Sunday, January 15th, 2017	
Course: Zero In on Tumor and Cancer NGS Data Analysis **Instructor**: Prof. Wang Lusheng **Place**: 204	
Session 1 **(10:00am – 12:00pm)**	**Virus Analysis in Cancer** Dr. Wenlong Jia
Session 2 **(14:00pm – 16:00pm)**	**Bioinformatics for Cancer Immunotherapy** Dr. Miao Li

Monday, January 16th, 2017		
08:30am - 09:00am	Opening Remarks	
09:00am - 10:00am	**Application of NGS and bioinformatics in response of infectious disease outbreaks**	
	Keynote Speech: Dr. Tong Yi-Gang	
10:00am - 10:25am	Coffee Break (Lobby)	
Parallel Session	**Session 1: Genomic Data Analysis** **(Session Chair: Prof. Byung-Jun Yoon)**	**Session 2: Protein functions** **(Session Chair: Prof. Dimitris Papamichail)**
10:25am - 10:50am	**Efficient Algorithms for Genomic Duplication Models** (Jarosław Paszek and Pawel Gorecki)	**Investigation and identification of protein carbonylation sites based on position-specific amino acid composition and physicochemical features** (Fergie Joanda Kaunang, Chien-Hsun Huang, Hui-Ju Kao, Kai-Yao Huang, Hsin-Yao Wang, Jang-Jih Lu and Tzong Yi Lee)
10:50am - 11:15am	**Visualization of consensus genome structure without using a reference genome** (Ipputa Tada, Yasuhiro Tanizawa and Masanori Arita)	**Predicting protein-binding regions in RNA using nucleotide profiles and compositions** (Daesik Choi, Byungkyu Park, Hanju Chae, Wook Lee and Kyungsook Han)
11:15am - 11:40am	Coffee Break (Lobby)	
11:40am - 12:05am	**Genome Rearrangement with ILP** (Tom Hartmann, Nicolas Wieseke, Roded Sharan, Martin Middendorf and Matthias Bernt)	**A sequence-based method to predict the impact of regulatory variants using random forest** (Qiao Liu and Rui Jiang)
12:05am - 12:30pm	**PECC: correcting contigs based on paired-end read distribution** (Min Li, Xiaodong Yan, Junwei Luo, Fangxiang Wu, Yi Pan and Jianxin Wang)	**Revealing Common Disease Mechanisms Shared by Tumors of Different Tissues of Origin through Semantic Representation of Genomic Alterations and Topic Modeling** (Vicky Chen, John Paisley and Xinghua Lu)
12:30pm - 14:30pm	Complimentary Lunch	
14:30pm - 15:30pm	**From Genotype to Phenotype: A Five-track Species-focused Biology Converges the Complexity of Life**	
	Keynote Speech: Prof. Jun Yu	
15:30pm - 15:55pm	Coffee Break (Lobby)	

Parallel Session	**Session 3: Evolution** **(Session Chair: Prof. Tzong Yi Lee)**	**Session 4: NGS data Analysis** **(Session Chair: Prof. Kyungsook Han)**
15:55pm - 16:20pm	**Gene Tree Construction and Correction using SuperTree and Reconciliation** (Manuel Lafond, Cedric Chauve, Nadia El-Mabrouk and Aïda Ouangraoua)	**Fuwa: a decision-tree-based fast variant caller for next-generation sequencing data** (Zhentang Li, Yi Wang and Fei Wang)
16:20pm - 16:45pm	**Live Phylogeny with Polytomies: Finding the Most Compact Parsimonious Trees** (Dimitris Papamichail, Angela Huang, Edward Kennedy, Jan-Lucas Ott, Andrew Miller and Georgios Papamichail)	**Optimal hybrid sequencing and assembly: feasibility conditions for accurate genome reconstruction and cost minimization strategy** (Chun-Chi Chen, Noushin Ghaffari, Xiaoning Qian and Byung-Jun Yoon)
16:45am - 17:10am	Coffee Break (Lobby)	
17:10pm - 17:35pm	**Evolutionary model for the statistical divergence of paralogous and orthologous gene pairs generated by whole genome duplication and speciation** (Yue Zhang, Chunfang Zheng and David Sankoff)	**A framework for space-efficient read clustering in metagenomic samples** (Jarno Alanko, Djamal Belazzougui, Fabio Cunial and Veli Mäkinen)
17:35pm - 18:00pm	**A Program to Compute the Soft Robinson–Foulds Distance between Phylogenetic Networks** (Bingxin Lu, Louxin Zhang and Hon Wai Leong)	**A Feature Sampling Strategy for Analysis of High Dimensional Genomic Data** (Jie Zhang, Zhigen Zhao, Kai Zhang and Zhi Wei)
18:00pm - 20:00pm	On-site Banquet with Dinner Speech (open and complimentary to all registered attendees) Speaker	

Tuesday, January 17th, 2017		
Parallel Session	**Session 5: Virus Analysis and Horizontal Gene Transfer** **(Session Chair: Prof. Leong Hon Wai)**	**Session 6: Parallel Tools and non-omics Data** **(Session Chair: Prof. Limsoon Wong)**
09:00am - 09:25am	**BATVI: Fast, Sensitive and Accurate Detection of Virus Integrations** (Chandana Tennakoon and Wing-Kin Sung)	**Parallel Identification of Variable-length Patterns for Large-scale Prediction of Protein-protein Interactions Using MapReduce** (Lun Hu, Xiaohui Yuan, Pengwei Hu and Keith C. C. Chan)
09:25am - 09:50am	**Inferring gene-species assignments in the presence of horizontal gene transfer** (Agnieszka Mykowiecka, Pawel Gorecki)	**P-Hint-Hunt: A Deep Parallelized Whole Genome DNA Methylation Detection Tool** (Ming Gao, Xiangke Liao, Chengkun Wu, Wenqiang Yu and Shaoliang Peng)
09:50am - 10:15am	**Prediction of virus-host infectious association by supervised learning methods** (Mengge Zhang, Lianping Yang, Jie Ren, Nathan Ahlgren, Jed Fuhrman and Fengzhu Sun)	**A novel wearable device for continuous, non-invasion blood pressure measurement** (Qin Xin, Jianping Wu and Ke Xu)
10:15am - 10:40am	Coffee Break (Lobby)	
Parallel Session	**Session 7: Analysis Tools and Statistical Methodology Development** **(Session Chair: Prof. Dongbo Bu)**	**Session 8: Analysis Tools** **(Session Chair: Prof. Yang Yang)**

10:40am - 11:05am	**AfterQC: Automatic Filtering, Trimming, Error Removing and Quality Control for Fastq Data** (Shifu Chen, Tanxiao Huang, Yanqing Zhou, Mingyan Xu and Jia Gu)	**Local-Nearest-Neighbors-Based Feature Weighting for Gene Selection** (Shuai An, Jun Wang and Jinmao Wei)
11:05am - 11:30am	**Reviving the two-state Markov chain approach** (Andrzej Mizera, Jun Pang and Qixia Yuan)	**Analyzing low-pass whole genome sequencing of over 140,000 individuals from throughout China** (Siyang Liu, Shujia Huang, Xin Jin and the Chinese Millionome Consortium)
11:30am - 11:55am	**DTL Reconciliation Repair** (Weiyun Ma, Dmitriy Smirnov and Ran Libeskind-Hadas)	
11:55am -14:00pm	Complimentary Lunch	
Parallel Session	**Session 9: 3D structures** **(Session Chair: Dr. Tianhai Tian)**	**Session 10: miRNA Analysis** **(Session Chair: Prof. Wing-Kin Sung)**
14:00pm - 14:25pm	**Receptor-guided 3D-QSAR studies, Molecular Dynamics Simulation and Free energy calculations of Btk kinase inhibitors.** (Pavithra Balasubramanian, Anand Balupuri and Seung Joo Cho)	**Identifying miRNA sponge modules using biclustering and regulatory scores** (Junpeng Zhang, Thuc Le, Lin Liu and Jiuyong Li)
14:25pm - 14:50pm	**SheddomeDB: the ectodomain shedding database for membrane-bound shed markers** (Wei-Sheng Tien, Jun-Hong Chen and Kun-Pin Wu)	**A clustering-based approach for the identification of microRNA combinatorial biomarkers** (Yang Yang, Ning Huang, Luning Hao and Wei Kong)
14:50pm - 15:15pm	**Improving prediction of burial state of residues by exploiting correlation among residues** (Hai'E Gong, Haicang Zhang, Chao Wang, Shiwei Sun, Wei-Mou Zheng, Dongbo Bu and Jianwei Zhu)	**Plant miRNAs found in human circulating sys-tem provide evidences of cross kingdom RNAi** (Yu-Chen Liu and Hsien-Da Huang)
15:15pm - 15:30pm	Coffee Break (Lobby)	
Parallel Session	**Session 11: Analysis** **(Session Chair: Dr. Lun Hu)**	**Session 12: Proteomics** **(Session Chair: Dr. Shifu Chen)**
15:30pm - 15:55pm	**An integrated approach with new strategies for QSAR models and lead optimization** (Hui-Hui Hsu, Li-Jen Chang and Jinn-Moon Yang)	**Using the entrapment sequence method as a standard to evaluate key steps of proteomics data analysis process** (Xiao-dong FENG, Li-wei LI, Jian-hong Zhang, Yun-ping ZHU, Cheng CHANG, Kun-xian SHU and Jie MA)
15:55pm - 16:20pm	**Negative Sampling with Multi-Layer Perceptron for Biological Event Trigger Identification** (Nan Jiang, Wenge Rong, Yifan Nie, Yikang Shen and Zhang Xiong)	**DISC: Disulfide Linkage Characterization from Tandem Mass Spectra** (Yi Liu, Weiping Sun, Baozhen Shan and Kaizhong Zhang)
16:20pm - 16:45pm	**Mathematical modelling for variations of inbreeding populations fitness with single and polygenic traits** (Shuhao Sun, Fima Klebaner and Tianhai Tian)	**Protein complex-based analysis is resistant to the obfuscating consequences of batch effects --- A case study in clinical proteomics** (Wilson Wen Bin Goh and Limsoon Wong)
16:45pm - 18:00pm	Poster Session / Exhibition	

Wednesday, January 18th, 2017

Parallel Session	**Session 13: Analysis Tools** **(Session Chair: Dr. Zeng Tao)**	**Session 14: Molecular Diagnosis with Omics Data** **(Session Chair: Prof. Shuqin Zhang)**
08:30am - 08:55am	**A statistical method for the conservative adjustment of false discovery rate (q-value)** (Yinglei Lai)	**Discovering DNA methylation patterns for long non-coding RNAs associated with cancer subtypes** (Xiaoke Ma, Liang Yu, Peizhuo Wang and Xiaofei Yang)
08:55am - 09:20am	**Feature Selection Based on AUC and Variable Complementarity** (Lei Sun, Jun Wang and Jinmao Wei)	**Staged heterogeneity learning to identify conformational B-cell epitopes from antigen sequences** (Jing Ren, Jiangning Song, John Ellis and Jinyan Li)
09:20am - 09:45am	**Pysim-sv: a package for simulating structural variation data with GC-biases** (Yuchao Xia, Yun Liu, Minghua Deng and Ruibin Xi)	**GQSAR Modeling and Combinatorial library generation of 4-phenylquinazoline-2-carboxamide derivatives as Antiproliferative Agents in Human Glioblastoma Tumors** (Debolina Goswami, Sukriti Goyal, Salma Jamal, Ritu Jain, Divya Wahi and Abhinav Grover)
09:45am - 10:10am	**A computational method for estimating the PCR duplication rate in DNA and RNA-seq experiments** (Vikas Bansal)	**Gene Expression Profiling of Tumor Associated Macrophage after Exposure to Single Dose Irradiaiotn** (Wei-Hsiang Kung, Ching-Fang Yu, Andy Chi-Lung Lee, Chi-Dung Yang, Yu-Chen Liu, Fang-Hsin Chen and Hsien-Da Huang)
10:10am - 10:35am	Coffee Break (Lobby)	
Parallel Session	**Session 15: Networks and Interactions** **(Session Chair: Dr. Ruibin Xi)**	**Session 16: Network Analysis** **(Session Chair: Prof. Jinyan Li)**
10:35am - 11:00am	**Prior knowledge guided active modules identification: an integrated multi-objective approach** (Weiqi Chen, Jing Liu and Shan He)	**Comparative network stratification analysis for identifying functional interpretable network biomarkers** (Zhang Chuanchao, Liu Juan, Shi Qianqian, Zeng Tao and Chen Luonan)
11:00am - 11:25am	**An empirical fuzzy multifactor dimensionality reduction method for detecting gene-gene interactions** (Sangseob Leem and Taesung Park)	**Construction of Condition-specific Pathway Interaction Network by Computing Shortest Paths on Weighted PPI** (Ji Hwan Moon, Sangsoo Lim, Kyuri Jo, Sangseon Lee, Seokjun Seo and Sun Kim)
11:25am - 11:50am	**Node-based differential network analysis in genomics** (Xiao-Fei Zhang, Le Ou-Yang and Hong Yan)	**Active module identification in intracellular networks using a memetic algorithm with a new binary decoding scheme** (Dong Li, Zhisong Pan, Guyu Hu, Zexuan Zhu and Shan He)
11:50am - 12:15pm	**Selecting High-Quality Negative Samples for Effectively Predicting Protein-RNA Interactions** (Zhanzhan Cheng, Kai Huang, Shuigeng Zhou, Hui Liu, Yang Wang and Jihong Guan)	**Drug-target Interaction Prediction by Integrating Multiview Network Data** (Shuqin Zhang, Limin Li and Michael Kwok-Po Ng)
12:15pm -14:30pm	Complimentary Lunch (Lobby)	
14:30pm – 15:30pm	Closing Remarks, Award Ceremony and Raffle Drawing (See You Next Year!)	