


The 15th Korea-Japan-China Bioinformatics Symposium 2017



 **June 21-22, 2017** The 15th KJC Bioinformatics Symposium, Seoul, Korea
<http://cjk-bioinfo.org/2017>

Korean Bioinformation Center (KOBIC) is pleased to host "The 15th Korea-Japan-China Bioinformatics Symposium" in Seoul, Korea on June 21-22, 2017. We hope that the symposium will be a prime channel to promote collaboration in bioinformatics in our region.

Outline

Venue

Koreana Hotel, Seoul



Schedule

June 20 (Tue): Arrival

June 21 (Wed): Symposium

June 22 (Thu): Symposium

June 23 (Fri): Departure

Organizers

Korean Bioinformation Center (KOBIC) at Korea Research Institute of Bioscience and Biotechnology (KRIBB)

National Institute of Genetics (NIG)

Shanghai Center for Bioinformation Technology (SCBIT)

Participants


- Ten presenters from each of the three countries, 30 in total.
 - A keynote speaker from each country will give 40-min presentation (35-min talk and 5-min Q&A).
 - Remaining nine speakers from each country will give 20-min presentation (15-min talk and 5-min Q&A).
- A mini poster session for students is also held.

Cost


The attendance fee is free. Local lodging and meals will also be provided by Korea, the hosting country of this year.


Participants

Speakers


 China			
Zhiwei Cao	Professor	Tongji University	Searching synergistic drug combinations to treat cancer
Tao Huang	Associate Professor	Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences	Deciphering the mechanisms of complex diseases using machine learning and network analysis approaches
Yixue Li (Keynote speaker)	Professor	Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences	Genomic analysis reveals hypoxia adaptation in the Tibetan Mastiff by introgression of the gray wolf from the Tibetan plateau
Guangrong Qin	Assistant Professor	Shanghai Center for Bioinformation Technology	Pan-cancer study from multiple omics data analysis
Yi Shi	Assistant Professor	Shanghai Jiao Tong University	Chromatin 3D structure and cancer typing via deep learning
Xiaofeng Song	Professor	Nanjing University of Aeronautics and Astronautics	Circular RNA profile in gliomas and human tissues
Chaochun Wei	Professor	Shanghai Jiao Tong University	Pan-genome analysis of ~3000 rice genomes
Lu Xie	Professor	Shanghai Center for Bioinformation Technology	Drug synergy study based on network and multi-level annotation


Zhi Xie	Professor	Sun Yat-sen University	Tissue-based map of the mouse translome
Yu Xue	Professor	Huazhong University of Science and Technology	PTM bioinformatics

 Japan			
Takashi Gojobori (Keynote speaker)	Professor	KAUST / Waseda University	Arabia Felix: A genomic history of Middle-East human populations and its application to precision medicine
Tadashi Imanishi	Professor	Tokai University School of Medicine	Medical applications of genome sequencing technologies and bioinformatics
Ituro Inoue	Professor	National Institute of Genetics	May the sequencing force be with you
Hideaki Kanzawa-Kiryama	Research Scientist	National Museum of Nature and Science	Genomic insights into the relationship between Neolithic Japanese hunter-gatherer, Jomon, and modern East Eurasians
Takashi Makino	Associate Professor	Tohoku University	Duplicated genes maintained after whole genome duplications and their relation to human disorders
Katsuhiko Mineta	Senior Research Scientist	KAUST	Shotgun metagenomics of the Red Sea: microbial profiling toward the comparative metagenomics
Yasukazu Nakamura	Professor	DDBJ Center at National Institute of Genetics	Cost and value in data curation for genome databases
Hirofumi Nakaoka	Assistant Professor	National Institute of Genetics	Allele specific functional genomics in the post-GWAS era
Naruya Saitou	Professor	National Institute of Genetics	Genomic history of modern humans in East Eurasia
Yoko Satta	Professor	The Graduate University for Advanced Studies (SOKENDAI)	Phylo-demographic study of primates: problems of the mutation rate and an ancestral population size


 Korea			
Daehyun Baek	Assistant Professor	Seoul National University	General rules for functional microRNA targeting
Jung Kyoong Choi	Associate Professor	KAIST	Convolutional neural networks predict causal regulatory variants
Sungwon Jung	Assistant Professor	Gachon University	Network model-based pathway activity quantification and considerations in personalized drug-response prediction for cancer
Sangsoo Kim	Professor	Soongsil University	A few examples of association rule mining in bioinformatics
Sanguk Kim (Keynote speaker)	Professor	POSTECH	Evolution of the genotype-phenotype relationship of human disease genes
Sangwoo Kim	Assistant Professor	Yonsei University	Accurate detection of low-level somatic mutations using next generation sequencing
Sun Kim	Professor	Seoul National University	Analysis of omics data on the time and phenotype dimensions
Insuk Lee	Professor	Yonsei University	Network-based augmenting and interpreting disease genomics data
Semin Lee	Assistant Professor	UNIST	Somatic mutations in single neurons
Jin-Wu Nam	Associate Professor	Hanyang University	High-confidence coding and noncoding transcriptome maps

Poster presenters

 Japan			
Junpei Ito	Graduate Student	National Institute of Genetics	Systematic identification of regulatory elements derived from human endogenous retroviruses
Yasuhiro Katahira	Graduate Student	Tokai University School of Medicine	Dramatically increased myelopoiesis in the bone marrow of EBV-infected humanized NOG mice
Kumiko Nishiyama	Graduate Student	The Graduate University for Advanced Studies (SOKENDAI)	An analysis of variation in human dyslexia related genes and association with writing systems
Wanjing Zheng	Graduate Student	The Graduate University for Advanced Studies (SOKENDAI)	Molecular evolution of avian RIG-I-like receptor family

 Korea			
Tae-Rim Lee	Graduate Student	Soongsil University	R shiny based interactive visualization application for DEG analysis and GWAS
Chaeyeong Choi	Graduate Student	Soongsil University	Discovery of candidate biomarkers using regulatory network analysis of lung cancer RNA-seq data

Staffs

 Korea		
Ryan Woonbong Kim	Director	KOBIC
Seungwoo Hwang	Senior Researcher	KOBIC

Program

All the program activities are held in the State Room at the 7th floor of Koreana Hotel.

Tuesday, June 20, 2017: Arrival		
-18:00	Hotel check-in	Lobby
18:00-20:00	Dinner (for those who arrived).	Royal Room (Fl.7)

Wednesday, June 21, 2017: Symposium Day 1		
-08:30	Breakfast (hotel guests only)	Danube restaurant (Fl.2)
08:30-09:00	Registration and poster mounting	State Room (Fl.7)
09:00-09:20	Greetings and announcements	
Session 1: Population genomics		
09:20-10:00	Keynote presentation 1: Takashi Gojobori, KAUST / Waseda University Arabia Felix: A genomic history of Middle-East human populations and its application to precision medicine	
10:00-10:20	Talk 1: Katsuhiko Mineta, KAUST Shotgun metagenomics of the Red Sea: microbial profiling toward the comparative metagenomics	
10:20-10:40	Talk 2: Hideaki Kanzawa-Kiriyama, National Museum of Nature and Science Genomic insights into the relationship between Neolithic Japanese hunter-gatherer, Jomon, and modern East Eurasians	
10:40-11:00	Taking group picture, tea break, and poster mounting	
11:00-11:20	Talk 3: Chaochun Wei, Shanghai Jiao Tong University Pan-genome analysis of ~3000 rice genomes	
11:20-11:40	Talk 4: Yoko Satta, The Graduate University for Advanced Studies (SOKENDAI) Phylo-demographic study of primates: problems of the mutation rate and an ancestral population size	
11:40-12:00	Talk 5: Naruya Saitou, National Institute of Genetics Genomic history of modern humans in East Eurasia	

12:00-13:30	Lunch	A restaurant outside the hotel (3-minute walk)
Session 2: Transcriptome		State Room (Fl.7)
13:30-13:50	Talk 6: Zhi Xie, Sun Yat-sen University Tissue-based map of the mouse transcriptome	
13:50-14:10	Talk 7: Xiaofeng Song, Nanjing University of Aeronautics and Astronautics Circular RNA profile in gliomas and human tissues	
14:10-14:30	Talk 8: Jin-Wu Nam, Hanyang University High-confidence coding and noncoding transcriptome maps	
14:30-14:50	Talk 9: Daehyun Baek, Seoul National University General rules for functional microRNA targeting	
14:50-15:30	Tea break and poster presentation	
	Steering Committee Meeting	
Session 3: Machine learning and algorithms		
15:30-15:50	Talk 10: Yi Shi, Shanghai Jiao Tong University Chromatin 3D structure and cancer typing via deep learning	
15:50-16:10	Talk 11: Tao Huang, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences Deciphering the mechanisms of complex diseases using machine learning and network analysis approaches	
16:10-16:30	Talk 12: Sun Kim, Seoul National University Analysis of omics data on the time and phenotype dimensions	
16:30-16:50	Talk 13: Jung Kyoon Choi, KAIST Convolutional neural networks predict causal regulatory variants	
16:50-17:10	Talk 14: Sangsoo Kim, Soongsil University A few examples of association rule mining in bioinformatics	
17:10-17:20	Tea break	

17:20-18:00	Keynote presentation 2: Yixue Li, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences Genomic analysis reveals hypoxia adaptation in the Tibetan Mastiff by introgression of the gray wolf from the Tibetan plateau	
18:00-19:30	Dinner	A restaurant outside the hotel (1-minute walk)

Thursday, June 22, 2017: Symposium Day 2		
-09:00	Breakfast (hotel guests only)	Danube restaurant (Fl.2)
Session 4: Pathway and network		State Room (Fl.7)
09:00-09:40	Keynote talk 3: Sanguk Kim, POSTECH Evolution of the genotype-phenotype relationship of human disease genes	
09:40-10:00	Talk 15: Sungwon Jung, Gacheon University Network model-based pathway activity quantification and considerations in personalized drug-response prediction for cancer	
10:00-10:20	Talk 16: Lu Xie, Shanghai Center for Bioinformation Technology Drug synergy study based on network and multi-level annotation	
10:20-10:40	Talk 17: Insuk Lee, Yonsei University Network-based augmenting and interpreting disease genomics data	
10:40-11:00	Tea break	
Session 5: Medical genomics, disease, and protein bioinformatics		
11:00-11:20	Talk 18: Tadashi Imanishi, Tokai University School of Medicine Medical applications of genome sequencing technologies and bioinformatics	
11:20-11:40	Talk 19: Guangrong Qin Pan-cancer study from multiple omics data analysis	
11:40-12:00	Talk 20: Takashi Makino, Tohoku University Duplicated genes maintained after whole genome	

	duplications and their relation to human disorders	
12:00-13:00	Lunch	Lunchbox at hotel
13:00-13:20	Talk 21: Yu Xue, Huazhong University of Science and Technology PTM bioinformatics	State Room (Fl.2)
13:20-13:40	Talk 22: Zhiwei Cao, Tongji University Searching synergistic drug combinations to treat cancer	
Session 6: Sequencing and genomics		
13:40-14:00	Talk 23: Sangwoo Kim, Yonsei University Accurate detection of low-level somatic mutations using next generation sequencing	
14:00-14:20	Talk 24: Semin Lee, UNIST Somatic mutations in single neurons	
14:20-14:40	Tea break	
14:40-15:00	Talk 25: Hirofumi Nakaoka, National Institute of Genetics Allele specific functional genomics in the post-GWAS era	
15:00-15:20	Talk 26: Yasukazu Nakamura, DDBJ Center at National Institute of Genetics Cost and value in data curation for genome databases	
15:20-15:40	Talk 27: Ituro Inoue, National Institute of Genetics May the sequencing force be with you	
15:40-15:50	Closing	
15:50-17:20	Break	Free time
17:30-18:30	Dinner (for those who stay)	A restaurant outside the hotel (3-minute walk)

Friday, June 23, 2017: Departure		
-10:00	Breakfast	Danube restaurant (Fl.2)
-12:00	Check-out from hotel. Late check-out is maybe available free of charge. Ask hotel check-in counter at the time of check-in.	

Travel Information

Which airport to use? (Incheon or Gimpo)

Both Incheon and Gimpo international airports have flights from China and Japan, so you can use either one of them.

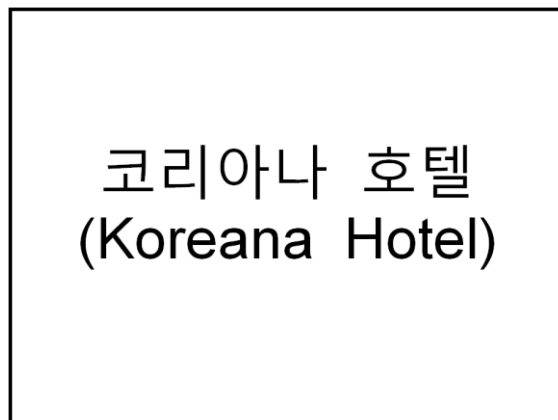
Airport	Scale	Distance to Koreana Hotel	Transportation to Koreana Hotel
Incheon Airport	Larger and newer	60km	Both taxi and limousine bus are available. Taxi: costs around 70,000 Won (430 Yuan / 7,000 Yen) Limousine bus: costs 16,000 Won (100 Yuan / 1,600 Yen)
Gimpo Airport	Smaller and older	20km	Only taxi is available, costing around 30,000 Won (190 Yuan / 3,000 Yen).

Taking a taxi to the hotel

(1) Take a taxi other than black-colored ones. DO NOT get a black taxi, which is twice as expensive as taxis of all other colors.



(2) Bring the printout of this to show to the taxi driver



Taking a limousine bus: Incheon Airport -> Koreana Hotel

See this instruction:

http://cjk-bioinfo.org/2017/Taking_a_limousine_bus_to_Koreana_Hotel.pdf

Taking a limousine bus: Koreana Hotel -> Incheon Airport

On your way back home, you can also use the limousine bus from Koreana Hotel back to Incheon Airport. You can buy the bus ticket right at Koreana Hotel reception desk. Purchasing in advance is recommended to secure seats.

Bus stop is right in front of the hotel.



There is a bus in every 20-30 minutes.

인 천 공 항		To Incheon Airport									
05시	06시	07시	08시	09시	10시	11시	12시	13시	14시	15시	16시
05:17	06:07	07:07	08:22	09:12	10:02	11:12	12:12	13:12	14:17	15:17	16:07
05:42	06:27	07:32	08:47	09:37	10:27	11:32	12:32	13:32	14:37	15:42	16:32
	06:47	07:57			10:52	11:52	12:52	13:52	14:57		16:57

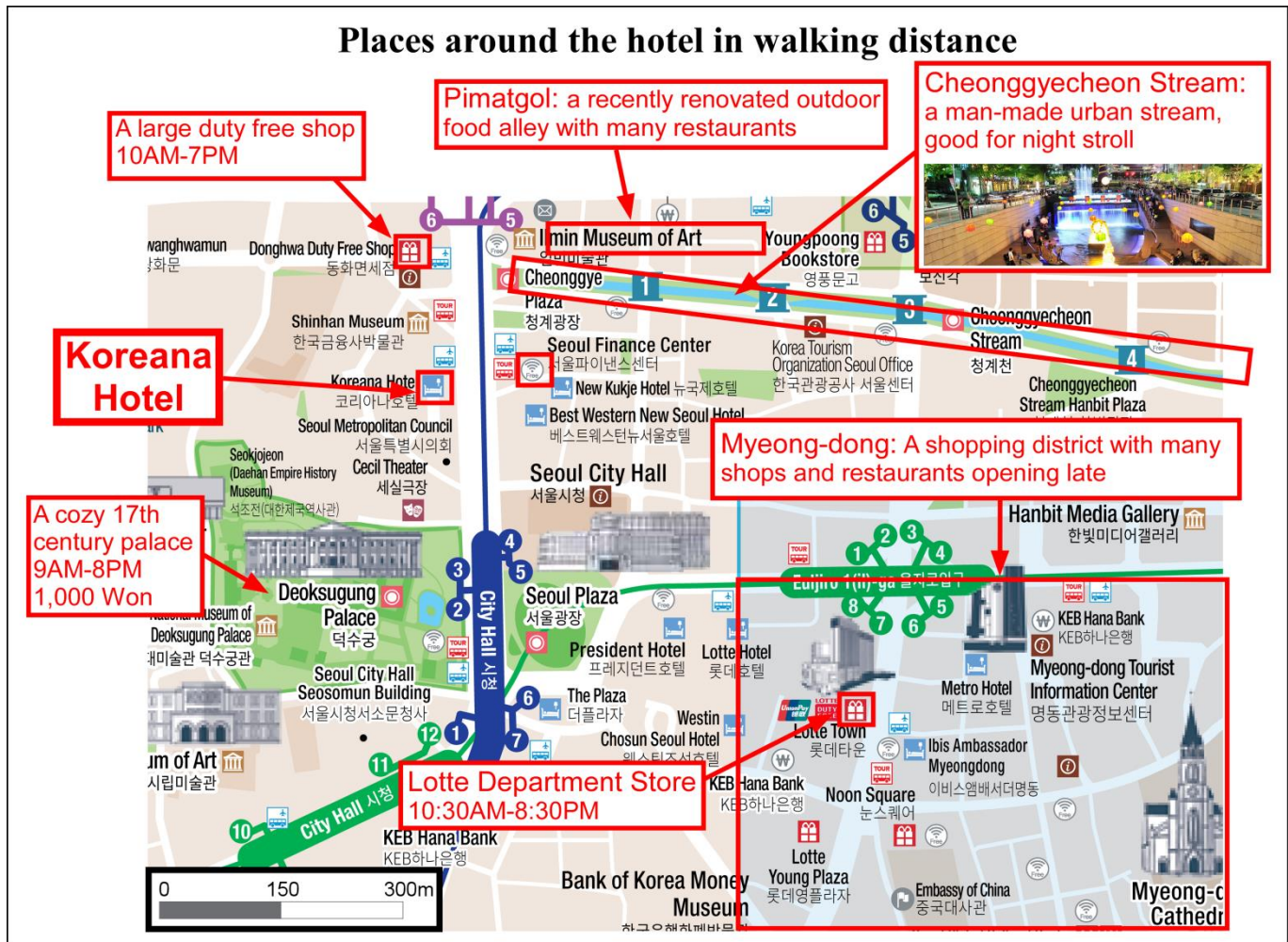
※ 본 시간표는 부득이한 사유로 변경될 수 있습니다.
Schedules are subject to change without prior notice

After Koreana Hotel, there are three stops in downtown Seoul, the fourth (and the last) stop being Incheon Airport.



Shopping and sightseeing around the hotel

At the heart of downtown Seoul, there are many shopping and sightseeing places around the hotel within walking distance. Some of the most nearby places are summarized below.



Also refer to the high resolution PDF map of downtown Seoul:

http://cjk-bioinfo.org/2017/Downtown_Seoul_map.pdf

Contact

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