

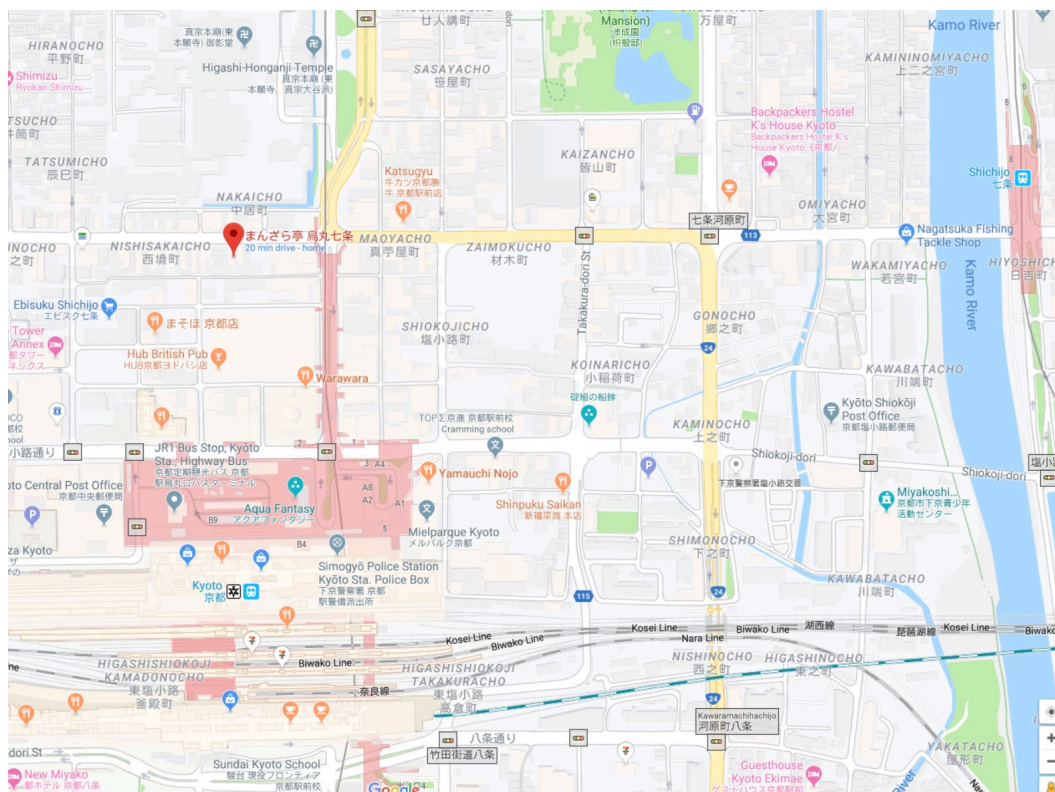
Program

Monday July 15th

9:10-10:10	Invited Talk 1
	Accountable machine learning for safe genome engineering and biotechnology <i>James Zou</i>
10:40-12:10	Oral Session 1
P1	A multi-class decision tree for identifying cell clusters marker genes in single-cell RNAseq analysis <i>Ahmed Youssef, Jing Zhang, Eric Reed, Zhe Wang, Evan Johnson, Stefano Monti, Gary Benson and Joshua Campbell</i>
P2	Fast and robust multi-view multi-task learning via group sparsity <i>Lu Sun, Canh Hao Nguyen and Hiroshi Mamitsuka</i>
P3	Modelling the transfer kinetics of Fipronil from feed to eggs of laying hens <i>Pietro Gerletti, Hans Mielke, Robert Pieper, Monika Lahrssen-Wiederholt, Thomas Kuhl, Max von Kleist and Jorge Numata</i>
12:10-14:00	Lunch & Poster Session <i>Hybrid space (leave posters here until Wednesday)</i>
14:00-15:30	Oral Session 2
P4	Single cell RNA sequencing reveals lung cancer-associated alterations in bronchial cell subpopulations in the mainstem bronchus <i>Xingyi Shi, Grant E. Duclos, Joshua D. Campbell, Yaron Gesthalter, Patrick Autissier, Yves M Dumas, Robert Terrano, Gang Liu, Marc E Lenburg, Avrum Spira and Jennifer Beane</i>
P5	Analysis of Tara Oceans omics data reveals eukaryotic plankton viruses related to carbon export flux and efficiency <i>Hiroto Kaneko, Romain Blanc-Mathieu, Hisashi Endo and Hiroyuki Ogata</i>
P6	Simulating single-cell RNA-seq data from bulk experiments <i>Lam-Ha Ly and Martin Vingron</i>
16:00-17:00	Oral Session 3
P7	ADAPTIVE: leArning DAta-dePendenT, concIse molecular Vectors for fast, accurate metabolite identification from tandem mass spectra <i>Dai Hai Nguyen, Canh Hao Nguyen and Hiroshi Mamitsuka</i>
P8	The transcriptome dynamics of the cell cycle <i>Daniel Schwabe, Sara Formichetti, Martin Falcke and Nikolaus Rajewsky</i>

Tuesday July 16th

9:10-10:10	Invited Talk 2 Metagenomic and metabolomic analyses reveal dynamic shifts in gut microbiota along the adenoma-carcinoma sequence in colorectal cancer <i>Takuji Yamada</i>
10:40-12:10	Oral Session 4
P9	Single-cell spatial reconstruction reveals zonation of xenobiotic-responsive lncRNAs (xeno-lncs) in mouse liver <i>Kritika Karri and David J. Waxman</i>
P10	Extracting boolean rules from trained neural networks <i>Pengyu Liu, Avraham A. Melkman and Tatsuya Akutsu</i>
P11	Computational analysis of the impact of MYCN on the metabolism of neuroblastoma cells <i>Mareike Simon, Uwe Benary, Katharina Baum, Britta Tjaden, Alexander Schramm and Jana Wolf</i>
12:10-13:00	Lunch
13:30-18:00	Excursion <i>Higashiyama walk</i>
18:30-20:30	Banquet dinner (map below) Manzara Nanajo https://manzara-nanajo.owst.jp



Wednesday July 17th

9:10-10:10	Invited Talk 3
	Time series anomaly detection using deep learning <i>See-Kiong Ng</i>
10:40-12:10	Oral Session 5
P12	Evaluation of assemblers and development of metagenome analysis pipeline for gut virome <i>Yasumasa Kimura, Kosuke Fujimoto, Satoru Miyano, Satoshi Uematsu and Seiya Imoto</i>
P13	Seasonal dynamics of a proposed group of giant viruses and bloom forming eukaryotic phytoplankton <i>Prodinger Florian, Endo Hisashi, Li Yanze, Tominaga Kento, Tatsuhiro Isozaki, Gotoh Yasuhiro, Yoshida Takashi and Ogata Hiroyuki</i>
P14	Reverse engineering of neuroblastoma signaling networks <i>Mathurin Dorel and Nils Blüthgen</i>
12:10-14:00	Lunch & Poster Session <i>(Please take down posters by 15:30)</i>
14:00-15:30	Oral Session 6
P15	Prediction of blood test values under different lifestyle scenarios using time-series electronic health record <i>Takanori Hasegawa, Rui Yamaguchi, Masanori Kakuta, Satoru Miyano, Shigeyuki Nakaji and Seiya Imoto</i>
P31	Multi-scale network biology & decoding of network attacking mutations rewiring cancer <i>Rune Linding</i>
P16	Quantitative insights into the cyanobacterial cell economy: from single cells to growth in a light-limited chemostat <i>Marjan Faizi and Ralf Steuer</i>
16:00-16:10	Closing Ceremony