

## Department of Integrative Genomics

Professor: Hiroyuki Ogata,

Assistant Professor: Romain Blanc-Mathieu, Hisashi Endo



### Research Projects:

Our laboratory aims to understand the diversity and functioning of complex living systems based on large scale life science data towards application in biomedical sciences and environmental conservation. We develop new bioinformatics methods allowing integrated analyses of molecular data such as drug structure, metabolites, and genomic information and higher level knowledge about cells, organisms, populations and environments. Current research projects involve viral and microbial genomics, prediction of drug-microbiome interactions, and investigation of the functional link between microorganisms and the environmental changes.

#### 1. Genomics of viruses

Viruses are generally considered as small biological objects with only a handful of genes sufficient for their rapid replication. However, relatively large viruses such as herpesviruses and poxviruses possess a few hundreds genes. Furthermore, recent studies have revealed the existence of much larger viruses encoding more than 300 up to 2,500 genes. Such giant viruses, comparable to cells in their dimension, show a huge genomic diversity. Including these giant viruses, viruses possess various mechanisms to evade host defense systems and to reprogram intracellular machinery of their hosts for their replication. Viruses are also considered to contribute to the evolution of their hosts through horizontal gene transfer and the host-parasite arms race. However, our knowledge on viruses is limited compared to the knowledge on cellular organisms. We are interested in revealing functions of their genomes and the roles of viruses in various ecosystems through comparative genomics. We also develop new bioinformatics methods helping such comparative genomics.

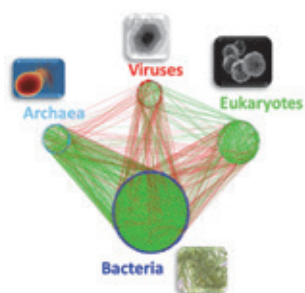
#### 2. Interactions between microbial communities and their environments

Bacteria and unicellular eukaryotes play important roles in various environments. We study microorganisms (from viruses, bacteria, unicellular eukaryotes

to zooplankton) in animal gut and marine ecosystems in terms of their community structure and functioning. Our focus is on the characterization of their diversity and the interactions among them as well as the relationships between the dynamics of microbial communities under varying environmental conditions. Our research interests include the identification of enzymes and secondary metabolites with new pharmacological activity from large scale genetic data.

#### 3. Integration of chemical, genomics, and biomedical knowledge for biomedical sciences and environmental preservation

To help the research communities in genomics and biomedical sciences, we develop a suite of bioinformatics tools and various databases through an integrated web environment named GenomeNet (<http://www.genome.jp/>). GenomeNet integrates major molecular biology databases such as the KEGG database (<http://www.kegg.jp/>) developed in Kyoto University, as well as other databases of genes, proteins, enzyme reactions, metabolic compounds, drugs, and drug side effects. Currently, we put much effort in integrating metagenomic data generated at a population level (e.g. Human microbiomes) or at a global scale (e.g. *Tara* Oceans expedition data). We also started an integrated database project for proteomics data from various species including human. Certain pathogens evade the host immune system by altering the surface proteins ("antigenic variation"), but its mechanism is still unclear. In this regard, we collect and organize the information of antigenic variations and relevant gene families to uncover the mechanism and to utilize it in clinical practice (varDB, <http://www.vardb.org/>). These resources are freely available through GenomeNet to the communities. We also develop various bioinformatics and statistical methods for medical and pharmacological sciences such as prediction methods for the side effects of drugs.



Prediction of species interaction networks



Prediction of drug-drug interactions

#### Recent publications

- Yoshikawa G., Blanc-Mathieu R., Song C., Kayama Y., Mochizuki T., Murata K., Ogata H., Takemura M.; Medusavirus, a novel large DNA virus discovered from hot spring water. *J. Virol.*, **93**, e02130-18 (2019).
- Li Y., Hingamp P., Watai H., Endo H., Yoshida T., Ogata H.; Degenerate PCR primers to reveal the diversity of giant viruses in coastal waters. *Viruses*, **10**, 496 (2018).
- Endo H., Ogata H., Suzuki K.; Contrasting biogeography and diversity patterns between diatoms and haptophytes in the central Pacific Ocean. *Sci. Rep.*, **8**, 10916 (2018).
- Yoshida T., Nishimura Y., Watai H., Haruki N., Morimoto D., Kaneko H., Honda T., Yamamoto K., Hingamp P., Sako Y., Goto S., and Ogata H.; Locality and diel cycling of viral production revealed by a 24 h time course cross-omics analysis in a coastal region of Japan. *ISME J.*, **12**, 1287-1295 (2018).