Hyunkyung KIM

Computational Biologist

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Research Interests

Research interests focusing on understanding genetic mechanisms of complex diseases using computational approaches

Research Experience

Diabetes Research Center, Massachusetts General Hospital — *Boston, MA*

Bioinformatics Specialist / Supervisor: Dr. Miriam Udler — *July 2019 - Present*

- Developed and coordinated a high-throughput genetic variant processing pipeline in Perl and R and identified shared biological pathways among cardiometabolic diseases from associations between variants and phenotypes based on a soft clustering method
- Chosen to present genetic clustering results of Type 2 Diabetes at *American Diabetes Association* and *International Genetic Epidemiology Society* virtual meetings

Quackenbush Laboratory, Harvard School of Public Health — *Boston, MA*

Graduate Researcher / Advisor: Dr. John Quackenbush — *September 2018 - May 2019*

- Constructed separate gene regulatory networks for male and female cases and normal samples in head & neck cancer RNA-seq data from TCGA using PANDA (Passing Attributes between Networks for Data Assimilation) package in R
- Identified differential modularity associated with defense response and immune system process between male and female gene regulatory networks in head & neck cancer using ALPACA (ALtered Partitions Across Community Architectures) package in R

Division of Clinical Bioinformatics, Seoul National University Hospital — *Seoul, Korea*

Research Intern / Advisor: Dr. Kwangsoo Kim — *June - July 2018*

- Constructed and analyzed gene interaction networks among differentially expressed genes in thyroid cancer in Python using co-expression information from TCGA thyroid cancer RNA-seq data
- Built gene regulatory networks of different subtypes (classical and follicular) of thyroid cancer using PANDA package in R to compare the key genes of thyroid cancer subtypes

Data Engineering Laboratory, Yonsei University — *Seoul, Korea*

Research Assistant / Advisor: Dr. Sanghyun Park — *July 2014 - December 2015*

- Performed literature review of current text mining techniques for inferring hidden relationships from biological literature
- Developed a novel movie recommender system in Java that applies rating tendencies of users by normalizing scores using users' past rating history
- Presented key findings of movie recommender system at *Proceedings of Korea Computer Congress* and published a manuscript in *Journal of Database Research* in Korea

Education

Harvard T.H. Chan School of Public Health — *Boston, MA*

Master of Science in Computational Biology and Quantitative Genetics — *September 2017 - May 2019*

- Relevant courseworks: Regression analysis, Genomic data manipulation, Computing skills for biomedical informatics, Epidemiologic research methods, Data mining and risk prediction

Yonsei University — *Seoul, Korea*

Bachelor of Science in Computer Science — *March 2011 - August 2016*

- Relevant courseworks: Engineering information processing, Probability and statistics, Software capstone design, Data structures, Data mining, Artificial intelligence

Skills

Programming Skills	R, Perl, Python, SQL, JAVA, C++, SAS, Stata and cluster computing
Language Skills	Fluent in English (TOEFL: 102 / GRE: Verb 158, Quant 170, Writing 4.0) and intermediate level in Chinese (Chinese Proficiency Test, Level 4: 272/300)
Soft Skills	Accomplished team player, effective communicator, highly adaptable, keen learner, well organized and results-oriented

Publications

- **Hyunkyung Kim**, Kenneth Westerman, Marcin von Grotthuss, Josep Mercader, Jaegil Kim, Kyle Gaulton, Joshua Chiou, Jose Florez, Alisa Manning, and Miriam Udler, "Multi-trait Cluster Analysis Using High-throughput Variant Preprocessing Pipeline Reveals Shared Mechanistic Pathways among Cardiometabolic Diseases," 2021. (Manuscript in preparation)
- **Hyunkyung Kim**, Kenneth Westerman, Marcin von Grotthuss, Josep Mercader, Jaegil Kim, Kyle Gaulton, Joshua Chiou, Jose Florez, Alisa Manning, and Miriam Udler, "Expanded Genetic Clustering of T2D Variants Using a High-throughput Variant Preprocessing Pipeline Reveals Novel Clusters Representing Potential Mechanistic Pathways," 2021. (Manuscript in preparation)
- Melissa Zhao, Yushi Tang, **Hyunkyung Kim**, and Kohei Hasegawa, "Machine Learning With K-Means Dimensional Reduction for Predicting Survival Outcomes in Patients With Breast Cancer," *Cancer Informatics*, 2018.
- **Hyunkyung Kim**, Hyunjin Kim, and Sanghyun Park, "Movie Recommendation Method Using Score Normalization Based on User Rating Tendency," *Journal of Database Research*, 2016. (in Korean)

Conference Presentations

- **Hyunkyung Kim**, Marcin von Grotthuss, Josep Mercader, Jaegil Kim, Kyle Gaulton, Joshua Chiou, Jose Florez, Alisa Manning, and Miriam Udler, "Expanded clustering of Type 2 diabetes genetic loci using high throughput approach," *International Genetic Epidemiology Society 2020* (Poster)
- **Hyunkyung Kim**, Marcin von Grotthuss, Josep Mercader, Jaegil Kim, Kyle Gaulton, Joshua Chiou, Jose Florez, Alisa Manning, and Miriam Udler, "High Throughput Approach Enables Expanded Clustering of Type 2 Diabetes Genetic Loci Informed by Phenotypic Associations," *American Diabetes Association 2020* (Poster)
- **Hyunkyung Kim**, Hyunjin Kim, and Sanghyun Park, "Movie Recommendation Method Using User Rating Tendency Based on Rating Difference between Items," *Proceedings of Korea Computer Congress 2015*, Jeju, Korea (Poster)

Awards

2017 **Harvard Chan Central Grant,** Harvard Chan School of Public Health *Boston, MA*

Other Experience

Korea Institute of Patent Information *Seoul, Korea*

Staff - Patent Translation *March - June 2017*

- Translated Korean Patent Cooperation Treaty (PCT) international patent application documents in order to protect domestic intellectual property rights, and to utilize and broaden Korean patent information through removal of a language barrier