



## FRIDAY, NOVEMBER 1

**Keynote Lecture 1 / OIST Presidential Lecture** Time: 10:50-12:10 / Venue: Auditorium

**Chair:** Tadashi Yamamoto (OIST/JST, Japan)



**KL-01 Deep Learning for Medical Imaging**

Lily Peng (Google AI Healthcare, USA)



Dale Webster (Google AI Healthcare, USA)

## TUESDAY, NOVEMBER 5

**Keynote Lecture 02**

Time: 9:40-11:00 / Venue: Auditorium

**Chair:** Shinya Kuroda (The University of Tokyo, Japan)



**KL-02 Nobel Turing Challenge: Creating the Engine for Scientific Discovery**

Hiroaki Kitano (OIST/SBI, Japan)

## FRIDAY, NOVEMBER 1

### Plenary Lecture 01

Time: 12:10-12:50 / Venue: Auditorium

Chair: Uwe Sauer (ETH Zurich, Switzerland)



#### PL-01 Trans-omic Analysis of Insulin Action

Shinya Kuroda (The University of Tokyo, Japan)

### Plenary Lecture 02

Time: 17:40-18:20 / Venue: Auditorium

Chair: Mariko Okada (Osaka University, Japan)



#### PL-02 Mining non-oncogene addiction for cancer therapy

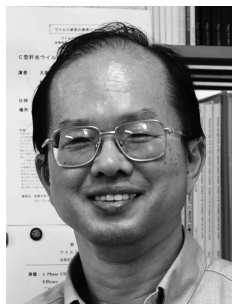
Hsueh-Fen Juan (Department of Life Science, Graduate Institute of Biomedical  
Electronics and Bioinformatics, National Taiwan University, Taiwan)

## SATURDAY, NOVEMBER 2

### Plenary Lecture 03

Time: 9:00-9:40 / Venue: Auditorium

Chair: Miki Ebisuya (EMBL Barcelona, Spain)



#### PL-03 The mechanism of the somite segmentation clock

Ryoichiro Kageyama (Kyoto University, Japan)



## Plenary Lecture 04

Time: 9:40-10:20 / Venue: Auditorium

**Chair:** Silvia Santos (Francis Crick Institute, UK)



### PL-04 Deciphering mechanisms regulating erythropoiesis – From the single cell to the patient level

Ursula Klingmüller (German Cancer Research Center, Germany)

## Plenary Lecture 05

Time: 17:40-18:20 / Venue: Auditorium

**Chair:** Yuichi Taniguchi (RIKEN BDR, Japan)



### PL-05 Deciphering developmental patterning with deep neural network

Chao Tang (Center for Quantitative Biology and School of Physics, Peking University, China)

## SUNDAY, NOVEMBER 3

## Plenary Lecture 06

Time: 9:00-9:40 / Venue: Auditorium

**Chair:** Katsuyuki Yugi (RIKEN IMS, Japan)



### PL-06 Global redox proteome and phosphoproteome analysis reveals novel insights into the Insulin Signaling Network

David E James (Charles Perkins Centre, School of Life & Environmental Science,  
School of Medicine, University of Sydney, Australia)

## Plenary Lecture 07

Time: 9:40-10:20 / Venue: Auditorium

**Chair:** Michael Tyers (University of Montreal, Canada)



**PL-07 From phenotypes to pathways: global exploration of cellular systems using yeast functional genomics**

Brenda J Andrews (The Donnelly Centre, University of Toronto, Canada)

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# MONDAY, NOVEMBER 4

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## Plenary Lecture 08

Time: 9:00-9:40 / Venue: Auditorium

**Chair:** Kim Avrama Blackwell (George Mason University, USA)



**PL-08 Systems Biology of Reinforcement Learning**

Kenji Doya (OIST, Japan)

## Plenary Lecture 09

Time: 9:40-10:20 / Venue: Auditorium

**Chair:** Tadashi Yamamoto (OIST/JST, Japan)



**PL-09 Impact of PD-1 deficiency on microbiome and brain**

Sidonia Fagarasan (Laboratory for Mucosal Immunity, RIKEN IMS, Japan)



## Plenary Lecture 10

Time: 17:40-18:20 / Venue: Auditorium

**Chair:** Brenda Andrews (University of Toronto, Canada)



### PL-10 Charting the chemical-genetic interaction landscape of human cells through genome-wide CRISPR screens

Michael Tyers (Institute for Research in Immunology and Cancer, University of Montreal, Canada)

## TUESDAY, NOVEMBER 5

## Plenary Lecture 11

Time: 9:00-9:40 / Venue: Auditorium

**Chair:** Mariko Okada (Osaka University, Japan)



### PL-11 Our first choices: decoding signals during developmental transitions

Silvia Santos (Francis Crick Institute, UK)

## FRIDAY, NOVEMBER 1

### Luncheon Seminar 01

Time: 13:00-14:00 / Venue: Auditorium

**Chair:** Shuichi Onami (RIKEN, Japan)



#### LS-01 Networked biophotonics for image analysis beyond imaging

Sadao Ota (Research Center for Advanced Science and Technology, The University of Tokyo, Japan)

## SATURDAY, NOVEMBER 2

### Luncheon Seminar 02

Time: 13:00-14:00 / Venue: Auditorium

**Chair:** Matthias Heinemann (University of Groningen, Netherland)



#### LS-02 Uncovering DNA grammar using deep learning

Aleksej Zelezniak (Chalmers University of Technology, Sweden)



## SUNDAY, NOVEMBER 3

### Luncheon Seminar 03

Time: 13:00-14:00 / Venue: Auditorium

**Chair:** Samson Fong (UC San Diego, USA)



#### LS-03 Accelerating life sciences by AI and robotic biology

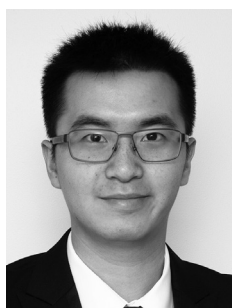
Koichi Takahashi (RIKEN BDR, Japan)

## MONDAY, NOVEMBER 4

### Luncheon Seminar 04

Time: 13:00-14:00 / Venue: Auditorium

**Chair:** Koichi Takahashi (RIKEN QBIC, Japan)



#### LS-04 Towards “Visible” Artificial Intelligence for Cancer Precision Medicine

Samson Fong<sup>1,2</sup>

(<sup>1</sup> Department of Medicine, University of California San Diego, USA)

(<sup>2</sup> Department of Bioengineering, University of California San Diego, USA)

### Luncheon Seminar 05

Time: 13:00-14:00 / Venue: B250

**Chair:** Hiroaki Kitano (SBI, Japan)

#### LS-05 Quantitative, population-level microbiome monitoring - the Flemish Gut Flora project

Jeroen Raes<sup>1,2</sup>

(<sup>1</sup> Department of Microbiology and Immunology, Rega Institute for Medical Research, KU Leuven-University of Leuven, Belgium)

(<sup>2</sup> VIB Center for Microbiology, Leuven, Belgium)

**Sponsored:** TSUMURA



## FRIDAY, NOVEMBER 1

### Multiscale Systems Biology

Time: 15:30-17:30 / Venue: Auditorium

**Chair:** Uwe Sauer (ETH Zurich, Switzerland)

Ayako Yachie-Kinoshita (SBI, Japan)

**1PS1-01 Boolean signaling inputs control predictable cell fate transitions in mouse pluripotency**

15:30

Ayako Yachie-Kinoshita (SBI, Japan)

**1PS1-02 From cells to tissue: continuum mechanics for tissue and cell population** Shuji Ishihara, Philippe Marcq, Kaoru Sugimura

15:50

Shuji Ishihara (The University of Tokyo, Japan)

**1PS1-03 A hybrid mathematical model of the interplay between keratinocyte differentiation and skin barrier function to understand epidermal homeostasis**

16:10

Elisa Domínguez-Hüttinger (Centre for Mathematical Sciences, National Autonomous University of Mexico, Mexico)

**1PS1-04 Deep Decoding of Network Rewiring Mutations in Cancer**

16:30

Rune Linding (Humboldt University of Berlin, Germany)

**1PS1-05 Noise==Function: Is Single-cell Expression Variability Functionally Important?**

16:50

James Cai (Texas A&M University, United States)

**1PS1-06 Towards high-resolution whole-body cell lineage tracing of mammalian development using an evolving DNA barcode technology**

17:10

Nanami Masuyama (Synthetic Biology Division, Research Center for Advanced Science and Technology, The University of Tokyo, Japan)

### Methodological Developments for Systems Biology

Time: 15:30-17:30 / Venue: B250

**Chair:** Yong Wang (CAS-AMSS, China)

Atsushi Mochizuki (Kyoto University, Japan)

**1PS2-01 Interpretating genetic variants by gene regulatory network**

15:30

Yong Wang (Academy of Mathematics and Systems Science, China)

**1PS2-02 Statistical test of structured continuous trees based on discordance matrix**

15:50

Xiangqi Bai (Academy of Mathematics and System Science, Chinese Academy of Sciences, China)

**1PS2-03 Information-theoretic causality predicts proteomic control of clinical parameters and reveals cancer network biomarkers**

16:10

Ian Overton (Queen's University Belfast, University of Edinburgh, United Kingdom)





**1PS2-04 Understanding the System Dynamics of Mitochondrial Retrograde Signaling from a Differential Equation-based Framework**  
16:30

Shao-Ting Chiu (National Taiwan University, Taiwan)

**1PS2-05 Model-based identification of ErbB network principles among cell types**

16:50

Hiroaki Imoto (Laboratory of Cell Systems, Institute for Protein Research, Osaka University, Japan)

**1PS2-06 Origin of adaptation and modularity in chemical reaction networks**

17:10

Atsushi Mochizuki (Kyoto University, Japan)

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## SATURDAY, NOVEMBER 2

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### Big Data, AI & Laboratory Automation

Time: 10:50-12:50 / Venue: Auditorium

**Chair:** Ross D. King (The University of Manchester and Alan Turing Institute, UK)

Jun Seita (RIKEN, Japan and Stanford University, USA, Japan)

**2PS1-01 Towards the Automation of Systems Biology**

10:50

Ross D. King (The University of Manchester and Alan Turing Institute, UK)

**2PS1-02 Mechanistic Models of Ligand-induced Programmed Cell Death Fates**

11:20

Carlos Lopez (Vanderbilt University, United States)

**2PS1-03 Machine learning diagnosis of multiple liver-related diseases by exhaled breath gas components**

11:38

Shingo Shirone (Nara Institute of Science and Technology, Japan)

**2PS1-04 Combining interpretable machine learning with high dimensional multi-omics data from laboratory evolution**

11:56

Junichiro Iwasawa (Department of Physics, The University of Tokyo, Japan)

**2PS1-05 A human reference interactome map reveals cellular context-specific biological mechanisms.**

12:14

Dae-Kyum Kim (University of Toronto, Canada)

**2PS1-06 Deep Learning approaches for reliable quantification of multi-omics cell imaging datasets to interrogate RNA and protein spatial and temporal subcellular interactions**

12:32

Emmanuel Bouilhol (University of Bordeaux - Bordeaux Bioinformatics Center; University of Bordeaux - CNRS, LaBRI, France)

## Modeling Networks and Circuits

Time: 10:50-12:50 / Venue: B250

**Chair:** Luonan Chen (Shanghai Institutes for Biological Sciences, CAS, China)

Matteo Barberis (University of Surrey, UK)

**2PS2-01 A Novel and Robust Molecular Design Synchronizing Transcriptional with Cell Cycle Oscillators**

10:50

Matteo Barberis (University of Surrey, United Kingdom)

**2PS2-02 Success of oscillations in negative feedback gene regulatory networks is determined by degradation rate uniformity**

11:10

Ruben Perez-Carrasco (University College London, United Kingdom)

**2PS2-03 Synchronization condition for hydrodynamically coupled Stokes spheres under external flow**

11:30

Yuki Izumida (The University of Tokyo, Japan)

**2PS2-04 Model-driven Design of *Mycoplasma pneumoniae* for vaccine production**

11:50

Erika Gaspari (Laboratory of Systems and Synthetic Biology, Wageningen University & Research, Wageningen, the Netherlands, Netherlands)

**2PS2-05 Modelling cell type-specific signalling networks by mass cytometry in colorectal cancer organoids**

12:10

Thomas Sell (Charité Berlin, Germany)

**2PS2-06 Dynamic network biomarkers detect tipping points of diseases by quantifying their early-warning signals as general dynamic biomarkers**

12:30

Luonan Chen (Shanghai Institutes for Biological Sciences, CAS, China)

## Quantitative Systems Biology

Time: 15:30-17:30 / Venue: Auditorium

**Chair:** Matthias Heinemann (University of Groningen, Netherland)

Kwang-Hyun Cho (KAIST, Korea)

**2PS3-01 A system of coupled oscillators driving the cell cycle**

15:30

Matthias Heinemann (Molecular Systems Biology, University of Groningen, Netherland)

**2PS3-02 A parallel cell-cycle entry pathway with inverted G1 signaling and alternate point of no return**

15:50

Tobias Meyer (Stanford University, United States)

**2PS3-03 Mechanism of Jet lag: Mathematical and Experimental Study**

16:10

Hiroshi Kori (The University of Tokyo, Japan)

**2PS3-04 Optical control of cell signaling with red/far-red light in human cells, fission yeast, and worms**

16:30

Kazuhiro Aoki (National Institutes of Natural Sciences, National Institute for Basic Biology, Japan)



## 2PS3-05 Bistability in ferroptosis leads to an irreversible switch

16:50 Pedro Mendes (University of Connecticut, United States)

## 2PS3-06 Tradeoffs between growth and adaptability shape microbial phenotypes

17:10 Markus Basan (Harvard University, United States)

## Synthetic Biology

Time: 15:30-17:30 / Venue: B250

**Chair:** Matthew Wook Chang (National University of Singapore, Singapore)

Miki Ebisuya (EMBL Barcelona, Spain)

## 2PS4-01 Engineering microbes to rewire host-microbiome interactions

15:30 Matthew Wook Chang (National University of Singapore, Singapore)

## 2PS4-02 A CRISPR–barcode technology to isolate a target clone from a heterogeneous cell population

Soh Ishiguro (Research Center for Advanced Science and Technology, The University of Tokyo., Japan)

## 2PS4-03 Comparing burden on a single cell with cell consortia using two-stage substrate conversion

Zoltan Tuza (Imperial College London, United Kingdom)

## 2PS4-04 Perfusable synthetic self-organized vascular network - experiment and modeling

16:25 Takashi Miura (Kyushu University, Japan)

## 2PS4-05 The development of the intestinal circadian clock and its roles in intestinal organoids

16:50 Christian Hong (University of Cincinnati, United States)

## 2PS4-06 Human Time vs. Mouse Time with Recapitulated Systems

17:05 Miki Ebisuya (EMBL Barcelona, Spain)

## SUNDAY, NOVEMBER 3

## Systems Medicine and Healthcare

Time: 10:50-12:50 / Venue: Auditorium

**Chair:** Nathan Price (Institute for Systems Biology, USA)

Reiko Tanaka (Imperial College London, UK)

## 3PS1-01 Longitudinal Deep Phenotyping of Thousands of People: Insights for Precision Medicine

Nathan Price (Institute for Systems Biology, USA)

## 3PS1-02 Mechanistic modelling towards designing personalised treatment strategies for eczema

Reiko Tanaka (Department of Bioengineering, Imperial College London, UK)

**3PS1-03 Data-driven study of cancer evolution and implications in precision oncology**

11:38 Jiguang Wang (The Hong Kong University of Science and Technology, Hong Kong)

**3PS1-04 eBrain: a Three Dimensional Simulation Tool to Study Drug Delivery in the Brain.**

12:02 Yaki Setty (Gateway Institute for Brain Research, Israel)

**3PS1-05 Discovering the genes mediating the interactions between chronic respiratory diseases in the human interactome**

12:26 Enrico Maiorino (Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, United States)

**Developmental Systems Biology**

Time: 10:50-12:50 / Venue: B250

**Chair:** Mary N. Teruel (Stanford University, USA)

Kaoru Sugimura (Kyoto University, Japan)

**3PS2-01 A gradual increase in the duration of an extended G1 period enables stochastic competition between the decision to terminally differentiate or enter the next cell cycle**

10:50 Mary N. Teruel (Dept. of Chemical and Systems Biology, Stanford University, USA)

**3PS2-02 Comprehensive determination of logic functions for genes that initiate expression in early ascidian embryos**

11:14 Yutaka Satou (Kyoto University, Japan)

**3PS2-03 Precision of Tissue Patterning is Controlled by Dynamical Properties of Gene Regulatory Networks**

11:38 Edgar Herrera Delgado (The Francis Crick Institute & King's College London, United Kingdom)

**3PS2-04 Computational modeling and experiments of cell wrapping: dissecting the mechanisms of endothelial cell coverage by pericytes.**

12:02 Kei Sugihara (Kyushu University Graduate School of Medical Sciences, Japan)

**3PS2-05 Planar polarization of the multi-ciliated planarian epidermis by body plan landmarks**

12:26 Lutz Brusch (Technische Universität Dresden, Center for Information Services and High Performance Computing, Dresden, Germany)

**Systems Biology for Neurosciences and Neural Circuits**

Time: 10:50-12:50 / Venue: C210

**Chair:** Kim Avrama Blackwell (George Mason University, USA)

Erik De Schutter (OIST, Japan)

**3PS3-01 AMPA-type glutamate receptor subunits in the synapse turnover by monomer diffusion; unraveling by single-molecule tracking**

10:50 Jyoji Morise (Division of Human Health Sciences, Graduate School of Medicine, Kyoto University, Japan)

**3PS3-02 Nanoscale analysis of neuronal spine synapses**

11:10 Shigeo Okabe (The University of Tokyo, Japan)



## 3PS3-03 The role of dopamine and post-synaptic signaling molecules in synaptic plasticity

11:30

and relapse to alcohol use

Kim Avrama Blackwell (George Mason University, Department of Bioengineering, USA)

## 3PS3-04 Chronometabolism in diurnal primates and nocturnal rodents

11:50

Hitoshi Okamura (Kyoto University, Japan)

## 3PS3-05 Modeling Purkinje neuron activity in 3D morphologies at the nanoscale

12:10

Alexey Martyushev (Okinawa Institute of Science and Technology Graduate University OIST, Japan)

## 3PS3-06 Individuality in the neural network dynamics in *C. elegans*

12:30

Yuichi Iino (The University of Tokyo, Japan)

# MONDAY, NOVEMBER 4

## Systems Biophysics

Time: 10:50-12:50 / Venue: Auditorium

**Chair:** Yuichi Taniguchi (RIKEN BDR, Japan)

Chao Tang (Peking University, China)

## 4PS1-01 Cooperative reliable response from sloppy gene expression dynamics

10:50

Masayo Inoue (Meiji University, Japan)

## 4PS1-02 Kinetic uncertainty relations for the control of stochastic reaction networks

11:14

Jiawei Yan (Harvard University, United States)

## 4PS1-03 A Theoretical Approach to Understand the Role of the Retention Mechanism in the Rejuvenation Process

11:38

Barbara Schnitzer (University of Gothenburg, Sweden)

## 4PS1-04 Controlling cell fate specification system by key genes determined from network structure

12:02

Kenji Kobayashi (Department of Zoology, Graduate School of Science, Kyoto University, Japan)

## 4PS1-05 Computational analysis of nuclear division dynamics in early *C. elegans* embryos

12:26

Koji Kyoda (RIKEN Center for Biosystems Dynamics Research, Japan)

## EcoSystems Biology

Time: 10:50-12:50 / Venue: B250

**Chair:** Edda Klipp (Humboldt-Universität zu Berlin, Germany)

Evan P. Economo (OIST, Japan)

## 4PS2-01 Modeling of yeast growth, division and stress response with focus on difference in the behavior of a single cell and the population

10:50

Edda Klipp (Humboldt-Universität zu Berlin, Theoretical Biophysics, Germany)

**4PS2-02 Mathematical interaction model of nasal pathogen interaction**

11:15 Reihaneh Mostolizadeh (University of Tübingen, Germany)

**4PS2-03 Analysis of phenotypic constraints by high-throughput laboratory evolution of *Escherichia coli***

11:40 Chikara Furusawa (Center for Biosystems Dynamics Research, RIKEN, Japan)

**4PS2-04 The traditional Japanese medicine (Kampo) Bofutsushosan as an anti-obesity medication: possible involvement of gut microbiota**

12:05 Mitsue Nishiyama (Tsumura Kampo Research Laboratories, Tsumura and Co., Japan)

**4PS2-05 The methyl cycle is a conserved regulator of biological clocks**

12:20 Jean-Michel Fustin (Kyoto University, Graduate School of Pharmaceutical Sciences, Laboratory of Molecular Metabolism, Japan)

**4PS2-06 A data-based mathematical model predicts dynamic trajectories of a protected plant community under different conservation regimes**

12:35 Jaime Acosta (Science Faculty, National Autonomous University of Mexico, Mexico)

**Single-cell Systems Biology**

Time: 15:30-17:30 / Venue: Auditorium

**Chair:** Roy Wollman (UCLA, USA)

Wataru Fujibuchi (Kyoto University, Japan)

**4PS3-01 Deciphering Cell States: the relationship between single-cell gene expression and phenotypic heterogeneity in calcium signaling**

15:30 Roy Wollman (University of California, USA)

**4PS3-02 Exploring universal aging dynamics using *Escherichia coli* as a model**

15:50 Yifan Yang (Weizmann Institute of Science, Israel)

**4PS3-03 Combining single cell and cell population based analysis identifies mechanisms leading to Acetaminophen-induced inhibition of cell cycle progression in hepatocytes**

16:10 Artyom Vlasov (German Cancer Research Center (DKFZ), Germany)

**4PS3-04 Inferring activity and targets of enhancers in single cells through single-cell enhancer RNA analysis**

16:30 Haruka Ozaki (Bioinformatics Laboratory, Faculty of Medicine, University of Tsukuba, Japan)

**4PS3-05 Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM**

16:50 Andrei Zinovyev (Institut Curie, France)

**4PS3-06 Multiscale clonal model of Germinal Center B cell differentiation**

17:10 Maria Rodriguez Martinez (IBM, Zurich Research Laboratory, Switzerland)



## Multi-omics

Time: 15:30-17:30 / Venue: B250

**Chair:** Jason W Locasale (Duke University, USA)

Katsuyuki Yugi (RIKEN IMS, Japan)

**4PS4-01 Trans-omic analysis of the central metabolism of *Saccharomyces cerevisiae* by integration of metabolome, metabolic flux, and proteome data**

15:30

Fumio Matsuda (Osaka University, Japan)

**4PS4-02 From protein translation to fluxes – quantitative systems biology of yeast stress responses**

15:50

Petri-Jaan Lahtvee (University of Tartu, Estonia)

**4PS4-03 Unraveling the impact of compensatory evolution on metabolic divergence**

16:10

Dorottya Kalapis (HAS, Biological Research Centre, Hungary)

**4PS4-04 Unraveling acetogen gas fermentation using quantitative systems biology**

16:30

Kaspar Valgepea (ERA Chair in Gas Fermentation Technologies, Institute of Technology, University of Tartu, Estonia)

**4PS4-05 Systems Biology of Herbal Medicine: Elucidating the complex interactions between traditional herbal medicine and endogenous biological systems**

16:50

Akinori Nishi (Tsumura Kampo Research Laboratories, Tsumura and Co., Japan)

**4PS4-06 Quantitative approaches to understanding metabolism in cancer**

17:10

Jason W Locasale (Department of Pharmacology and Cancer Biology, Duke University School of Medicine, USA)



## FRIDAY, NOVEMBER 1

Time: 14:10-15:30 / Venue: Tunnel Gallery

### Big Data, AI & Laboratory Automation

- 1P-001 Deep Learning-based quantitative evaluation of early embryo in infertility treatments**  
Yuta Tokuoka (Keio University, Japan)
- 1P-002 Accurate Prediction of Kinase-Substrate Networks Using Knowledge Graphs**  
Dirk Fey (Systems Biology Ireland, Ireland)
- 1P-003 Cell Image Segmentation Using Attention Module at Each Layer**  
Daisuke Matsuzuki (Meijo University, Japan)
- 1P-004 Image Translation for Cell Image Segmentation Using Deep Learning**  
Sota Kato (Meijo University, Japan)
- 1P-005 Subcellular mitochondria structure prediction in label-free microscope images using convolutional neural networks**  
Chan-Min Hsu (National Taiwan University, Taiwan)

### Developmental Systems Biology

- 1P-006 Theoretical tool bridging cell polarities with development of robust morphologies**  
Silas Boye Nissen (Niels Bohr Institute, University of Copenhagen, Denmark)
- 1P-007 Vascular intraluminal pressure inhibits angiogenic branch elongation**  
Koichi Nishiyama (Kumamoto University, Japan)
- 1P-008 Force-sensitivity of alpha-catenin and epithelial morphogenesis**  
Shigenobu Yonemura (Tokushima University Graduate School of Medical Science, Japan)
- 1P-009 Perivascular pericytes facilitate endothelial branch elongation in angiogenesis: possible involvement of biomechanical mechanisms**  
Yasuyuki Hanada (Nagoya University, Kumamoto University, Japan)
- 1P-010 Vascularization of a tumor spheroid in a microfluidic device to investigate flow-effects on growth and drug delivery**  
Yuji Nashimoto (Tohoku University, Japan)

### Methodological Developments for Systems Biology

- 1P-011 Towards a physiological scale of vocal fold agent-based biological models: sensitivity analysis, calibration and validation**  
Nicole Y. K. Li-Jessen (McGill University, Canada)





- 1P-012 Regulating *Pseudomonas aeruginosa* Biofilm using Spatio-Temporal Cellular Automata**  
Kumar Selvarajoo (Agency for Science, Technology & Research (A\*STAR), Singapore)
- 1P-013 The 'rubber band method' of ranking network mechanisms rather than claiming the single best: *E. coli*'s active ammonium transport is 130 times better than the passive transport network**  
Kazuhiro Maeda (Kyushu Institute of Technology, Japan)
- 1P-014 A distributed computing framework to reconstruct lineage trees of millions of sequences**  
Naoki Konno (The University of Tokyo, Japan)
- 1P-015 Quantification of the methylation-based cellular memory in *Escherichia coli* chemotaxis**  
Jürgen Pahle (Heidelberg University, Germany)
- 1P-016 A Semigroup Formalism for Biochemical Reaction Networks**  
Dimitri Loutchko (The University of Tokyo, Japan)
- 1P-017 Vesicle modeling extension to reaction-diffusion simulator STEPS**  
Iain Hepburn (Okinawa Institute of Science and Technology Graduate University, Japan)

## Modeling Networks and Circuits

- 1P-018 High Throughput Genome-Scale Metabolic Model Reconstruction and Reconciliation with Tn-seq Data**  
Jose Faria (Data Science and Learning, Argonne National Laboratory, Argonne, IL, United States)
- 1P-019** Withdrawn
- 1P-020 Genetic interactions derived from high-throughput phenotyping of 7,350 yeast cell cycle mutants**  
Jenna Gallegos (Colorado State University, United States)
- 1P-021 Detecting the early-warning signal of the critical transition for complex diseases**  
Pei Chen (South China University of Technology, China)
- 1P-022 In silico lymphangiogenesis: Development of an intracellular network model of receptor trafficking and signaling pathway in lymphatic endothelial cells**  
Sophie Bekisz (University of Liege, Belgium)
- 1P-023 A whole cell modeling of bacteria from genomic sequence**  
Kazunari Kaizu (RIKEN Center for Biosystems Dynamics Research, Japan)

- 1P-024 Ensemble boolean modeling sheds light on the molecular mechanisms of tumor invasion**  
Vincent Noel (Institut Curie, PSL Research University, Mines Paris Tech, Inserm, France)
- 1P-025 Scalable Simulation of Biochemical Models with PySB**  
Alexander Lubbock (Vanderbilt University, United States)
- 1P-026 Modeling signal transduction networks in heterogeneous colon cancer using single cell modelling**  
Nils Blüthgen (Charite, Germany)
- 1P-027** Withdrawn
- 1P-028 Mathematical modeling for endothelial cell migration during sprouting angiogenesis**  
Tatsuya Hayashi (Faculty of Information Science and Technology, Hokkaido University, Japan)
- 1P-029 Hematopoiesis modeling and applications**  
Nathaniel Mon Pere (Interuniversity Institute of Bioinformatics in Brussels, ULB-VUB, Brussels, Belgium)
- 1P-030 Modeling of infection in a growing plaque to quantify role of amino acid mutations in GP of filovirus**  
Kwangsu Kim (Department of Biology, Faculty of Sciences, Kyushu University, Japan)
- 1P-031 In silico and in vivo experiments reveal mechanism of centrosome positioning during mitosis**  
Yoshitaka Yamazaki (Center for Biosciences and Informatics, Graduate School of Fundamental Science and Technology, Keio University, Japan)
- 1P-032 Post-transcriptional regulation, noise and spatial transcript localization of small RNA-controlled genes in an Escherichia coli stress response network**  
Rinat Goren (Weizmann Institute of Science, Israel)
- 1P-033 Development of an in silico chondrocyte via mechanistic and data-driven modeling for the study Osteoarthritis progression and the identification of potential intervention targets.**  
Raphaëlle Lesage (Katholieke Universiteit Leuven, Belgium)
- 1P-034 Synthetic genetic networks based on neural models in living cells**  
Ramez Daniel (Technion- Israel Institute of Technology, Israel)
- 1P-035 Viruses are modulators in the human molecular system**  
Vandana Ravindran (MRC-Centre for Virus Research University of Glasgow, United Kingdom)
- 1P-036 Investigating Pulsed Neural Network Structures in a Framework of Dynamical Bayesian Network by a Greedy Searching**  
Chaoyi Dong (Inner Mongolia University of Technology, China)
- 1P-037 Sensitivity analysis for elementary circuits in signal transduction model**  
Kentaro Inoue (University of Miyazaki, Japan)



## Multi-omics

- 1P-038 DEIso: a database for differentially expressed isoforms/genes in human cancers**  
Wei-Sheng Wu (National Cheng Kung University, Taiwan)
- 1P-039 Workflow for TF knockout simulations on transcriptome primed whole genome metabolic model reconstructions for 10 antibiotic resistant E. coli strains**  
Daria Gaidar (Saarland University, Germany)
- 1P-040 Time Series Transomics: Integrated analysis through multiple molecular layers**  
Fumiko Matsuzaki (Kyushu University, Japan)
- 1P-041 Prediction of pioneer transcription factors from DNA methylation profiles**  
Harukazu Suzuki (RIKEN IMS, Japan)
- 1P-042 Exploring the landscape of regulatory elements on promoter regions of cassava AGPase genes via TFBS scan and phylogenetic footprinting approach**  
Saowalak Kalapanulak (King Mongkut's University of Technology Thonburi, Thailand)
- 1P-043 Effect of Synechocystis-Hik28 deletion on photosynthetic activity and fatty acid profile under nitrogen and temperature stresses**  
Pavinee Rakruangdet (National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Thailand)
- 1P-044 Proteomic and phosphoproteomic profiling of lineage transition in mice from lung ADC to SCC represent molecular mechanism for drug resistance**  
Chen Li (Institute of Biochemistry and Cell Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, China)
- 1P-045 Interconnection of carbon- and nitrogen metabolism and its possible role in temperature stress response in Arthrospira (Spirulina) platensis C1**  
Apiradee Hongsthong (National Science and Technology Development Agency, Thailand)
- 1P-046 A trans omic analysis of insulin action in Drosophila S2R+ cells across phosphoproteome, protein-protein interactions, transcriptome, and metabolome**  
Akira Terakawa (The University of Tokyo, Japan)

## Multiscale Systems Biology

- 1P-047 Time-series analysis of the concentration changes of human blood metabolites and hormones after oral glucose ingestion**  
Suguru Fujita (The University of Tokyo, Japan)
- 1P-048 Deciphering Yeast Physiology by a Multi-scale Framework Integrating Cell Cycle and Metabolism**  
Matteo Barberis (University of Surrey, United Kingdom)

- 1P-049 Trans-omic analysis reveals different responses to glucose in the muscle during obesity**  
Miki Eto (The University of Tokyo, Japan)
- 1P-050 Metabolome analysis of glucose dose-dependent metabolism in mice liver**  
Yifei Pan (The University of Tokyo, Japan)
- 1P-051 Modeling the coupled within- to between-host dynamics of a viral infectious disease**  
Alexis Erich Almocera (Division of Physical Sciences and Mathematics, University of the Philippines Visayas, Miag-ao, Philippines)

## Quantitative Systems Biology

- 1P-052 Nitrogen limitation reveals large reserves in the metabolic and translational capacities of yeast**  
Rosemary Yu (Chalmers University of Technology, Sweden)
- 1P-053 Role of temporal waveform of biological rhythms and its quantification**  
Shingo Gibo (Interdisciplinary Theoretical and Mathematical Sciences Program, RIKEN, Japan)
- 1P-054 Metabolic flux changes over time and the regulatory mechanisms in insulin-stimulated adipocytes**  
Satoshi Ohno (Molecular Genetics Research Laboratory, Graduate School of Science, University of Tokyo, Japan)
- 1P-055 CRISPR-PCA screens highlight the contribution of protein context to the regulation of SRC Homology 3 (SH3) domains protein-protein interactions**  
Ugo Dionne (Laval University, Canada)
- 1P-056 Systematic Identification of Genes Whose Overexpression Works Adaptively Using the ADOPT System**  
Nozomu Saeki (Okayama University, Japan)
- 1P-057 Creating consortia metabolic models for Next Generation Probiotics**  
Isma Belouah (Tartu University Institute of Technology, Estonia)
- 1P-058 Large-scale morphological feature extraction by spherization and spherical harmonics decomposition from in vivo 3D migrating immune cells**  
Saori Uematsu (The University of Tokyo, Japan)
- 1P-059 Quantitative insights into the cyanobacterial cell economy**  
Marjan Faizi (Humboldt University Berlin, Germany)
- 1P-060** Withdrawn
- 1P-061 Environment-dependent binary protein interactome of a cell**  
Dayag Sheykhkarimli (Department of Molecular Genetics, University of Toronto; Donnelly Centre; Lunenfeld-Tanenbaum Research Institute, Canada)
- 1P-062 GB-X Map: Causal Pathways and Motifs common in IBD and Schizophrenia**  
Saptarshi Bej (University of Rostock, Institute of Computer Science, Department of Systems Biology and Bioinformatics, Germany)



## Systems Biophysics

- 1P-063 Allosteric regulation of Glutamate dehydrogenase deamination activity**  
Soumen Bera (Central University of Rajasthan, India, India)
- 1P-064 Essential role of cytoskeleton polarity for alignment and orientation of basal bodies in multi-ciliated cell**  
Toshinori Namba (The University of Tokyo, Japan)
- 1P-065 TPPP3 promotes microtubule networking adaptive to the external stress changes**  
Kazuhiro Oiwa (National Institute of Information and Communications Technology, Japan)
- 1P-066 Quantitative analysis of cellular dynamics in *C. elegans* embryos**  
Yusuke Azuma (RIKEN Center for Biosystems Dynamics Research, Japan)
- 1P-067 Evaluation of the time-delay effect of molecular surface diffusion due to positive Gaussian curvature of dendritic spine head**  
Kenji Kimura (Department of Micro Engineering, Graduate School of Engineering, Kyoto University, Japan)
- 1P-068 Signal transduction systems run by metastable molecular complexes: discoveries by single-molecule tracking**  
Akihiro Kusumi (Okinawa Institute of Science and Technology Graduate University, Japan)

## Systems Medicine and Healthcare

- 1P-069 Functional analysis of the MAPK scaffold KSR1 in malignant melanoma**  
Zhi Liu (Systems Biology Ireland, University College Dublin, Ireland)
- 1P-070 An in silico approach to identify potential interactors of toxic huntingtin proteins**  
Do Young Hyeon (Seoul National University, South Korea)
- 1P-071 The innate immune response to respiratory fungal infections: a systems medicine approach**  
Reinhard Laubenbacher (University of Connecticut School of Medicine, United States)
- 1P-072 Personalized Microbiota Dynamics for Disease Classification**  
Xiangtian Yu (Shanghai Jiao Tong University Affiliated Sixth People's Hospital, Shanghai, China)
- 1P-073 Trans-omic analysis reveals allosteric and gene regulation-axes for altered glucose-responsive liver metabolism associated with obesity**  
Toshiya Kokaji (Department of Biological Sciences, Graduate School of Science, University of Tokyo., Japan)
- 1P-074 Pan-Cancer Analyses Reveal Signaling Entropy Features associated with Tumor Stemness, Metastasis and Prognosis**  
Rong Zeng (Shanghai Institute of Biochemistry and Cell Biology, CAS, China)

- 1P-075 Comprehensive metabolite profiling of traditional herbal medicine in human plasma: from metabolites to phenotypes**  
Katsuya Ohbuchi (Tsumura & Co., Japan)
- 1P-076 Predicting the responsiveness of targeted anti-cancer drugs based on signal flow distribution by mapping genomic data onto the topological signaling network**  
Yunseong Kim (Laboratory for Systems Biology and Bio-Inspired Engineering, KAIST, South Korea)
- 1P-077 On the prediction of protein abundance from RNA**  
Rasmus Magnusson (Linköping University, Sweden)
- 1P-078 The methodological trends of traditional herbal medicine employing network pharmacology methods**  
Won-Yung Lee (College of Korean Medicine, Gachon University, South Korea)

## Methodological Developments for Systems Biology

- 1P-079 Design and construction of novel one-carbon assimilation pathways**  
Hongwu Ma (Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, China)
- 1P-080 GlycoMaple for global mapping of glycosylation pathways in human-derived cells**  
Morihiisa Fujita (Jiangnan University, China)
- 1P-081 OpenCOR: a modelling environment for reproducible science**  
Alan Garny (The University of Auckland, New Zealand)

## Modeling Networks and Circuits

- 1P-082 Hepatocyte growth factor increases glycolytic flux in HepG2 cells by inducing gene expression of multiple isoforms of hexokinase and glucose transporter type 1**  
Irina Titkova (German Cancer Research Center (DKFZ), Germany)
- 1P-083 A landscape view on the interplay between EMT and cancer metastasis**  
Chunhe Li (Fudan University, China)
- 1P-084 Error-speed correlations in biopolymer synthesis**  
Davide Chiuchiù (Okinawa Institute for Science and Technology, Japan)

## Quantitative Systems Biology

- 1P-085 The role of sigma factors in circadian transcriptional output networks of unicellular cyanobacteria**  
Koji Kawasaki (Department of Electrical Engineering and Bioscience, Waseda University, Japan, Japan)



## SATURDAY, NOVEMBER 2

Time: 14:10-15:30 / Venue: Tunnel Gallery

### Big Data, AI & Laboratory Automation

- 2P-001 FAIR data exchange in the life sciences by standardization of heterogenous data and models**  
Martin Golebiewski (HITS gGmbH, Germany)
- 2P-002 The JSBML Project: A Fully Featured Java API for Working with Systems Biological Models**  
Andreas Dräger (Computational Systems Biology of Infection and Antimicrobial-Resistant Pathogens, University of Tübingen, Germany)
- 2P-003 SSBD: an open public database of microscopy images and quantitative data of biological dynamics facilitating the reuse and reanalyze of biological data**  
Kenneth Ho (RIKEN Center for Biosystems Dynamics Research (BDR) , Japan)
- 2P-004 ProtFunAI - An artificial intelligence for prediction of protein function from protein sequence alone**  
Torbjörn E. M. Nordling (Department of Mechanical Engineering, National Cheng Kung University, Taiwan)
- 2P-005 Estimation of intracellular key enzymes by applying machine learning algorithm**  
Kakeru Kosaka (Nara Institute of Science and Technology, Japan)

### Developmental Systems Biology

- 2P-006 Maternal factors involved in developmental buffering**  
Atsuko Sato (Ochanomizu University, Japan)
- 2P-007 Reconstruction and understanding of long-term microvascular remodeling in a microfluidic platform**  
Takanori Sano (Kyushu University, Japan)
- 2P-008 A microfluidic chip to evaluate the role of pericytes and fluid flow in vascular development**  
Scott Erickson (Kyoto University, Japan)
- 2P-009 Inferring gene regulatory network and differentiation dynamics of human embryonic stem cell**  
Yukitaka Isaka (RIKEN and The University of Tokyo, Japan)
- 2P-010 On-chip 3D biomimetic model to reconstitute vital phenomena with vascular and interstitial flow**  
Sanshiro Hanada (Kumamoto University, Japan)

## EcoSystems Biology

- 2P-011 A Theory on the Survival of Species in a Microbial Aquatic Food Web with Chytrids**  
Alexis Erich Almocera (Division of Physical Sciences and Mathematics, University of the Philippines Visayas, Miag-ao, Philippines)
- 2P-012 Identification of microbial community functioning for sulfide removal and electricity generation in microbial fuel cell: Application for wastewater treatment of canned pineapple factory in Thailand**  
Nattawet Sriwichai (King Mongkut's University of Technology Thonburi, Thailand)
- 2P-013 Identification of mutations conferring resistance to anti-tuberculosis drugs by laboratory evolution of non-pathogenic Mycobacterium on agar plate**  
Tomoya Maeda (RIKEN Center for Biosystems Dynamics Research, Japan)

## Methodological Developments for Systems Biology

- 2P-014 Tools for scalable simulation and parameter estimation of ordinary differential equation models**  
Daniel Weindl (Helmholtz Zentrum München, Germany)
- 2P-015 BioModels Parameters: A resource to search and retrieve parameters from published systems models**  
Rahuman Sheriff (European Bioinformatics Institute - European Molecular Biology Laboratory (EMBL-EBI), United Kingdom)
- 2P-016 Efficient parameter estimation methods for integration of qualitative data in quantitative models**  
Leonard Schmiester (Helmholtz Zentrum München, Germany)
- 2P-017 SABIO-RK: a comprehensive reaction kinetics information system**  
Andreas Weidemann (HITS gGMBH, Germany)
- 2P-018 Automated search of a minimal set of adjustable parameters optimizing constrained kinetic model of metabolism**  
Egils Stalidzans (University of Latvia, Latvia)
- 2P-019 Deciphering animal decision making by inverse reinforcement learning**  
Honda Naoki (Kyoto University, Japan)
- 2P-020 E-Cell System version 4: An integrated platform for cell simulations**  
Kozo Nishida (RIKEN Center for Biosystems Dynamics Research, Japan)

## Modeling Networks and Circuits

- 2P-021 Establishment and Maintenance of two opposing transcriptional states during random X-chromosome inactivation**  
Verena Mutzel (Max Planck Institute for Molecular Genetics, Germany)





- 2P-022** Withdrawn
- 2P-023** **Discrete empirical interpolation for model reduction in biological systems**  
Neveen Ali Salem Eshtewy (Freie Universität Berlin, Germany)
- 2P-024** **Model-driven Safety-by-design in Synthetic Biology**  
Erika Gaspari (Laboratory of Systems and Synthetic Biology, Wageningen University & Research, Wageningen, the Netherlands, Netherlands)
- 2P-025** **Automatic Adaptive Refinement of Bayesian Networks for Biomarker Discovery from Heterogeneous Healthcare Data**  
Ann-Kristin Becker (University Medicine Greifswald, Germany)
- 2P-026** **Deciphering the differential NF- $\kappa$ B activity regulation due to different post-translational modifications of NF- $\kappa$ B complex subunits**  
Ahmed Mobeen (CSIR - Institute of Genomics and Integrative Biology; Academy of Scientific & Innovative Research (AcSIR), India)
- 2P-027** **Exploring glioblastoma cell state dynamics using single cell lineage tracing**  
Ida Larsson (Uppsala University, Sweden)
- 2P-028** **The polarising world of Cdc42: the importance of geometry in cell division**  
Johannes Borgqvist (University of Gothenburg, Sweden)
- 2P-029** Withdrawn
- 2P-030** **Cost-speed trade-off and optimal strategies for biochemical regulation**  
Ken-Ichi Hironaka (The University of Tokyo, Japan)
- 2P-031** **Mathematical modelling of the interplay between early viral replication and immune signalling**  
Darius Schweinoch (University Medicine Greifswald, Institute of Bioinformatics, Germany)
- 2P-032** **Growth-coupled overproduction is theoretically possible for most metabolites in *Saccharomyces cerevisiae* under anaerobic condition**  
Takeyuki Tamura (Kyoto University, Japan)
- 2P-033** **Non-sinusoidal waveform in biological rhythms and a method to predict a black box using its waveform**  
Gen Kurosawa (RIKEN iTHEMS, Japan)
- 2P-034** **Alteration in MicroRNA dynamics fine-tunes Nanog expression heterogeneity**  
Tagari Samanta (INDIAN INSTITUTE OF TECHNOLOGY BOMBAY, India)
- 2P-035** Withdrawn
- 2P-036** **Atlas of Cancer Signaling Network: a resource of multi-scale biological maps to study disease mechanisms**  
Inna Kuperstein (Institut Curie, France)

**2P-037 A Realistic Spatial Model of the Complete Synaptic Vesicle Cycle**

Andrew Gallimore (Okinawa Institute of Science and Technology Graduate University, Japan)

2P-038 Withdrawn

**2P-039 A hybrid mathematical model for design and optimization of tamoxifen treatment in MCF-7 breast cancer cells**

Elisa Domínguez-Hüttinger (Centre for Mathematical Sciences, National Autonomous University of Mexico, Mexico)

2P-040 Withdrawn

## Multi-omics

**2P-041 Differential trans-omic networks in the liver and muscles between healthy and obese mice**

Riku Egami (Department of Computational Biology and Medical Sciences, Graduate School of Frontier Sciences, University of Tokyo, Japan)

2P-042 Withdrawn

**2P-043 Sequential pattern fusion analysis for brain evolution analysis by cross-species and cross-tissues omics data**

Tao Zeng (Key Laboratory of Systems Biology, SIBS, CAS, China)

**2P-044 Genome-wide CRISPR screen identifies TMEM41B as a gene required for autophagosome formation**

Keigo Morita (Department of Biochemistry and Molecular Biology, Graduate School of Medicine, Japan)

**2P-045 Bioinformatic pipeline aided proteome-wide analysis for deciphering bioactive peptides from the Spirulina proteins**

Jittisak Senachak (National Center for Genetic Engineering and Biotechnology, Thailand)

**2P-046 Comprehensive characterization of 'chromatome' by SWATH-MS**

Atsushi Hatano (RIKEN Center for Integrative Medical Sciences, Japan)

**2P-047 Comparative genomics of two tardigrades with different cryptobiotic capacities**

Yuki Yoshida (Keio University, Japan)

## Quantitative Systems Biology

**2P-048 Multi-dimensional analysis of NF- $\kappa$ B nuclear dynamics**

Johannes Nicolaus Wibisana (Osaka University, Japan)

**2P-049 A NF- $\kappa$ B - p38 MAPK crosstalk shapes oscillatory gene expression**

Hiroki Michida (Osaka University, Japan)

**2P-050 Hsp90-dependent strain-specific differential gene expression is common in yeast populations**

Po-Hsiang Hung (Institute of Molecular Biology, Academia Sinica, Taiwan)



- 2P-051 Systems-level modelling of meiosis regulatory network**  
Prakrati Dangarh (International Institute of Information and Technology, Hyderabad, India)
- 2P-052 Controlling biological networks using Boolean algebra**  
Chun-Kyung Lee (Department of Bio and Brain Engineering, Korea Advanced Institute of Science and Technology (KAIST), Korea)
- 2P-053 Predicting cell-line specific drug response profiles from analysis of the pan-cancer genetic regulatory network**  
Yun-Won Kang (Korea Advanced Institute of Science and Technology, South Korea)
- 2P-054 Carbon Flux Partition Underlying Storage Root Growth of Cassava Variety KU50 Inferred by Transcriptome-Integrated Metabolic Model**  
Ratchaprapa Kamsen (King Mongkut's University of Technology Thonburi, Thailand)
- 2P-055 High-resolution live-cell imaging analysis in the formative process of coordinated airway ciliary beating**  
Satoshi Konishi (Osaka University, Kyoto University, Japan)
- 2P-056 A Multi-layer Analysis of Signal-dependent Cell Cycle Progression**  
Kyoichi Ebata (Laboratory of Cell Systems, Institute for Protein Research, Osaka University, Japan)
- 2P-057 Absolute Quantification of the Mitochondrial Proteome Reveals the Dual Role in Diauxic growth of *Saccharomyces cerevisiae***  
Carl Malina (Department of Biology and Biological Engineering, Chalmers University of Technology, Sweden)
- 2P-058 Proteome Re-Allocation Towards Amplified Translational Machinery as the Limiting Factor for Increased Growth Rate of Amino Acid Supplemented *Saccharomyces cerevisiae*.**  
Johan Björkeroth (Chalmers University of Technology, Sweden)

## Single-cell Systems Biology

- 2P-059 A multi-omic approach to predict gene expression and specific metabolic function from label-free spectral imaging of living cells.**  
Arno Germond (RIKEN, Japan)
- 2P-060 Modelling of single-cell mass cytometry data to unravel breast cancer heterogeneity**  
Maria Rodriguez Martinez (IBM, Zurich Research Laboratory, Switzerland)
- 2P-061 Multi-step structure of cell fate decisions in murine neural crest**  
Peter Kharchenko (Harvard University, United States)
- 2P-062 Single-cell information analysis reveals small intracellular and large intercellular variations increase cellular information capacity**  
Takumi Wada (The University of Tokyo, Japan)

## Synthetic Biology

- 2P-063 Engineering 16-repeats PUF proteins to sequence-specifically manipulate RNA functions**  
Miki Imanishi (Kyoto University, Japan)
- 2P-064 A single base editor for simultaneous C:G to T:A and A:T to G:C mutations**  
Rina Sakata (The University of Tokyo, Japan)
- 2P-065 Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)**  
Daniel Evans-Yamamoto (Research Center for Advanced Science and Technology, The University of Tokyo, Japan)
- 2P-066 Systematic perturbation of yeast essential genes using base editing**  
Philippe Després (IBIS, Université Laval, Canada)
- 2P-067 Barcode Split Genetics (BSG) Public-key Cryptography**  
Sean Leo Kito Okawa (Research Center for Advanced Science and Technology, The University of Tokyo, Japan)
- 2P-068 A genome-wide CRISPR screen reveals novel genetic vulnerabilities to telomerase inhibition and telomere erosion**  
Lea Harrington (University of Montreal, Canada)

## Systems Biophysics

- 2P-069 Transient dimerization of a postsynaptic cell adhesion molecule neuroligin and its implications in the regulation of trans-synaptic adhesion**  
Saahil Acharya (Okinawa Institute of Science and Technology (OIST), Japan)
- 2P-070 Transient hetero-dimerization of opioid receptors (GPCRs) and their formation mechanisms revealed by single-molecule tracking**  
Peng Zhou (Membrane Cooperativity Unit, Okinawa Institute of Science and Technology Graduate University (OIST), Japan)
- 2P-071 Feedback design for desynchronization based on the analysis of the Sakaguchi-Kuramoto model**  
Ayumi Ozawa (Ochanomizu University, Japan)
- 2P-072 N-terminal region of Drosophila Argonaute2 can form amyloid fibrils**  
Haruka Narita (The University of Tokyo, Japan)
- 2P-073 Single-molecule tracking of the RNA cleavage and the dissociation driven by silkworm PIWI-clade Argonaute Siwi and RNA helicase Vasa**  
Sotaro Uemura (The University of Tokyo, Japan)



## Systems Medicine and Healthcare

- 2P-074** Computational modeling identifies optimal use of EGFR tyrosine kinase inhibitors for lung cancer patients with EGFR mutations  
Hiroshi Haeno (The University of Tokyo, Japan)
- 2P-075** Variant effect mapping of coding mutations in the human low density lipoprotein receptor (LDLR) gene  
Atina Cote (University of Toronto, Canada)
- 2P-076** Metabolic Network Modelling of Neuro-Psychiatric Disorders  
Sai Teja Reddy Moolamalla (International Institute of Information Technology, India)
- 2P-077** A missense variant effect map for the human MTHFR gene in two common genetic backgrounds  
Jochen Weile (The Donnelly Centre & Lunenfeld-Tanenbaum Research Institute; University of Toronto, Canada)
- 2P-078** Metabolic Fingerprint of Hepatic Tumor Cells  
Gerda Schicht (Department of Hepatobiliary Surgery and Visceral Transplantation, University Hospital Leipzig, Germany)
- 2P-079** Dynamic modelling of cancer signalling for improved patient stratification  
Dirk Fey (Systems Biology Ireland, Ireland)
- 2P-080** Quantification of heterogeneity of gastric cancer tumors based on Matrix-Assisted Laser Desorption Ionization or MALDI data using Machine Learning  
Majid Abedi (Helmholtz Centre for Infection Research (HZI), Braunschweig Integrated Centre of Systems Biology (BRICS), Germany)
- 2P-081** Immuno-metabolic target discovery using integrated metabolic maps (imMAPS)  
Keng Soh (Rheos Medicines, Inc, United States)

## EcoSystems Biology

- 2P-082** A novel keystone species in the rhizosphere microbiome of tomato that contributes to bacterial wilt resistance  
Jihyun F. Kim (Yonsei University, South Korea)

## Methodological Developments for Systems Biology

- 2P-083** The Center for Reproducible Biomedical Modeling  
David Nickerson (The University of Auckland, New Zealand)
- 2P-084** Pathway-specific model estimation for improved pathway annotation by network crosstalk  
Miguel Castresana Aguirre (Stockholm university, Sweden)

**2P-085 CodonAdjust: a software to design codon nucleotide compositions for generating mutagenesis libraries**

Thuy Duong Nguyen (National Institute of Advanced Industrial Science and Technology, AI Research Center, Japan)

## **Systems Biophysics**

**2P-086 Optimal information processing of time-varying signals through metastable states at criticality**

Akhilesh P. Nandan (Max Planck Institute of Molecular Physiology, Germany)

## **Systems Medicine and Healthcare**

**2P-087 What do we really mean by Health?: On the way towards Precision Health**

Gokhan Ertaylan (Flemish Institute for Technological Research (VITO) , Netherlands)



## MONDAY, NOVEMBER 4

Time: 14:10-15:30 / Venue: Tunnel Gallery

### Big Data, AI & Laboratory Automation

- 4P-001 Automatic tumor identification from ultrasonic liver images using deep learning**  
Kenji Karako (Department of Human and Engineered Environmental Studies, Graduate School of Frontier Sciences, The University of Tokyo, Japan)
- 4P-002 Medical image segmentation by CNN using the relationship between features of different layers**  
Yuki Hiramatsu (Meijo University, Japan)
- 4P-003 Classification of Pluripotent genes using Machine Learning Techniques**  
Saurabh Kumar (IIIT Bhubaneswar, India)

### Developmental Systems Biology

- 4P-004 Planar cell polarity-dependent distribution of apical microtubules in tracheal multiciliated cells**  
Shogo Nakayama (Dept. of Bio Sci., Grad. Sch. of Medicine, Osaka University, Japan)
- 4P-005 Analysis of shear stress for angiogenic sprouting using on-chip microvascular model**  
Ryuji Yokokawa (Kyoto University, Japan)
- 4P-006 Thymocytes reprogram in the face of progenitor shortage**  
Adrien Jolly (DKFZ, Germany)

### EcoSystems Biology

- 4P-007 Development of Novel Immunoassay using a recombinant scFv Antibody Specific to Potato Leafroll Virus**  
Mi-Gi Lee (Biocenter, Gyeonggido Business & Science Accelerator, South Korea)
- 4P-008 Chromosome-scale comparative sequence analysis among *Oikopleura dioica* individuals sampled from globally distributed locations**  
Aleksandra Bliznina (Okinawa Institute of Science and Technology Graduate University, Japan)
- 4P-009 SPADE for exploring periodic sequence repeats as potential genome editing modules**  
Hideto Mori (Synthetic Biology Division, Research Center for Advanced Science and Technology, The University of Tokyo, Japan)
- 4P-010 The zooplankton *Oikopleura dioica* from the point of view of systems biology**  
Charles Plessy (Okinawa Institute of Science and Technology Graduate University (OIST), Japan)

## Methodological Developments for Systems Biology

- 4P-011 Visualizing Metabolic Network Dynamics through Time-Series Metabolomics Data**  
Andreas Dräger (Computational Systems Biology of Infection and Antimicrobial-Resistant Pathogens, University of Tübingen, Germany)
- 4P-012 Mining of cell-intrinsic core-regulatory circuits driving tumor-related phenotypes with the I3-OncoNet cycle**  
Mohamed Elati (Université de Lille, France)
- 4P-013 Diverse metabolic modeling capabilities and its use of scientific applications in KBase**  
Janaka Edirisinghe (Argonne National Laboratory, United States)
- 4P-014 Benchmarking Time-Series Data Discretization on Reverse Engineering Methods**  
Paola Vera-Licona (Center for Quantitative Medicine, University of Connecticut School of Medicine, United States)
- 4P-015 Integrative workflow of modelling and parameter estimation for quantitative multicellular systems biology**  
Jörn Starruß (TU Dresden, Germany)
- 4P-016 “GlycoSim”: a web tool for modeling and simulation of glycan biosynthesis pathways**  
Sachiko Akase (Bioinformatics Department, Graduate School of Engineering, SOKA University, Japan)
- 4P-017** Withdrawn
- 4P-018 Computing all possible cell differentiation pathways from time-series data**  
Zoltan Tuza (Imperial College London, United Kingdom)

## Modeling Networks and Circuits

- 4P-019 Validity of quasi-steady-state approximation for a Michaelis-Menten-type reaction in regulatory reaction networks**  
Takashi Naka (Kyushu Sangyo University, Japan)
- 4P-020 Effects of 1-Methyltryptophan on the kynurenine pathway in pigs**  
Dana Kleimeier (Institute of Bioinformatics, University Medicine Greifswald, Germany)
- 4P-021 Disease-gene prioritization by link prediction identifies candidate genes for complex disease.**  
Ilyes Abdelhamid (Channing Division of Network Medicine, Brigham and Women's Hospital, Harvard Medical School, United States)
- 4P-022 A novel approach for the generation of disease specific genetic interaction data using gene-based statistical epistasis**  
Sathish Periyasamy (Queensland Brain Institute; Queensland Centre for Mental Health Research, Australia)
- 4P-023** Withdrawn





- 4P-024 Local-community network automata modelling based on length three-paths for prediction of complex network structures in protein interactomes, food webs and more**  
Ilyes Abdelhamid (Channing Division of Network Medicine, Brigham and Women's Hospital, Harvard Medical School, United States)
- 4P-025 A stochastic spatial model of the vesicular trafficking of AMPA-receptors**  
Sarah Nagasawa (Okinawa Institute of Science and Technology, Japan)
- 4P-026 The Systems Biology Graphical Notation: a standardised representation of biological maps**  
Andreas Dräger (Computational Systems Biology of Infection and Antimicrobial-Resistant Pathogens, University of Tübingen, Germany)
- 4P-027 Reconstruction of Boolean gene regulatory network model based on pseudotime analysis of single-cell RNA-Seq data**  
Hoon-Min Kim (Korea Advanced Institute of Science and Technology, South Korea)
- 4P-028 Development of simultaneous measurement system for transcription and RNA degradation rates using modified nucleic acid**  
Kentaro Kawata (The University of Tokyo, Japan)
- 4P-029 Integrating statistical methods and modeling approaches reveals the synergistic transcriptional control mechanism of the primary B cell**  
Sufeng Chiang (Genome and Systems Biology Degree Program, National Taiwan University and Academia Sinica, Taiwan)
- 4P-030 Probabilistic critical controllability analysis on protein interaction network integrating normal brain aging gene expression profiles**  
Eimi Yamaguchi (Toho University, Japan)
- 4P-031 An Integer Linear Programming-based Approach for Identifying Driven Nodes in Complex Networks**  
Yuma Shinzawa (Toho University, Japan)
- 4P-032 A computational method to infer consensus formation processes during cell differentiation**  
Shinji Nakaoka (Hokkaido University, Japan)
- 4P-033 Random responses to specific stimuli, modelling the  $\sigma^B$  mediated stress response in *B. Subtilis***  
Torkel Loman (University of Cambridge, United Kingdom)
- 4P-034 MODELING THE IMPACT OF DOUBLE X-DOSAGE ON SIGNALING PATHWAYS IMPLICATED IN PLURIPOTENCY**  
Zeba Sultana (Max Planck Institute for Molecular Genetics, Berlin, Germany)
- 4P-035 Regulatory networks driving circRNA expression in breast cancer**  
Wanwan Feng (CAS-MPG Partner Institute for Computational Biology (PICB), Chinese Academy of Sciences (CAS), China)

- 4P-036 Computational model to predict O-linked glycosylation of glycoprotein PSGL-1 in CHO cells**  
Thukaa Kuoka (Graduate School of Engineering, SOKA University, Japan)
- 4P-037 Analyzing whole-brain dynamics of *C. elegans* with statistical approach**  
Yuko Murakami (Kyushu University, Japan)
- 4P-038 A Framework for Building Models for Biomolecular Systems from Experimental Data Automatically**  
Zoltan Tuza (Imperial College London, United Kingdom)
- 4P-039 Molecular Interpolation of multi dimensional space to predict Monomeric high scaled Enzymatic protein from NEAT Neural Networks**  
Lokesh Thangamani (Bharathiar University, India)

## Multi-omics

- 4P-040 Comprehensive detection of group II intron sequences from genome data and their phylogenetic profiles in bacteria**  
Masahiro C. Miura (Keio University, Japan)
- 4P-041 Identifying Potential Candidate Genes by Combining Gene Regulatory and Protein-Protein Interaction Networks Using a Multiplex PageRank Algorithm**  
Annika Röhl (Harvard University, United States)
- 4P-042 Generating hypothesis from microRNA - mRNA expression data using the smirk R package.**  
Krutik Patel (Newcastle University, United Kingdom)
- 4P-043 piRScan: a webserver to predict piRNA targeting sites and to avoid transgene silencing in *C. elegans***  
Wei-Sheng Wu (Dept. of Electrical Engineering, Nat'l Cheng Kung University, Taiwan)
- 4P-044 Transcriptomic and metabolic integrative study inferring the dynamics of cyanogenic glucoside biosynthesis in developing storage roots of cassava**  
Wanatsanan Siriwat (King Mongkut's University of Technology Thonburi, Thailand)
- 4P-045 Using multi-omics approaches to identify pathogenic pathways associated with systematic vasculitis**  
Tai-Ming Ko (National Chiao Tung University, Taiwan)
- 4P-046 Automated Reconstruction, Evaluation and Comparison of Diverse Genome-Scale Fungal Metabolic Models**  
Janaka Edirisinghe (Argonne National Laboratory, United States)



## Quantitative Systems Biology

- 4P-047 Feedback control of evolutionary trajectory of bacterial cells on fitness landscape**  
Atsushi Shibai (RIKEN, Japan)
- 4P-048 Sporadic gene expression dynamics : a clever strategy for virus persistence**  
Shingo Iwami (Kyushu University, Japan)
- 4P-049 Apical cytoskeleton mediates coordinated beating of cilia in tracheal multiciliated cells for apical functioning of epithelia**  
Sachiko Tsukita (Teikyo University, Osaka University, Japan)
- 4P-050** Withdrawn
- 4P-051 Reversion of Chemoresistance in a Triple Negative Breast Cancer Subtype**  
Paola Vera-Licona (Center for Quantitative Medicine, UConn Health, United States)
- 4P-052** Withdrawn
- 4P-053 Signaling network of apoptosis/necroptosis in bortezomib and oncolytic virus therapy and miR-451-LKB1-AMPK-Oct1 signaling in glioblastoma**  
Yangjin Kim (Konkuk University Ohio State University, South Korea)
- 4P-054 Revealing the functional role of FABP5 in stratification of lung cancer patients**  
Pouyan Ghaffari (Technical University of Denmark, Denmark)
- 4P-055 Comparative transcriptome analysis of idiopathic pulmonary fibrosis and lung cancer**  
Yosui Nojima (National institutes of biomedical innovation, health and nutrition, Japan)
- 4P-056 A Computational Model for Programmed Necrosis in Cancer**  
Iman Tavassoly (Icahn School of Medicine at Mount Sinai, United States)
- 4P-057 Wnt/beta-catenin modulates lung adeno-to-squamous transdifferentiation**  
Zhaoyuan Fang (Shanghai Institute of Biochemistry and Cell Biology, China)

## Single-cell Systems Biology

- 4P-058 Single-cell frequency response of intracellular signal transduction based on live-cell active sensing and nonlinear system identification**  
Katsuyuki Kunida (Graduate School of Science and Technology, and Data Science Center, Nara Institute of Science and Technology, Japan)
- 4P-059 Bioinformatic processing of single-cell RNA-seq data for genome-wide parameter estimation upon eukaryotic gene expressions**  
Keita Iida (Osaka University, Japan)
- 4P-060 rCASC, Reproducible Classification Analysis of Single Cell sequencing data**  
Luca Alessandri (Department of Molecular Biotechnology and Health Sciences, University of Torino, Italy)

**4P-061 Thermodynamically motivated cell segmentation for single-cell modeling of GAL1 in yeast**

Cheng-Hui Chen (National Cheng Kung University, Taiwan)

**4P-062 A Systems Biology Study on Parkinson's Disease Based on Single Cell RNA Sequencing in Drosophila Model**

Zhirong Sun (School of Life Sciences, Tsinghua University, China)

## **Systems Biology for Neurosciences and Neural Circuits**

**4P-063 Astrocyte Neuron Simulation Environment Platform: ANSEP**

Andres Pinzón Velasco (Universidad Nacional de Colombia, Colombia)

**4P-064 Circuit-level analysis of deviance detection and adaptation by in vivo calcium imaging of mouse auditory cortex**

Shunsuke Mizutani (Department of Cellular Neurobiology, Graduate School of Medicine and Faculty of Medicine, The University of Tokyo, Japan)

**4P-065 Computational geometry analysis of spine morphology in living neurons**

Yutaro Kashiwagi (The University of Tokyo, Japan)

**4P-066 Circadian characteristics of behavioral and physiological rhythms in diurnal primate common marmosets (*Callithrix jacchus*).**

Iori Murai (Graduate School of Pharmaceutical Sciences, Kyoto University, Japan)

**4P-067 Whole-brain imaging reveals dynamical structure of neural signaling in *C. elegans***

Taichi Isaka (Ibaraki University, Japan)

**4P-068 Does maternal rhythm affect the development of circadian rhythm of the offspring?**

Keiko Tominaga (Osaka University, Japan)

## **Systems Biophysics**

**4P-069 RNA helicase DDX43 drives Ago3-dependent piRNA biogenesis in ping-pong cycle**

Ryo Murakami (The University of Tokyo, Japan)

**4P-070 A pipeline of bio-image informatics for whole-brain imaging of *C. elegans* and analysis of the neural activity**

Yu Toyoshima (The University of Tokyo, Japan)

**4P-071 Numerical simulation of multiciliated cells cilia translational and rotational self-organization by the interaction with the apical cytoskeleton and asymmetric time-dependent boundary conditions**

Fermin Franco Medrano (Osaka University, Japan)

**4P-072 Simulation of live-cell imaging system reveals hidden uncertainties in cooperative binding measurements**

Masaki Watabe (RIKEN Center for Biosystems Dynamics Research, Japan)



**4P-073 Phase-field modeling for 3D dynamics in macropinocytosis**

Nen Saito (The University of Tokyo, Japan)

## Systems Medicine and Healthcare

**4P-074 Individual gene expression profiles identify responders and non-responders to Imatinib in severe asthmatics.**

Seung Han Baek (Channing Division of Network Medicine, Brigham and Women's Hospital and Harvard Medical School, United States)

**4P-075 Novel relationship between osteoporosis and genes: potential role of Vit. D metabolism and sex hormone**

Sang Wook Kang (Dankook University, South Korea)

**4P-076 DrugComb: an integrative cancer drug combination data portal.**

Bulat Zagidullin (University of Helsinki, Finland)

**4P-077 Integrative analysis of multi-Omics data reveals that the dysregulation of splicing related proteins in prostate cancer is controlled by FOXA1**

Marco Del Giudice (Italian Institute for Genomic Medicine, Italy)

**4P-078 Evaluation of enhanced intracellular delivery of doxorubicin in metastatic cancer cells by systems Biology approach**

Dongqing Wei (Shanghai Jiao Tong University, China)

**4P-079 Translational Informatics and Systems Healthcare in the Era of 5G Networks**

Bairong Shen (West China Hospital, Sichuan University, China)

**4P-080 Ambient MS-based tissue profiling for assistance on neurosurgery operations of brain cancer**

Anatoly Sorokin (Moscow Institute of Physics and Technology, Russia)

**4P-081 Towards discovery of human disease mechanisms by graph-based contextual integration of 'omics signatures.**

Artem Lysenko (RIKEN, Japan)

## Big Data, AI & Laboratory Automation

**4P-082 The generalized relationship between gene intrinsic properties and phenotypic features revealed by multi-omic big data mining**

Dong Yang (Institute of Lifeomics, AMMS, China, China)

**4P-083 Detection and quantification of necrosis in glioma using deep learning on whole slide images**

Hanli Huang (The Hong Kong University of Science and Technology, Hong Kong)

## Methodological Developments for Systems Biology

- 4P-084 Improved gene regulatory network inference with consensus methods**  
Thomas Hillerton (Stockholm University, Sweden)
- 4P-085 A Benchmark Study Highlighting the Importance of Perturbation Design for Accurate Gene Regulatory Network Inference**  
Deniz Seçilmiş (Stockholm Bioinformatics Center, Science for Life Laboratory, Department of Biochemistry and Biophysics, Stockholm University, Sweden)
- 4P-086 Integrated networks in *Salmonella* research**  
Márton Ölbei (Earlham Institute, Norwich and Quadram Institute Biosciences, Norwich, UK)

## Systems Biology for Neurosciences and Neural Circuits

- 4P-087 Neural synchrony as a coupling mechanism of multi-agent systems**  
Ana Lucia Valencia (UNAM, Mexico)
- 4P-088 Self-optimization in biologically-inspired topologies: the case of the *C. elegans* connectome**  
Alejandro Ehecátl Morales Huitrón (Universidad Nacional Autónoma de México, Mexico)



**Workshop 01 Precision Network Medicine in the era of big data!**

Date: October 31, 2019, 9:00-18:00 Venue: Auditorium

Organizer: Amitabh Sharma (Harvard Medical School)

**Workshop 02 BioNetVisA: from biological network reconstruction to data visualization and analysis in molecular biology and medicine**

Date: October 31, 2019, 9:00-18:00 Venue: B250

Organizer: Inna Kuperstein (Institut Curie)

**Workshop 03 Singularity Biology: small elements change the function of the whole systems**

Date: October 31, 2019, 9:00-14:00 Venue: Meeting room 1

Organizer: Shuichi Onami (RIKEN BDR)

**Workshop 04 Trans-Omics workshop – The 3rd International Symposium for Trans-Omics –**

Date: October 31, 2019, 14:00-18:00 Venue: Meeting room 1

Organizer: Shinya Kuroda (The University of Tokyo)

**Workshop 05 Qualitative computational modeling for biological networks**

Date: October 31, 2019, 9:00-18:00 Venue: Meeting room 3

Organizer: Adrien Faure/Denis Thieffry (Yamaguchi University/Univ Paris-Saclay)

**Workshop 06 KBase: free, open platform for genomics analysis of microbes, plants, and their communities**

Date: October 31, 2019, 9:00-12:00 Venue: Meeting room 4

Organizer: Jose P. Faria (Argonne National Laboratory)

**Workshop 07 Putting metabolomic data into context: An introduction to the Virtual Metabolic Human database ([www.vmh.life](http://www.vmh.life)) and metabolic modeling**

Date: October 31, 2019, 14:00-18:00 Venue: Meeting room 4

Organizer: Cyrille C. Thinnes (Universte du Luxembourg)

**Tutorial 01 Advanced Modelling with COPASI**

Date: October 31, 2019, 9:00-13:00 Venue: C209

Organizer: Sven Sahle (Universitat Heidelberg)

**Tutorial 02 COMBINE & de.NBI Tutorial: Modelling and Simulation Tools in Systems Biology**

Date: October 31, 2019, 9:00-18:00 Venue: C210

Organizer: Martin Golebiewski (HITS gGmbH)