

Table of Contents

Part I iCBBE 2013 Conference Schedule	2
Part II Plenary Speech.....	4
Part III Oral Sessions	9
Oral Session 1: Bioinformatics	9
Oral Session 2: Bioinformatics and Biomedical Engineering.....	10
Oral Session 3: Biomedical Engineering	11
Part IV Instructions for Presentations	13
Part V Hotel Information	14
Contact Us	14

Part I iCBBE 2013 Conference Schedule

Registration September 26~28, 2013

Registration Time	Date	Location:
14:00-18:00	September 26, 2013	
08:00-18:00	September 27, 2013	1 st Floor, Beijing Yanshan Hotel
08:00-14:00	September 28, 2013	

Friday Morning, September 27

Time	Activity	Location: PLUM BLOSSOM ROOM (沁梅厅) 2 nd Floor, Beijing Yanshan Hotel
08:20-08:30	Opening Ceremony	
08:30-09:10	Plenary Speech: Modeling Dynamics of Cell-fate Speaker: Prof. Michael Q. Zhang , University of Texas at Dallas, USA	
09:10-09:50	Plenary Speech: Molecular Networks for Interpretation and Prediction in Biology Speaker: Prof. Edwin Wang , National Research Council Canada/McGill University, Canada	
09:50-10:30	Plenary Speech: Testing Threshold-Dependent Model for Cell Fate Controlling during Drosophila Embryogenesis Speaker: Dr. Feng Liu , Princeton University, USA	
10:30-10:50	Coffee Break	
10:50-11:30	Plenary Speech: When Modern Computational Systems Biology Meets Ancient Traditional Chinese Medicine Speaker: Prof. Calvin Yu-Chian Chen , China Medical University	
11:30-12:10	Plenary Speech: Gene Networks and Drivers of Inflammation in Complex Human Diseases Speaker: Prof. Bin Zhang , Icahn School of Medicine at Mount Sinai, USA	

Friday Noon, September 27

12:00 – 13:30	Lunch Buffet	Location: VISTA CAFÉ (雅景咖啡厅) 1 st Floor, Beijing Yanshan Hotel
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Friday Afternoon, September 27

Time	Activity (Coffee Break 15:40 – 16:00)	Location: 2 nd Floor Beijing Yanshan Hotel
14:00-18:00	Oral Session 1: Bioinformatics	PLUM BLOSSOM ROOM (沁梅厅)

Friday Evening, September 27

18:00 -19:00	Dinner Buffet	Location: VISTA CAFÉ (雅景咖啡厅) 1 st Floor, Beijing Yanshan Hotel
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Saturday Morning, September 28

Time	Activity	Location: ORCHID ROOM (雅兰厅) 2 nd Floor, Beijing Yanshan Hotel
08:30-09:10	Plenary Speech: TBD Speaker: Prof. Collin M. Stultz , Massachusetts Institute of Technology, USA	
9:10-09:50	Plenary Speech: Findings from the third Critical Assessment of Genome Interpretation, CAGI 2013, a community experiment to evaluate phenotype prediction. Speaker: Prof. Steven Brenner , UC Berkeley, USA	
09:50-10:10	Coffee Break	

Saturday Morning, September 28

Time	Activity	Location: Beijing Yanshan Hotel
10:10-12:00	Oral Session 2: Bioinformatics and Biomedical Engineering	ORCHID ROOM (雅兰厅) 2 nd Floor

Saturday Noon, September 28

12:00 -13:30	Lunch Buffet	Location: VISTA CAFÉ (雅景咖啡厅) 1 st Floor, Beijing Yanshan Hotel
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Saturday Afternoon, September 28

Time	Activity (Coffee Break 15:40 – 16:00)	Location: Beijing Yanshan Hotel
14:00-18:00	Oral Session 3: Biomedical Engineering	ORCHID ROOM (雅兰厅) 2 nd Floor

Sunday Morning, September 29

Conference Tour

Registration for tour on September 28 from 8:30 to 11:00

Part II Plenary Speech

Plenary Speech: Modeling Dynamics of Cell-fate

Speaker: Prof. Michael Q. Zhang, University of Texas at Dallas, USA

Time: 08:30-09:10, September 27, 2013

Location: PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

Understanding the principles of cell-fate determination and dynamics is fundamentally important in quantitative biology of development and differentiation in metazoans. Exploring general rules of the interplay between gene regulation networks and cell-cell communication/tissue environment can provide valuable insight to the mechanism of cell-fate maintenance or changes. I will describe our recent works with two examples: one is to model the dynamics of iPSC reprogramming by Yamanaka factors or epigenetic perturbation; another is to model the dynamics of cancer stem cells.

Plenary Speech: Molecular Networks for Interpretation and Prediction in Biology

Speaker: Prof. Edwin Wang, National Research Council Canada/McGill University, Canada

Time: 09:10-09:50, September 27, 2013

Location: PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

It is challenging in interpreting omic data (i.e., deep sequencing, array, and large-scale genetic screenings) to get insights and generate testable hypotheses. Further, it is even harder to use these data to make predictions. We have proposed and applied molecular networks to reach these goals. I will illustrate these points using a few examples: RNA-seq data analysis of wheat embryogenesis, gene co-expression networks and metabolic networks of wheat embryogenesis, predicting network genes for improving yields of crops, understanding of crop trait-driving events in a network context to predict plant trait-driving genes by combining SNP data, and finally identifying functional network modules for crop traits.

Plenary Speech: Testing Threshold-Dependent Model for Cell Fate Controlling during *Drosophila* Embryogenesis

Speaker: Dr. Feng Liu, Princeton University, USA

Time: 09:50-10:30, September 27, 2013

Location: PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

Understanding the cell fate controlling in cellular programming and reprogramming is a key to tissue engineering and regenerative medicine. We choose *Drosophila* embryos as our model system to unravel the underlying mechanism for cellular programming during embryogenesis. As predicted by the threshold-dependent model, cell fate determination is executed by genetic networks that respond to absolute concentrations of transcription factors. To test this model, we manipulated the absolute concentration of the maternally supplied transcription factor Bicoid and measure the cell fate map shift in response to the Bicoid concentration perturbation. When we increase the overall amount of Bicoid 5-fold, Bicoid concentrations in cells at positions of the cephalic furrow, an early morphological marker, differ by a factor of two. This finding apparently contradicts the traditional threshold-dependent readout model, which predicts that the Bicoid concentrations at these positions should be identical. In contrast, Bicoid concentration at target gene expression boundaries is nearly unchanged during early developmental times, but adjusts dynamically toward the same 2-fold change as development progresses. Thus the cell fate map responds faithfully to Bicoid concentration during early development, in agreement with the threshold model, but subsequently partially adapts in response to altered Bicoid dosage, driving segmentation patterns towards their wild-type positions. This dynamic response requires other maternal regulators such as Torso and Nanos, suggesting that cell fate determination is established by the integration of multiple maternal inputs.

Plenary Speech: When Modern Computational Systems Biology Meets Ancient

Traditional Chinese Medicine

Speaker: Prof. Calvin Yu-Chian Chen, China Medical University

Time: 10:50-11:30, September 27, 2013

Location: PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

Though the single drug-single protein theory has served medical research well in the past, increasing evidence now reveals that such a reductionist approach is overly simplistic. Support for this is seen in the multiplex of genetic and epigenetic factors involved in complex multifactor diseases. Better understanding of human physiological inner

workings and disease networks has pushed for a re-evaluation of drug development principles. One concept that has emerged is the systems biology-based approach which integrates genomics, proteomics and metabolomics to enhance our understanding of the effects of a lead compound on whole pathways and networks rather than isolated protein targets, hereby increasing the success rate and decreasing the adverse effects of drugs. Interestingly, while the concept of viewing an illness as the collective expression of multiple imbalanced factors and using various treatments to “restore” balance to alleviate illness is relatively new to modern medicine practitioners, it is the central idea for TCM and the guiding concept for TCM formulations. Effectiveness of TCM formula is affected by the synergism of different components and largely dependent on the formula composition. The composition of a TCM formula follows set principles and has certain applicability. It is the practical adaptation of differential treatment. Therefore, its clinical application is not rigid and should change according to the progression of the illness, physical conditions, and age. When compositions of the primary medicinals are changed, the function of the TCM formula changes. There seems to be much similarity between TCM and systems biology. Both differ from the conventional bottom-up research approach by taking into account the entire biological system. Systems biology may be applied to “translate” TCM formula into logical, scientific information that can be communicated and generally applied. The question is how are we going about to do this?

Plenary Speech: Gene Networks and Drivers of Inflammation in Complex Human Diseases

Speaker: Prof. Bin Zhang, Icahn School of Medicine at Mount Sinai, USA

Time: 11:30-12:10, September 27, 2013

Location: PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

Inflammation plays a critical role in many complex diseases such as cancer, obesity, diabetes and neurodegenerative diseases. Large scale molecular profiling data from such diseases that were generated in the past decade further deepen our understanding of the mechanisms of inflammation underlying disease progression. Using a multiscale network approach, we systematically uncovered inflammation related gene networks as a causal factor for multiple complex human diseases. These inflammation networks in different diseases share certain topology and key regulators. Validation experiments support the causal role of many key regulators of inflammation in disease progression. These multiscale inflammation networks as well as their drivers may serve as predictive biomarkers and effective targets for therapeutic intervention.

Plenary Speech: TBD

Speaker: Prof. Collin M. Stultz, Massachusetts Institute of Technology, USA

Time: 08:30-09:10, September 28, 2013

Location: ORCHID ROOM (雅兰厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

TBD

Plenary Speech: Findings from the third Critical Assessment of Genome Interpretation, CAGI 2013, a community experiment to evaluate phenotype prediction.

Speaker: Prof. Steven Brenner, UC Berkeley, USA

Time: 09:10-09:50, September 28, 2013

Location: ORCHID ROOM (雅兰厅) 2nd Floor, Beijing Yanshan Hotel



Abstract

The Critical Assessment of Genome Interpretation (CAGI, 'kā-jē) is a community experiment to objectively assess computational methods for predicting the phenotypic impacts of genomic variation. In the experiment, participants are provided genetic variants and make predictions of resulting phenotype. These predictions are evaluated against experimental characterizations by independent assessors. A long-term goal for CAGI is to improve the accuracy of phenotype and disease predictions in clinical settings.

The third CAGI experiment (concluded in July 2013) consisted of ten diverse challenges. CAGI deliberately extends challenges from previous years, with the continuity allowing measurement of progress. For example, in the second CAGI, in a challenge to predict Crohn's disease from exomes, one group was able to identify 80% of affected individuals before the first false positive healthy person. In the third CAGI experiment, this challenge used an improved dataset, and several groups performed remarkably well, with one group achieving a ROC AUC of 0.94. The experiment also revealed important population structure to Crohn's disease in Germany.

For three years, CAGI has posed a challenge with Personal Genome Project (PGP) genome data. This year, two groups were able to successfully map a significant number of complete genomes to their corresponding trait profiles submitted by PGP participants. In the expanded challenge to predict benign versus deleterious variants in DNA double-strand break repair MRN genes—Rad50 (from last year), Mre11, and Nbs1—as determined by those that appear in a breast cancer case versus healthy control, predictions show how methods differ sharply in their effectiveness even amongst proteins in the same complex.

A new challenge this year was to use exomes from families with lipid metabolism disorders. In the case of hypoalphalipoproteinemia (HA), a company made predictions which showed how understanding the problem structure and employing an extensive knowledgebase led to remarkably good results. Another related challenge revealed a twist wherein real-world data differed sharply from theoretical models.

The other challenges were to predict which variants of BRCA1 and BRCA2 are associated with increased risk of breast cancer; to predict how variants in p53 gene exons affect mRNA splicing; to predict how well variants of a p16 tumor suppressor protein inhibit cell proliferation; and to identify potential causative SNPs in disease-associated loci.

Overall, CAGI revealed that the phenotype prediction methods embody a rich and diverse representation of biological knowledge, and they are able to make predictions that are highly statistically significant. However, we also found the accuracy of prediction on the phenotypic impact of any specific variant was unsatisfactory and of questionable clinical utility. The most effective predictions came from methods honed to the precise challenge, including the specific genes of interest as well as the problem context. Prediction methods are clearly growing in sophistication, yet there are extensive opportunities for further progress.

Complete information about CAGI may be found at <http://genomeinterpretation.org>.

Part III Oral Sessions

Oral Session 1: Bioinformatics

Session Chair: Dr. Hui Zhang, St. Jude Children's Research Hospital, Memphis U.S.A.

PLUM BLOSSOM ROOM (沁梅厅) 2nd Floor

Time: 14:00-18:00, Friday, Sept. 27

ID	Paper Title	Author	Affiliation
80136	Visual Composition of Complex Queries on an Integrative Genomic and Proteomic Data Warehouse	Francesco Pessina	Politecnico di Milano
80312	Integrative Self-Organizing Map – A Mean Pattern Model	ZiHua Yang	University of Queen Mary
80345	Splitting of Gaussian Models via Adapted BML Method Pertaining to Cry-Based Diagnostic System	Hesam Farsaie Alaie	Ecole de technologie superieure
80219	Prediction of Protein Tyrosine Nitrosylation Sites by Position-Specific Dipeptide Propensity	Yan Xu	University of Science and Technolgy
80023	Monte Carlo Simulation and a Review of the Physics of the Positron Annihilation Process in PET	Hamed Hamid Huhammed	Royal Institute of Technology KTH
80024	Skin Cancer Detection Using Temperature Variation Analysis	Ahmed M. Nasr Moustafa	Royal Institute of Technology KTH
80320	Structural Bioinformatics of Protein and DNA, as Early Stimulation in Basic Education of Rural and Indigenous Communities of Oaxaca	Susana Lozano-Muniz	Universidad del Papaloapan
80260	Semi-Global Inference in Phenotype-Protein Network	Siliang Xia	University of Stuttgart
80094	Semantic Similarity over Gene Ontology for Multi-label Protein Subcellular Localization	Man-Wai Mak	The Hong Kong Polytechnic University
80288	In Silico Molecular Interaction Studies of Suberoylanilide Hydroxamic Acid and its Modified Compounds with Histones Deacetylase Class II Homo sapiens as Curative Measure towards Cervical Cancer	Usman Sumo Friend Tambunan	University of Indonesia
80305	Data Fusion with Optimized Block Kernels in LS-SVM for Protein Classification	Li Liao	University of Delaware
80154	Developing Customized Evaluation Software for Clinical Trials: An Example with Obstructive Lung Diseases	Zhanqi Zhao	Furtwangen University
80341	Feature Extraction by Multi-scale Principal Component Analysis and Classification in Spectral Domain	Shengkun Xie	Ryerson University
80178	Mechanism of Cuff-less Blood Pressure Measurement Using MMSB	Yibin Li	Tsinghua University
80381	Htz1 deposition at certain genomic regions is regulated by histone chaperon Nap1	Liangqun Huang	Colorado State University
80307	Heart Rate Variability Applied to Short-Term Cardiovascular Event Risk Assessment	Simao Paredes	Polytechnic Institute of Coimbra (IPC/ISEC)
80379	Wireless and Battery-free Bladder Pressure Monitoring System	Li Chunchan	Capital Medica University

ID	Paper Title	Author	Affiliation
80382	Effect of Radiation Emitting devices like Mobile Phones, Computers and Laptops on people ?tests results of improvement in pulse rate after fixing Enviro Chip	Ajay Poddar	SYENERGY ENVIRONICS LTD.
80242	Study on Paths of Affect Factors on Adaption to University Life of Chinese International Students in Korea	Qin-Lan Lin	Beihua Uiniversity
80318	Model-based Analysis of Ventilation Inhomogeneity in Respiratory Mechanics	Kevin Meffray	Institute of Technical Medicine, Furtwangen University
80377	Proof of concept study to identify candidate biomarkers of fibrosis using high throughput peptide aptamermicroarray and validate by enzyme linked immunosorbant assay	Sam Straw	Scleroderma Research Centre

Plenary Session 2 & Oral Session 2: Bioinformatics and Biomedical

Engineering

Plenary Session 2 Session Chair: Prof. Kuo-Chen Chou, The Gordon Life Science Institute, USA

Oral Session 2 Session Chair: Dr. Thanh Hai Nguyen, International University

ORCHID ROOM (雅兰厅) 2nd Floor

Time: 8:30-12:00, Saturday, Sept. 28

ID	Paper Title	Author	Affiliation
VIP	TBD	Prof. Collin M. Stultz	Massachusetts Institute of Technology, USA
VIP	Findings from the third Critical Assessment of Genome Interpretation, CAGI 2013, a community experiment to evaluate phenotype prediction	Prof. Steven Brenner	UC Berkeley, USA
80084	Relationships Between A Thiol-Disulfide System and Liposoluble Antioxidants with Cytogenetic Indices in Humans Exposed to Low Doses Radiation	Ivanenko Galina	Russian Academy of Sciences Emanuel Institute of Biochemical Physics Moscow
80316	The Electrokinetic Characterization of Gold Nanoparticles, Functionalized with Cationic Functional Groups, and Its' Interaction with DNA	Geraldine Genevive Lazarus	University of Kwa-Zulu Natal
80352	Mean Threshold and ARNN Algorithms for Identification of Eye Commands in an EEG-Controlled Wheelchair	Thanh Hai Nguyen	International University
80054	Indoor Air Quality Study on Fiber Glass Industry	Amir Alhaddad	Kuwait University
80245	A System for Improving the Management of the Lesion and Test Images of Patients	Cho Sungbum	Asan Medical Center
80359	A Humerus Arterial Bleeding Simulation Model for Hemostasia	Ni Aijuan	Academy of Military Medical Sciences
80061	Study of Multimedia Technology in Posture Training for the Elderly	Chih-Chen Chen	Hwa Hsia Institute of Technology

ID	Paper Title	Author	Affiliation
80139	Using Variations of Somatosensory Evoked Potentials to Quantify Spinal Cord Injury Level	Hasan Mir	American University of Sharjah
80258	Combination of The Kinect with Virtual Reality in Balance Training for the Elderly	Wei-Min Hsieh	Hwa Hsia Institute of Technology
80335	Sleep Apnea Detection Using Adaptive Neuro Fuzzy Inference System	Cafer Avci	Yalova University
80333	Biaxial Constitutive Model of Active Coronary Media Based on Microstructural Information	Huan Chen	Indiana University Purdue University Indianapolis
80250	Contrast limited adaptive histogram equalization for qualitative enhancement of myocardial perfusion images	Neethu M.Sasi	Govt. Model Engineering College
80368	Studies on Prevention and Therapy for Mesothelioma, a Cancer Model of Gene-Environment Interaction	Haining Yang	University of Hawaii Cancer Center
80013	Treatment Principles of Obesity with Chinese Herbal Medicine: Literature Analysis by Text Mining	MIAO JIANG	China Academy of Chinese Medical Sciences

Oral Session 3: Biomedical Engineering

Session Chair: Dr. Shaomin Yan, Guangxi Academy of Sciences

ORCHID ROOM (雅兰厅) 2nd Floor

Time: 14:00-18:00, Saturday, Sept. 28

ID	Paper Title	Author	Affiliation
80158	Bone Regeneration Enhanced by Antigen-extracted Xenogeneic Cancellous Bone Graft with rhBMP-2 in Rabbits Mandibular Defect Repair	Renfa Lai	The 1st Affiliated Hospital of Jinan University, Guangzhou 510630, China
80254	Design of Real-time Document Control Based on Zigbee and Surface Electromyography (sEMG)	Wang Zhen	East China University of Science and Technology
80276	Assistive Navigation Device for Visually Impaired - A Study on Reaction Time to Tactile Modality Stimuli	Jing Yu	Furtwangen University
80289	A Study of Safety Evaluation Method for Medical Diagnostic Table	Xiaoyan Zhang	GE Hangwei HealthCare Co. Ltd
80027	Study on Mult-Exponential Inversion Method for NMR Relaxation Signals with Tikhonov Regularization	Shanshan Chen	Shanghai Medical Instrumentation College
80026	Compensation of Finite Bandwidth Effect by Using an Optimal Filter in Photoacoustic Imaging	Chen Zhang	Fudan University
80165	A New Approach to the Presentation of Myocardial SPECT Images	Niloufar Darvish	Royal Institute of Technology KTH
80176	An Adaptive Pulse Compression Filter for Ultrasound Contrast Harmonic Imaging	Jenho Tsao	National Taiwan University
80223	Multi-Layer Microbubbles by Microfluidics	Hongbo Zhang	East China of Science and Technology
80302	Cell Segmentation and Tracking in Microfluidic Platform	lipan ouyang	University of Winnipeg

ID	Paper Title	Author	Affiliation
80358	Design of Acoustic Radiation Force Excitation Module for Ultrasound Elastography	Mingbo Qiu	Shenzhen University
80117	Modeling and Simulation of Laparoscopic Tools for Autonomously Positioning Laparoscope in Laparoscopic Surgery	Said Megahed	Cairo University
80025	Identification of Atrial Fibrillation Using Complex Network Similarity	Yajuan Zhang	Fudan University
80066	Information Transfer Index-A Promising Measure of the Corticomuscular Interaction	Ping Xie	Yanshan University
80096	Emotional Speech Synthesis based on Prosodic Feature Modificaiton	Ling He	Sichuan University
80259	Cardiovascular Diseases Detecting via Pulse Analysis	Jingjing Xia	University of Winnipeg
80337	Performance Improvement with Combining Multiple Approaches to Diagnosis of Thyroid Cancer	Ahmet Akba	Yalova University
80344	Characterization of Pathologic Cries of Newborns Based on Fundamental Frequency Estimation	Yasmina Kheddache	Ecole de technologie superieure
80196	Triangle characters of Electrocardiogram for distinguishing states between exercise and relaxation	Yanjun Li	Biomedical Engineering Lab of China Astronaut Research and Training Center
80372	Design of a Noninvasive Bladder Urinary Volume Monitoring System Based on Bio-Impedance	Li Rihui	Sun Yat-Sen University
80339	Simulation of the Thermal and Mechanical Effects of a Planar Rectangular High Intensity Ultrasound Transducer to be Used for Destroying Atherosclerotic Plaque	Christakis Damianou	University of Technology
80340	Sonothromblysis in Combination With Thrombolytic Drugs in a Rabbit Model Using MRI-Guidance	Christakis Damianou	Cyprus University of Technology
80278	Matching DSIFT descriptors extracted from CSLM images	Stefan G. Stanciu	University Politehnica of Bucharest
80064	An Integrated Analysis of Aberrantly Expressed miRNA and mRNA Profiles Unveils a Robust Regulatory Network in HepG2 Cell	Sheng Yang	Nanjing Medical University
80361	Effects of Different Types of Verbal Activities on Heart Rate Variability	Ping Shi	University of Shanghai for Science and Technology
80224	Using Chou's pseudo amino acid composition for protein remote homology detection	Bin Liu	Harbin Institute of Technology Shenzhen Graduate School
80106	2-Dimensional HP Foldings of Dermaseptin-J2	Shaomin Yan	Guangxi Academy of Sciences
80257	A Restricted, Adaptive Threshold Segmentation Approach for Processing High-speed Image Sequences of the Glottis	Yuling Yan	Santa Clara University

Part IV Instructions for Presentations

Devices Provided by the Conference Organizing Committee:

- Laptops (with MS-office & Adobe Reader)
- Projectors & Screen
- Laser Sticks

Materials Provided by the Presenters:

- PowerPoint or PDF files

Duration of each Presentation:

- Oral Presentation: 15 - 20 Minutes of Presentation, 5 Minutes of Q & A
- Plenary Speech: 35- 40 Minutes of Presentation, 5 Minutes of Q & A

Part V Hotel Information

About Hotel

Located in Beijing's Zhongguancun Hi-tech Zone, the "Silicon Valley of China", Beijing Yanshan Hotel is in the neighbourhood of the North Third Ring Road and the Zhongguancun Street with convenient transport to the Capital Airport, Beijing Railway Station, National Library, Beijing TV Station and Shangdi Information Industry Base. Peking University, Qinghua University, Renmin University and many other famous universities as well as scientific and technical institutions are all in the vicinity. The Summer Palace and Yuanmingyuan — China's ancient royal gardens can be reached in several minutes' drive.

Address: No.38 A, Zhongguancun Street, Haidian District, Beijing
中国北京市海淀区中关村大街甲38号 (100086)

Homepage: <http://www.yanshanhotel.com/>

Telephone: (+86) 10 62563388

Facsimile: (+86) 10 62568640

How to Get to the Hotel

Please show the following message to the taxi driver if you cannot speak Chinese:

请送我到: 北京市海淀区中关村大街甲38号燕山大酒店

Contact Us

Secretary of Organizing Committee: Ms. Zhang

Telephone: +86- 13264702230

E-mail: submit@icbbe.org

NOTE