep neural network to identify sequences of plasmids, viruses, and proviruses, achieving high classification performance and enabling the discovery of millions of such genetic elements in large-scale datasets. (Nat Biotechnol: [10.1038/s41587-023-01953-y](#))

The comprehensive analysis of viruses associated with methanogenic archaea reveals a diverse range of viral sequences infecting these methane-producing microorganisms and highlights their potential roles in regulating methanogen communities and facilitating the development of genetic tools for further research. (Nat Microbiol: [10.1038/s41564-023-01485-w](#))

This study challenges the common assumption that viruses significantly outnumber cells on Earth, suggesting that in many non-aquatic environments, viruses only outnumber cells by a modest two-fold margin, using a metagenome-based method that accounts for various stages of virus replication and avoids potential false positives from traditional virus counting techniques. (ISME J: [10.1038/s41396-023-01431-y](#))

RNA Masonry is a computer program and web service, which automates the modeling of RNA 3D structures by assembling RNA fragments based on user-provided secondary structure constraints, tertiary contact restraints, and small-angle X-ray scattering data, addressing the need for efficient structure determination of new non-coding RNA sequences. (Bioinformatics: [10.1093/bioinformatics/btad527](#))

The study introduces Phables, a computational method for recovering complete phage genomes from fragmented viral metagenome assemblies, which outperforms existing tools by identifying more high-quality phage genomes and distinguishing variant phage genomes with a high degree of accuracy, addressing a significant challenge in phage genome recovery for advancing phage biology and diagnostic tool development. (Bioinformatics: [10.1093/bioinformatics/btad586](#))

Using electroporation to synchronously activate RIG-I, the study provides a high temporal resolution of the dynamics of cell-intrinsic innate immune signaling. Subsequently, a mathematical model was developed to simulate signaling downstream of dsRNA recognition by RIG-I and the feedback and signal amplification by IFN, offering insights into early events in virus infection and the host-virus interaction. (Life Sci Alliance: [10.26508/lsa.202302059](#))

The lncRNAs ANRIL and THRIL in the blood of moderate and severe COVID-19 patients are expressed significantly higher in severe cases compared to moderate cases and healthy individuals, suggesting their potential as circulating biomarkers for assessing the severity of the disease. (Virus Res: [10.1016/j.virusres.2023.199214](#))

The study employs complete genome sequencing strategies, including targeted enrichment, to investigate hepatitis E virus (HEV) sequence diversity in various samples, identifying potential novel subtypes, assessing intra-host diversity in a chronically infected patient, and revealing evidence of HEV compartmentalization, with implications for understanding virus diversity and potential resistance in HEV infections. (J Clin Virol: [10.1016/j.jcv.2023.105583](#))

The machine learning tool ConCreT, which was tested for the *Cressdnaviricota* phylum with over 98% accuracy, utilizes a 2D convolutional neural network to classify viruses, addressing the need for less computationally intensive tools capable of classifying viruses at the genus and species rank. (J Virol Methods: [10.1016/j.jviromet.2023.114789](#))

Reviews / Commentaries / Editorials / ...

"Giant viruses" of the phylum *Nucleocytoviricota* have evolved elaborate strategies for manipulation of their host's physiology, like the use of genes acquired from the host (viral homologs, "virologs") to promote viral propagation. The review covers recent findings of further virologs which include genes not typically found in viruses, and the evolutionary pathways to acquire those functional repertoires. (FEMS Microbiol Rev: [10.1093/femsre/fuad053](#))

The review describes the strategies used for the study of ancient viruses, along with their limitations, and provides a detailed account of what past viral infections have revealed about human history. (Annu Rev Virol: [10.1146/annurev-virology-111821-123859](#))

This review provides a comprehensive evaluation of 24 active virus databases, assessing their content, functionality, and adherence to FAIR principles, while also reviewing different types of errors, with the aim of assisting users in selecting appropriate virus databases and aiding database improvement, since the use of virus databases is crucial for advancing understanding of virus biology, evolution, transmission, and outbreak management. (Viruses: [10.3390/v15091834](#))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](#).

SARS-CoV-2


influenza

HIV

monkeypox

Tools and Resources

 [Virus tools website](#)

Tools that have been added to our [collection](#) this month, or have now been published. Tools developed by EVBC members are marked .

Multi-choice Viromics Pipeline (MVP): a pipeline of state-of-art tools to get from a set of contigs to a vOTU heatmap

vHULK: bacteriophage host prediction based on annotated genomic features and deep neural networks

INFH-VH: Kernelized Logistic Matrix Factorization based on Similarity Network Fusion for Predicting Virus-host Association

CHERRY: Computational methoD for accuratE pRediction of virus-pRokarYotic interactions using a graph encoder-decoder model

PHIS Detector: web tool to detect diverse *in silico* phage-host interaction signals

EVBC Special Issues

Special issue list

Diversity of bacteriophages and their contribution to improve animal, environmental, and human health

in *Sustainable Microbiology*

(Guest Editor: Darren Smith | Editorial Board incl. **Janina Rahlff**)

There is a global shift towards utilizing bacteriophages in the fight against antibiotic resistance, with discussions spanning academia, industry, and government. This series aims to cover various aspects of phage biology related to human, animal, or environmental health, supporting their international development and application.

Manuscript submission deadline:

1st January 2024

Upcoming Events

Subscribe to Calendar

We do not endorse any of the listings and do not take any responsibility for the accuracy of the information. EVBC members are involved in events marked ✨.

International Conference on Research in Computational Molecular Biology (RECOMB)

29 April – 02 May 2024 | Boston, MA, USA

Abstract submission deadline: 16 October 2023

Swedish Bioinformatics Workshop 2023

06–07 November | Stockholm, Sweden

Registration is free for students and postdocs

✨ Lars Juhl Jensen (keynote speaker)

viruses *in silico* lecture series

Register

This lecture is designed to keep you up to date with the latest developments in virus bioinformatics, especially new tools that might help you in your research.

You can already [register](#) for our upcoming lectures:

23. October 2023	Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine, Germany
20. November 2023	Anton Petrov, Riboscope Ltd., UK
19. December 2023	Dominik Heider, University of Marburg, Germany

If you are attending the "viruses in silico" lecture regularly and do not want to register every month, you can choose to be permanently registered. You will be added to the mailing list and receive the access details every month. You can unsubscribe at any time.

Vacancies

Find a job

The Systemsbiology Research group at Jena University Hospital is seeking applications for a **PhD Student or Postdoc position in bioinformatics**. The position is part of the Antivirus Pandemic Preparedness Platform (APPEAL), a new EU-funded project aimed at developing strategies for pandemic preparedness to combat viral infections. The research will involve the development of machine learning models for identifying druggable host dependency factors, studying molecular-level protein interactions and gene regulation, and integrating this data to identify potential drug targets for virus treatment.

New Members

EVBC members website

We are happy to welcome our new members:

- **Pakorn Aiewsakun**, Mahidol University, Thailand
- **Yulia Aleshina**, Sechenov First Moscow State Medical University, Russia
- **Poliane Alfenas-Zerbini**, Universidade Federal de Viçosa, Brazil
- **Ana Avellón**, Instituto de Salud Carlos III, Spain
- **Farzad Beikpour**, University of Bari Aldo Moro, Italy
- **Denis Beslic**, Robert Koch Institute, Germany
- **Nadja Brait**, University of Groningen, Netherlands
- **Achille Broggi**, Aix Marseille Université, France
- **Ravendra P. Chauhan**, Rhodes University, South Africa
- **Christian Eggeling**, Friedrich Schiller University Jena, Germany
- **Anh Ha**, Virginia Tech, United States
- **Erin Harvey**, The University of Sydney, Australia
- **William T Harvey**, University of Edinburgh, United Kingdom
- **Julia Hillung**, Institute for Integrative Systems Biology, Spain
- **Jiabin Huang**, University Medical Center Hamburg-Eppendorf, Germany
- **Chris Illingworth**, University of Glasgow, United Kingdom
- **Camille Melissa Johnston**, Statens Serum Institut, Denmark
- **Konda Reddy Karnati**, Bowie State University, USA
- **Juan Ledesma**, Instituto de Salud Carlos III, Spain
- **Hannelore Longin**, KU Leuven, Belgium
- **Dominik Lücking**, Max Planck Institute for Marine Microbiology, Germany
- **Alejandro Matía**, Stanford University, United States
- **So Nakagawa**, Tokai University School of Medicine, Japan
- **Maximilian Klaus Nocke**, Ruhr-Universität Bochum, Germany
- **Rhys Parry**, The University of Queensland, Australia
- **Rajesh Kumar Pathak**, Chung-Ang University, South Korea
- **Judit Penzes**, Rutgers University, United States
- **Aryan Rahimi Midani**, University of Würzburg, Germany
- **Shoichi Sakaguchi**, Osaka Medical and Pharmaceutical University, Japan
- **Lygeri Sakellaridi**, Julius Maximilian University of Würzburg, Germany
- **Timofey Skvortsov**, Queen's University Belfast, United Kingdom
- **Sandra Triebel**, Friedrich Schiller University Jena, Germany
- **Tomasz Wirecki**, IIMCB, Poland
- **Bishoy Maher Zaki**, MSA University, Egypt
- **F. Murilo Zerbini**, Universidade Federal de Viçosa, Brazil

The EVBC has now 311 members from 180 research institutions distributed over 44 countries worldwide.