

# Schedule

June 8, Friday (Chun Hui Yuan Resort)		
14:00 – 21:00	Registration & Reception	
18:00 – 20:00	Dinner	Four Seasons Hall
June 9, Saturday (Chun Hui Yuan Resort)		
8:40 – 8:50	Opening Remarks	Zi Jing Hall (1 <sup>st</sup> Floor)
8:50 – 10:10	Keynote & Invited Talk	Zi Jing Hall (1 <sup>st</sup> Floor)
8:50 – 9:40	<b>Keynote:</b> Xuegong Zhang (Tsinghua University): A primary view on single-cell bioinformatics	
9:40 – 10:10	<b>Invited:</b> Min Li (Central South University): De novo Genome Assembly by Using Statistical Characteristics of Paired-end Reads	
10:10 – 10:30	Coffer Break	
10:30 – 11:50	Parallel Sessions	
Session 1	Network Analysis & Modelling	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 2	Genomic Data Analysis	Meeting Room 12 (2 <sup>nd</sup> Floor)
12:00 – 14:00	<b>Lunch</b>	
14:00 – 17:40	Parallel Sessions	
Session 3	Network Analysis & Modelling	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 4	Genomic Data Analysis	Meeting Room 12 (2 <sup>nd</sup> Floor)
15:20 – 15:40	Coffer Break	
Session 5	Cancer Data Analysis	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 6	Structure & Interaction	Meeting Room 12 (2 <sup>nd</sup> Floor)
18:00 – 20:00	<b>Banquet</b>	
		Zi Jing Hall (1 <sup>st</sup> Floor)
June 10, Sunday (Chun Hui Yuan Resort)		
8:40 – 10:00	Keynote & Invited Talk	Zi Jing Hall (1 <sup>st</sup> Floor)
8:40 – 9:30	<b>Keynote:</b> Ying Xu (University of Georgia) : Searching for roots of cancer development through mining large scale cancer tissue data and modeling the chemistry of cellular base-acid homeostasis	
9:30 – 10:00	<b>Invited:</b> Xin Gao (King Abdullah University of Science and Technology): Gracob: a graph-based constant-column biclustering method for mining growth phenotype data	
10:00 – 10:20	Coffer Break	
10:20 – 11:55	Parallel Sessions	
Session 7	HPC & CryoEM	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 8	Machine & Deep Learning	Meeting Room 12 (2 <sup>nd</sup> Floor)
12:00 – 14:00	<b>Lunch</b>	
14:00 – 17:40	Parallel Sessions	
Session 9	Data Analysis & Methodology	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 10	Machine & Deep Learning	Meeting Room 12 (2 <sup>nd</sup> Floor)
Session 11	Structure & Interaction	Meeting Room 12 (2 <sup>nd</sup> Floor)
16:00 – 16:20	Coffer Break	
Session 12	Analysis and Visualization Tools	Meeting Room 3 (2 <sup>nd</sup> Floor)
Session 13	Cancer Data Analysis	Meeting Room 12 (2 <sup>nd</sup> Floor)
18:00 – 19:30	Dinner	
		Four Seasons Hall
June 11, Monday (Chun Hui Yuan Resort)		
8:30 – 9:30	Session 14: Gene Expression Data Analysis	Meeting Room 3 (2 <sup>nd</sup> Floor)
9:30 – 10:30	Session 15: RNA-Seq Data Analysis	Meeting Room 3 (2 <sup>nd</sup> Floor)
10:30 – 10:40	Closing Remarks	
		Meeting Room 3 (2 <sup>nd</sup> Floor)

# ISBRA 2018 Agenda

## June 8, Friday

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14:00pm to 21:00pm	Registration & Reception
18:00pm to 20:00pm	Dinner Four Seasons Hall

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## June 9, Saturday

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8:40am to 8:50am	Opening Remarks	Zi Jing Hall (1 <sup>st</sup> Floor)
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8:50am to 9:40am	<b>A primary view on single-cell bioinformatics</b> Xuegong Zhang (Tsinghua University) Session Chair: Yi Pan (Georgia State University)
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9:40am to 10:10am	<b>De novo genome assembly by using statistical characteristics of paired-end reads</b> Min Li (Central South University) Session Chair: Zhipeng Cai (Georgia State University)
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10:10am to 10:30am	Coffer Break
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10:30am to 11:50am	Session 1: Network Analysis & Modelling Session Chair: Le Zhang (Sichuan University) Meeting Room 3 (2 <sup>nd</sup> Floor)
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10:30am – 10:50am	<b>An improved particle swarm optimization with dynamic scale-free network for detecting multi-omics features (ID: 71)</b> Huiyu Li, Sheng-Jun Li, Junliang Shang, Jin-Xing Liu and Chun-Hou Zheng.
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10:50am – 11:10am	<b>PBMarsNet: a multivariate adaptive regression splines based method to reconstruct gene regulatory networks (ID: 100)</b> Siyu Zhao, Ruiqing Zheng, Xiang Chen, Yaohang Li, Fangxiang Wu, Min Li.
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11:10am – 11:30am	<b>Prediction of drug response with a topology based dual-layer network model (ID: 40)</b> Suyun Huang and Xingming Zhao.
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11:30am – 11:50am	<b>GRTR: drug-disease association prediction based on graph regularized transductive regression on heterogeneous network (ID: 52)</b> Qiao Zhu, Jiawei Luo, Pingjian Ding and Qiu Xiao.
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<b>10:30am to 11:50am</b>	<p>Session 2: Genomic Data Analysis</p> <p>Session Chair: Bingqiang Liu (Shandong University)</p> <p>Meeting Room 12 (2<sup>nd</sup> Floor)</p>	
10:30am – 10:50am	<p><b>Rextal: regional extension of assemblies using linked-reads (ID: 111)</b></p> <p>Tunazzina Islam, Desh Ranjan, Eleanor Young, Ming Xiao, Mohammad Zubair and Harold Riethman.</p>	
10:50am – 11:10am	<p><b>Bounds on identification of genome evolution pacemakers (ID: 108)</b></p> <p>Sagi Snir.</p>	
11:10am – 11:30am	<p><b>Predicting comorbid diseases with geometric embedding of human interactome (ID: 75)</b></p> <p>Pakeeza Akram and Li Liao.</p>	
11:30am – 11:50am	<p><b>Region-based interaction detection in genome-wide case-control studies (ID: 21)</b></p> <p>Sen Zhang, Ronald Cw Ma and Weichuan Yu.</p>	
<b>12:00pm to 14:00pm</b>	Lunch	Four Seasons Hall
<b>14:00pm to 15:20pm</b>	<p>Session 3: Network Analysis &amp; Modelling</p> <p>Session Chair: Xingming Zhao (Fudan University)</p> <p>Meeting Room 3 (2<sup>nd</sup> Floor)</p>	
14:00pm – 14:20pm	<p><b>Identification of methylation states of DNA regions for Illumina Methylation BeadChip (ID: 46)</b></p> <p>Ximei Luo, Yuming Zhao, Fang Wang and Guohua Wang.</p>	
14:20pm – 14:40pm	<p><b>Drug repositioning based on individual bi-random walks on a heterogeneous network (ID: 18)</b></p> <p>Yuehui Wang, Maozu Guo, Yazhou Ren, Lianyin Jia and Guoxian Yu.</p>	
14:40pm – 15:00pm	<p><b>Detecting differential consistency genes and network modules (ID:33)</b></p> <p>Jianwei Lu, Yao Lu, Yusheng Ding, Qingyang Xiao, Linqing Liu, Qingpo Cai, Yunchuan Kong, Yun Bai and Tianwei Yu.</p>	
15:00pm – 15:20pm	<p><b>Joint SNMF method for finding modules of multiple brain networks (ID: 102)</b></p> <p>Lingkai Tang, Yulian Ding and Fangxiang Wu.</p>	
<b>14:00pm to 15:20pm</b>	<p>Session 4: Genomic Data Analysis</p> <p>Session Chair: Min Li (Central South University)</p> <p>Meeting Room 12 (2<sup>nd</sup> Floor)</p>	
14:00pm – 14:20pm	<p><b>Identifying driver genes involving gene dysregulated expression, tissue-specific expression and gene-gene network (ID: 7)</b></p> <p>Junrong Song, Feng Wang, Wei Peng and Jianxin Wang.</p>	
14:20pm – 14:40pm	<p><b>Detecting horizontal gene transfer: a probabilistic approach (ID: 45)</b></p> <p>Gur Sevillya, Orit Adato and Sagi Snir.</p>	

14:40pm – 15:00pm	<b>HiSSI: high-order SNP-SNP interactions detection based on efficient significant pattern and differential evolution (ID: 26)</b> Xia Cao, Jie Liu, Maozu Guo and Jun Wang.
15:00pm – 15:20pm	<b>MetaMat: reference-free metagenomic binning by matrix deconvolution (ID: 74)</b> Terry Ma, Xin Xing and Di Xiao.
<b>15:20pm to 15:40pm</b>	Coffer Break
<b>15:40pm to 17:40pm</b>	Session 5: Cancer Data Analysis Session Chair: Dong Si (University of Washington) Meeting Room 3 (2 <sup>nd</sup> Floor)
15:40pm – 16:00pm	<b>An extension of deep pathway analysis: a pathway route analysis framework incorporating multi-dimensional cancer genomics data (ID: 105)</b> Yue Zhao.
16:20pm – 16:40pm	<b>Inferring dysregulated pathways of driving cancer subtypes through multi-omics integration (ID: 24)</b> Kai Shi, Lin Gao and Bingbo Wang.
16:40pm – 17:00pm	<b>The review of the major entropy methods and applications in biomedical signal research (ID: 9)</b> Guangdi Liu, Yuan Xia, Chuanwei Yang and Le Zhang.
17:00pm – 17:20pm	<b>Detecting circular RNA from high-throughput sequence data with De Bruijn graph (ID: 59)</b> Xin Li and Yufeng Wu.
17:20pm – 17:40pm	<b>A new method for mining information of co-expression network based on multi-cancers integrated data (ID: 51)</b> Mi-Xiao Hou, Ying-Lian Gao, Jin-Xing Liu, Jun-Liang Shang, Rong Zhu and Sha-Sha Yuan.
<b>15:40pm to 17:40pm</b>	Session 6: Structure & Interaction Session Chair: Jinxing Liu (Qufu Normal University) Meeting Room 12 (2 <sup>nd</sup> Floor)
15:40pm – 16:00pm	<b>KSIBW: predicting kinase-substrate interactions based on bi-random walk (ID: 49)</b> Qingfeng Chen, Canshang Deng, Jin Liu, Ruiqing Zheng, Jianxin Wang and Wei Lan.
16:20pm – 16:40pm	<b>XPredRBR: accurate and fast prediction of RNA-binding residues in proteins using extreme gradient boosting (ID: 87)</b> Lei Deng, Zuojin Dong and Hui Liu.
16:40pm – 17:00pm	<b>DDIGIP: predicting drug-drug interactions based on Gaussian interaction profile kernels (ID: 16)</b>

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Cheng Yan, Jianxin Wang, Fang-Xiang Wu and Yi Pan.

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17:00pm – 17:20pm **A novel multi-scale local sequence and structural representation for identifying protein-protein complexes (ID: 85)**

Fei Guo and Jijun Tang.

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17:20pm – 17:40pm **Novel inhibitors of BCL-ABR1 tyrosine kinase for chronic myeloid leukemia disease through fragment-based drug design (ID: 131)**

Satya Anindita, Atika Marnolia, Hersal Permana Putra, Muhammad Chandra Haikal and Usman Sumo Friend Tambunan.

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**18:00pm to 20:00pm** Banquet Zi Jing Hall (1<sup>st</sup> Floor)

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## June 10, Sunday

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**8:40am to 9:30am** **Searching for roots of cancer development through mining large scale cancer tissue data and modeling the chemistry of cellular base-acid homeostasis**

Ying Xu (University of Georgia & Jilin University)  
Session Chair: Alexander Zelikovsky (Georgia State University)  
Zi Jing Hall (1st Floor)

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**9:30am to 10:00am** **Gracob: a graph-based constant-column biclustering method for mining growth phenotype data**

Xin Gao (King Abdullah University of Science and Technology)  
Session Chair: Pavel Skums (Georgia State University)  
Zi Jing Hall (1st Floor)

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**10:00am to 10:20am** Coffer Break

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**10:20am to 11:55am** Session 7: HPC & CryoEM  
Session Chair: Guoxian Yu (Southwest University)  
Meeting Room 3 (2<sup>nd</sup> Floor)

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10:20am – 10:40am **On  $\$k$ -mismatch shortest unique substring queries using GPU (ID:95)**

Daniel W. Schultz and Bojian Xu.

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10:40am – 11:00am **Memory-efficient and stabilizing management system and parallel methods for RELION using CUDA and MPI (ID: 110)**

Jingrong Zhang, Zihao Wang, Yu Chen and Fa Zhang.

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11:00am – 11:20am **GPU accelerated ray tracing for the Beta-barrel detection from three-dimensional Cryo-EM map (ID: 115)**

Albert Ng, Adedayo Odesile and Dong Si.

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11:20am – 11:40am	<b>A pattern recognition tool for medium-resolution Cryo-EM density maps and low-resolution Cryo-ET density maps (ID: 138)</b> Qiao Zhu, Jiawei Luo, Pingjian Ding and Qiu Xiao. Devin Haslam, Salim Sazed and Jing He.
11:40am – 11:55am	<b>A fast genome sequence aligner based on minimal perfect hash algorithm realized with FPGA based heterogeneous computing platform (ID: 121)</b> Ke Huang, Shubo Yang, Zhaojian Luo, Ke Yang, Menghan Chen, Guopeng Wei and Jian Huang.
<b>10:20am to 11:55am</b>	Session 8: Machine & Deep Learning Session Chair: Jun Wang (Southwest University) Meeting Room 12 (2 <sup>nd</sup> Floor)
10:20am – 10:40am	<b>An integrative framework for combing sequence and epigenomic data to predict transcription factor binding sites using deep learning. (ID: 25)</b> Fang Jing, Shaowu Zhang, Zhen Cao and Shihua Zhang.
10:40am – 11:00am	<b>DEEPSEN: a new method for super-enhancer prediction based on convolutional neural network (ID: 44)</b> Hongda Bu, Jiaqi Hao, Yanglan Gan, Jihong Guan and Shuigeng Zhou.
11:00am – 11:20am	<b>Data-driven approach for understanding the mild cognitive impairment (ID: 55)</b> Bingchen Yu, Meng Han, Liyuan Liu, Liquan Bai, Yan Huang and Yi Liang.
11:20am – 11:40am	<b>A deep learning method for prediction of Benign Epilepsy with centrotemporal spikes (ID: 92)</b> Ming Yan, Yi Pan, Ling Liu and Sihan Chen.
11:40am – 11:55am	<b>LSTM recurrent neural networks for influenza trends prediction (ID: 123)</b> Liyuan Liu, Meng Han, Yiyun Zhou and Yan Wang.
<b>12:00pm to 14:00pm</b>	Lunch <span style="float: right;">Four Seasons Hall</span>
<b>14:00pm to 16:00pm</b>	Session 9: Data Analysis & Methodology Session Chair: Wei Peng (Kunming University of Science and Technology) Meeting Room 3 (2 <sup>nd</sup> Floor)
14:00pm – 14:20pm	<b>On approaching the one-sided exemplar adjacency number problem. (ID: 14)</b> Letu Qingge, Killian Smith, Sean Jungst and Binhai Zhu.
14:20pm – 14:40pm	<b>Prediction of type III secreted effectors based on word embedding for protein sequences (ID: 68)</b> Xiaofeng Fu, Yiqun Xiao and Yang Yang.

14:40pm – 15:00pm	<b>Extending the evolvability model to the prokaryotic world: simulations and results on real data (ID: 106)</b> Sagi Snir and Ben Yohay.
15:00pm – 15:20pm	<b>Jaccard/Tanimoto similarity test and estimation methods to evaluate species co-occurrences (ID:57)</b> Neo Christopher Chung, Błażej Miasojedow, Michał Startek and Anna Gambin.
15:20pm – 15:40pm	<b>A robustness metric for biological data clustering algorithms (ID:101)</b> Yuping Lu, Charles Phillips and Michael Langston.
15:40pm – 16:00pm	<b>Predicting opioid epidemic by using twitter data (ID: 137)</b> Yubao Wu, Pavel Skums, Alex Zelikovsky, David S. Campo and Xueting Liao.
<b>14:00pm to 16:00pm</b>	Session 10: Machine & Deep Learning / Session 11: Structure & Interaction Session Chair: Lei Deng (Central South University) Meeting Room 12 (2nd Floor)
14:00pm – 14:20pm	<b>Deep feature selection with application in neisseria gonorrhoeae antimicrobial resistance study (ID:116)</b> Jinhong Shi, Yan Yan, Michael Horsch, Mathew Links, Longhai Li and Antony Kusalik.
14:20pm – 14:40pm	<b>InvBFM: finding genomic inversions from high-throughput sequence data based on feature mining (ID: 97)</b> Zhongjia Wu, Yufeng Wu and Jingyang Gao.
14:40pm – 15:00pm	<b>Predicting gene-disease associations with manifold learning (ID: 134)</b> Ping Luo, Li-Ping Tian, Bolin Chen, Qianghua Xiao and Fangxiang Wu.
15:00pm – 15:20pm	<b>Sprites2: detection of deletions based on an accurate alignment strategy (ID: 38)</b> Zhen Zhang, Jianxin Wang, Junwei Luo, Juan Shang, Min Li, Fang-Xiang Wu and Yi Pan.
15:20pm – 15:40pm	<b>A biologically meaningful extension of the efficient method for deleterious mutations prediction in RNAs: insertions and deletions in addition to substitution mutations (ID: 120)</b> Alexander Churkin and Danny Barash.
15:40pm – 16:00pm	<b>Screening of sonic hedgehog (Shh) inhibitors in the hedgehog signaling pathway from traditional Chinese medicine (TCM) database through structure-based pharmacophore design. (ID: 129)</b> Ilmi Fadhilah Rizki, Mochammad Arfin Fardiansyah Nasution, Syafrida Siregar, Mega Maulina Ekawati and Usman Sumo Friend Tambunan.
<b>16:00pm to 16:20pm</b>	Coffer Break
<b>16:20pm to 17:40pm</b>	Session 12: Analysis and Visualization Tools

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Session Chair: Xiaohua Wan (ICT, CAS)  
Meeting Room 3 (2<sup>nd</sup> Floor)

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16:20pm – 16:40pm **CSA: a web service for the complete process of ChIP-Seq analysis (ID: 47)**  
Min Li, Li Tang, Fangxiang Wu and Yi Pan.

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16:40pm – 17:00pm **OffScan: a universal CRISPR off-target sites detection tool (ID: 107)**  
Yingbo Cui, Minxia Cheng, Jiaming Xu, Xiangke Liao and Shaoliang Peng.

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17:00pm – 17:20pm **GPRED-GC: a gene PREDiction model accounting for 5'-3' GC gradient (ID: 114)**  
Prapaporn Techa-Angkoon, Kevin Childs and Yanni Sun.

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17:20pm – 17:40pm **Cluster matching distance for rooted phylogenetic trees (ID: 60)**  
Jucheol Moon and Oliver Eulenstein.

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**16:20pm to 17:40pm** Session 13: Cancer Data Analysis  
Session Chair: Wei Lan (Guangxi University)  
Meeting Room 12 (2<sup>nd</sup> Floor)

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16:20pm – 16:40pm **MECoRank: cancer driver genes discovery simultaneously evaluating the impact of SNPs and differential expression on transcriptional networks (ID: 84)**  
Hui Ying, Wei Pi-Jing, Xia Junfeng and Zheng Chun-Hou.

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16:40pm – 17:00pm **Non-monotonic directional association test reveals high-quality putative cancer driver noncoding RNAs and biomarkers (ID: 43)**  
Hua Zhong and Mingzhou Song.

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17:00pm – 17:20pm **Identifying subtype specific network-biomarkers of breast cancer survivability (ID: 34)**  
Sheikh Jubair, Luis Rueda and Alioune Ngom.

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17:20pm – 17:40pm **Hierarchical similarity network fusion for discovering cancer subtypes (ID: 36)**  
Liu Shuhui and Shang Xuequn.

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**18:00pm to 19:30pm** Dinner Four Seasons Hall

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## June 11, Monday

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<b>8:30am to 9:30am</b>	Session 14: Gene Expression Data Analysis Session Chair: Shihua Zhang (AMSS, CAS) Meeting Room 3 (2 <sup>nd</sup> Floor)
8:30am – 8:50am	<b>Detecting diagnostic biomarkers of Alzheimer's disease by integrating gene expression data in six brain regions (ID: 2)</b> Lihua Wang and Zhi-Ping Liu.
8:50am – 9:10am	<b>Revealing the tipping points during infant brain development for human and chimpanzee by analysis of gene expression data (ID: 64)</b> Hui Tang, Ying Tang, Luonan Chen and Tao Zeng.
9:10am – 9:30am	<b>A framework using topological pathways for deeper analysis of transcriptome data (ID: 112)</b> Yue Zhao, Stephanie Piekos, Tham Hoang and Dong-Guk Shin.
<b>9:30am to 10:30am</b>	Session 15: RNA-Seq Data Analysis Session Chair: Fa Zhang (ICT, CAS) Meeting Room 3 (2 <sup>nd</sup> Floor)
9:30pm – 9:50pm	<b>Truncated robust principal component analysis and noise reduction for single cell RNA-seq data (ID: 79)</b> Krzysztof Gogolewski, Maciej Sykulski, Neo Christopher Chung and Anna Gambin.
9:50pm – 10:10pm	<b>Locality sensitive imputation for single-cell RNA-Seq data (ID: 109)</b> Marmar Moussa and Ion Mandoiu.
10:10pm – 10:30pm	<b>Identifying microRNA-gene networks specific to pathologic stages in colon cancer (ID: 54)</b> Benika Hall and Xinghua Shi.
<b>10:30am to 10:40am</b>	Closing Remarks

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# BEI JING CHUNHUIYUAN RESORT GENERAL LAYOUT

北京春晖园温泉度假酒店 平面示意图

