RECOMB 2017

The 21st Annual International Conference on
Research in Computational Molecular Biology

May 3-7, 2017

RECOMB-Seq 2017

The Seventh RECOMB Satellite Workshop on
Massively Parallel Sequencing

May 7-8, 2017

Sponsors

Croucher Foundation
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Welcome to
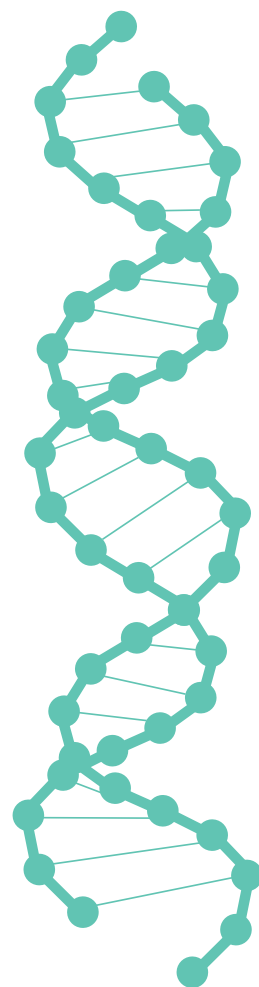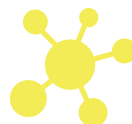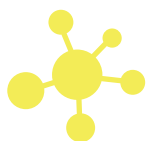## RECOMB & RECOMB-Seq 2017

On behalf of the local organizing committee, The University of Hong Kong and The Chinese University of Hong Kong, I welcome you to Hong Kong. Apart from attending the conference, I do wish that you will have the chance to explore our really wonderful city in your spare time.

RECOMB 2017 will be action-packed, consisting of a three-and-a-half-day conference program (May 4-7, 2017) followed by RECOMB-Seq 2017 with one-and-a-half-day workshop program (May 7-8, 2017). This program booklet gives you the agenda for both RECOMB and RECOMB-Seq. Note that, we have six keynotes for RECOMB (one in the morning and one in the afternoon on the first three days) and two keynotes for RECOMB-Seq (one on each day). Posters are divided into two parts (see the detailed schedule in this booklet).

Upon registration of attendance, you will receive the e-copy of the proceedings containing the accepted papers and the abstracts of the accepted posters. The meal tickets you receive will include one for the Banquet on May 5.

Please note that wireless Internet access is available throughout most of the campus of the Chinese University of Hong Kong (via eduroam if you have an account) or throughout the venue of the conference (the login and password are shown at "Others" section of this booklet and at the back of your conference badge).

Finally, I would like to take this opportunity to thank the many people who have contributed to RECOMB 2017 and RECOMB-Seq 2017. A special thanks should go to the Croucher Foundation for their generous support of the keynote speakers; ISCB for their kind support for student travel fellowship; and BGI and the Chinese University of Hong Kong for their kind support of the conference.

Enjoy the conference!

S.M. Yiu
RECOMB 2017 Conference Chair

Agenda at a Glance

Venue: Cheng Yu Tung (CYT) Building, The Chinese University of Hong Kong (CUHK)
RECOMB KT: Keynote, PT: Proceedings Talk, HT: Highlights Talk *(LT1, Level 1, CYT Building, CUHK)*

RECOMB-Seq KT: Keynote, RT: Regular Talk, ST: Short Talk *(LT6, Level 2, CYT Building, CUHK)*

	RECOMB		
	May 3 (Wed)	May 4 (Thu)	May 5 (Fri)
8:30 AM - 8:45 AM		Registration (RECOMB)	Registration (RECOMB)
8:45 AM - 9:00 AM		**Opening Remarks**	
9:00 AM - 10:00 AM		**S01: Precision Health [KT] Jun Wang**	**S07: Network and Pathways [KT] Ben Raphael**
10:00 AM - 10:20 AM		*Coffee break*	*Coffee break*
10:20 AM - 11:20 AM		S02: Sequencing I [PT] Mukherjee et al. [PT] Welch et al. [PT] Shlemov et al.	S08: Cancer I [PT] Dao et al. [PT] Zaccaria et al. [PT] Szczurek et al.
11:20 AM - 11:30 AM		*Break*	*Break*
11:30 AM - 12:30 PM		S03: Population and Disease Studies I [PT] Wu et al. [PT] Wang et al. [HT] Rahmani et al.	S09: Protein-DNA Interactions and Gene Regulation [PT] Zhao et al. [PT] Guo et al. [PT] Orenstein et al.
12:30 PM - 1:00 PM		*Lunch break (lunch provided)*	*Lunch break (lunch provided)*
1:00 PM - 2:00 PM			
2:00 PM - 3:00 PM		**S04: Translational Science [KT] Colin Collins**	**S10: Sequencing II [KT] Michael Schnall-Levin**
3:00 PM - 3:20 PM		*Coffee break*	*Coffee break*
3:20 PM - 4:20 PM		S05: Networks and Systems [PT] Ness et al. [PT] Wang et al. [PT] Luo et al.	S11: New Directions [PT] Li et al. [HT] Altenbuchinger et al. [PT] Keich et al. [PT] Zhang et al.
4:20 PM - 4:30 PM		*Break*	
4:30 PM - 5:00 PM		S06: Alignment, Search and Compression [PT] Solomon et al., Sun et al. [PT] Holley et al. [PT] Jain et al.	**Poster Session I**
5:00 PM - 5:30 PM			
5:30 PM - 6:00 PM			
6:00 PM - 6:30 PM	**Registration and Welcome Reception (Hyatt, Sha Tin)**		
6:30 PM - 7:00 PM			**Banquet (ClubONE on the Park, Science Park)**
7:00 PM - 9:00 PM			

RECOMB		
	RECOMB-Seq	
May 6 (Sat)	May 7 (Sun)	May 8 (Mon)
Registration (RECOMB)	Registration (RECOMB)	Registration (RECOMB-Seq)
S12: Early Cancer Detection and Therapy [KT] Joe Gray	S18: Metagenomics [PT] Popic et al. [PT] Ahn et al. [PT] Han et al.	**SS4 [KT] Sharon Aviran**
Coffee break	*Coffee break*	*Coffee break*
S13: Cancer II [PT] Rajaraman et al. [HT] Amar et al. [PT] Hristov et al.	S19: Protein Structure and Proteomics [PT] Ojewole et al. [HT] Wang et al. [HT] Kullanja et al.	SS5 [RT] Rozov et al. [RT] Sun et al. [RT] Durai et al.
Break	*Break*	*Break*
S14: Epigenomics [HT] Szalaj et al. [PT] Rahmani et al. [PT] Leung et al.	S20: Phylogenetics and Multiple Sequence Alignment [PT] Shekhar et al. [PT] Jansson et al. [PT] Deblasio et al.	SS6 [ST] Cairo et al. [ST] Nihalani et al. [ST] Chen et al. [ST] Quedenfeld et al. [ST] Yeo et al. [ST] Hashemi et al.
Lunch break (lunch provided)	**Awards Ceremony and Closing Remarks**	*Lunch break (lunch provided)*
	Registration (RECOMB-Seq)	
S15: IBM Watson in the Clinic [KT] Laxmi Parida	**Opening Remarks, SS1 [KT] Olga Troyanskaya**	SS7 [RT] Mandric et al. [RT] Bansal
Coffee break	*Coffee break*	*Coffee break*
S16: Population and Disease Studies II [PT] Huynh et al. [PT] Schweiger et al. [PT] Naseri et al.	SS2 [RT] Skums et al. [RT] Liu et al. [RT] Mariani et al.	**Poster Session (RECOMB-Seq I)**
Break	*Break*	*Break*
S17: Genome Data Structures [PT] Paten et al. [PT] Haussler et al. [PT] Pockrandt et al.	SS3 [ST] Ginart et al. [ST] Xin et al. [ST] Shao et al.	**Poster Session (RECOMB-Seq II)**
Poster Session II		

Detailed Schedule

RECOMB KT: Keynote, PT: Proceedings Talk, HT: Highlights Talk
Venue: LT1, Level 1 Cheng Yu Tung (CYT) Building, The Chinese University of Hong Kong (CUHK)

May 3, 2017 (Wednesday)

6:00 PM - 9:00 PM	**Registration and Welcome Reception** **(Regency Ballroom II, Hyatt Regency Hong Kong, Sha Tin)** *Address: 18 Chak Cheung Street, Sha Tin, N.T.*

May 4, 2017 (Thursday)

8:30 AM - 8:45 AM	Registration
8:45 AM - 9:00 AM	**Opening Remarks**
9:00 AM - 10:00 AM	**S01: Precision Health**
	[KT] Jun Wang (iCarbonX)
10:00 AM - 10:20 AM	*Coffee break*
10:20 AM - 11:20 AM	**S02: Sequencing I**
	[PT] Sudipto Mukherjee, Mark Chaisson, Sreeram Kannan and Evan Eichler **Resolving multicopy duplications de novo using polyploid phasing**
	[PT] Joshua Welch, Alexander Hartemink and Jan Prins **E Pluribus Unum: United States of Single Cells**
	[PT] Alexander Shlemov, Sergey Bankevich, Andrey Bzikadze, Yana Safonova and Pavel Pevzner **Reconstructing antibody repertoires from error-prone immunosequencing datasets**
11:20 AM - 11:30 AM	*Break*
11:30 AM - 12:30 PM	**S03 Population and Disease Studies I**
	[PT] Yue Wu, Farhad Hormozdiari, Jong Wha J Joo and Eleazar Eskin **Improving imputation accuracy by inferring causal variants in genetic studies**
	[PT] Xiaoqian Wang, Li Shen and Heng Huang **Longitudinal Genotype-Phenotype Association Study via Temporal Structure Auto-Learning Predictive Model**
	[HT] Elior Rahmani, Noah Zaitlen, Yael Baran, Celeste Eng, Donglei Hu, Joshua Galanter, Sam Oh, Esteban Burchard, Eleazar Eskin, James Zou and Eran Halperin **Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies**
12:30 PM - 2:00 PM	*Lunch break (lunch provided)*
2:00 PM - 3:00 PM	**S04: Translational Science**
	[KT] Colin Collins (Vancouver Prostate Centre)
3:00 PM - 3:20 PM	*Break*
3:20 PM - 4:20 PM	**S05: Networks and Systems**
	[PT] Robert Osazuwa Ness, Karen Sachs, Parag Mallick and Olga Vitek **A Bayesian Active Learning Experimental Design for Inferring Signaling Networks**
	[PT] Yijie Wang, Dong-Yeon Cho, Hangnoh Lee, Brian Oliver and Teresa Przytycka **NetREX: Network Rewiring using EXpression - Towards Context Specific Regulatory Networks**
	[PT] Yunan Luo, Xinbin Zhao, Jingtian Zhou, Jinling Yang, Yanqing Zhang, Wenhua Kuang, Jian Peng, Ligong Chen and Jianyang Zeng **A Network Integration Approach for Drug-Target Interaction Prediction and Computational Drug Repositioning from Heterogeneous Information**
4:20 PM - 4:30 PM	*Break*

4:30 PM - 5:30 PM	**S06: Alignment, Search and Compression**
	[PT] Brad Solomon and Carl Kingsford **Improved Search of Large Transcriptomic Sequencing Databases Using Split Sequence Bloom Trees** joint with Chen Sun, Robert Harris, Rayan Chikhi and Paul Medvedev **Allsome Sequence Bloom Trees**
	[PT] Guillaume Holley, Roland Wittler, Jens Stoye and Faraz Hach **Dynamic Alignment-free and Reference-free Read Compression**
	[PT] Chirag Jain, Alexander Dilthey, Sergey Koren, Srinivas Aluru and Adam Phillippy **A Fast Approximate Algorithm for Mapping Long Reads to Large Reference Databases**

May 5, 2017 (Friday)

8:30 AM - 9:00 AM	Registration
9:00 AM - 10:00 AM	**S07: Network and Pathways**
	[KT] Ben Raphael (Princeton)
10:00 AM - 10:20 AM	*Coffee break*
10:20 AM - 11:20 AM	**S08: Cancer I**
	[PT] Phuong Dao, Yoo-Ah Kim, Damian Wojtowicz, Sanna Madan, Roded Sharan and Teresa Przytycka **BeWith: A Between-Within Method for Module Discovery in Cancer using Integrated Analysis of Mutual Exclusivity, Co-occurrence and Functional Interactions**
	[PT] Simone Zaccaria, Mohammed El-Kebir, Gunnar Klau and Ben Raphael **The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-Sample Bulk Sequencing Tumor Data**
	[PT] Ewa Szczurek and Dariusz Matlak **Epistasis in genomic and survival data of cancer patients**
11:20 AM - 11:30 AM	*Break*
11:30 AM - 12:30 PM	**S09: Protein-DNA Interactions and Gene Regulation**
	[PT] Jingkang Zhao, Dongshunyi Li, Jungkyun Seo, Andrew Allen and Raluca Gordan **Quantifying the impact of non-coding variants on transcription factor-DNA binding**
	[PT] Yuchun Guo, Kevin Tian, Haoyang Zeng and David K. Gifford **K-mer Set Memory (KSM) motif representation enables accurate prediction of the impact of regulatory variants**
	[PT] Yaron Orenstein, Ryan Kim, Polly Fordyce and Bonnie Berger **Joker de Bruijn: sequence libraries to cover all k-mers using joker characters**
12:30 PM - 2:00 PM	*Lunch break (lunch provided)*
2:00 PM - 3:00 PM	**S10: Sequencing II**
	[PT] Michael Schnall-Levin (10X Genomics)
3:00 PM - 3:20 PM	*Coffee break*
3:20 PM - 4:30 PM	**S11: New Directions**
	[PT] Zhen Li, Sheng Wang, Yizhou Yu and Jinbo Xu **Predicting membrane protein contacts from non-membrane proteins by deep transfer learning**
	[HT] Michael Altenbuchinger, Thorsten Rehberg, Helena Zacharias, Frank Stämmler, Katja Dettmer, Daniela Weber, Andreas Hiergeist, André Gessner, Ernst Holler, Peter Oefner and Rainer Spang **Reference point insensitive molecular data analysis**
	[PT] Uri Keich and William Stafford Noble **Progressive calibration and averaging for tandem mass spectrometry statistical confidence estimation: Why settle for a single decoy?**

[PT] Sai Zhang, Hailin Hu, Jingtian Zhou, Xuan He, Tao Jiang and Jianyang Zeng

ROSE: a deep learning based framework for predicting ribosome stalling

4:30 PM - 6:00 PM   **Poster Session I**

Banquet (ClubONE on the Park, Science Park) *[ticket required]*

Address: Shop061-066, G/F, Building 12W, No.12 Science Park West Avenue, Hong Kong Science Park, Shatin, N.T.
- Coaches will start departing at the entrance of CYT during 6:00 PM – 6:30 PM.
- Transportation from ClubONE on the Park to University MTR Station will be provided after the banquet.

6:30 PM - 9:00 PM   **Banquet (ClubONE on the Park, Science Park)** *[ticket required]*

May 6, 2017 (Saturday)

8:30 AM - 9:00 AM	Registration
9:00 AM - 10:00 AM	**S12: Early Cancer Detection and Therapy**

[KT] Joe Gray (OHSU)

10:00 AM - 10:20 AM	*Coffee break*
10:20 AM - 11:20 AM	**S13: Cancer II**

[PT] Ashok Rajaraman and Jian Ma

Towards Recovering Allele-specific Cancer Genome Graphs

[HT] David Amar, Shai Izraeli and Ron Shamir

Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications

[PT] Borislav Hristov and Mona Singh

Network-based coverage of mutational profiles reveals cancer genes

11:20 AM - 11:30 AM	*Break*
11:30 AM - 12:30 PM	**S14: Epigenomics**

[HT] Przemyslaw Szalaj, Zhonghui Tang, Paul Michalski, Michal Pietal, Michal Sadowski, Oskar Luo, Yijun Ruan and Dariusz Plewczynski

3D-GNOME: high-resolution model of chromatin looping architecture in human genome

[PT] Elior Rahmani, Regev Schweiger, Liat Shenhav, Eleazar Eskin and Eran Halperin

A Bayesian Framework for Estimating Cell Type Composition from DNA Methylation Without the Need for Methylation Reference

[PT] Michael Leung, Andrew Delong and Brendan Frey

Inference of the Human Polyadenylation Code

12:30 PM - 2:00 PM	*Lunch break (lunch provided)*
2:00 PM - 3:00 PM	**S15: IBM Watson in the Clinic**

[KT] Laxmi Parida (IBM)

3:00 PM - 3:20 PM	*Coffee break*
3:20 PM - 4:20 PM	**S16: Population and Disease Studies II**

[PT] Linh Huynh and Fereydoun Hormozdiari

Ultra-accurate complex disorder prediction: case study of neurodevelopmental disorders

[PT] Regev Schweiger, Eyal Fisher, Elior Rahmani, Liat Shenhav, Saharon Rosset and Eran Halperin

Using stochastic approximation techniques to efficiently construct confidence intervals for heritability

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[PT] Ardalan Naseri, Xiaoming Liu, Shaojie Zhang and Degui Zhi

Ultra-fast Identity by Descent Detection in Biobank-Scale Cohorts using Positional Burrows–Wheeler Transform

4:20 PM - 4:30 PM	*Break*
4:30 PM - 5:30 PM	**S17: Genome Data Structures**

[PT] Benedict Paten, Adam Novak, Erik Garrison, Eric Dawson and Glenn Hickey

Superbubbles, Ultrabubbles and Cacti

[PT] David Haussler, Maciej Smuga-Otto, Benedict Paten, Adam Novak, Sergei Nikitin, Maria Zueva and Miagkov Dmitrii

A flow procedure for the linearization of genome variation graphs

[PT] Christopher Pockrandt, Marcel Ehrhardt and Knut Reinert

EPR-dictionaries: A practical and fast data structure for constant time searches in unidirectional and bidirectional FM-indices

5:30 PM - 7:00 PM	**Poster Session II**

May 7, 2017 (Sunday)

8:30 AM - 9:00 AM	Registration
9:00 AM - 10:00 AM	**S18: Metagenomics**

[PT] Victoria Popic, Volodymyr Kuleshov, Michael Snyder and Serafim Batzoglou

GATTACA: Lightweight metagenomic binning using Kmer Counting

[PT] Soyeon Ahn and Haris Vikalo

aBayesQR: A Bayesian method for reconstruction of viral populations characterized by low diversity

[PT] Wontack Han, Mingjie Wang and Yuzhen Ye

A concurrent subtractive assembly approach for identification of disease associated sub-metagenomes

10:00 AM - 10:20 AM	*Coffee break*
10:20 AM - 11:20 AM	**S19: Protein Structure and Proteomics**

[PT] Adegoke Ojewole, Jonathan Jou, Vance Fowler and Bruce Donald

BBK* (Branch and Bound over K*): A Provable and Efficient Ensemble-Based Algorithm to Optimize Stability and Binding Affinity over Large Sequence Spaces

[HT] Sheng Wang, Siqi Sun, Zhen Li, Renyu Zhang and Jinbo Xu

Folding Large Proteins by Ultra-Deep Learning

[HT] Vikram Alva Kullanja, Johannes Söding and Andrei Lupas

A vocabulary of ancient peptides at the origin of folded proteins

11:20 AM - 11:30 AM	*Break*
11:30 AM - 12:30 PM	**S20: Phylogenetics and Multiple Sequence Alignment**

[PT] Shubhanshu Shekhar, Sebastien Roch and Siavash Mirarab

Species tree estimation using ASTRAL: how many genes are enough?

[PT] Jesper Jansson, Andrzej Lingas, Ramesh Rajaby and Wing-Kin Sung

Determining the Consistency of Resolved Triplets and Fan Triplets

[PT] Dan Deblasio and John Kececioglu

Boosting alignment accuracy by adaptive local realignment

12:30 PM - 1:00 PM	**Awards Ceremony and Closing Remarks**

RECOMB-Seq KT: Keynote, RT: Regular Talk, ST: Short Talk
Venue: LT6, Level 2, Cheng Yu Tung (CYT) Building, The Chinese University of Hong Kong (CUHK)

May 7, 2017 (Sunday)

1:00 PM - 2:00 PM	Registration
2:00 PM - 3:00 PM	**Opening Remarks**
	SS1
	[KT] Olga Troyanskaya (Princeton)
3:00 PM - 3:20 PM	*Coffee break*
3:20 PM - 4:20 PM	**SS2**

[RT] Pavel Skums, Alex Zelikovsky, Sergey Knyazev, Igor Mandric, Zoya Dimitrova, Sumathi Ramachandran, David Stiven Campo Rendon, Leonid Bunimovich, Elizabeth Costenbader, Connie Sexton, Siobhan O'Connor, Guo-Liang Xia and Yury Khudyakov
QUENTIN: accurate reconstruction of disease transmissions from viral quasispecies genomic data

[RT] Xinan Liu, Ye Yu, Jinpeng Liu, Chen Qian and Jinze Liu
A Novel Data Structure to Support Ultra-fast Taxonomic Classification of Metagenomic Sequences with k-mer Signatures

[RT] Luca Mariani, Kathryn Weinand, Anastasia Vedenko, Luis A. Barrera and Martha L. Bulyk
Transcription factor-8mer glossary with GENRE genomic background enables precise identification of lineage-specific coregulators

4:20 PM - 4:30 PM	*Break*
4:30 PM - 5:00 PM	**SS3**

[ST] Tony Ginart, Kaiyuan Zhu, Joseph Hui, Ibrahim Numanagic, David Tse, Thomas Courtade and Cenk Sahinalp
Genomic Reads Forests for Compressed Representation of High Throughput Sequence Data

[ST] Hongyi Xin, Jeremie Kim, Sunny Nahar, Can Alkan and Onur Mutlu
LEAP: A Generalization of the Landau-Vishkin Algorithm with Custom Gap Penalties

[ST] Mingfu Shao and Carl Kingsford
Theory and Algorithm for the Minimum Path Flow Decomposition Problem

May 8, 2017 (Monday)

8:30 AM - 8:45 AM	Registration
9:00 AM - 10:00 AM	**SS4**
	[KT] Sharon Aviran (UC Davis)
10:00 AM - 10:20 AM	*Coffee break*
10:20 AM - 11:20 AM	**SS5**

[RT] Roye Rozov, Gil Goldshlager, Ron Shamir and Eran Halperin
Faucet: streaming de novo assembly graph construction

[RT] Zhe Sun, Ting Wang, Ke Deng, Xiao-Feng Wang, Robert Lafyatis, Ying Ding, Ming Hu and Wei Chen
DIMM-SC: A Dirichlet mixture model for clustering droplet-based single cell transcriptomic data

[RT] Dilip Durai and Marcel Schulz
In-silico read normalization using set multicover optimization

11:20 AM - 11:30 AM	*Break*

11:30 AM - 12:30 PM	**SS6**

[ST] Massimo Cairo, Paul Medvedev, Nidia Obscura Acosta, Romeo Rizzi and Alexandru I. Tomescu
Faster Omnitig Listing for Safe and Complete Contig Assembly

[ST] Rahul Nihalani, Sriram P. Chockalingam, Shaowei Zhu, Vijay Vazirani and Srinivas Aluru
Probabilistic Estimation of Overlap Graphs for Large Sequence Datasets

[ST] Xintong Chen, Oscar Rodriguez, Matthew Pendleton, Bojan Losic and Ali Bashir
TransPac: transposon detection and characterization from long-reads

[ST] Jens Quedenfeld and Sven Rahmann
Variant tolerant read mapping using min-hashing

[ST] Sarah Yeo, Lauren Coombe, Justin Chu, Rene Warren and Inanc Birol
ARCS: Assembly Roundup by Chromium Scaffolding

[ST] Abolfazl Hashemi, Banghua Zhu and Haris Vikalo
A Tensor Factorization Framework for Haplotype Assembly of Diploids and Polyploids

12:30 PM - 2:00 PM	*Lunch break (lunch provided)*
2:00 PM - 3:00 PM	**SS7**

[RT] Igor Mandric, Sergey Knyazev and Alex Zelikovsky
Repeat-aware evaluation of scaffolding tools

[RT] Vikas Bansal
An accurate algorithm for the detection of DNA fragments from dilution pool sequencing experiments

3:00 PM - 3:20 PM	*Coffee break*
3:20 PM - 4:20 PM	**Poster Session (RECOMB-Seq I)**
4:20 PM - 4:30 PM	*Break*
4:30 PM - 5:30 PM	**Poster Session (RECOMB-Seq II)**

RECOMB Keynote Speakers

Colin Collins

Colin Collins is a Senior Research Scientist at the Vancouver Prostate Centre and a Director of The Laboratory for Advanced Genome Analysis (LAGA). His current research is best described as translational genomics where mathematics, genomics, computer science, and clinical science converge in diagnostics and therapeutics. His past work as a member of the UCSF Prostate SPORE has resulted in identification of a suite of DNA based biomarkers that show promise for predicting a patient's risk of progression and metastasis. He also invented and patented End Sequence Profiling (ESP) the forerunner of modern paired-end sequencing. ESP as a technique has helped determining the physical structure, complexity, and mutation load of tumor genomes and directly detecting fusion genes and transcripts. He has also worked on integrating array-based technologies and next generation sequencing technologies to radically cut costs and make very large-scale tumor genome projects and personalized oncology a reality. He holds multiple patents, and has received numerous awards including the California Cancer Research Programs Cornelius L. Hopper Scientific Achievement Award for Innovation.

Joe W. Gray

Dr. Joe W. Gray, a physicist and an engineer by training, is a Professor and Gordon Moore Endowed Chair, Biomedical Engineering Department, the Director, Center for Spatial Systems Biomedicine, and the Associate Director for Biophysical Oncology, Knight Cancer Institute at the Oregon Health & Science University. He is also Emeritus Professor, University of California San Francisco; and Senior Scientist, Lawrence Berkeley National Laboratory. He is Principal Investigator of the National Cancer Institute /Integrative Cancer Biology Program (ICBP) Center for Cancer Systems Biology (CCSB) aimed at understanding and modeling of RTK signaling, PI of a project to contribute to further development of the NIH Library of Integrated Network-based cellular signatures (LINCS) by developing a dataset and computational strategy to elucidate how microenvironmental signals affect cell intrinsic intracellular transcriptional- and protein-defined molecular networks to generate experimentally durable therapies for patients, PI of a Brenden Colson Center for Pancreatic Health that provides support for a broad-based, team approach to finding causes, early detection and improvement of clinical care for pancreatic diseases including pancreatitis and pancreatic cancer, and PI of a Susan G. Komen project to identify the mechanisms by which ERBB2+ breast cancer cells escape inhibition by ERRB2-targeted therapies. Dr. Gray's work is described in over 400 publications and in 73 US patents. He is a Fellow of the American Association for the Advancement of Science and the American Institute for Medical and Biological Engineering, an elected a member of the Institute of Medicine of the National Academy of Sciences, a member of the National Institutes of Health, Frederick Advisory Committee to the Director of the National Cancer Institute, a Fellow of the American Association of Cancer Research Academy, and US Councilor on the Board of the Radiation Effects Research Foundation (RERF), Hiroshima, Japan.

Laxmi Parida

Dr. Laxmi Parida is a Distinguished Research Scientist and heads the Computational Genomics at the IBM Thomas J. Watson Research Center, USA. She is a visiting professor at the Courant Institute of Mathematical Sciences, New York. She is the currently leading the science teams in the personalized cancer medicine system "Watson for Genomics" and the "Sequence the Food Supply Chain Consortium" across multiple IBM labs in different geographies. Over the last 10 years, she also led the IBM Science team in the Cacao Consortium (with MARS, USDA) and the Genographic Project with National Geographic. Her research areas include population genomics, cancer genomics, plant genomics, bioinformatics algorithms and topological data analysis. She has published over 150 peer-reviewed research papers; edited 5 volumes and authored a monograph on pattern discovery in bioinformatics. She holds over 35 US patents. She is on the advisory board of NYU Engineering School and editorial board of BMC Bioinformatics, Journal of Computational Biology and an Associate Editor, IEEE/ACM Transactions on Computational Biology and Bioinformatics and SIAM Journal of Discrete Mathematics.

Ben Raphael

Ben Raphael is a Professor in the Department of Computer Science at Princeton University. His research focuses on the design of algorithms for genome sequencing and interpretation. Recent interests include structural variation in human and cancer genomes, and network/pathway analysis of genetic variants. He received his S.B. in Mathematics from MIT, Ph.D. in Mathematics from the University of California, San Diego (UCSD), and completed postdoctoral training in Bioinformatics and Computer Science at UCSD. He is the recipient of the NSF CAREER award, a Career Award from the Burroughs Wellcome Fund, and a Sloan Research Fellowship.

RECOMB-Seq Keynote Speakers

Michael Schnall-Levin

Michael Schnall-Levin is the Vice President of Computational Biology and Applications at 10x Genomics. His broad aim is to use new technology to improve our understanding of the genome and to improve human health. Before joining 10x Genomics, Michael was an NSF postdoctoral fellow with Eric Lander at the Broad Institute where he worked on developing novel applications of DNA sequencing technologies. Prior to that, Michael worked at Foundation Medicine, where he developed some of the early algorithms to accurately detect mutations in patient tumor samples. Michael earned his PhD in Mathematics from MIT, where he was both a Hertz fellow and NDSEG fellow, and his BA in Physics from Harvard College.

Jun Wang (王俊)

Jun Wang (王俊) is the founder and CEO of iCarbonX. He earned a bachelor's degree in artificial intelligence and a Ph.D. in bioinformatics from Peking University. In 1999, Dr. Wang co-founded BGI, which is now widely recognized as one of world's premier research facilities committed to excellence in genome sciences. During this time, Dr. Wang managed three rounds of fundraising (about 1B$ in total), and acquired a U.S. public company, Complete Genomics. He summarizes the vision of iCarbonX as "both life sciences and genomics have now run into a bottleneck in handling data from tens of thousands of samples. AI and machine learning could do something with big data and for people's health." He was recognized with numerous awards and nominations, such as His Royal Highness Prince Foundation, and "Fortune's 40 under 40" by Fortune Magazine (2013) and Highly Cited Researchers 2015" by Thomson Reuters.

Olga Troyanskaya

Olga Troyanskaya is a professor at the Lewis-Sigler Institute for Integrative Genomics and the Department of Computer Science at Princeton University, where she has been on the faculty since 2003. In 2014 she became the deputy director of Genomics at the Center for Computational Biology at the Flatiron Institute, a part of the Simons Foundation in NYC. She holds a Ph.D. in Biomedical Informatics from Stanford University, has been honored as one of the top young technology innovators by the MIT Technology Review, and is a recipient of the Sloan Research Fellowship, the National Science Foundation CAREER award, the Overton award from the International Society for Computational Biology, and the Ira Herskowitz award from the Genetic Society of America.

Sharon Aviran

Sharon Aviran is broadly interested in statistical models and algorithms, applied to problems in genomics, functional genomics, and molecular systems engineering. Her current research interests lie in developing computational methods for analyzing RNA structure mapping experiments and in modeling and analysis of next-generation sequencing-based protocols. Before joining UC Davis, she was a postdoc at the Center for Computational Biology at UC Berkeley, where she worked with Lior Pachter. At Berkeley she also worked with the teams of Adam Arkin and David Schaffer on analyzing HIV's evolutionary population dynamics when the virus is exposed to novel gene therapies. Prior to that, she obtained her Ph.D. in information theory and communication systems at UCSD, under the supervision of Paul Siegel and Jack Wolf. Sharon's PhD work dealt with the design and analysis of error-correcting codes and signal processing methods for digital storage devices, such as CDs, DVDs, and disk drives. She has also worked in the telecom and software industries for several years and obtained her Master's in discrete optimization from the Technion, where she worked with Shmuel Onn. Her research and industrial experience span both theoretical and applied work, in the areas of bioinformatics, applied mathematics, algorithmics and systems engineering.

Poster Session Schedule

Venue:
The Gastronomy Club, Level 5, Cheng Yu Tung (CYT) Building, The Chinese University of Hong Kong (CUHK)

Poster Session	Posters	Date	Display time
RECOMB I	Odd numbered	May 5 (Fri)	4:30 PM - 6:00 PM
RECOMB II	Even numbered	May 6 (Sat)	5:30 PM - 7:00 PM
RECOMB-Seq I	Even numbered	May 8 (Mon)	3:20 PM - 4:20 PM
RECOMB-Seq II	Odd numbered	May 8 (Mon)	4:30 PM - 5:30 PM

List of Posters

1. Jiaan Dai, Fengchao Yu, Ning Li and Weichuan Yu
   Is it feasible to only use tags in database search for PTM-invariant peptide identification? --- A simulation-based study

2. Fengchao Yu, Ning Li and Weichuan Yu
   ECL 2.0: Exhaustively Identifying Cross-Linked Peptides with a Linear Computational Complexity

3. João Herminio Martins Da Silva, Disraeli Vasconcelos, Lia Pinho and Beatriz Chaves
   De novo Receptor-Based Design of new Integrin Beta 1 Inhibitors and in silico ADMET methods evaluation

4. Natalie Fox, Emilie Lalonde, Julie Livingstone, Julia Hopkins, Yu-Jia Shiah, Vincent Huang, Takafumi Yamaguchi, Veronica Sabelnykova, Lawrence Heisler, Michael Fraser, Theodorus van der Kwast, Robert Bristow and Paul Boutros
   Integrated somatic subtypes of localized prostate cancer with prognostic implications

5. Robert Brown, Eleazar Eskin and Bogdan Pasaniuc
   Haplotype-based eQTL Mapping Increases Power to Identify eGenes

6. Thahmina Ali, Baekdoo Kim, Carlos Lijeron and Konstantinos Krampis
   Xplore-seq: a comprehensive, standardized and scalable method to transcriptomic profiling as a clinically-useful application

7. Serghei Mangul, Igor Mandric, Alex Zelikovsky and Eleazar Eskin
   Profiling adaptive immune repertoires across multiple human tissues by RNA Sequencing

8. Jing Qin, Yaohua Hu, Jen-Chih Yao, Yiming Qin, Ka Hou Chu and Junwen Wang
   Group Sparse Optimization: An Integrative OMICs Method to Predict Master Transcription Factors for Cell Fate Conversion

9. Jennifer Zou, Farhad Hormozdiari, Jason Ernst, Jae-Hoon Sul and Eleazar Eskin
   Leveraging allele-specific expression to improve fine-mapping for eQTL studies

10. Luca Alessandri and Raffaele Calogero
    CASC: Classification Analysis of Single Cell Sequencing Data

11. Nan Papili Gao, S.M Minhaz Ud-Dean and Rudiyanto Gunawan
    SINCERITIES: Inferring gene regulatory net-works from time-stamped single cell transcrip-tional expression profiles

12. Feng Yang, Wei Zeng, Ke Liu, Guangbin Wang, Zhengwen Li, Keli Huang and Nini Rao
    The Roles of Signal Pathways mediated by AF-VHD-related microRNA combinations in Development from VHD to AF-VHD

13. Egor Dolzhenko, Joke J.F.A. van Vugt, Subramanian S. Ajay, Ryan Taft, David R. Bentley, Jan H. Veldink and Michael A. Eberle
    Detection of long repeat expansions from PCR-free whole-genome sequence data

14. Andreas Dwi Maryanto Gunawan, Bingxin Lu, Hon Wai Leong and Louxin Zhang
    Computer Program for Verification of Phylogenetic Networks

15. Vera Kaiser and Colin Semple
    Diversity of mutational loads at CTCF binding sites predicts foci of dysregulated expression

16. Dong-Jun Lee and Hyeon-So Gi
    Comparative transcriptome analysis of resistant and susceptible Korea rice genotype in response to bakanae disease

17. Thrasyvoulos Karydis and Joseph M. Jacobson
    Learning hierarchical motif representations for protein analysis, search and design

18. Jie Ren, Fengzhu Sun, Nathan A Ahlgren, Jed A Fuhrman and Yang Young Lu
    VirFinder: a novel k-mer based tool for identifying viral sequences from assembled metagenomic data

19. Dat Duong, Lisa Gai, Sagi Snir, Eun Yong Kang, Buhm Han, Jae Hoon Sul and Eleazar Eskin
    Applying meta-analysis to Genotype-Tissue Expression data from multiple tissues to identify eQTLs and increase the number of eGenes

20. Ruban Durairaj D, Murugesh Easwaran and Shanmughavel P
    Molecular docking and dynamics simulation studies of Antitubercular compounds with Enoyl-ACP reductase enzyme of MDR-Tuberculosis

21. Luming Meng, Wenjun Xie, Sirui Liu, Ling Zhang and Yiqin Gao
    Chromatin modeling reveals segregation of chromosome characteristics and fuctions in 3D space

22. Harry Taegyun Yang, Serghei Mangul, Noah Zaitlen, Sagiv Shifman and Eleazar Eskin
    Repeat Elements Profile Across Different Tissues in GTEx Samples

23. Ung-Han Yoon, Jaecheol Jeong, Jang-Ho Hahn, Jung-Wook Yang, Tae-Ho Kim, Hyeong-Un Lee, Young-Ju Seol, Sang-Sik Nam, Sang-Soo Kwak and Tae-Ho Lee
    Structural and evolutionary analysis of sweetpotato chloroplast genomes

24. Roven Rommel Fuentes, Dmytro Chebotarov, Sean Smith, Jorge Duitama, Marghoob Mohiyuddin, Ramil Mauleon, Andrey Grigoriev, Rod Wing and Nickolai Alexandrov
    Discovery of Structural Variants in 3,024 Rice Genomes

25. Magdalena Strauss, Lorenz Wernisch and John Reid
    New MCMC methods for pseudo-time estimation using Gaussian processes

26. Yali Xiao, Ssu-Min Fang, Yun-Hsin Tsou, Cheng-Fang Tsai and Pei-Chun Chang
    The Potential Inhibitors in Chinese Traditional Medicine for Bcr-AblT315I Mutation of Chronic Myelogenous Leukemia

27. Chalida Rangsiwutisak, Treenut Saithong and Saowalak Kalapanulak
    Exploring the landscape of regulatory elements on non-coding regions of cassava genome via motif-based screening

28. Zhun Miao and Xuegong Zhang
    A new differential expression analysis method for single-cell RNA-Seq data

29. Robert Schöpflin and Martin Vingron
    Interactive visualization of Hi-C data and epigenetic marks

30. Sang Chun, Caitlin Rodriguez, Ryan Mills and Peter Todd
    Regulation of Differentiation in SH-SY5Y Neuroblastoma Cells by Translation of Upstream Open Reading Frames

31. Jian-Ying Chiu, Tse-Ching Ho, Syun-Wun Liang and Yen-Hua Huang
    Quality assessment of genome assembly generated by the third-generation sequencing platform PacBio and an online editor for continuous update of genome annotation

32. Michael Altenbuchinger, Philipp Schwarzfischer, Thorsten Rehberg, Jörg Reinders, Christian W. Kohler, Wolfram Gronwald, Julia Richter, Monika Szczepanowski, Neus Masqué-Soler, Wolfram Klapper, Peter J. Oefner and Rainer Spang
    Molecular signatures that can be transferred across different omics platforms

33. Xin Li, Chong Chu, Jingwen Pei, Ion Mandoiu and Yufeng Wu
    CircMarker: A Fast and Accurate Algorithm for Circular RNA Detection

34. Lisa Gai, Dat Duong and Eleazar Eskin
    Finding associated variants in genome-wide associations studies on multiple traits

35. Gongchao Jing, Jian Xu and Xiaoquan Su
    Microbiome Search Engine: Enabling Rapid Microbiome Samples Search In Large-scale Database

36. Diya Sen, Mathu Malar Chandrababunaidu and Sucheta Tripathy
    An efficient contamination removal tool for improving prokaryotic genome assembly

37. Dan Huang, Fu Yan Hu and Nelson Tang
    Splicing aberration of TP53 transcripts in cancers: mechanisms and effects

38. Alexey Morgunov, Alexander Gunnarsson, Norbert Fehér and Madan Babu
    Investigating residue coevolution in proteins from a structural perspective

39. Gregory Smith, Alan Stern and Marc Birtwistle
    Inferring Dynamic Network Architecture from Time Series Perturbation Data

40. Daniel Hogan, Bharathi Vellalore, Ronald Geyer and Anthony Kusalik
    SeqMiner: A Weka package for mining phage display sequence data

41. Chao Sima, Shanaz Ghandhi, Sally A. Amundson, David J. Brenner and Michael Bittner
    Feature reduction for practical radiation biodosimetry using combined approach of gene co-expression network and pathway knowledge

42. Kimberly Mackay, Christopher Eskiw and Anthony Kusalik
    3D Yeast Genome Prediction with Constraint Logic Programming

43. Jae Hyeon Oh, Tae Ho Lee, Chang Kug Kim, Lee Dong-Jun and Dowan Kim
    Transcripsome and metabolism studies to identify alkaloid biosynthesis genes in poppies

44. Wendao Liu, Zhun Miao and Xuegong Zhang
    Assessing mRNA integrity of single-cell RNA-Seq data using mRIN

45. Alden King-Yung Leung, Nana Jin, Kevin Y. Yip and Ting-Fung Chan
    OMView: a comprehensive visualization suite for interpreting optical mapping data

46. Heng Xiong, Dongbing Liu and Leo Lee
RED-ML: a novel, effective RNA editing detection method based on machine learning

47. Dawn Chen and Ming-Jing Hwang
Reducing Runtime in CONTRAlign by Feature Reduction

48. Yu-Chieh Liao and Hsin-Hung Lin
drVM: detect and reconstruct known viral genomes from metagenomes

49. Kuei-Ling Sun, Onkar Singh and Emily Chia-Yu Su
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50. Xiang-Tian Yu, Jin-Song Zhang, Shao-Yan Sun, Tao Zeng and Luonan Chen
Individual-specific edge network analysis for disease prediction

51. Juan Zhao, Yiwei Zhou, Xiujun Zhang and Luonan Chen
Part mutual information for quantifying direct associations in networks

52. Dowan Kim, Jae-Hyeon Oh, Dong-Jun Lee, Chang-Kug Kim and Tae-Ho Lee
Transcriptome analysis in some varieties of Papaver rhoeas

53. Hojin Gwak and Mina Rho
ABCProfiler: a program for Alignment Based Clustering and taxonomy Profiling

54. Jehyun Jeon and Mina Rho
Modular type I PKS cluster in sediment microbiomes

55. Julian Zaugg, Yosephine Gumulya and Mikael Bodén
Learning From Sequence-Activity Data - Predicting Enantioselectivity of an Epoxide Hydrolase

56. Julian Zaugg, Yosephine Gumulya, Mikael Bodén and Alpeshkumar Malde
Using Theory to Reconcile Experiments: Understanding the Origin of Enantioselectivity of Epoxide Hydrolase

57. Ingoo Lee and Hojung Nam
Identification of drug-target interactions using weighted interactome network

58. Kavya Vaddadi, Naveen Sivadasan, Kshitij Tayal and Rajgopal Srinivasan
Sequence Alignment on Directed Graphs

59. Naveen Sivadasan, Rajgopal Srinivasan and Kshama Goyal
Kmerlight: fast and accurate k-mer abundance estimation

60. Kang Ning, Shaojun Yu and Maozhen Han
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61. Przemyslaw Szalaj, Zhonghui Tang, Yijun Ruan and Dariusz Plewczynski
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62. Mika Gustafsson
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63. Saad Mneimneh and Syed Ali Ahmed
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64. Bingxin Lu and Hon Wai Leong
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65. Wanatsanan Siriwat, Saowalak Kalapanulak and Treenut Saithong
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66. Shah Md. Shahik, Md. Saiful Islam, Md Sohel and Mohd. Omar Faruk Sikder
Mining the Proteome of Fusobacterium nucleatum subsp. nucleatum ATCC 25586 for Potential Therapeutics Discovery: An In Silico Approach

67. Abhishek Das, Subhadeep Das, Samrat Ghosh and Sucheta Tripathy
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68. Alexander Shlemov, Alexey Gurevich, Alla Mikheenko, Anastasiia Abramova, Anton Korobeynikov, Hosein Mohimani and Pavel Pevzner
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69. Heeju Noh, Ziyi Hua and Rudiyanto Gunawan
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70. Kui Hua and Xuegong Zhang
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71. Jongsoo Keum and Hojung Nam
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72. Sajad Mirzaei and Yufeng Wu
RENT+: An Improved Method for Inferring Local Genealogical Trees from Haplotypes with Recombination

73. Mohammadhossein Moeinzadeh, Jun Yang and Martin Vingron
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74. Jingwen Pei and Yufeng Wu
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76. Chirag Jain, Luis M. Rodriguez, Alexander Dilthey, Adam Phillippy, Kostas Konstantinidis and Srinivas Aluru
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77. Chong Chu, Jingwen Pei and Yufeng Wu
An improved approach for reconstructing consensus repeats from short sequence reads

78. Chong Chu, Xin Li and Yufeng Wu
GAPPadder: A Sensitive Approach for Closing Gaps on Draft Genomes with Short Sequence Reads

79. Chen Yang, Readman Chiu, Daniel MacMillan, Zhuyi Xue, Rene Warren and Inanc Birol
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80. Cenk Sahinalp
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81. Alexander Shlemov, Sergey Bankevich, Andrey Bzikadze and Yana Safonova
Antibody repertoire construction for organisms with unknown germline V/J genes

82. Sergey Bankevich, Alexander Shlemov, Andrey Bzikadze and Yana Safonova
Antibody repertoire construction from short HiSeq Rep-Seq reads

83. Sergey Bankevich, Alexander Shlemov, Andrey Bzikadze and Yana Safonova
Antibody repertoire construction from Ion Torrent Rep-seq reads

84. Andrey Bzikadze, Sergey Bankevich, Alexander Shlemov and Yana Safonova
AntEvolo: a novel approach for clonal analysis of antibody repertoires

85. Yue Wu, Eleazar Eskin and Sriram Sankararaman
Improving imputation by maximizing power

86. Rayan Chikhi, Charles Deltel, Guillaume Rizk, Claire Lemaitre, Pierre Peterlongo, Kristoffer Sahlin, Lars Arvestad, Paul Medvedev and Dominique Lavenier
High-quality, fast, and memory-efficient assembly of metagenomes and large genomes using Minia-pipeline

87. Luiz Carlos Irber Junior, C. Titus Brown and Tim Head
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88. Andrzej Kloczkowski, Girik Malik and Anirban Banerji
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89. Sheida Hayati and Antonina Mitrofanova
Computational approaches to identify alternative splice variants as biomarkers of disease progression and drug resistance in Acute Myeloid Leukemia

90. Praveen Kumar, Murugesh Easwaran, Nilavamuthan Chandrasekaran and Shanmughavel Piramanayagam
Molecular Insights of Peptide Folding Propensities for Cancer Drug Target Improvisation and Anti Microbial Peptide Library

91. R. Gonzalo Parra, Nikolaos Papadopoulos, Laura Ahumada-Arranz and Johannes Soeding
scTree: reconstructing complex cellular lineage trees from single-cell RNA-seq data

92. Eric Ho
IDICAP2: An Improved Tool for Integrating Drug Intervention Based on Cancer Panel

93. Pravin Dudhagara, Anjana Ghelani and Rajesh Patel
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94. Weronika Wronowska, Krzysztof Gogolewski, Bogdan Lesyng and Anna Gambin
PARP inhibition cytotoxicity or cytoprotection - inferring molecular pathways heterogeneity from transcriptional data

95. Nazar Zaki and Chandana Tennakoon
BioCarian: A Search Engine for Performing Exploratory Searches of Biological Databases

96. Sunhye Park, Young Chan Park, Kiejung Park and In-Song Koh
A comprehensive variation analysis based on whole-genome of 62 Koreans and constructing Korean variome database called as HYKVB

97. Camille Scott and C. Titus Brown
Characterizing RNA-seq assembly graphs: when is enough, enough?

98. Sean La, Ehsan Haghshenas and Cedric Chauve
An analysis of PacBio long read correction algorithms on simulated data using LRCstats

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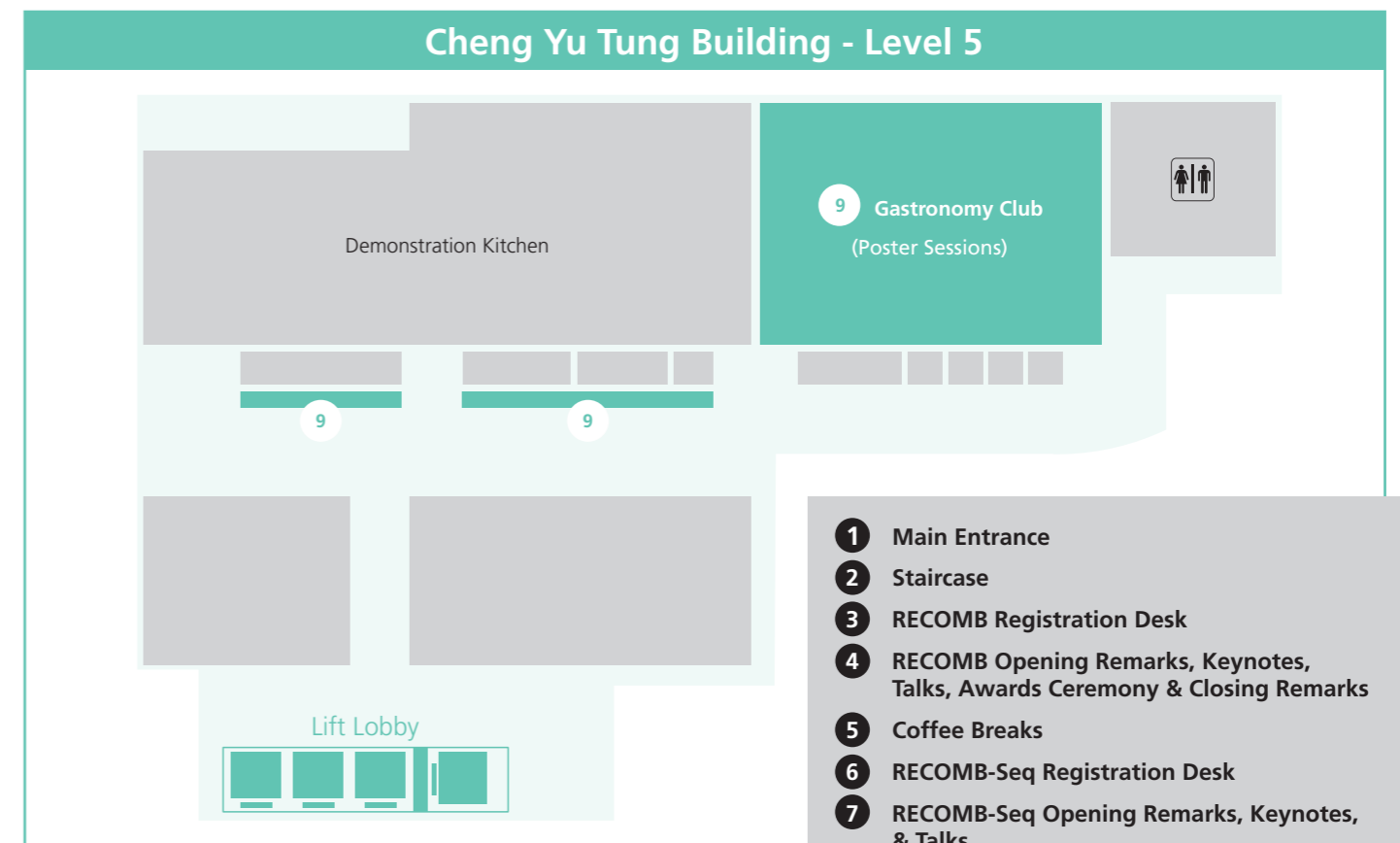
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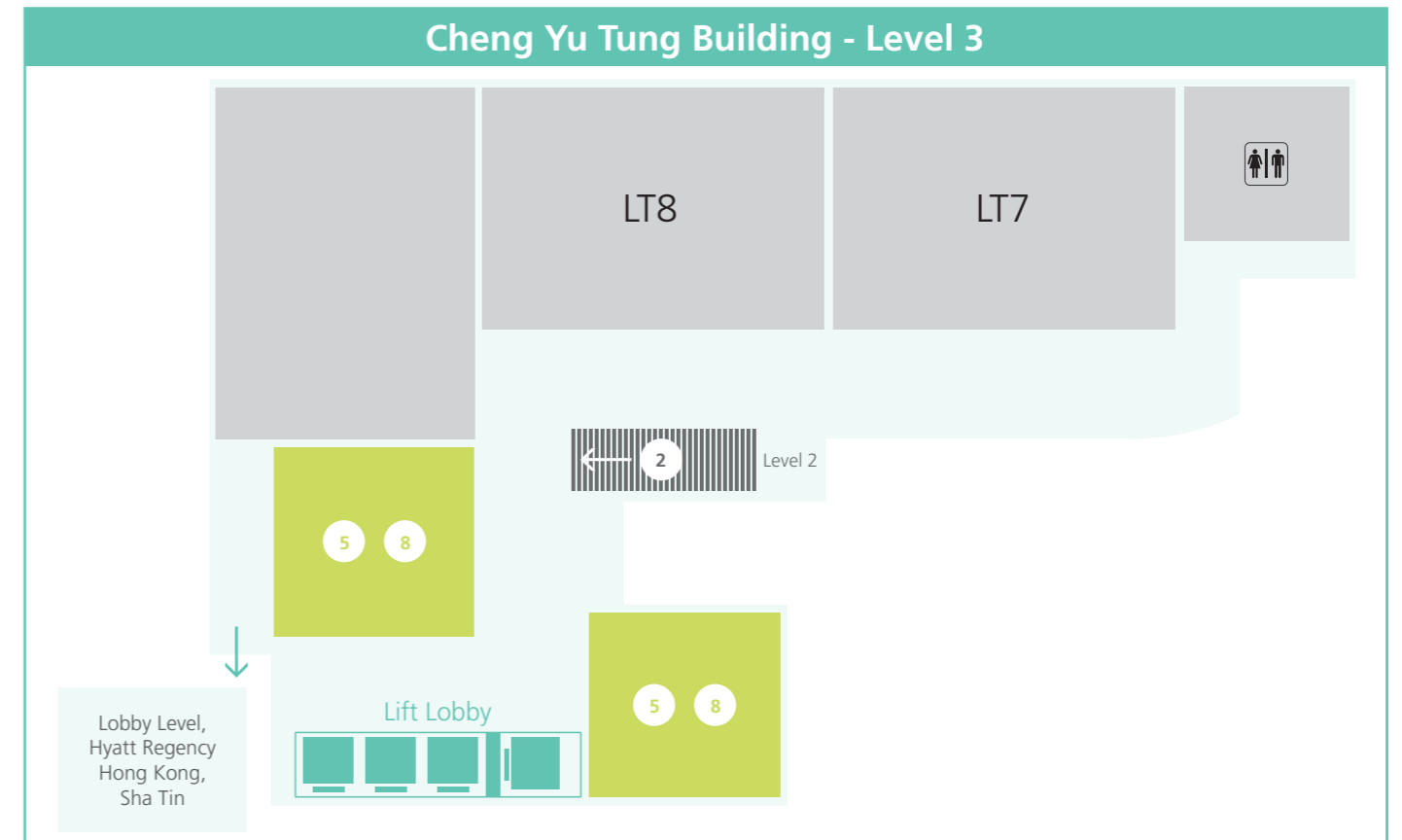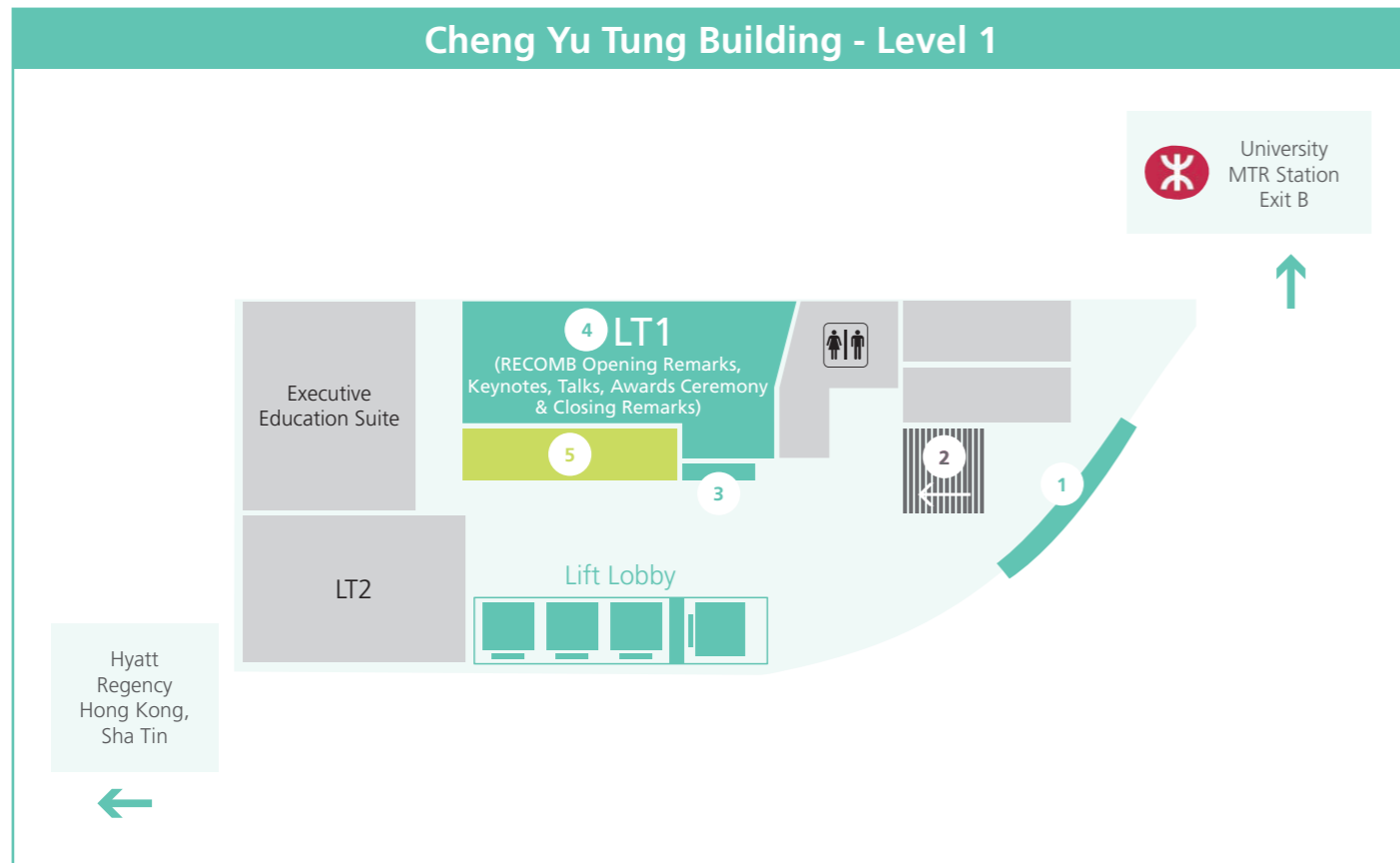
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Executive Education Suite

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(RECOMB Opening Remarks, Keynotes, Talks, Awards Ceremony & Closing Remarks)

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3

2

1

LT2

Lift Lobby

Hyatt Regency Hong Kong, Sha Tin

Cheng Yu Tung Building - Level 3

LT8

LT7

2 Level 2

5 **8**

Lobby Level, Hyatt Regency Hong Kong, Sha Tin

Lift Lobby

5 **8**

Cheng Yu Tung Building - Level 2

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213 214 215 216

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(RECOMB-Seq Opening Remarks, Keynotes & Talks)

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2 Level 1

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Lift Lobby

Cheng Yu Tung Building - Level 5

Demonstration Kitchen

9 **Gastronomy Club**
(Poster Sessions)

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Lift Lobby

1 **Main Entrance**

2 **Staircase**

3 **RECOMB Registration Desk**

4 **RECOMB Opening Remarks, Keynotes, Talks, Awards Ceremony & Closing Remarks**

5 **Coffee Breaks**

6 **RECOMB-Seq Registration Desk**

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Conference Venue:
Cheng Yu Tung Building
The Chinese University of Hong Kong

University MTR Station
Exit B

Hyatt Regency Hong Kong,
Sha Tin

P Carpark

CUHK Campus Map
www.cuhk.edu.hk/english/campus/cuhk-campus-map.html

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Transportation to banquet venue from the conference site and return on May 5
Banquet venue: ClubONE on the Park, Science Park *[ticket required]*
Address: Shop 061-066, G/F, Building 12W, No.12 Science Park West Avenue, Hong Kong Science Park, Shatin, N.T.
- Coaches will start departing at the entrance of Cheng Yu Tung Building (CYT) during 6:00 PM - 6:30 PM
- Transportation from ClubONE on the Park to University MTR Station will be provided after the banquet

Other restaurants
- You can obtain more information about the other restaurants at the Chinese University of Hong Kong at *www.cuhk.edu.hk/english/campus/accommodation.html* (under the section "Living On Campus > Restaurants")
- You can also find a lot of local restaurants and food shops in the Shatin district, which is two train stations away from the University MTR Station

Interesting places to visit

Ocean Park
www.oceanpark.com.hk

Giant Buddha/Po Lin Monastery at Lantau Island
www.plm.org.hk/eng/home.php

Hong Kong Wetland Park
www.wetlandpark.gov.hk/en

The Peak Tower, Hong Kong
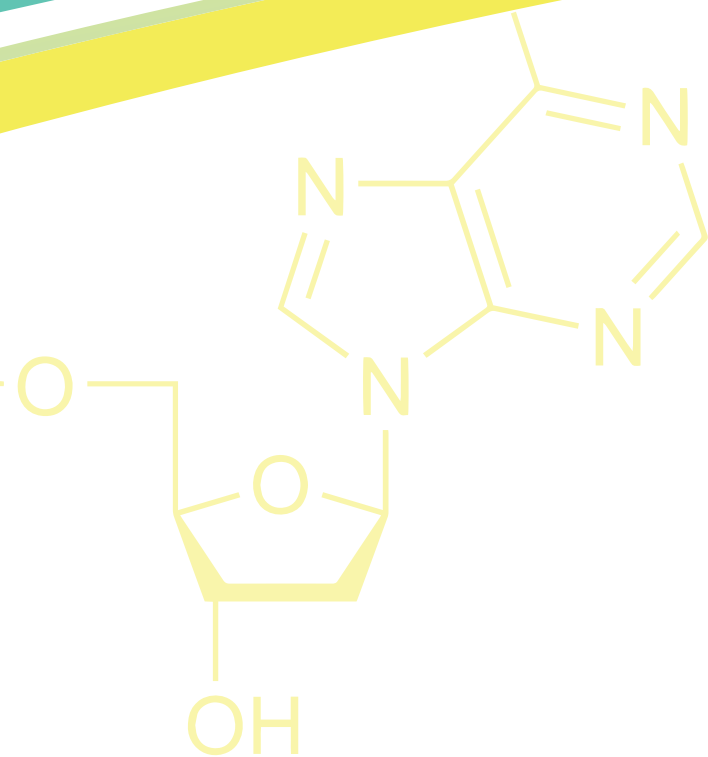*www.thepeak.com.hk*

Hong Kong Disneyland
www.hongkongdisneyland.com

Hiking Trails in Hong Kong
hiking.gov.hk/eng

You can obtain more information at:
www.discoverhongkong.com/eng/index.jsp