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For more frequent updates, please follow us on Twitter [EVirusBioinfC](https://twitter.com/EVirusBioinfC).

Recent Selected Publications by EVBC Members

The long-term genetic stability and individual specificity of the human gut microbiome. *Cell* [10.1016/j.cell.2021.03.024](https://doi.org/10.1016/j.cell.2021.03.024)

Enteric viruses evoke broad host immune responses resembling those elicited by the bacterial microbiome. *Cell Host Microbe* [10.1016/j.chom.2021.03.015](https://doi.org/10.1016/j.chom.2021.03.015)

Primate phageomes are structured by superhost phylogeny and environment. Now published in *PNAS* [10.1073/pnas.2013535118](https://doi.org/10.1073/pnas.2013535118)

The dinucleotide composition of the Zika virus genome is shaped by conflicting evolutionary pressures in mammalian hosts and mosquito vectors. *PLoS Biol* [10.1371/journal.pbio.3001201](https://doi.org/10.1371/journal.pbio.3001201)

The virome of German bats: comparing virus discovery approaches. *Sci Rep* [10.1038/s41598-021-86435-4](https://doi.org/10.1038/s41598-021-86435-4)

A Roadmap for Genome-Based Phage Taxonomy. *Viruses* [10.3390/v13030506](https://doi.org/10.3390/v13030506)

Metagenomic Snapshots of Viral Components in Guinean Bats. *Microorganisms* [10.3390/microorganisms9030599](https://doi.org/10.3390/microorganisms9030599)

Establishment of *Culex modestus* in Belgium and a Glance into the Virome of Belgian Mosquito Species. *mSphere* [10.1128/mSphere.01229-20](https://doi.org/10.1128/mSphere.01229-20)

Recommendations for the introduction of metagenomic next-generation sequencing in clinical virology, part II: bioinformatic analysis and reporting. *J Clin Virol* [10.1016/j.jcv.2021.104812](https://doi.org/10.1016/j.jcv.2021.104812)

ViralON2: a short- and long-read sequencing and informatics workflow to study the genomic diversity of viruses in nature. Now published in *PeerJ* [10.7717/peerj.11088](https://doi.org/10.7717/peerj.11088)

Bayesian Phylogeographic Analysis Incorporating Predictors and Individual Travel Histories in BEAST. *Curr Protoc* [10.1002/cpz1.98](https://doi.org/10.1002/cpz1.98)

Reviews

Targeting the DEAD-Box RNA Helicase eIF4A with Rocaglates-A Pan-Antiviral Strategy for Minimizing the Impact of Future RNA Virus Pandemics. Now published in *Microorganisms* [10.3390/microorganisms9030540](https://doi.org/10.3390/microorganisms9030540)

Mechanisms of Hepatitis C Virus Escape from Vaccine-Relevant Neutralizing Antibodies. *Vaccines* [10.3390/vaccines9030291](https://doi.org/10.3390/vaccines9030291)

Novel opportunities for NGS-based one health surveillance of foodborne viruses. *One Health Outlook* [10.1186/s42522-020-00015-6](https://doi.org/10.1186/s42522-020-00015-6)

 [EVBC publications website](#)

New Members

We are happy to welcome our new members:

Daniel Carrillo Bautista, Utrecht University, NL | **Simon Dellicour**, Université Libre de Bruxelles, BE | **Andrei Deviatkin**, Sechenov University, RU | **Celeste Donato**, Murdoch Children's Research Institute, AU | **Ernestina Hauptfeld**, Utrecht University, NL | **Spyros Lytras**, University of Glasgow, UK | **Björn Meyer**, Institut Pasteur, FR | **Krupa Parmar**, Helmholtz Centre for Environmental Research- UFZ, DE | **Muriel Ritsch**, Friedrich Schiller University Jena, DE | **Simon Roux**, DOE Joint Genome Institute, US | **Hanspeter Stalder**, University of Bern, CH | **Lore Van Espen**, KU Leuven, BE | **Ling-yi Wu**, Utrecht University, NL

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viruses *in silico* | EVBC Lectures

Genomic surveillance of SARS-CoV-2 at the Robert Koch Institute: an overview and bioinformatics edge cases

17. May 2021 | 04–05pm CEST

online

Dr. Martin Hölzer, Robert Koch Institute, Germany

In mid-January, the Federal Ministry of Health issued a decree requiring laboratories to submit reconstructed SARS-CoV-2 genomes to the RKI to improve genomic surveillance. The number of sequences increased tremendously. Reconstructed genomes of virus-positive samples sequenced directly at RKI further enrich this set. This lecture will discuss the various bioinformatics tasks and challenges involved in the daily reconstruction, quality control, annotation, profiling, and clustering of these sequences and discuss important bioinformatics edge cases that, if not addressed appropriately, may even lead to misclassification of variants or virus lineages of concern.

 [Register](#)

EVBC Special Issues

Endogenous Retroviruses: Contribution to Human Evolution and Physiopathology.

This special issue in *Biology* (guest edited by EVBC member R. J. Gifford) will provide an updated survey of ERV interplay with the host biology, with particular attention to clarifying fundamental misconceptions and outlining current controversies regarding the evolutionary origins of ERVs in the human genome and their possible contributions to human evolution and pathogenesis.

Deadline:

10 December 2021

Molecular Epidemiology, Host Genetic Factors, and Viral Hepatitis Related Liver Diseases.

This special issue in *Pathogens* (guest edited by EVBC member D. Todt) will cover aspects of the pathogenesis, immunology, epidemiology, diagnosis, treatment, and prevention of viral hepatitis.

Deadline:

31 December 2021

Virus Bioinformatics 2022

This Special Issue in *Viruses* (guest edited by ViBioM 2022 Organizing Team) is published alongside ViBioM 2022 and covers papers dealing with the recent advancements and current understanding of computational aspects of virology.

Deadline:

30 April 2022

 [More special issues by EVBC members](#)