Keynote Talk

Keynote Talk 1

23rd Oct. 10:30-11:30 Large Theatre

Prediction of cancer-associated metabolites and their application for drug targeting system

Hyun Uk Kim

Department of Chemical and Biomolecular Engineering and
Graduate School of Engineering Biology,
Korea Advanced Institute of Science and Technology (KAIST)

The utilization of bio big data through computational models can help predict biomarkers and drug targets for a range of diseases. In the case of cancer, a substantial amount of bio big data has been deposited, including patient-specific omics data (e.g., RNA-seq data) and medical data (e.g., survival data). In this talk, I will elaborate a computational workflow where transcriptome and mutation data from cancer patients, along with genome-scale metabolic models (GEMs), have been used to predict potential biomarkers known as oncometabolites. Oncometabolites exhibit pro-oncogenic functions when they accumulate abnormally in cancer cells, and they are generated upon mutations in a metabolic gene. GEM is a computational model that allows predicting entire metabolic reaction fluxes. I will also showcase the application of this computational workflow to predict drug targets effective for high-risk bladder cancer patients, showing poor prognosis. The predicted drug targets were validated using in vitro and in vivo studies. Ongoing efforts in generating and applying meaningful bio big data, alongside the proper use of computational models, will revolutionize our approaches to addressing medical problems.

Keynote Talk 2

24th Oct. 9:30-10:30 Large Theatre

How far are we from designing an antibody therapeutic on a computer?

Charlotte Deane MBE

Professor of Structural Bioinformatics, University of Oxford

Antibodies play a key role in the immune system and our response to vaccines, and have shown great promise as biotherapeutics. The development of new biotherapeutics typically takes many years and requires over $1bn in investment. Computational methods and in particular, machine learning, have shown great promise for increasing the speed and reducing the cost of biotherapeutic development. In this talk I will describe some of the novel computational tools and databases we are pioneering in biotherapeutics from accurate rapid structure prediction to the prediction of their affinity and binding, looking at both their promise and limitations.

Keynote Talk 3

24th Oct. 13:45-14:45 Large Theatre

Evolution of SARS-CoV-2 and beyond

Kei Sato

Professor, Division of Systems Virology, Institute of Medical Science,
The University of Tokyo, Japan.
Representative Director, G2P-Japan Association

SARS-CoV-2, the causative agent of COVID-19, emerged at the end of 2019. During its global spread over the past 3 years, SARS-CoV-2 has been highly diversified, and these SARS-CoV-2 variants have been considered to be the potential threats to the human society. In order to elucidate the virological characteristics of newly emerging SARS-CoV-2 variants in real-time, I launched a consortium called "The Genotype to Phenotype Japan (G2P-Japan)" in January 2021. With the colleagues who joined the G2P-Japan consortium, we have revealed the virological characteristics of SARS-CoV-2 variants. In May 2023, WHO declared the end of the Public Health Emergency of International Concern (PHEIC) for COVID-19. However, "the next pandemic" will come in the future, and we need to gather our wisdom learned from the COVID-19 pandemic for the preparedness of future pandemic. Here, I will talk about our findings on SARS-CoV-2 variants and future perspectives to combat the outbreaks and pandemic that will happen in the future.

Keynote Talk 4

25th Oct. 9:30-10:30 Large Theatre

Using bioinformatics to identify new regulatory mechanisms related to RNA m^{6}A modification

Xiujie Wang

Institute of Genetics and Developmental Biology,
Chinese Academy of Sciences

The application of various types of omics studies has produced huge amount of data,which enabled researchers to identify new regulatory mechanisms using bioinformatics. By integration of bioinformatic analysis with experimental studies, we focused on deciphering the regulatory mechanisms and biological functions of N6-methyladenosine (m^{6}A) modification, which is the most abundance modification on mRNAs. We discovered that the selectivity of m^{6}A modification sites is partially regulated by miRNAs via sequencing pairing, revealing a novel function of miRNAs in regulating mRNA epigenetic modification. We also systematically characterized the distribution feature and dynamic changes of m^{6}A modification sites in mouse brain during learning process. Intriguingly, we found that the formation of m^{6}A modification can enhance the efficacy of hippocampus-dependent memory consolidation by facilitating the translation of early-response genes, yet excessive training can compensate the function of m^{6}A in regulating long term memory formation. We also revealed novel functions of a m^{6}A reader protein, YTHDC1, in regulating embryonic brain development.