

Bioinformatics Center

– Chemical Life Science –



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*New Research Field
Development Project

Students

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Guest Research Associate

DEMORY, David (Ph. D.) CNRS – BIOM Laboratory, France, 18 February 2024–6 March 2024

Scope of Research

We are interested in understanding the functioning and evolution of biological systems at varying scales from tiny microbes up to the Earth's environment, by leveraging rapidly accumulating big data in life science and bioinformatics approaches. We currently focus on 1) the evolution of viruses and their links to the origin of life, 2) microbial ecology in different ecosystems, and 3) the development of bioinformatics methods and biological knowledge resources for biomedical and industrial applications. To fuel these research activities, we take part in environmental sampling campaigns such as *Tara Oceans*. Our resources and developed tools are accessible through GenomeNet (www.genome.jp) to scientific communities and the public.



KEYWORDS

GenomeNet Bioinformatics Environmental Genomics Virology Molecular Evolution

Recent Selected Publications

Zhang, L.; Meng, L.; Fang, Y.; Ogata, H.; Okazaki, Y., Spatiotemporal Dynamics of Giant Viruses within a Deep Freshwater Lake Reveal a Distinct Dark-Water Community, *ISME J.*, **18** (1), wrae182 (2024).
Wu, J.; Meng, L.; Gaïa, M.; Hikida, H.; Okazaki, Y.; Ogata, H., Gene Transfer Among Viruses Substantially Contributes to Gene Gain of Giant Viruses, *Mol. Biol. Evol.*, **41**, msae161 (2024).
Kijima, S.; Hikida, H.; Delmont, T. O.; Gaïa, M.; Ogata, H., Complex Genomes of Early Nucleocytoviruses Revealed by Ancient Origins of Viral Aminoacyl-tRNA Synthetases, *Mol. Biol. Evol.*, **41**, msae149 (2024).
Zhao, H.; Meng, L.; Hikida, H.; Ogata, H., Eukaryotic Genomic Data Uncover an Extensive Host Range of Mirusviruses, *Curr. Biol.*, **34**, 2633-2643.e3 (2024).
Ban, H.; Endo, H.; The EukBank Team; Kuwata, A.; Ogata, H., Global Distribution and Diversity of Marine Parmales, *Microbes Environ.*, **39**, ME23093 (2024).
Nishimura, Y.; Yamada, K.; Okazaki, Y.; Ogata, H., DiGAlign: Versatile and Interactive Visualization of Sequence Alignment for Comparative Genomics. *Microbes Environ.*, **39**, ME23061 (2024).