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Selected Publications by EVBC Members

[📖 All publications on Pubmed](#)

ShapeSorter: a fully probabilistic method for detecting conserved RNA structure features supported by evolutionary and SHAPE-probing evidence without employing the thermodynamic strategy. (Nucleic Acids Res: [10.1093/nar/gkac405](#))

Predicting the evolution of the Lassa virus endemic area and population at risk: introduced into a new suitable region, the spread might remain spatially limited over the first decades. (Nat Commun: [10.1038/s41467-022-33112-3](#))

Deep neural network program based on natural language processing to precisely classify the superkingdom and phylum of DNA sequences taxonomically without the need for a known representative relative from a database. (PNAS: [10.1073/pnas.2122636119](#))

Examination of the viral content of diverse human-pathogenic fungi in a clinical biobank identified numerous viral genomes, including one lineage previously not known to infect fungi. (Microbiol Spectr: [10.1128/spectrum.01610-22](#))

Bidirectional Interactions between Arboviruses and the Bacterial and Viral Microbiota in *Aedes aegypti* and *Culex quinquefasciatus*. (mBio: [10.1128/mbio.01021-22](#))

MetaPhage: an comprehensive, automated reads-to-report pipeline for analyzing, annotating, and classifying bacteriophages in metagenomics sequencing data, that streamlines the use of multiple phage miners and generates an exhaustive report. (mSystems: [10.1128/msystems.00741-22](#))

Arbovirus-vector protein interactomics identifies Loquacious as a co-factor for dengue virus replication in *Aedes* mosquitoes. (PLoS Pathog: [10.1371/journal.ppat.1010329](#))

Computational workflow for predicting viral hosts from complex metagenomic datasets. (Virus Evol: [10.1093/ve/veac087](#))

Varidnaviruses in the Human Gut: complementing the existing knowledge of the human gut virome by exploring a group of viruses that has been virtually overlooked in previous work. (Viruses: [10.3390/v14091842](#))

Machine learning for cell type classification from single nucleus RNA sequencing data. (PLoS One: [10.1371/journal.pone.0275070](#))

PathoLive is a real-time diagnostics pipeline for the detection of pathogens from clinical samples hours before sequencing has finished. (Life: [10.3390/life12091345](#))

Reviews / Commentaries / Editorials

Summary of the Bayesian phylogenetic framework and conceptualization of a variety of methods to improve posterior approximations via Markov chain Monte Carlo sampling. (Philos Trans R Soc Lond B Biol Sci: [10.1098/rstb.2021.0242](#))

The global virome: How much diversity and how many independent origins? (Environ Microbiol: [10.1111/1462-2920.16207](#))

Recent findings about signals able to trigger prophage induction in the gut. (Mol Microbiol: [10.1111/mmi.14983](#))

Aquatic Flaviviruses: recent findings indicate that a range of flaviviruses are also present in aquatic environments, both marine and freshwater. (J Virol: [10.1128/jvi.00439-22](#))

Preprints

VIRify: an integrated detection, annotation and taxonomic classification pipeline using virus-specific protein profile hidden Markov models. (bioRxiv: [10.1101/2022.08.22.504484](#))

PepGM: A probabilistic graphical model for taxonomic inference of viral proteome samples with associated confidence scores. (bioRxiv: [10.1101/2022.09.21.508832](#))

SARS-CoV-2

Evolutionary remodelling of N-terminal domain loops fine-tunes SARS-CoV-2 spike. (EMBO Rep: [10.15252/embr.202154322](#))

Computational pipeline dedicated to reference-free high-throughput comparative analysis of 3D RNA structures to predict the three-dimensional structures of 5'- and 3'-untranslated regions (UTRs) of the SARS-CoV-2 genome. (Int J Mol Sci: [10.3390/ijms23179630](#))

Contributions of adaptation and purifying selection to SARS-CoV-2 evolution. (bioRxiv: [10.1101/2022.08.22.504731](#))

The SARS-CoV-2 Spike Protein Mutation Explorer for science communication and education: interactive 3D molecular models and animations to explain and improve public understanding of SARS-CoV-2 spike protein variants and VOCs. (bioRxiv: [10.1101/2022.09.09.507349](#))

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 in a journal. Tools developed by EVBC members are marked [✳](#).

✳ **BERTax:** Taxonomic Classification of DNA sequences.

✳ **Cov2Tree:** explore a phylogenetic tree with more than a million SARS-Cov-2 sequences.

✳ **CoVariants:** Real-time updates and information about key SARS-CoV-2 variants, plus the scripts that generate this information.

✳ **MetaPhage:** nextflow pipeline for automatic phage discovery.

✳ **PathoLive:** real-time diagnostics pipeline for the detection of pathogens from clinical samples.

✳ **PepGM:** A probabilistic graphical model for taxonomic inference of viral proteome samples with associated confidence scores.

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

Vacancies

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Joint PhD position in two groups headed by Bas E. Dutilh (at Utrecht University and Friedrich Schiller University Jena): **Evolution of Crassvirales in the context of their hosts**. In this project, you will use phylome analysis to elucidate the evolutionary history of bacteriophages in the Crassvirales order and discover potential host links.

Application deadline: **19 October 2022**

PhD position in the Computational Biology Group of Niko Beerenwinkel at ETH Zurich in **analyzing viral sequencing data to improve HIV diagnostics**. The goal is to develop computational methods for viral NGS data that enable DNA-based HIV drug resistance testing, to test the method on a large clinical dataset, and to devise a novel genotypic HIV-1 DNA drug resistance test.


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 .

VEGA, Viral EcoGenomics & Applications

06–07 October 2022 | Berkeley, US and virtual


 S. Roux (organizer)

Virus Genomics and Evolution

09–11 November 2022 | Wellcome Genome Campus, UK and Virtual

Registration deadline (in-person): **11 October 2022**

Registration deadline (virtual): **01 November 2022**

 E. Thomson (Programme Committee), E. Hodcroft, P. Lemey (speakers)

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.

The viruses within: endogenous viral elements as genomic fossils to explore the deep-evolutionary history of viruses

24 October 2022 | 04–05 pm CEST online

Sebastian Lequime, University of Groningen, The Netherlands

Endogenous viral elements are integrations of full or partial viral genomes in their host nuclear genome. EVEs can shed light on the deep evolutionary history of viruses, ancestral host ranges, and ancient viral-host interactions. In this presentation, Sebastian Lequime will use viruses from the Flaviviridae family as an example. Through a comprehensive *in silico* screening of a large dataset of available mammalian genomes, they identified two novel Flaviviridae-like EVE.

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](#).

RNA viruses in metatranscriptomes - dawn of a new age?

12 October 2022 | 04-05 pm CEST online

Uri Neri, Tel Aviv University, Israel

High-throughput RNA sequencing offers broad opportunities to explore the Earth RNA virome. Mining 5,150 diverse metatranscriptomes uncovered >2.5 million RNA virus contigs, which corresponds to a 5-fold increase of the known RNA virus diversity. Uri Neri will speak about gene content analysis, extended RdRP phylogeny, new putative additional virus phyla, classes and orders, identification of CRISPR spacer matches and bacteriolytic proteins.

ViBioM 2023

 [Save the date](#)



We are happy to announce further keynote speakers:



Ana B. Abecasis

Institute for Hygiene and Tropical Medicine, NOVA University of Lisbon, Portugal



Emma Thomson

MRC-University of Glasgow Centre for Virus Research, United Kingdom

EVBC Special Issues

 [Special issue list](#)

Special issues edited by EVBC members:

Drivers of Evolution of Animal RNA Viruses, Volume II in *Viruses*
(edited by **A. Fusaro**)

Deadline: **31 October 2022**

Member Profile: Sebastian Lequime



Name: Sebastian Lequime
Position: tenure-track assistant professor
Research focus: RNA virus ecology and evolution



What do you love about viruses?

How efficient they are given the relatively small size of their genomes (especially RNA viruses) and the very strong evolutionary pressures.

Who is your favourite scientist and why?

Alexandre Yersin, a scientist from the early era of microbiology who lived an amazing life, somewhere between being a medical doctor, a microbiologist, and an adventurer in South-East Asia.

On what topic could you give a 30-minute presentation without any preparation?

Evolution of RNA viruses

What are you currently learning?

Dutch, and how to navigate in academia

If you could create a new invention, what would it be?

An AI that would take care of the most boring parts of my work, so I can focus on the exiting parts!

What is the coolest thing about your research?

Untargeted metagenomics has revealed/reveals how little we know about the diversity of viruses in nature. What is still missing is now to understand the ecology of these viruses; how do they transmit? what influence their distribution? what is their host range?

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

Pay more attention to maths! Mathematics, models, statistics are everywhere, and mastering at least some part of it makes you a more complete scientist.

Is there anything else you would like to share with other EVBC members?

Happy to receive any request for help or collaboration on topics linked to RNA virus evolution and ecology!

Member Profile: Kevin Lamkiewicz



Name: Kevin Lamkiewicz
Position: PostDoc/Junior Group Leader, FSU Jena
Research focus: *in silico* analyses of viral RNA-RNA- and RNA-protein interactions; evolution of RNA secondary structures



[Full interview online](#)

What do you love about viruses?

From a computational point of view, it is their small genomes. You can work with viral sequences on nearly every laptop and make cool science nearly everywhere without having to worry much about RAM or hard drive storage. From a more biological point of view, I love all the different molecular mechanisms and strategies viruses employ during infection. There is always something new that amazes me when I am introduced to new viral species.

Who is your favourite scientist and why?

No idea, honestly. Back when I was a teenager, there might have been an answer to that question. Nowadays, I find it hard to determine a "favourite" scientist just based on their scientific career and results. But I do have a deep respect for all the people that did stuff without actually knowing what is going on. People discovered DNA back in 1868 and worked with it without knowing what it really is or does until roughly 100 years later. How amazing - and somewhat unimaginable - is that?

What are you currently learning?

Many things about RNA-protein interactions in general. And I am trying to learn the Julia language for potential cloud computing use-cases.

If you could create a new invention, what would it be?

Teleportation. Do I have to explain that...?

What is the coolest thing about your research?

This may sound a bit lurid, but the fact that a single-point mutation in the non-coding region of the viral genome can lead to a stop of replication fascinates me very much.

What do people think about you that isn't true?

That I am in love with alignments; and that I am named after the movie "Home alone"

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

I don't think I would be working on another topic. Molecular biology has always fascinated me and with new technologies, such as direct RNA sequencing, there are a lot of new research questions that need attention (RNA modifications, structure landscapes of molecules, interaction dynamics, ...)