

Bioinformatics Seminar Series

Hosted by ICR-KUBIC and NPO Bioinformatics Japan

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14:00-15:00 at CB207

Contact: Hiroyuki Ogata (ogata@kuicr.kyoto-u.ac.jp)

The ocean microbiome as a treasure trove for novel taxa, enzymes and bioactive compounds

Shinichi Sunagawa

Associate Professor, Microbiome Research, Department of Biology (D-BIOL), ETH Zürich

Ocean microbes are phylogenetically and metabolically diverse. Exploring this diversity for yet unknown taxa and biochemistry has been greatly accelerated by cultivation-independent DNA sequencing of microbial communities in bulk (metagenomics) or as single cells. However, the requirement for genome-resolved information has limited (i) the identification and host assignment of biosynthetic gene clusters (BGCs) that encode enzymes and the synthesis of chemical compounds, including biotechnological and therapeutic leads. Here, we analyzed metagenomic data from decades of ocean sampling efforts to reconstruct 26,293 genomes that uncovered 2,700 previously unknown species and integrated these data with publicly available reference and single-cell genomes to compile the Ocean Microbiomics Database. Mining this database for BGCs revealed *Ca. Eudoremicrobiaceae*, a new family of bacteria with an unparalleled biosynthetic diversity in the open ocean. By biochemically characterizing two BGCs, we found an unusual bioactive chemical structure and an unexpected enzymatic reaction. These examples demonstrate the current limitations of computational predictions by sequence homology alone. This work highlights the promise of environmental genomics for discovering new microbial products and advancing current models of planetary-scale microbial distributions.