1st International Symposium on Aihara Moonshot Project

June 6th – 8th, 2022

This symposium is motivated by our aim to "Realization of Ultra-Early Disease Prediction and Intervention by 2050" as the Moonshot Goal 2, which is supported by MOONSHOT Research & Development Program at the Japan Science and Technology Agency (JST). In this symposium, we would like to discuss how we can detect a "pre-disease" state, which has not yet been precisely defined but suggested as the risky state approaching the timing leaving the normal state of health. Precision medicine at a very early stage is targeted by detection of pre-disease states. For this purpose, we would like to exchange our recent research progresses, including personalized medicine, biological and mathematical modeling, control theory, and data analysis.

Organizers : Keita Iida, Koji Noshita, and Shingo Iwami

For Registration:

https://u-tokyo-ac-jp.zoom.us/webinar/register/WN_H1l-qa12SlmanmaYsj22sQ

Program（JST）

6th June

15:00 - 15:10	*Welcome* **Gen Sobue**
15:10 - 15:20	*Welcome* **Masato Wakayama**
15:20 - 15:40	*Opening remark* **Kazuyuki Aihara**
15:40 - 16:10	*"Identification and control of brain dynamics underpinning neuropsychiatric conditions"* **Takamitsu Watanabe**
	Break
16:30 - 17:00	*"Phenotyping studies using morphometric descriptors for multi-omics analysis"* **Koji Noshita**
	Break
17:10 - 18:00	*"What TDA can say about the morphology of diseased neurons"* **David Beers**
	Break
19:10 - 20:00	*"Topological Flow Data Analysis for Blood Flows Inside a Heart"* **Takashi Sakajo**
20:00 - 20:50	*"Modelling dynamics in the presence of bounded noise"* **Jeroen S.W. Lamb**

7th June

15:00 - 15:30	*"Predicting diseases by dynamic network biomarker with network fluctuations"* **Luonan Chen**
	Break
15:40 - 16:30	*"Nonequilibrium phase transitions and critical phenomena"* **Eckehard Schöll**
	Break
17:00 - 17:50	*"Mechanisms of protective immunity in SARS-CoV-2 infection"* **Miles Davenport**
	Break
18:00 - 18:30	*"Modeling and characterizing vaccine-elicited antibody responses"* **Shingo Iwami**
	Break
19:30 - 20:20	*"From mechanisms to prediction: Designing personalised treatment strategies for eczema"* **Reiko Tanaka**
20:20 - 20:50	*"Statistical genetics, disease biology, drug discovery, and personalized medicine"* **Yukinori Okada**

8th June

15:00 - 15:50	*"Non-genetic heterogeneity arising from biological networks"* **Mariko Okada**
	Break
16:00 - 16:30	*"Re-stabilization of gene network systems via pole placement with HDLSS data"* **Xun Shen**
	Break
17:00 - 17:50	*"Can we define attractor states in biology?"* **Kumar Selvarajoo**
	Break
18:00 - 18:30	*"Understanding the disease-triggering inter-organ crosstalk using a genetic animal model"* **Kazutaka Akagi**
	Break
19:30 - 20:20	*"Two new ideas for dynamical time-series analysis"* **Hiroshi Kokubu**
20:20 - 20:50	*"Clustering single-cell and spatial transcriptomes through multifaceted biological aspects"* **Keita Iida**
20:50 - 21:00	*Closing remark*