OIST OKINAWA INSTITUTE OF SCIENCE AND TECHNOLOGY

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OSAKA UNIVERSITY

A Recipe for Scientific Synergy — Series 3 —

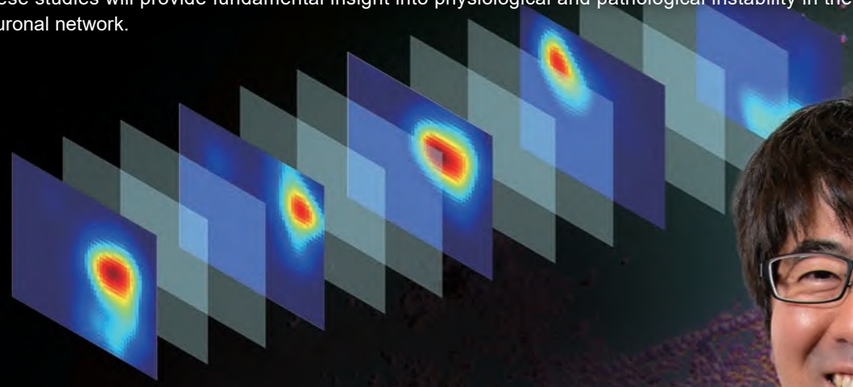
2022 Thu. Oct. 20th 14:00-15:30 Zoom

Meeting ID: 973 9704 6616
Passcode: 240236

Moderator
Dean of Research
Professor, Genomics and Regulatory Systems Unit
Dr. Nicholas Luscombe

Dynamic Nature of Memory Representation and the Hippocampal Network

Memories are encoded through long-lasting changes in the network of the brain. These memory traces can interfere with each other and therefore lead to instability of the representations. Indeed, a previous study discovered that instability is preferentially embedded within spatial maps in memory engram cells in the hippocampus even though their activity is still functionally linked to memory-relevant behaviors (Tanaka et al., 2018). Notably, higher instability of place cells is often observed in aberrant network states caused by various factors, including aging, stress, or epileptic seizure, which cause memory impairments. These studies highlight two distinct types of instability leading to the opposite outcomes of hippocampal memory. In my talk, I will introduce our unpublished studies aiming at 1) elucidation of neuronal underpinning that survives extreme plasticity yet supports memory and 2) development of a novel approach to reset the aberrant network state. These studies will provide fundamental insight into physiological and pathological instability in the neuronal network.



Assistant Professor
Memory Research Unit,
Okinawa Institute of Science and Technology (OIST)

Dr. Kazumasa Tanaka

Kazumasa Z. Tanaka received Ph.D. from the University of California, Davis, in 2015. After working as a Special Post-Doctoral Researcher and SPD JSPS research fellow at McHugh lab in RIKEN Center for Brain Science, he became an assistant professor leading Memory Research Unit at OIST.

Interpreting population genomics data at single variant resolution

Although genome-wide association studies (GWAS) have identified large numbers of regions in the genome associated with complex traits, elucidating truly causal variant(s) at single variant resolution remains challenging, since each “region” typically contains thousands of variants in linkage disequilibrium (LD).
In this talk, I will introduce three approaches to prioritize causal variants, enabling characterization of their functions in the context of human biology:
i. Utilizing the genome Aggregation Database (gnomAD) for variant interpretation from population frequency data.
ii. Estimating the probability of a variant being causal to a phenotype under sparse model (statistical fine-mapping).
iii. Functionally-informed fine-mapping utilizing deep-neural network based epigenetic features.
Finally, I will discuss recent application of statistical fine-mapping on multi-omics data from COVID-19 infected individuals including 359 severe and 106 non-severe cases, highlighting the presence of COVID-19 severity-interaction expression quantitative loci (ieQTLs).

Associate Professor
Department of Statistical Genetics
Osaka University Graduate School of Medicine

Dr. Qingbo S. Wang

Qingbo “Seiha” Wang completed his undergraduate study majoring in bioinformatics at University of Tokyo in 2016. He then started Ph.D. study at the division of biomedical informatics at Harvard University. Working in Daniel MacArthur lab, he contributed to development of the world’ s largest human genome Aggregation Database (gnomAD). He also demonstrated a novel framework to interpret human non-coding genetic variation in Hilary Finucane lab. After completing his Ph.D. in May 2021, he joined Osaka University Graduate School of Medicine as an Associate Professor in Yukinori Okada lab, where he continues his journey to understand human genetic variation.