



Ohio State University - Center Of Microbiome Science

Viromics Workshop Webinar Series

October 13-15, 2021

Foreword

As the microbiome has gained increasing attention across ecosystems ranging from oceans and soils to humans and bioreactors, so too have the viruses that infect these microbiota. Since 2013, we have run in-person training workshops in viral ecology, with viromics taking center stage since 2016. This has introduced hundreds of trainees to the challenges and opportunities that come with studying viruses in complex communities, and gave rise to 'iVirus', our virus ecogenomics platform on NSF's CyVerse Cyberinfrastructure and DOE's KBase. Different to past workshops, this one focuses less on an overview of viral ecogenomics and instead on a deep dive of several timely topics where we will hear from the experts building the tools, and then open the floor for 'discussion' — all held virtually to make as broadly accessible as possible. Enjoy!

- Matt Sullivan

Agenda

(All times are Eastern Standard Time)

October 13 - Session 1: Virus Identification Tools

- 1 pm.** Welcome & introduction - *Matt Sullivan* (Ohio State U., USA)
- 1:30 pm.** VIBRANT - *Karthik Anantharaman* (U. of Wisconsin-Madison, USA)
- 1:50 pm.** Cenote-Taker2 - *Mike Tisza* (NIAID-NIH, USA)
- 2:10 pm.** VirSorter2 - *Simon Roux* (Joint Genome Institute, USA)
- 2:30 - 3:30 pm.** Q&A and panel discussion

October 14 - Session 2: Virus Classification Tools

- 1 pm.** Introduction - *Evelien Adriaenssens* (Quadram Institute, UK)
- 1:30 pm.** VPF-Class - *Joan Carles Pons* (Balearic Islands U., Spain)
- 1:50 pm.** VIRIDIC & VirClust - *Cristina Moraru* (U. of Oldenburg, Germany)
- 2:10 pm.** vConTACT2 - *Ben Bolduc* (Ohio State U., USA)
- 2:30 - 3:30 pm.** Q&A and panel discussion

October 15 - Session 3: Virus Databases

- 1 pm.** Introduction - *Joanne Emerson* (U. of California, Davis, USA)
- 1:15 pm.** IMG/VR - *Simon Roux* (Joint Genome Institute, USA)
- 1:40 pm.** EBI and MGnify - *Rob Finn* (EBI)
- 2:05 pm.** EVBC's coming platform - *Manja Marz* (Friedrich Schiller U. Jena, Germany)
- 2:30 - 3:30 pm.** Q&A and panel discussion

Useful links:

- For technical issues and general questions, please contact Olivier (zablocki.4@osu.edu) or Brittany (fonner.11@osu.edu)
- This agenda can also be found at <https://u.osu.edu/coms/1059-2/>

Suggested Reading

- Adriaenssens, E., & Brister, J. R. (2017). How to name and classify your phage: an informal guide. *Viruses*, 9(4), 70. [LINK](#)
- Turner, D., Kropinski, A. M., & Adriaenssens, E. M. (2021). A roadmap for genome-based phage taxonomy. *Viruses*, 13(3), 506. [LINK](#)
- Kieft, K., Zhou, Z., & Anantharaman, K. (2020). VIBRANT: automated recovery, annotation and curation of microbial viruses, and evaluation of viral community function from genomic sequences. *Microbiome*, 8(1), 1-23. [LINK](#)
- Jang, H. B., Bolduc, B., Zablocki, O., Kuhn, J. H., Roux, S., Adriaenssens, E. M., ... & Sullivan, M. B. (2019). Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. *Nature biotechnology*, 37(6), 632-639. [LINK](#)
- Bolduc, B., Jang, H. B., Doucier, G., You, Z. Q., Roux, S., & Sullivan, M. B. (2017). vConTACT: an iVirus tool to classify double-stranded DNA viruses that infect Archaea and Bacteria. *PeerJ*, 5, e3243. [LINK](#)
- Mitchell, A. L., Almeida, A., Beracochea, M., Boland, M., Burgin, J., Cochrane, G., ... & Finn, R. D. (2020). MGnify: the microbiome analysis resource in 2020. *Nucleic acids research*, 48(D1), D570-D578. [LINK](#)
- Moraru, C., Varsani, A., & Kropinski, A. M. (2020). VIRIDIC—A novel tool to calculate the intergenomic similarities of prokaryote-infecting viruses. *Viruses*, 12(11), 1268. [LINK](#)
- Moraru, C. (2021). VirClust—a tool for hierarchical clustering, core gene detection and annotation of (prokaryotic) viruses. *bioRxiv*. [LINK](#)
- Pons, J. C., Paez-Espino, D., Riera, G., Ivanova, N., Kyrpides, N. C., & Lladrés, M. (2021). VPF-Class: taxonomic assignment and host prediction of uncultivated viruses based on viral protein families. *Bioinformatics*. [LINK](#)
- Roux, S., Enault, F., Hurwitz, B. L., & Sullivan, M. B. (2015). VirSorter: mining viral signal from microbial genomic data. *PeerJ*, 3, e985. [LINK](#)
- Guo, J., Bolduc, B., Zayed, A. A., Varsani, A., Dominguez-Huerta, G., Delmont, T. O., ... & Roux, S. (2021). VirSorter2: a multi-classifier, expert-guided approach to detect diverse DNA and RNA viruses. *Microbiome*, 9(1), 1-13. [LINK](#)
- Roux, S., Páez-Espino, D., Chen, I. M. A., Palaniappan, K., Ratner, A., Chu, K., ... & Kyrpides, N. C. (2021). IMG/VR v3: an integrated ecological and evolutionary framework for interrogating genomes of uncultivated viruses. *Nucleic acids research*, 49(D1), D764-D775. [LINK](#)
- Tisza, M. J., & Buck, C. B. (2021). A catalog of tens of thousands of viruses from human metagenomes reveals hidden associations with chronic diseases. *Proceedings of the National Academy of Sciences*, 118(23). [LINK](#)
- Tisza, M. J., Belford, A. K., Dominguez-Huerta, G., Bolduc, B., & Buck, C. B. (2021). Cenote-Taker 2 democratizes virus discovery and sequence annotation. *Virus evolution*, 7(1), veaa100. [LINK](#)

Speakers



Evelien Adriaenssens, Quadram Institute, UK

I am a molecular and computational microbiologist with a passion for everything viral. I started my research career at the University of Leuven (KU Leuven, Belgium) investigating the use of bacteriophages (viruses of bacteria) as a biological control agent in potato plant production. During my time as a postdoc (University of Pretoria, South Africa & University of Liverpool, UK), I specialised in viromics or viral metagenomics, to elucidate viral community diversity in a range of habitats, including hot and cold deserts, and the freshwater-marine continuum as impacted by wastewater.

I joined the Quadram Institute in January 2019 as a Career Track Group Leader, where my group is investigating the role of viruses, in particular bacteriophages, in the human gut. We investigate how these viruses interact with bacteria, other microorganisms and the human host system. We aim to elucidate the role of viruses in the healthy gut across life. We are also heavily involved in virus taxonomy, creating a genomic framework with which to understand global viral diversity. We further aim to use newly isolated bacteriophages in the biocontrol of pathogenic bacteria in the fight against antimicrobial resistance and for the modulation of the microbiome to improve gut health.

I am the Chair of the Bacterial Viruses Subcommittee of the International Committee on Taxonomy of Viruses (ICTV).

Website: [link](#)

Google scholar: [link](#)

Twitter: @EvelienAdri

Workshop session: Virus classification



Karthik Anantharaman, University of Wisconsin-Madison, USA

I am an Assistant Professor in the Department of Bacteriology at the University of Wisconsin-Madison. My interdisciplinary research program focuses on understanding the cycling of sulfur and nutrients, with a strong emphasis on the microbial and viral processes that transform them in environmental and human systems. Our research uses a combination of omics, experimental, and field-based approaches to investigate the interplay between the microbiome, virome, biogeochemistry, and human health.

Website: [link](#)

Google scholar: [link](#)

Twitter: @KarthikGeomicro

Workshop session: Virus identification



Ben Bolduc, Ohio State University, USA

I am a Research Scientist working in the labs of Drs. Matthew Sullivan and Virginia Rich in the Department of Microbiology at The Ohio State University. I started my path towards virology at Montana State University, where I focused on traditional molecular biology approaches studying viruses in Yellowstone National Park. Towards the end of my PhD training, I decided to make the transition from wet lab to bioinformatics, where I worked on understanding viral community structure of the Yellowstone habitats - combining both lab and informatic approaches. I joined the Sullivan lab in 2015 as a Postdoc, where I focused on developing network-based approaches to solve virus classification problems as well as designing a multidisciplinary and multiscale database. I lead the iVirus efforts to provide viral ecology-focused tools and datasets across the NSF-funded CyVerse and DOE-funded Knowledgebase ("KBbase) cyberinfrastructures, as well as manage the iVirus website and maintain the numerous apps developed by, or integrated by, iVirus.

Website: [link](#)

Google scholar: [link](#)

Workshop session: Virus classification



Joanne Emerson, University of California, Davis, USA

I am an Assistant Professor in the Department of Plant Pathology at UC Davis, and my group uses a variety of omic and bioinformatic approaches to study soil viral communities in natural and managed ecosystems. I have been working in the general field of microbial ecology and metagenomics since 2004, with a focus on viromics since 2008.

Website: [link](#)

Google Scholar: [link](#)

Twitter: @jemersonmicro

Workshop session: Virus databases



Rob Finn, EMBL-EBI, UK

I am a team leader of the Microbiome Informatics Team at EMBL's European Bioinformatics Institute. This team produces MGnify, a major open access platform for the archiving, assembly and analysis platform of microbiome-derived sequence data (metabarcoding, metagenomic, and metatranscriptomic). My team has pioneered the development and provision of new tools and analysis pipelines and the production of comprehensive collections of metagenome assembled genomes (MAGs) to the scientific community at large. My research team has conducted major surveys of the human gut microbiome, covering both prokaryotes and phages. I am co-lead of ELIXIR's Microbiome Community and a member of the Genome Standards Consortium.

Website: [link](#)

Google scholar: [link](#)

Twitter: @robdfinn

Workshop session: Virus databases



Manja Marz, Friedrich Schiller University Jena, Germany

I studied biology and computer science in Edinburgh, Darmstadt and Leipzig where I received my diplomas in Biology 2005 and in Computer Science in 2006. At the University Leipzig in the group of Peter Stadler I conducted my dissertation research on homology-based identification of non-coding RNA genes (2009). After two years as a group leader for “RNA Bioinformatics” at the Philipps-University Marburg I was appointed Junior-Professor for “High Throughput Sequence Analysis” at the Friedrich-Schiller University Jena in 2012. In 2015 I was promoted to the full

Professorship. My research focuses on RNA viruses, RNA structures and non-coding RNAs.

Website: [link](#)

Research Networks: [EVBC](#) and [ITN Viroinf](#) and [NFDI4Microbiota](#)

ResearchGate: [link](#)

Workshop session: Virus databases



Cristina Moraru, University of Oldenburg, Germany

I’m a senior scientist at the Institute for Chemistry and Biology of the Marine Environment (ICBM), in Oldenburg, Germany, where I’m leading my own “marine phages” group. I’ve started my scientific carrier by developing Fluorescence *in situ* Hybridization (FISH) methods to detect genes in microbial cells, as a PhD student in the group of Rudi Amann, at the Max Plank Institute for Marine Microbiology, Bremen. This is how, together with the groups of Matthew Sullivan and Rudi Amann, I have

worked on the development of phageFISH and related methods, for detection of viruses infecting prokaryotic and eukaryotic cells. And, because viruses are really cool, at some point during my postdoc I have moved from wetlab method development to viral ecology, and therefore, also to bioinformatics. In my group at ICBM Oldenburg, we are looking at viruses infecting marine heterotrophic bacteria, as for example those in the *Roseobacter Group*. We isolate many new viruses, which need to be classified to better understand their diversity. To help my students with the classification and genomic analysis, I’m continuously developing bioinformatics tools, as for example VIRIDIC and VirClust, which later on I make available for the larger community use.

Website: <http://moraru-phage-lab.icbm.de/>

Twitter: @CristinaMorar20

Workshop session: Virus classification



Joan Carles Pons, Balearic Islands University, Spain

I am a Mathematician and I received my PhD in Mathematics in 2016 working on problems related to phylogenetic networks. For the past two years, I've served as a tenure-track associate professor in the Department of Mathematics and Computer Science at the University of the Balearic Islands (UIB), Spain. I belong to the Computational Biology and Bioinformatics (BIOCOM) research group. My research interests include graph theory, combinatorics, phylogenetics and, recently, after a research stage at JGI, I'm also working on virus classification and mathematical analysis of metaviromes.

Website: [link](#)

Google Scholar: [link](#)

Twitter: @joancarles_pons

Workshop session: Virus classification



Simon Roux, DOE Joint Genome Institute, USA

At the DOE Joint Genome Institute, I lead the Viral Genomics group where we explore viruses of microbes and their impacts on ecosystems using (mostly) fancy 'omics tools. Our current projects include the study of viral diversity and virus:host interactions in soil and freshwater environments, along with the development of new bioinformatics tools and experimental protocols to probe and characterize uncultivated viruses. We also assist users of the JGI Metagenome Program with their analysis, including identification of viral sequences, functional annotation, taxonomic classification, etc. The long-term goal of my research is to better understand the ecological and evolutionary drivers of virus:host dynamics in natural microbial communities.

Website: [link](#) / [link](#)

Google scholar: [link](#)

Twitter: @simroux_virus

Workshop session: Virus classification, Virus databases



Matt Sullivan, Ohio State University, USA

Matthew Sullivan is a Professor at The Ohio State University in the Departments of Microbiology and Civil, Environmental and Geodetic Engineering, and the founding director of the Center of Microbiome Science. His research aims to quantitatively explore the roles of microbial viruses in global ocean biogeochemical cycling, thawing permafrost, and the human gut. As a Gordon and Betty Moore Foundation Investigator, he has helped lay the foundation for modern, quantitative viral ecology. Specifically, he has helped develop a quantitative viral metagenomic sample-to-sequence pipeline and community-available informatics platforms to analyze such data, significantly expanded our understanding of the global virosphere through illuminating ‘viral dark matter’, and pioneered numerous experimental and informatic approaches to link and explore virus-host interactions. Complementarily, he has recently and extensively developed new environmental model phage-host systems for hypothesis-generating and testing to better elucidate mechanisms of phage-host interactions.

Website: [link](#) / [link](#)

Google scholar: [link](#)

Twitter: @Lab_Sullivan

Workshop session: Welcome and introduction



Mike Tisza, NIAID-NIH, USA

I received my B.A in biology and English literature from Augustana College in 2012 and my PhD in molecular biology and genomics from Johns Hopkins University in 2020. During my PhD I worked as a Johns Hopkins-NIH partnership program fellow, conducting my dissertation research on virus discovery at the National Cancer Institute under Dr. Chris Buck. Since 2020, I’ve been working as a postdoc at the National Institute of Allergy and Infectious diseases with Dr. John Dekker. I’m interested in microbial genomes, mobile genetic elements, epigenetics of microbes, genetic “dark matter”, and understanding how accessory genes regulate microbial physiology and phenotypes. I currently live with my family in Washington, DC.

Website: [link](#)

Google scholar: [link](#)

Twitter: @MikeTisza

Workshop session: Virus discovery

Organizing Committee

Evelien Adriaenssens, Quadram Institute, UK
Ben Bolduc, Ohio State University, USA
Joanne Emerson, University of California, Davis, USA
Manja Marz, Friedrich Schiller University Jena, Germany
Simon Roux, DOE Joint Genome Institute, USA
Matt Sullivan, Ohio State University, USA
Ben Temperton, University of Exeter, UK
Arvind Varsani, Arizona State University, USA

Coordination & Logistics

Olivier Zablocki, Ohio State University, USA
Brittany Fonner, Ohio State University, USA

Sponsors



What's next?

Please look forward to our upcoming early career researcher viromics webinar series to launch later this fall, and to the next in-person Viromics workshop in May 2022.