

## APBC2019 Program

Day 0: Sunday, January 13, 2019		
08:20-08:40	Tutorial Registration	
08:40-10:10	Transcriptome Analysis (Part I) <a href="#">Cheng Li</a> , <a href="#">Peking University</a>	
10:10-10:30	Tea Break	
10:30-12:00	Transcriptome Analysis (Part II)	
12:00-14:00 Lunch		
14:00-15:30	Metagenomics (Part I) <a href="#">Rohan Williams</a> National University of Singapore	Gene-Regulatory Network (Part I) <a href="#">Yong Wang</a> Institute of Applied Math., CAS.
15:30-16:00	Tea Break	
16:00-17:30	Metagenomics (Part II)	Gene-Regulatory Network (Part II)
16:00-18:30	<b>Conference Registration (IEC Lobby)</b>	

† International Exchange Center Lobby

Day 1: Monday, January 14, 2019		
08:00-09:00	Registration (IEC Lobby)	
09:00-09:15	Welcome Speech (Main Hall)	
09:15-10:15 Plenary Session	<p style="text-align: center;">Ming Li Discovering Neoantigens Chair TBA</p>	
10:15-10:50	Group photo, tea break	
Parallel Session	Genome I Chair TBA	Data I Chair TBA
10:50-11:10	(P49) Identification of trans-eQTLs using mediation analysis with multiple mediators	(P54) Improving the sensitivity of detecting long read overlaps using grouped short k-mer matches
11:10-11:30	(Highlight) Machine Learning Algorithms for Modeling 3D Chromosome Structures	(P30) Signal enrichment of metagenome sequencing reads using topological data analysis
11:30-11:50	(P141) A secure SNP panel scheme using homomorphically encrypted K-mers without SNP calling on the user side	(P46) Automatic localization and identification of Mitochondria in cellular electron Cryo-Tomography using Faster-RCNN
12:00-14:00	Lunch	
Parallel Session	Proteins I Chair TBA	Genome II Chair TBA
14:00-14:20	(P145) De Novo glycan structural identification from mass spectra using tree merging strategy	(Highlight) Detection and analysis of ancient segmental duplications in mammalian genomes
14:20-14:40	(P134) Prediction of FMN Binding Sites in Electron Transport Chain based on 2-D CNN and PSSM Profiles	(P117) Sorting Signed Permutations by Inverse Tandem Duplication Random Losses
14:40-15:00	(Highlight) AuTom-dualx: a toolkit for fully automatic fiducial marker-based alignment of dual-axis tilt series with simultaneous reconstruction	(P53) A distance-type measure approach to the analysis of copy number variation in DNA sequencing data
15:00-15:20	(P140) Constructing optimal energy functions for protein structure prediction using reverse Monte Carlo sampling	(P113) Branching out to speciation with a Birth-and-Death model of fractionation: the <i>Malvaceae</i>
15:20-15:40	Tea break	
Parallel Session	Systems I Chair TBA	Genes and RNAs I Chair TBA
15:40-16:00	(P56) Predicting drug-target interaction network using deep learning model	(P149) Detecting virus-specific effects on post-infection temporal gene expression
16:00-16:20	(P79) Identifying mutated driver pathways in cancer by integrating multi-omics data	(P9) RCPred: RNA Complex Prediction as a constrained maximum weight clique problem
16:20-16:40	(P18) Modelling the role of dual specificity phosphatases in Herceptin resistant breast cancer cell lines	(P25) ReactIDR: Evaluation of the statistical reproducibility of high-throughput structural analyses for a robust RNA reactivity classification
16:40-17:00	(P41) Prediction of drug-disease associations based on ensemble meta paths and singular value decomposition	(Highlight) The functional study of non-coding elements by integrating of 3D and 1D genome information
17:00-18:00	Poster Session (posters with odd ID)	

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Day 2: Tuesday, January 15, 2019		
09:00-10:00 Plenary Session	<p style="text-align: center;"><b>Fengzhu Sun</b>            Statistical and Computational Approaches for the Identification            of Novel Viruses and Virus-host Interactions  <b>Chair TBA</b></p>	
10:00-10:30	Tea break	
Parallel Session	<b>Genome III</b> <b>Chair TBA</b>	<b>Data II</b> <b>Chair TBA</b>
10:30-10:50	(P126) Meta-Network: Optimized species-species network analysis for microbial communities	(P108) SplicedFamAlign: CDS-to-gene spliced alignment and identification of transcript orthology groups
10:50-11:10	(P89) Towards optimal decomposition of Boolean networks	(P124) Large-scale 3D chromatin reconstruction from chromosomal contacts
11:10-11:30	(P31) Fusing gene expression and transitive protein-protein interaction for gene regulatory networks	(P86) Estimating the total genome length of a metagenomic sample using K-mers
11:30-11:50	(P100) Anti-TNF- $\alpha$ treatment-related pathways and biomarkers revealed by transcriptome analysis in Chinese Psoriasis patients	(P67) Ultrafast clustering of single-cell flow cytometry data using FlowGrid
12:00-14:00	Lunch	
Parallel Session	<b>Data III</b> <b>Chair TBA</b>	<b>Genome IV</b> <b>Chair TBA</b>
14:00-14:20	(P5) SCOUT: A new algorithm for the inference of pseudo-time trajectory using single-cell data	(P87) GPU accelerated sequence alignment with traceback for GATK HaplotypeCaller
14:20-14:40	(P80) ENIGMA: An enterotype-like unigram mixture model for microbial association analysis	(P20) The unconstrained diameters of the duplication-loss cost and the loss cost
14:40-15:00	(P109) Extending liquid association to explore mediated co-varying dynamics in marine microbial community	(P21) Reconciliation reconsidered: In search of a most representative reconciliation in the Duplication-Transfer-Loss model
15:00-15:20	(P150) Microbiota in the apical root canal system of tooth with apical periodontitis	(P104) Multiple optimal reconciliations under the duplication-loss-coalescence model
15:20-15:40	Tea break	
Parallel Session	<b>Proteins II</b> <b>Chair TBA</b>	<b>Genome V</b> <b>Chair TBA</b>
15:40-16:00	(P73) Network-based characterization of drug-protein interaction signatures with a space-efficient approach	(P129) Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues
16:00-16:20	(Highlight) iEKPD 2.0: an update with rich annotations for eukaryotic protein kinases, protein phosphatases and proteins containing phosphoprotein-binding domains	(P148) Identification of Hürthle cell cancers: solving a clinical challenge with genomic sequencing and a trio of machine learning algorithms
16:20-16:40	(P19) Protein complex detection based on flower pollination mechanism in multi-relation reconstructed dynamic protein networks	(Highlight) Resilience of human gut microbial communities for the long stay with multiple dietary shifts
16:40-17:00	(P38) A class imbalance-aware Relief algorithm for the classification of tumors using microarray gene expression data	(P29) DeepHistone: a deep learning approach to predicting histone modifications
17:00-18:00	Poster Session (posters with even ID)	
18:00-20:00	Banquet and Business Meeting	

Day 3: Tuesday, January 16, 2019		
09:00-10:00 Plenary Session	<b>Ron Shamir</b> Integrated analysis of cancer data and precision medicine <b>Chair TBA</b>	
10:00-10:30	Tea break	
Parallel Session	Systems II <b>Chair TBA</b>	Genes and RNAs II <b>Chair TBA</b>
10:30-10:50	(P143) Boolean network modeling of $\beta$ -cell apoptosis and insulin resistance in Type 2 diabetes mellitus	(P33) FCMDAP: Using miRNA family and cluster information to improve the prediction accuracy of disease related miRNAs
10:50-11:10	(P139) Discovery of perturbation gene targets via free text metadata mining in Gene Expression Omnibus	(P26) GNE: A deep learning framework for gene network inference by aggregating biological information
11:10-11:30	(P127) Automatic hierarchy classification in venation networks using directional morphological filtering for hierarchical structure traits extraction	(Highlight) De novo haplotype reconstruction in viral quasispecies using paired-end read guided path finding
11:30-11:50	(Highlight) Comprehensive identification of peptides in tandem mass spectra using an efficient open search engine	(P23) DeGSM: memory scalable construction of large scale de Bruijn graph
12:00-14:00	Lunch	
Parallel Session	Genome VI <b>Chair TBA</b>	Systems III <b>Chair TBA</b>
14:00-14:20	(P24) MRCNN: A deep learning model for regression of genome-wide DNA methylation	(P146) A fast and efficient count-based matrix factorization method for detecting cell types from single-cell RNAseq data
14:20-14:40	(P84) TSEE: an elastic embedding method to visualize the dynamic gene expression patterns of time series single-cell RNA sequencing data	(P34) Predicting disease-related phenotypes using an integrated phenotype similarity measurement based on HPO
14:40-15:00	(P62) A new class of super-enhancers associated with fast recovery of 3D chromatin loops	
15:00-15:30	<b>Award Ceremony and Closing Remarks</b>	