

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

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

Selected Publications by EVBC Members

 [All publications on Pubmed](#)

NetoVIR protocol: powerful method for detecting viral pathogens in amniotic fluid samples, demonstrating its accuracy in identifying cytomegalovirus and parvovirus B19 and suggesting its potential for uncovering unexpected pathogens associated with fetal abnormalities in future applications. (*J Med Virol*: [10.1002/jmv.29045](#))

This study explores the largely uncharted rumen virome by analyzing 975 rumen metagenomes to create a global rumen virome database (RVD), identifying a wide range of viral species and their potential influence on the rumen microbiome and ecosystem. (*Nat Commun*: [10.1038/s41467-023-41075-2](#))

Estimating the ratio of viruses to cells in the environment is complex, with varying results depending on methods used, but metagenomic approaches offer a promising yet still uncertain perspective to complement traditional microscopy-based counts in understanding virus-host interactions in different ecosystems. (*ISME J*: [10.1038/s41396-023-01468-z](#))

MARVD2: upgraded tool employing a random forest machine learning algorithm significantly enhances the identification of archaeal viruses in datasets, addressing the previous limitations in distinguishing between bacterial and archaeal viruses and allowing for improved scalability, usability, and flexibility in archaeal

virus discovery. (*ISME Commun*: [10.1038/s43705-023-00295-9](#))

ASFV unexpectedly diversified into five distinct lineages with multiple variants, including a frameshift mutation in the DNA polymerase PolX gene O174L, raising concerns about the potential impact on the ASFV pandemic and emphasizing the importance of genomic surveillance and monitoring for future changes in the virus. (*Emerg Microbes Infect*: [10.1080/22221751.2022.2146537](#))

Computational pipeline for accurately characterizing viral communities, capable of identifying and classifying both prokaryotic and eukaryotic viruses, with an average accuracy of 86.6%, and it substantially improves taxonomic classifications, demonstrating its effectiveness in various metagenomic datasets. (*PLoS Comput Biol*: [10.1371/journal.pcbi.1011422](#))

A new inference pipeline for phylogenetic probit models is introduced, utilizing Zigzag Hamiltonian Monte Carlo (Zigzag-HMC) and a joint sampling scheme to achieve a 5-fold speedup compared to the previous state-of-the-art approach (BPS), making it feasible to analyze large-scale datasets and explore dependencies between mixed-type biological traits while considering evolutionary relationships between specimens. (*PLoS Comput Biol*: [10.1371/journal.pcbi.1011419](#))

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

Workshop Automating Virus Taxonomy 2023 in Jena

 [More Info](#)

On 31 July - 2 August 2023, the [ICTV](#), [EVBC](#), and [NFDI4Microbiota](#) co-organised a Workshop **Automating Virus Taxonomy** in Jena. There were almost 400 registrations from 46 countries on all continents (except Antarctica) highlighting the huge interest in this important topic from a global community of virus taxonomy enthusiasts. The current virus taxonomy is characterised by a patchwork of methods that capture the features of different viral lineages. However, these methods are not reproducibly implemented, making it difficult to classify unknown viral sequences, such as those derived from metagenomics data. On the first two days of the Jena Workshop, virology experts explained how they classified divergent types of viruses, and bioinformaticians presented methods to cluster and classify viral sequences. On the third day, a group of enthusiasts rolled up their sleeves during the Hands-On Workshop, consisting of a Snakemake tutorial and creating pipelines to automate classification. We are pleased to share the results of the hackathon: two Snakemake workflows for Caudoviricetes classification that follow best coding practices! Take a peek at the [mashup-phage](#) and [download-and-reannotation-of-phage-genomes](#) workflows on the [GitHub repository of the ICTV Virus Bioinformatics Enthusiasts Group](#). The Snakemake material and slides are available [here](#) and [here](#). If you are interested in viewing the slides and/or recordings of other presentations, please contact the organizers.

ICTV/EVBC Workshop on




**Automating
Virus Taxonomy**

31 July – 2 August 2023

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 .

1st Workshop "Young PI" of the Society of Virology (GfV)


11 – 12 Dezember 2023 | Marburg, Germany

The goal of the working group is to provide knowledge that facilitates the transition from bench to successful leadership of one's own working group. Therefore the Young PI working group organizes meetings and workshops where important tips, tricks and soft skills are imparted. [Register here](#) (limited availability)

European Study Group on the Molecular Biology of Picornaviruses (EUROPIC)

02 – 06 June 2024 | Jyväskylä, Finland

Europic is the world premier virology conference that focuses on studies of picornaviruses, covering picornavirus diversity and evolution, pathogenesis, virus-cell interactions, immunological aspects, virus structure, molecular mechanisms of the viral life cycle, treatment and prevention among others. [More details here](#).

 Petri Susi (scientific board)

ECR Viromics Webinar Series

 [Register](#)

This lecture for early career researchers studying viruses in complex communities is organized together with the [Center of Microbiome Science](#) at Ohio State University and the [NSF EMERGE Biology Integration Institute](#).

A global virome of methanogenic archaea highlights novel diversity and adaptations to the gut environment

13 September 2023 | 04-05 pm CET

[online](#)

Sofia Medvedeva, Institut Pasteur, Paris, France

Vacancies

 [Find a job](#)

Frontend development of virus database and community engagement. The NFDI4Microbiota and FSU Jena are looking for a post-doctoral researcher or PhD candidate to join the database development team to develop and maintain the front-end website of the virus database, create analysis workflows and communicate with bioinformaticians, virologists and other researchers to get user feedback.


Application deadline:


01 November 2023


PhD Student in Data Science / Computational Biology / Bioinformatics at the Clinic for Pneumology of the Hannover Medical School, Germany for the Implementation, development and extension of methods for single cell RNA-seq and spatial transcriptomics processing and analysis. Application deadline: **17 September 2023**

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 .

 **MArVD2:** Metagenomic Archaeal Virus Detector.

 **VIRify:** detection of phages and eukaryotic viruses from metagenomic and metatranscriptomic assemblies.