

Send us your news to [evbc@uni-jena.de](mailto:evbc@uni-jena.de).

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

### Selected Publications by EVBC Members

[All publications on Pubmed](#)

Major updates to the European Nucleotide Archive's services and infrastructure that have been delivered in 2021. (Nucleic Acids Res: [10.1093/nar/gkab1051](https://doi.org/10.1093/nar/gkab1051))

MODOMICS: a database of RNA modification pathways including SARS Cov-2 NSP proteins involved in the capping of viral RNA. (Nucleic Acids Res: [10.1093/nar/gkab1083](https://doi.org/10.1093/nar/gkab1083))

Skin Microbial Genome Collection provides a genome-centric view of the microbial populations found on the skin, incl. 6,935 quality-filtered viral sequences. (Nat Microbiol: [10.1038/s41564-021-01011-w](https://doi.org/10.1038/s41564-021-01011-w))

After initial introduction out of China, the US acted as an important source of PEDV introductions into Japan, Korea, China and Mexico. (Mol Biol Evol: [10.1093/molbev/msab364](https://doi.org/10.1093/molbev/msab364))

Updated parameter values of a mathematical model of African horse sickness virus resulted in an increase in the number of host deaths, decrease in the duration of the outbreak, and greater prevalence in vectors. (Transbound Emerg Dis: [10.1111/tbed.14420](https://doi.org/10.1111/tbed.14420))

ICTV summary on the family *Retroviridae*. (J Gen Virol: [10.1099/jgv.0.001712](https://doi.org/10.1099/jgv.0.001712))

A signaling pathway-driven bioinformatics pipeline to quickly identify candidate therapeutics for future emerging infectious diseases. (F1000Res: [10.12688/f1000research.52412.2](https://doi.org/10.12688/f1000research.52412.2))

### Reviews / Commentaries / Editorials

Chaos game representation is a powerful method in bioinformatics in many different applications, including alignment-free classification of viruses. (Comput Struct Biotechnol J: [10.1016/j.csbj.2021.11.008](https://doi.org/10.1016/j.csbj.2021.11.008))

Bioinformatics of virus taxonomy: Advancing tools will be critical for improving taxa demarcation across the virosphere and resolving rank origins in research that may also inform experimental virology. (Curr Opin Virol: [10.1016/j.coviro.2021.11.003](https://doi.org/10.1016/j.coviro.2021.11.003))

Editorial overview: Virus bioinformatics - empowering genomics of pathogens, viromes, and the virosphere across divergence scales. (Curr Opin Virol: [10.1016/j.coviro.2021.12.001](https://doi.org/10.1016/j.coviro.2021.12.001))

### Preprints

Evaluation of multiple ORF-calling programs for viral genome annotation suggests need for improved programs to deal with RNA viruses. (bioRxiv: [10.1101/2021.12.11.472104](https://doi.org/10.1101/2021.12.11.472104))

TreeKnit, a method that infers ancestral reassortment graphs (ARG) from two segment trees to identify reassortment events from viral sequence data. (bioRxiv: [10.1101/2021.12.20.473456](https://doi.org/10.1101/2021.12.20.473456))

DNA methylation patterns are associated with ecological changes and virus-host dynamics in the marine microbiome. (bioRxiv: [10.1101/2021.11.30.470565](https://doi.org/10.1101/2021.11.30.470565))

### viruses *in silico* | EVBC Lectures

[Register](#)

#### Behind the scenes: Estimating infectiousness throughout SARS-CoV-2 infection course

24. January 2022 | 04–05 pm CET online  
Dr. Terry Jones, Charité – Universitätsmedizin Berlin, Germany

Although post facto studies have revealed the importance of SARS-CoV-2 transmission from presymptomatic, asymptomatic, and mildly symptomatic cases, the virological basis of their infectiousness remains largely unquantified. Two elementary parameters for quantifying viral infection and shedding are viral load and whether samples yield a replicating virus isolate in cell culture. In this talk, Terry Jones will tell the back story of [this paper](#) and the challenges associated with processing and interpreting messy data.

### Tools and Resources

[Virus tools website](#)

**MODOMICS:** database of RNA modification pathways.

**Pathway2Targets:** predicting therapeutics against emerging infectious diseases.

**TreeKnit:** infer Ancestral Reassortment Graphs for segmented genomes.

### ViBioM 2022

[Register](#)

Registration for ViBioM 2022 in Valencia is still open. We will keep you updated regarding the SARS-CoV-2 (Omicron) situation.

**We look forward to receiving your submissions for giving a talk at ViBioM 2022.**

Deadline: **31 January 2022**

### Vacancies


[Find a job](#)

Chair for Methods in Medical Informatics, Department of Computer Science at the University of Tübingen is currently looking for a **Post-doc for AI in Infection Research (COVID-19)** starting as soon as possible. Application deadline: **09 January 2022**

The newly established Viral Ecology and Omics group at FSU Jena, Germany, is looking for a **Bioinformatic Programmer/Data Steward** to support the dry lab activities of our group. Application deadline: **16 January 2022**

### Upcoming Events

[Subscribe to Calendar](#)

EVBC does not endorse any of the listings. EVBC members are involved in events marked .

#### 31st Annual Meeting of the Society for Virology

30 March–2 April 2022 | Munich, Germany

Abstract submission deadline: **09 January 2022**

Registration opening: **January 2022**

**Don't forget to suggest speakers for our ECR Viromics Webinar Series. Registration now open.**

Please see the [back of the newsletter](#) to get to know our members!

Board of Directors

Martin Beer, Li Deng, Bas E. Dutilh, Philippe Le Mercier, Manja Marz, Volker Thiel

[✉ evbc@uni-jena.de](mailto:evbc@uni-jena.de)

[☎ +49-3641-9-46482](tel:+49-3641-9-46482)

[🌐 http://evbc.uni-jena.de/](http://evbc.uni-jena.de/)

[📍 Leutrargaben 1, 07743 Jena](#)