

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

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

Selected Publications by EVBC Members

 [EVBC publications website](#)

Genomes of Zaire ebolavirus from resurgence in 2021 form a well-supported phylogenetic cluster with previous outbreak and considerably lower divergence. (*Nature* [10.1038/s41586-021-03901-9](https://doi.org/10.1038/s41586-021-03901-9))

Examination of phylogenetically distinct MERS-CoV lineages for phenotypic characteristics: Lineage 5 viruses replicate more efficiently, lung cell immune responses are lower, and lineage 5 is more resistant to interferon pretreatment. (*Nat Commun* [10.1038/s41467-021-25519-1](https://doi.org/10.1038/s41467-021-25519-1))

New model for estimating viral time scales estimates the date of diversification of hepatitis C virus genotypes to be 423,000 years before present and the most recent common ancestor of sarbecoviruses to be 21,000 years ago. (Now published in *Curr Biol* [10.1016/j.cub.2021.08.020](https://doi.org/10.1016/j.cub.2021.08.020))

Metagenomics is a promising approach to test for multiple pathogens simultaneously in patients with meningitis and encephalitis and detecting geographically relevant infectious CNS diseases. (*mBio* [10.1128/mBio.01143-21](https://doi.org/10.1128/mBio.01143-21))

Up-regulated interferon-stimulated genes encoding antiviral proteins have a distinctive nucleotide composition (highly CpG-suppressed). (*PLoS Biol* [10.1371/journal.pbio.3001352](https://doi.org/10.1371/journal.pbio.3001352))

Methodology for comparing mutational networks in different HIV-1 subtypes to infer the temporal progression of mutations conferring

resistance to the protease inhibitor lopinavir. (*PLoS Comput Biol* [10.1371/journal.pcbi.1008363](https://doi.org/10.1371/journal.pcbi.1008363))

New machine learning approach to explore potential functional associations between prokaryotic Virus Orthologous Groups placed 95.6 % of the previously unannotated pVOGs in a functional context. (*BMC Bioinformatics* [10.1186/s12859-021-04343-w](https://doi.org/10.1186/s12859-021-04343-w))

Reviews / Commentaries / Editorials

Overview of new approaches that elucidate the composition of viral ribonucleoproteins. (*Trends Biochem Sci* [10.1016/j.tibs.2021.08.002](https://doi.org/10.1016/j.tibs.2021.08.002))

Review on genetic data from RSV revealed gaps in whole-genome data to study global RSV evolution, data from low- and middle-income countries and data from global surveillance programs. (*Rev Med Virol* [10.1002/rmv.2284](https://doi.org/10.1002/rmv.2284))


Preprints

Timeline of flavivirus evolution: the family is at least 100 million years old. The main subgroups originate early in animal evolution and broadly co-diverge with animal phyla. (*bioRxiv* [10.1101/2021.09.19.460981](https://doi.org/10.1101/2021.09.19.460981))

The endemic area of Lassa virus may expand well beyond West Africa in the next decades, putting hundreds of million more people at risk of infection. (*bioRxiv* [10.1101/2021.09.22.461380](https://doi.org/10.1101/2021.09.22.461380))

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

Save the date: 30 Mar – 2 Apr 2022 | Munich, Germany

5th Workshop on Virus Dynamics

4 – 6 Oct 2021 | online

Viromics Workshop Webinar Series

13 – 15 Oct 2021 | online

 Evelien Adriaenssens, Manja Marz, Simon Roux, Ben Temperton

viruses *in silico* | EVBC Lectures

 [Register](#)

Viromics: from virus discovery to viral ecology

25. October 2021 | 04–05 pm CEST

online

Dr. Bas Dutilh, Utrecht University, Netherlands

The greatest terra incognita in biology is the world of the viruses. In recent years, tens of thousands of viruses have been discovered using viromics, but for most of them we have no idea of their ecological roles. I will use the story of crAssphage to illustrate the developments in the viromics field.

As feedback from our member survey, we have been asked by several people for profiles of our members (in particular in those pandemic times where it is hard to meet people in person). Please see the [back of the newsletter](#) to get to know our members!

ViBioM 2022

 [Register](#)

Registration for ViBioM 2022 in Valencia is now open for everyone.

We are happy to announce an amazing lineup of keynote speakers: Evelien Adriaenssens | Francois Balloux | Emma Hodcroft | Philippe Lemey | Andrew Rambaut | Daniel Streicker | Matt Sullivan | Friedemann Weber

 [Submit abstract and/or application for PhD Travel Award](#)

EVBC Special Issues

 [Special issue list](#)

Virus Bioinformatics 2022

In parallel to ViBioM 2022, we run a special issue in MDPI Viruses, which is guest edited by the conference organizers. We encourage you to publish your work in this Special Issue and present it at ViBioM 2022. However, this is not an obligation for publication. Deadline: **30 April 2022**

Tools and Resources

 [Virus tools website](#)

MC-CBN performs large-scale inference on conjunctive Bayesian networks.

PoW model calculates the time to the most recent common ancestor of virus species across all Baltimore groups from the maximum clade credibility distance tree.

PVOGs functional associations is an automated and reproducible pipeline for predicting functional associations between pVOGs.

Member Profile: Brett Pickett



Name: Brett Pickett

Position: Assistant Professor, Microbiology and Molecular Biology Department, Brigham Young University, Provo, United States

Research topic: Human transcriptional response to infectious diseases, comparative genomics, RNA-squencing



What do you love about viruses?

Their ability to cause so much damage to a cell with relatively little genetic material.

Who is your favourite scientist and why?

My favorite scientist was Robert Koch because his postulates gave rise to modern infectious disease research.

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

Host transcriptional response to infectious pathogens.

What is your favourite way to spend a day off?

I love spending time with my family.

What is the coolest thing about your research?

We are now able to use RNA-seq data to predict existing drugs that can be repurposed as therapeutics against viral disease. Up to 80 % of our predicted drugs are validated in the literature.

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

We would love to become more proficient at using CRISPRi/a systems to screen host genes in human cells.

What was your biggest achievement / your biggest failure?

One of my biggest achievements was interacting with many talented researchers throughout my training. My biggest failure was not learning how to code earlier in life.

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

Keep moving forward (and buy Amazon stock).

What would you like to share with other EVBC members?

We are DEFINITELY willing to work with potential collaborators!

Member Profile: Alexandros Stamatakis



Name: Alexandros Stamatakis

Position: Full Professor, Scientific Computing Group, Heidelberg Institute for Theoretical Studies, Heidelberg, Germany

Research topic: Computational molecular evolution



What do you love about viruses?

That you can observe evolution in real time.

Who is your favourite scientist and why?

Joe Felsenstein, he introduced the phylogenetic likelihood model.

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

Phylogenetic Inference.

What is your favourite way to spend a day off?

Hiking in the mountains of Crete.

What are you currently learning?

Ancient DNA challenges and archeology.

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

An AI-based system to automatically handle all academic and private administration tasks.

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

Earthquake prediction.

What is the coolest thing about your research?

Developing useful software for biologists that can yield new insights - enabling science.

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

That I spend my whole time in front of a computer.

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

I would like to get more deeply involved in software verification & software quality assessment.

What was your biggest achievement / your biggest failure?

The development of the RAxML software for phylogenetic inference / all the bugs I managed to implement in RAxML.

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

Minoan Culture.

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

Be more relaxed about things.

What would you like to share with other EVBC members?

Apart from my lab in Germany, I am now also co-directing an ancient DNA lab in Crete, Greece, so if there is interest in ancient Virus research let me know.