

Simon Roux

DOE Joint Genome Institute, Lawrence Berkeley National Laboratory

EDUCATION

- PhD: Bioinformatics, Ecology and Evolutionary Biology 2010 - 2013
Viral diversity, ecology, and evolution from community to genotype scale
Laboratoire Micro-organismes : Génome and Environment, Université Blaise Pascal,
CNRS UMR 6023, Clermont-Ferrand, France
- M.S.: Data Analysis and Modeling applied to Life Sciences 2008 - 2010
Université Blaise Pascal, Clermont-Ferrand, France
- B.S.: Biology 2005 - 2008
Université Blaise Pascal, Clermont-Ferrand, France

PROFESSIONAL APPOINTMENTS

- Research Scientist – DOE Joint Genome Institute 2017 - present
Virus discovery, viral ecogenomics, and virus–host interactions.
Lawrence Berkeley National Laboratory, Berkeley, CA
- Postdoctoral Researcher – Tucson Marine Phage Lab (a.k.a. Sullivan's Lab) 2013 - 2017
Global viral diversity and virus–host dynamics.
University of Arizona, Tucson, AZ (2013-2015)
Ohio State University, Columbus, OH (2015-2017)

SELECTED PUBLICATIONS

- Roux S**, Krupovic M, ... [8 authors] ..., Eloë-Fadrosh EA. Cryptic inoviruses revealed as pervasive in bacteria and archaea across Earth's biomes. *Nature Microbiology* 2019
- Roux S**. A Viral Ecogenomics Framework To Uncover the Secrets of Nature's "Microbe Whisperers". *mSystems* 4 (3). 2019
- Roux S**, Trubl G, Goudeau D, ... [11 authors] ..., Eloë-Fadrosh EA. Optimizing de novo genome assembly from PCR-amplified metagenomes. *PeerJ* 7:e6902 2019
- Jang HB, Bolduc B, Zablocki O, Kuhn JH, **Roux S**, ... [6 authors] ..., Sullivan MB. Taxonomic assignment of uncultivated prokaryotic virus genomes is enabled by gene-sharing networks. *Nature Biotechnology* 2019
- Gregory A*, Zayed AA*, Conceição-Neto N, ... [24 authors] ..., **Roux S**, Sunagawa S, Wincker P, Sullivan MB. Marine viral macro- and micro-diversity from pole to pole. *Cell* 177 (5) 2019
- Mizuno CM, Guyomar C, **Roux S**, ... [5 authors] ..., Krupovic M. Numerous cultivated and uncultivated viruses encode ribosomal proteins. *Nature Communications* 10 (1) 2019
- Roux S**, ... [58 authors] ..., Eloë-Fadrosh EA. Minimum Information about Uncultivated Virus Genomes (MIUViG): a community consensus on standards and best practices for describing genome sequences from uncultivated viruses. *Nature Biotechnology* 37 2019

- Roux S**, Brum JR. A viral reckoning: Viruses emerge as essential manipulators of global ecosystems. *Environmental Microbiology Reports* 11 (1) 2018
- Daly RA, **Roux S**, ... [11 authors] ..., Wilkins M. Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing, *Nature Microbiology* 3 2018
- Solden LM, **Roux S**, ... [13 authors] ..., Wrighton KC. Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. *Nature Microbiology* 3 (11) 2018
- Martins PD, Danczak RE, **Roux S**, ... [4 authors] ..., Wilkins MJ. Viral and metabolic controls on high rates of microbial sulfur and carbon cycling in wetland ecosystems. *Microbiome* 6 (1) 2018
- Borton MA, Hoyt DW, **Roux S**, ... [14 authors] ..., Wrighton KC. In vitro interactions scaled to in situ conditions: microorganisms predict field scale biogeochemistry in hydraulically fractured shale. *PNAS* 115 (28) 2018
- Tschitschko B, Erdmann S, DeMaere MZ, **Roux S**, ... [6 authors] ..., Cavicchioli R. Genomic variation and biogeography of Antarctic haloarchaea. *Microbiome*. 6 (1) 2018
- Emerson JB, **Roux S**, ... [16 authors] ..., Sullivan MB. Host-linked soil viral ecology along a permafrost thaw gradient. *Nature Microbiology*. 3 (8) 2018
- Eichorst S, Trojan D, **Roux S**, Herbold C, Rattei T, Woebken D. Genomic insights into the Acidobacteria reveal strategies for their success in terrestrial environments. *Environmental Microbiology*. 20 (3), 1041-1063 2018
- Roux S**, Chan LK, Egan R, Malmstrom R, McMahon KD, Sullivan MB. Ecogenomics of virophages and their giant virus hosts assessed through time series metagenomics. *Nature Communications*. 8 (1), 858 2017
- Roux S**, Emerson JB, Eloie-Fadrosch EA, Sullivan MB. Benchmarking viromics: an in silico evaluation of metagenome-enabled estimates of viral community composition and diversity. *PeerJ*. 5, e3817 2017
- Vik DR, **Roux S**, Brum JR, Bolduc B, Emerson JB, Padilla CC, Stewart FJ, Sullivan MB. Putative archaeal viruses from the mesopelagic ocean. *PeerJ*, 5, e3428 2017
- Enault F, Briet A, Bouteille L, **Roux S**, Sullivan MB, Petit MA. Phages rarely encode antibiotic resistance genes: a cautionary tale for virome analyses. *The ISME journal*. 11 (1), 237-47 2017
- Roux S**, ... [7 authors] ..., Sullivan MB. Towards quantitative viromics for both double-stranded and single-stranded DNA viruses. *PeerJ*. 4, e2777 2016
- Roux S**, ... [23 authors] ..., Sullivan MB. Ecogenomics and biogeochemical impacts of globally abundant ocean viruses. *Nature*. 537:689-93 2016
- Brum JR*, Ignacio-Espinoza J-C*, Kim EH*, Trubl G, Jones RM, **Roux S**, VerBerkmoes NC, Rich VI, Sullivan MB. Illuminating structural proteins in viral metagenomic 'dark matter'. *PNAS*. 113(9), 2436-2441. [*co-first authors, listed alphabetically] 2016
- Guidi L*, Chaffron S*, Bittner L*, Eveillard D*, Larhlimi L, **Roux S**, ... [33 authors] ..., Gorsky G. Plankton networks driving carbon export in the oligotrophic ocean. *Nature*. 532, 465-70. [*co-first authors] 2016
- Roux S**, Enault F, Ravet V, Colombet J, Bettarel Y, Auguet JC, Bouvier T, Soizick L, Vellet A, Prangishvili D, Forterre P, Debroas D, Sime-Ngando T. Analysis of metagenomic data reveals common features of halophilic viral communities across continents. *Environmental Microbiology*. 18 (3), 889-903. 2016

- Roux S**, Hallam SJ, Woyke T, Sullivan MB. Viral dark matter and virus–host interactions resolved from publicly available microbial genomes. *eLIFE*. 4, e08490 2015
- Brum JR*, Ignacio-Espinoza J-C*, **Roux S***, ... [28 authors] ..., Sullivan MB. Patterns and ecological drivers of ocean viral communities. *Science*. 348 (6237), 1261498 [***co-first authors, listed alphabetically**] 2015
- Lima-Mendez G*, Faust K*, Henry N*, ... [5 authors] ..., **Roux S**, ... [36 authors] ..., Sullivan MB, Bowler C, Karsenti E, de Vargas C, Raes J. Top-down determinants of community structure in the global plankton interactome. *Science*. 348 (6237), 1262073 [***co-first authors**] 2015
- Villar E, Audic S, ... [23 authors] ... **Roux S**, ... [19 authors] ... Sullivan MB, Sunagawa S, Wincker P, Zingone A, Karsenti E, Not F, Hingamp P, Iudicone D. Environmental characteristics of Agulhas rings affect inter-ocean plankton transport. *Science*. 348 (6237), 1261447 2015
- Roux S**, Enault F, Hurwitz BL, and Sullivan MB. VirSorter: mining viral signal from microbial genomic data. *PeerJ*. 3, e985 2015
- Roux S**, Enault F, Ravet V, Pereira O, and Sullivan MB. Genomic characteristics and environmental distributions of the uncultivated Far-T4 phages. *Frontiers in microbiology*. 6, 199 2015
- Roux S**, Hawley AK, Torres Beltran M, Scofield M, Schwientek P, Stepanauskas R, Woyke T, Hallam S, Sullivan MB. Cultivation-independent exploration of SUP05 virus-host interactions in a model Oxygen Minimum Zone. *eLIFE*. 3, e03125. 2014
- Roux S**, Tournayre J, Mahul A, Debroas D and Enault F. Metavir 2: Comparison of viral metagenomes and analysis of assembled datasets. *BMC Bioinformatics*. 15 (76) 2014
- Roux S**, Krupovic M, Debroas D, Forterre P and Enault F. Assessment of viral community functional potential from viral metagenomes may be hampered by contamination with cellular sequences. *Open Biology*. 3 (130160) 2013
- Roux S**, Enault F, Bronner G, Vaulot D, Forterre P and Krupovic M. Chimeric viruses blur the border between the major groups of eukaryotic single-stranded DNA viruses. *Nature Communications*. 4 (2700) 2013
- Roux S**, Enault F, Robin A, Ravet V, Personnic S, Theil S, Colombet J, Sime-Ngando T, Debroas D. Assessing the Diversity and Specificity of Two Freshwater Viral Communities through Metagenomics. *PLoS ONE*. 7 (3), e33641 2012
- Roux S**, Faubladiere M, Mahul A, Paulhe N, Bernard A, Debroas D, Enault F. Metavir: a web server dedicated to virome analysis. *Bioinformatics* 27 (21), 3074-5 2011

Manuscripts in revision

GRANTS & FELLOWSHIPS

Grants

- LBNL Early Career (\$157,563), “High-throughput resolution of virus-host linkages”, 2018 - 2019
- NSF BioOce Grant (\$851,485), “Ecological impacts and drivers of double-stranded DNA viral communities in the global oceans”, PI Matthew B Sullivan, co-wrote the grant application as “key personnel”. 2015 - 2018
- DGA (French Defense Procurement Agency) PhD grant (\$56,348), “Development of 2010 - 2013

bioinformatics tools for viral metagenomics analysis”.

Award

Best oral presentation (SVSAE, Clermont-Ferrand, France), “Redefining a viral family with complete genomes assembled from viral metagenomes: the case of *Microviridae*”. 2012

CONFERENCE AND WORKSHOP PRESENTATIONS

Invited talk

Roux S. Viral ecogenomics: exploring viral diversity and virus-host interactions from metagenomes. *MAC-EPID Symposium, U Michigan, Ann Arbor, MI* 2019

Roux S. Viral ecogenomics: exploring viral diversity and virus-host interactions from metagenomes. *NASA Workshops Without Walls: Astrovirology, Online workshop* 2019

Roux S. Establishing standards and best practices for describing genome sequences of uncultivated viruses (MIUViGs). *GSC20, San Diego, CA* 2018

Roux S. Viruses of microbes and their impacts on microbial metabolic networks. 5th *International Symposium on Microbial Sulfur Metabolism (ISMSM-5), Vienna, Austria* 2018

Roux S. Exploring viral dark matter through time-series metagenomes: the case of freshwater virophages. *Ringberg Symposium on Giant Virus Biology, Germany* 2017

Roux S. Exploration, classification, and characterization of environmental viral genomes. *FASEB Virus structure and assembly, Steamboat Springs, CO* 2016

Roux S. Ecogenomics and biogeochemical impacts of globally abundant ocean viruses. *ASLO 2016 Summer meeting, Santa Fe, NM* 2016

Roux S. Exploring viral diversity through (meta-) genomics. “*Computational Life Sciences*” seminars, *University of Vienna, Austria* 2015

Roux S. Promises and Pitfalls of Viromics analyses, hands-on with Metavir. *A viromics workshop: Tools and Trick to see the 'Virus' in diverse sequence datasets, ASM 2014, Boston, MA* 2014

Roux S, Debroas D, Mahul A, Enault F. Metavir, a web server dedicated to virome analysis : presentation & hands-on training. *Environmental Virology Workshop, Tucson, AZ* 2013

Selected abstracts (international conferences)

Roux S. Cryptic Inoviruses are Pervasive in Bacteria and Archaea across Earth's Biomes. *Multi 'omics for microbiomes, PNNL, Richland, WA* 2019

Roux S. Cryptic Inoviruses are Pervasive in Bacteria and Archaea across Earth's Biomes. *ASM Microbe 2019, San Francisco, CA* 2019

Roux S. The broad diversity, host range, and functional repertoire of the cryptic inoviruses. *Viral EcoGenomics and Applications 2018.* 2018

Roux S. Exploring viral dark matter through time-series metagenomes: the case of freshwater virophages. *NeLLi 2017: From New Lineages to New Functions* 2017

Roux S. Ecogenomics and biogeochemical impacts of globally abundant ocean viruses. *ISME 2016* 2016

Roux S, Brum JR, Ignacio-Espinoza JC, Enault F, Hallam SJ, Woyke T, Sullivan MB. How to swim and not drown in the ocean of viral unknowns. *ASM General Meeting, New Orleans (Poster)* 2015

Roux S , Hurwitz B, Chourasiya D, Sullivan MB. Promises and Pitfall of Virome Bioinformatics Analyses. <i>Viruses of Microbes III</i> , Zurich, Switzerland	2014
Roux S , Hawley AK, Torres Beltran M, Scofield M, Schwientek P, Stepanauskas R, Woyke T, Hallam S, Sullivan MB. Cultivation-independent exploration of SUP05 virus-host interactions in a model Oxygen Minimum Zone. <i>Viruses of Microbes III</i> , Zurich, Switzerland (Poster)	2014
Roux S. , Enault F., Ravet V., Mahul A., Sime-Ngando T., Debroas D. Assessment of viral communities richness, diversity, and biogeography through viromes comparative analyses. <i>Viruses of microbes</i> . Bruxelles, Belgique. (Poster)	2012
Roux S , Enault F, Robin A, Ravet V, Personnic S, Theil S, Colombet J, Sime-Ngando T, Debroas D. Metagenomic analysis of the viral communities from temperate freshwater lakes. <i>Viruses of the environment</i> . Heidelberg, Germany	2011

STUDENTS MENTORED (as primary, day-to-day supervisor)

Gareth Trubl, 5 th year graduate student. “Pioneering soil viromics to elucidate virus impacts on soil ecosystem services” (SCGSR award)	2018
Myriam Labbe, 2 nd year graduate student. “Diversity and dynamics of viruses in freshwater systems” (FRQNT and Sentinelle Nord grants, Canada)	2018
Maureen Berg, 1 st year postdoctoral student. “High-throughput resolution of virus-host linkages”	2018-2020
Collin Nisler, rotation graduate student, Biophysics department, OSU “Identifying structural genes from newly discovered abundant ocean viruses”	2016
Guilhem Doulcier, senior master student from ENS Paris “Automatic taxonomic affiliation via <i>Guilt by contig association</i> in viral metagenomic data”.	2014
Hugo Doré, senior master student from ENS Lyon “Infection of <i>Cellulophaga baltica</i> 38 by phage ϕ 38:1 – a multi -omics approach”	2014
Jeremy Tournayre, master student from Université Blaise Pascal “Analysis of viral communities from ancient lake sediments”.	2013

TEACHING EXPERIENCE

Workshop organization and teaching

MGM workshop @ JGI	2016 - 2019
Viromics workshop @ The Ohio State University	2017
Teaching assistant for undergraduate and graduate bioinformatics classes	2010 - 2013

SERVICE TO THE PROFESSION

Conference organization: Viral EcoGenomics and Applications (VEGA) symposium. Hosted by the DOE Joint Genome Institute, Hilton San Francisco	2018
Manuscript review: The ISME Journal; Environmental Microbiology; PLoS One; Frontiers In Microbiology; Applied and Environmental Microbiology; Fungal Biology; Aquatic Microbial Ecology; Genomics, Proteomics & Bioinformatics; Infection, Genetics and Evolution; FEMS Microbiology Reviews; Scientific Reports; BMC Genomics; Nucleic Acids Research.	2013 - present
Grant proposal review: UK Biotechnology and Biological Sciences Research Council.	2013 - present

Community-available tool (design and maintenance): Metavir, web server dedicated to virome analysis (<http://metavir-meb.univ-bpclermont.fr>). VirSorter, high-throughput for the automatic detection of viral signal in sequencing datasets (<https://github.com/simroux/VirSorter>). Lead of a community-wide initiative to establish standards for the analysis and report of genomes from uncultivated viruses, in the framework of the Genomic Standards Consortium (<http://gensc.org>). 2011 - present

SELECTED MEDIA COVERAGE

<i>Learning to see</i> , Chris Edwards, Communications of the ACM	2018
<i>The virome hunters</i> , Charles Schmidt, Nature Biotechnology	2018
<i>Machine learning spots treasure trove of elusive viruses</i> , Amy Maxmen, Nature News	2018
<i>A sea of viruses</i> , Noah Baker, Nature Podcast	2016
<i>What are viruses up to?</i> , Liz Kalaugher, Environmental Research Web	2016
<i>Scientists Unearth a Trove of New Bacteria-Killing Viruses</i> , Shara Tonn, Wired	2015
<i>Scientists Sample the Ocean and Find Tiny Additions to the Tree of Life</i> , Karen Weintraub, The New York Times	2015