

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](#)

A new deep mutational scanning platform based on non-replicative pseudotyped lentiviruses directly quantifies how large numbers of spike mutations impact antibody neutralization and pseudovirus infection. (Cell: [10.1016/j.cell.2023.02.001](https://doi.org/10.1016/j.cell.2023.02.001))

Serum antibodies elicited by first-generation smallpox vaccines can neutralize the current Monkeypox more than 40 years after vaccine administration. (J Med Virol: [10.1002/jmv.28643](https://doi.org/10.1002/jmv.28643))

In mosquitoes, the piRNA pathway has unique functions in antiviral defense, with core piRNA clusters enriched for non-retroviral endogenous viral elements, and identifies transcriptional readthrough as a conserved mechanism for piRNA biogenesis in several vector mosquitoes, which could allow adaptation to environmental challenges such as virus infection. (Cell Rep: [10.1016/j.celrep.2023.112257](https://doi.org/10.1016/j.celrep.2023.112257))

Versatile tool for detecting promising antimicrobial peptide candidates, which uses pruning methods to evaluate ensemble classifiers made of different peptide encodings and base models. (BioData Min: [10.1186/s13040-022-00317-7](https://doi.org/10.1186/s13040-022-00317-7))

The family of archaeal L7Ae proteins uniquely inhibit the splicing biology of *Orthomyxoviridae* members, including influenza A virus, influenza B virus, and Salmon isavirus, revealing a common strategy to coordinate their replication cycle. (J Virol: [10.1128/jvi.01813-22](https://doi.org/10.1128/jvi.01813-22))

A novel coronavirus was identified and genetically characterized in the European badger, which clustered as outgroup and potentially belongs to a new genus Epsilon coronavirus, emphasizing the need for continued surveillance of diverse coronaviruses with unknown zoonotic and epizootic potential. (Infect Genet Evol: [10.1016/j.meegid.2023.105406](https://doi.org/10.1016/j.meegid.2023.105406))

Preprints

New assembly workflow HYPFA utilizes long-read assemblies in combination with short-read sequencing to resolve phage direct terminal repeats (DTRs) and correct errors, emphasizing the importance of careful phage assembly curation before comparative genomics. (bioRxiv: [10.1101/2023.03.09.531871](https://doi.org/10.1101/2023.03.09.531871))

Investigation of diversity and activity of environmental DNA and RNA viruses across seasonal changes in a snow-dominated mountainous watershed identified a large number of taxonomically divergent viruses. (bioRxiv: [10.1101/2023.03.06.531389](https://doi.org/10.1101/2023.03.06.531389))

geNomad is a classification and annotation framework that identifies sequences of plasmids and viruses, provides functional gene annotation and taxonomic assignment, and detects proviruses integrated into host genomes with high precision. (bioRxiv: [10.1101/2023.03.05.531206](https://doi.org/10.1101/2023.03.05.531206))

Three novel crAssphage species isolated from wastewater and infecting the bacterial host *Bacteroides cellulosilyticus* WH2 have a conserved gene arrangement with known crAssphages, but gene similarity within phages belonging to the same taxa was highly variable. (bioRxiv: [10.1101/2023.03.05.531146](https://doi.org/10.1101/2023.03.05.531146))

Massively parallel algorithms that take advantage of graphics processing units (GPUs) to calculate the gradient of the log-likelihood with respect to all branch-length-specific parameters, resulting in many fold higher speedups over previous CPU implementations, enabling more efficient inference techniques for phylogenetic models with increasing number of sequences. (arXiv: [10.48550/arXiv.2303.04390](https://arxiv.org/abs/10.48550/arXiv.2303.04390))

Novel tool Magnipore searches for significant signal shifts between samples of Oxford Nanopore data from similar or related species and detected 55 mutations and 15 sites that hint at differential modifications between SARS-CoV-2 Alpha and Delta. (bioRxiv: [10.1101/2023.03.17.533105](https://doi.org/10.1101/2023.03.17.533105))

The Read Annotation Tool (RAT) now integrates read-based taxonomic profiling, assembly, and binning of metagenome-assembled genomes (MAGs) to enhance read annotation and provides an accurate and comprehensive view of the microbiome. (bioRxiv: [10.1101/2023.03.22.533753](https://doi.org/10.1101/2023.03.22.533753))

Hybrid parasites of the zoonotic disease cutaneous leishmaniasis in Peru and Bolivia were geographically and ecologically dispersed and commonly infected from a pool of genetically diverse viruses, which increased the frequency of endosymbiotic interactions known to play a key role in disease severity. (bioRxiv: [10.1101/2023.03.24.534103](https://doi.org/10.1101/2023.03.24.534103))

Proof-of-principle for predicting earlier time for decision-making based on Illumina sequencing cycles for pathogen diagnosis using a machine learning approach, which can save several hours of turnaround time. (bioRxiv: [10.1101/2023.03.07.530760](https://doi.org/10.1101/2023.03.07.530760))

Publication shortcuts: If you would like us to add a shortcut to a specific virus (family) or topic, drop us an [email](mailto:evbc@uni-jena.de).

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 .

 **DRAMv:** annotation of metagenomic assembled genomes and VirSorter identified viral contigs.

 **geNomad:** Identification of mobile genetic elements.


 **iVirus 2.0:** central and accessible analytical platform for studying how (dsDNA) viruses impact diverse microbial ecosystems.

MaGplotR: analysis and visualization of multiple MaGeCK screen datasets through aggregation.

 **NGS-BiClass:** Predicting Decision-Making Time for Diagnosis over NGS Cycles.

PhageDPO: prediction of depolymerases in bacteriophage genomes using machine learning methods.

Pharokka: bacteriophage annotation tool.

 **RAT:** Read Annotation Tool integrating metagenome-assembled genomes.

VPF-Class: taxonomic assignment and host prediction of uncultivated viruses based on viral protein families.

EVBC Special Issues

 [Special issue list](#)


For our special issue **Virus Bioinformatics 2023** running alongside ViBioM 2023, we have vouchers available for EVBC members. Get in contact if you are interested!

New papers published:

Validation of HIV-1 MA Shell Structural Arrangements and Env Protein Interactions Predict a Role of the MA Shell in Viral Maturation
[10.3390/v15040893](https://doi.org/10.3390/v15040893)

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 Intelligent Systems for Molecular Biology (ISMB)

23–27 July 2023 | Lyon, France

Submission deadline: **20 April 2023**

ViBioM 2023

 [Register](#)



We are happy to let you know, that we have received 60 high-quality submissions for presenting at ViBioM 2023. The decisions and a preliminary schedule will be announced this week. We look forward to meeting you in Valencia! [Registration is still open.](#)

We are pleased to announce the final speaker in our list of keynote speakers:

The promise and pitfalls of prophages.

Robert Edwards

Flinders University, Adelaide, Australia



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](#).

Unearthing Climate Impacts on Soil Viruses

05 April 2023 | 04-05 pm CET

Ruonan Wu, Pacific Northwest National Laboratory, USA

[online](#)

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.

TBA

24 April 2023 | 04 pm CEST

Masayuki Horie, Osaka Metropolitan University, Japan

[online](#)

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

28. August 2023 Dominik Heider, University of Marburg, Germany

23. October 2023 Gabriel da Luz Wallau, Bernhard Nocht Institute for Tropical Medicine, 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.

EVBC Workshops

 [Register](#)

Nanopore Sequencing workshop

26. – 28. April 2023 | Jena, Germany

This workshop is offered by the [Bioinformatics Core Facility Jena](#).

Preliminary workshop outline:

Day 1 (Introduction): Details about the Nanopore sequencing technology and a general overview of sequencing approaches.

Day 2 (Sequencing): Introduction and specifics about sample (DNA/RNA) extraction and library preparation, and a demonstration of a sequencing run and real-time analysis during sequencing.

Day 3 (Data analysis): Introduction to the command line and Bash as well as installation and configuration of the needed software tools using Conda. Base calling, read quality control, read processing, read mapping, genome/transcriptome assembly, and modification calling

If you are interested in participating, you can register [via email](#).

Vacancies

 [Find a job](#)

The group of Prof. Dr. Manja Marz in the Department of RNA Bioinformatics & High-Throughput Analysis at the Friedrich Schiller University Jena is looking for a **Junior research group leader and a PhD student in molecular biology**.

Starting date:

01 October 2023

The Robert Koch Institute is looking for **multiple bioinformaticians within the public health sector** within the MF 1 "Genome Competence Center" in Berlin-Mitte to help establishing a national integrated molecular surveillance (IMS) of public health-relevant pathogens.

Application deadline:

17. April 2023

Member Profile: Peter Simmonds



Name: Peter Simmonds
Position: Professor of Virology,
University of Oxford
Research focus: virus
pathogenesis and evolution



[Full interview online](#)

What do you love about viruses?

I'm not sure "love" is the right word - I think I just grew to like viruses eventually, as my original involvement in them was really just chance. [...]

What are you currently learning?

Spare moments learning Python 3 - part of a project to bring obscure single OS sequence analysis software (eg. SSE) to a wider community platform.

What is the coolest thing about your research?

Virus classification, which I am often associated with after HCV is definitely not cool, and not sure it's actually research! I think previous work, and in my case hopefully future work (grant gods permitting) on cellular pathways that restrict viruses at the level of nucleotide composition and RNA structure. These include ZAP and RNA editing pathways and represent major extensions to existing ideas about innate immunity and are collectively pretty cool. The shaping effect these have on RNA virus evolution is pretty cool too.

For which project idea are you looking for a cooperation partner?

The extent to which of host cell editing of RNA viruses can restrict their replication and host ranges and the ways in which viruses can evade these potentially highly potent antiviral pathways. Well explored for HIV-1 and other retroviruses but the pathways and mechanisms likely go wider into RNA viruses too. A combination of wet-lab virology, immunology, bioinformatics and evolutionary biology.

If you had the option to advise a younger version of yourself, what would that be?

A rather difficult question and criticism of my younger persona is not intended! However (as general advice that I have always followed - no really!), it's important to be effective and thorough in what you do and publish, use multiple approaches to address a problem (they can't all get stuck at the same time), and learn from others working in your field rather than competing with them. Develop and maintain broader interests in your subject, but at the same time don't be "a jack of all trades, a master of none". And showing my age, it's your family and friends who will care for you and miss you when you've left, not the Infection and immunity Board of Wellcome Trust, or the Nuffield Department of Medicine, so keep a perspective on the things that really matter.

Member Profile: Arif Nur Muhammad Ansori



Name: Arif Nur Muhammad Ansori
Position: Researcher and Assistant Lecturer, Universitas Airlangga, Indonesia
Research focus: Virology, zoonotic diseases, bioinformatics, molecular biology



[Full interview online](#)

What do you love about viruses?

It's very mysterious!

Who is your favourite scientist and why?

Robert Koch and Christiaan Eijkman. They are part of Indonesia history of medical sciences. In the late 18th century, they did various projects in Dutch East Indies (presently Indonesia).

On what topic could you give a 30-min talk without preparation?

All about SARS-CoV-2 and COVID-19.

What is your favourite way to spend a day off?

Doing yoga, photography, and cooking :)

If you could create a new invention, what would it be? Invention which can control the virulent viruses so that it could be developed as a therapeutic agent against various deadly diseases.

What is the most interesting question or challenge in science that is still unanswered?

Is it possible to cross another dimension?

What is the coolest thing about your research?

Dealing with a novel virus like SARS-CoV-2 requires us to constantly adjust our research and public health questions to the rapidly changing state of the field. In addition, it's also important to aware that in the near future, novel viruses will continue to surprise us and prepared to begin new partnerships with scientists around the globe and outside of our discipline. However, working in a novel viruses is very interdisciplinary, which I enjoy a lot since 2020.

What was your most surprising scientific finding?

I was able to unlock the whole-genome sequence of Indonesian SARS-CoV-2 isolates and to construct the pattern of spike glycoprotein as an antigen to induce the dendritic cells.

For which project idea are you looking for a cooperation partner?

Genome editing of virulent viruses to construct vaccines or therapeutic agents.

If you were completely free to choose a scientific topic to work on, which would it be?

Whole-genome sequencing of novel viruses.

What else you would like to share with other EVBC members?

"Fall down seven times, stand up eight" – Japanese Proverb