GENOMES & AI: FROM PACKING TO REGULATION
October 2-4, 2019, Singapore
Venue: Shaw Foundation Alumni House, National University of Singapore

Day 0: (Oct 1, 2019)		
18.30-20.30	Welcome Reception at The Mechanobiology Institute	
Day 1: (Oct 2, 2019)		
08.30-09.20	Registration	
09.20-09.30	**Caroline Uhler** Massachusetts Institute of Technology, USA	*Opening remarks*
Session-I	**Chair: Lior Pachter, California Institute of Technology, USA**	
09.30-10.00	**Timm Schroeder** ETH Zurich, Switzerland	*Long-term single-cell quantification: New tools for old questions*
10.00-10.30	**Barbara Engelhardt** Princeton University, USA	*Rethinking distal genetic regulation of gene expression*
10.30-10.45	**Yongdae Shin*** Seoul National University, South Korea	*The mechanical interplay of Nuclear Condensates and Genome revealed by Optogenetics*
10.45-11.15	Tea Break	
11.15-11.45	**Vadim Backman** Northwestern University, USA	*Bridging chromatin nanoimaging and molecular modeling: Chromatin packing as a regulator of transcriptional heterogeneity in carcinogenesis*
11.45-12.00	**Hisae Tateishi-Karimata*** (FIBER) Konan University, Japan	*Effects of malignant alteration in cancer cells on the DNA G-quadruplex formation and transcript mutations*
12.00-12.30	Lightning talks from poster presenters-Session I	
12.30-14.30	Lunch and Posters	
Session-II	**Chair: Vadim Backman, Northwestern University, USA**	
14.30-15.00	**Caroline Uhler** Massachusetts Institute of Technology, USA	*From Single-Cell Data to Computational Models of Genome Packing and Regulation*
15.00-15.30	**Shyam Prabhaka**r Genome Institute of Singapore, Singapore	*Algorithms for Single Cell Omics*
15.30-15.45	**Karren Yang*** Massachusetts Institute of Technology, USA	*Single-Cell Data Integration using Representation Learning*
15.45-16.15	Tea Break	
16.15-16.45	**Lani Wu** University of California, San Francisco, USA	*Single-cell cancer fate decisions after non-lethal dose of chemotherapy*
16.45-17.15	**Gustavo Stolovitzky** IBM Research, USA	*Intracellular noise and intercellular diversity: from causal network inference to single cell response to chemical perturbations*
17.15-17.30	**Saradha Venkatachalapathy*** Mechanobiology Institute-NUS, Singapore	*Multivariate analysis of fibroblast activation in engineered 3D tumor microenvironments*
17.30 onwards	Outing & Dinner (own)	

Day 2: (Oct 3, 2019)		
Session-III	**Chair: Timm Schroeder, ETH Zurich, Switzerland**	
09.30-10.00	**Jennifer Listgarten** University of California, Berkeley, USA	*Accelerating protein and molecule engineering with machine learning approaches*
10.00-10.30	**Steven Altschuler** University of California, San Francisco, USA	*Dissecting network crosstalk in intestinal epithelial tissue, one cell at a time*
10.30-10.45	**Yuguang Mu*** Nanyang Technological University, Singapore	*OnionNet: a multiple-layer inter-molecular contact based convolutional neural network for protein-ligand binding affinity prediction*
10.45-11.15	Tea Break	
11.15-11.45	**Marco Foiani** IFOM-FIRC Institute of Molecular Oncology, Italy	*Coordinating chromosome replication forks with gene transcription*
11.45-12.00	**Greg-Tucker-Kellogg*** National University of Singapore, Singapore	*Transcription factor inference from transcript start-site level differential expression analysis*
12.00-12.15	**Eddy Pang*** National University of Singapore, Singapore	*Dynamic changes in 3D chromatin structure during EMT in ovarian cancer*
12.15-12.45	Lightning talks from poster presenters-Session II	
12.45-14.30	Lunch and Posters	
14.30 onwards	Free Time/Singapore Sightseeing (own)	

Day 3: (Oct 4, 2019)		
Session-IV	**Chair: Lani Wu, University of California, San Francisco, USA**	
09.30-10.00	**Long Cai** California Institute of Technology, USA	*Spatial Genomics: single cell in situ RNA analysis by seqFISH*
10.00-10.15	**Justine Seow*** Genome Institute of Singapore, Singapore	*Cellular plasticity associated gene regulatory networks at single cell resolution*
10.15-10.30	**Doorgesh Sharma Jokhun*** Mechanobiology Institute-NUS, Singapore	*Nuclear morphometrics and chromatin condensation patterns as Disease Biomarkers*
10.30-10.45	**Winston Koh*** Molecular Engineering Lab, Singapore	*Model based clustering and annotation of single cell omics data for inference of tumour clonality and tumour-infiltrating myeloid cells identity*
10.45-11.15	Tea Break	
11.15-11.45	**Meromit Singer** Harvard University, USA	*Characterization to function: prediction of marker panels from single-cell transcriptomics data*
11.45-12.15	**Kim-Chuan Toh** National University of Singapore, Singapore	*Inference of spatial organizations of chromosomes from Hi-C data by a semidefinite programming approach*
12.15-12.30	**Etienne ROUTHIER*** Sorbonne Université, France	*Studying the effects of single mutations on nucleosome positioning with deep neural network*
12.30-14.30	Lunch and Posters	
Session-V	**Chair: Barbara Engelhardt, Princeton University, USA**	
14.30-15.00	**María Rodríguez Martínez** IBM Research, Zurich	*Multiscale clonal model of Germinal Center B cell differentiation*
15.00-15.30	**Francesco Ferrari** IFOM-FIRC Institute of Molecular Oncology, Italy	*Novel solutions for mapping chromatin 3D architecture rearrangements*
15.30-15.45	**Anastasiya Belyaeva*** Massachusetts Institute of Technology, USA	*Addressing Challenges in Analysis of Hi-C Data: From Gene Clusers to Diploid Organization and Cell Sub-populations*
15.45-16.15	Tea Break	
16.15-16.45	**Lior Pachter** California Institute of Technology, USA	*Applications and implications of modular efficient processing of single-cell RNA-seq*
16.45-17.15	**G.V. Shivashankar** Mechanobiology Institute-NUS, Singapore & IFOM, Italy	*Mechano-Genomics and Cell-Fate Decisions*
17.15-17.30	**G.V. Shivashankar**	*Awards & Closing Remarks*
End of Meeting		

* selected short talks from contributed abstracts