

HEEWON SEO, MS, PhD

101 College Street, PMCRT 11-410 • Toronto, ON M5G 1L7
(416) 879-6775 • Heewon.Seo@lootpiz.com

SUMMARY

Skilled bioinformatician in biomedical science with experience analyzing thousands of whole-genomes, exomes, and transcriptomes to discover molecular biomarkers for precision therapeutics and novel synergistic drug combinations for determining best treatment strategies via advanced statistical analysis and predictive modelling methods.

AREAS OF EXPERTISE

- Development of new tools and advanced statistical models for biomedical big data analysis
- Rapid construction of complex computational pipelines and their optimization
- Experience in working in high performance computing environments (on-premise and cloud)

EDUCATION

PhD in Medical Science (Biomedical Informatics) *Sep 2012 - Feb 2018*
Seoul National University College of Medicine, Seoul, Korea
Thesis: Methods for Variant- and Gene-based Analysis for Pharmacogenomics Research.

MS in Medicine (Biomedical Informatics) *Sep 2010 - Aug 2012*
Seoul National University College of Medicine, Seoul, Korea
Thesis: Loss of Function Gene-set Analysis of Personal Genome using Pathway-disease Similarity.

BS in Computer Science *Mar 2004 - Feb 2010*
Sejong University, Seoul, Korea
*GPA: 4.37/4.5, **Summa Cum Laude**, achieved the early graduation of excellent students within 3 years*

RESEARCH/WORK EXPERIENCE

Postdoctoral Fellow *Jan 2018 - Present*
Princess Margaret Cancer Centre, University Health Network, Toronto, Canada

- Developed the largest integrated database in high-throughput drug combination studies, SYNERGxDB (<http://SYNERGxDB.ca/>), and integrated high-dimensional molecular profiles of the corresponding preclinical models
- Discovered two synergistic drug combinations and four meaningful expression-based biomarkers via statistical analysis in personalized medicine
- Built predictive models using several machine learning algorithms of cancer treatment response using transcriptomic data
- Created a semi-automatic analysis tool on Microsoft Azure using Jupyter Notebook for exploring large pharmacogenomics datasets
- Built a translational framework for precision cancer medicine using a compendium of preclinical multimodal pharmacogenomics datasets and large clinical patients cohorts
- Devised an online tool to report significant biomarkers using a semi-automation system for better data representation and easier data investigation with multiple levels of granularity

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RESEARCH/WORK EXPERIENCE (Cont'd)

- Performed meta-analysis of pancreatic cancer cell lines to discover expression-based biomarkers predictive of drug responses in order to improve current treatment strategies
- Analyzed multiple preclinical models including patient-derived cell lines and organoids in single or pairwise drug testing and their molecular profiles (feature space exceeding 50K)
- Identified two promising drug resistance biomarkers that may help patients overcome drug resistance in combination with inhibitors in pancreatic cancer

Visiting Researcher

Jan 2018 - Present

Ontario Institute for Cancer Research (OICR), Toronto, Canada

- Analyzed large scale genomic and clinical data with appropriate statistical methods in order to identify gemcitabine resistance biomarkers in pancreatic cancer cohorts
- Discovered gemcitabine resistance biomarkers to select drugs (i.e., inhibitors) that sensitize gemcitabine resistance in pancreatic cancer and validated in patient-derived organoids
- Conducted survival meta-analysis to validate the biomarkers in multiple pancreatic cancer cohorts to improve patient outcomes
- Participated in the molecular tumour board of the COMPASS (Changes and Characteristics of Genes in Patients With Pancreatic Cancer for Better Treatment Selection) trial

Doctoral Researcher

Sep 2012 - Dec 2017

Seoul National University College of Medicine, Seoul, Korea

- Successfully found pharmaco-genes and -variants that have an association with mercaptopurine-induced neutropenia or busulfan-induced hepatotoxicity in paediatric cancer patients and ritodrine-induced pulmonary oedema in pregnant women
- Identified favourable prognostic markers of survival in allogeneic hematopoietic stem cell transplantation patients in donor exomes
- Solely developed a pharmacogenomics analysis platform for the analysis and interpretation of patient genomes and exomes in order to identify drug side effect associated genes and variants
- Built a computational gene-level approach to aggregate the impact of heterogeneous variants in sequencing data
- Analyzed whole-genome, whole-exome, targeted panels, whole-transcriptome, small RNAs, and microarray data with clinical information across platforms (i.e., Ion Proton, Complete Genomics, and Illumina)
- Localized big open public omics datasets such TCGA (The Cancer Genome Atlas), 1KGP (1000 Genomes Project), ADSP (Alzheimer's Disease Sequencing Project), and SFARI (Simons Foundation Autism Research Initiative)
- Doubled as a Server Administrator who was responsible for setting up and maintaining large-scale servers (472 cores, 4.25 TB RAM) and storage (756 TB) in Network/Lustre/Fraunhofer File Systems

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PUBLICATIONS

- **SYNERGxDB: an Integrative Pharmacogenomic Portal to Identify Synergistic Drug Combinations for Precision Oncology.** Heewon Seo[†], Denis Tkachuk, Chantal Ho, Anthony Mammoliti, Aria Rezaie, Seyed Ali Madani Tonekaboni, and Benjamin Haibe-Kains* *Nucleic Acids Res* 2020
- **Discovery of Donor Genotype Associated with Long-term Survival of Patients with Hematopoietic Stem Cell Transplantation in Refractory Acute Myeloid Leukemia.** Chan-Young Ock[†], Heewon Seo[†], Dae-Yoon Kim, Byung Joo Min, Yoomi Park, Hyun Sub Cheong, Eun-Young Song, Inho Kim, Sung-Soo Yoon, Ju Han Kim*, and Youngill Koh* *Leuk Lymphoma* 2018;60(7):1775-1781
- **Deleterious Genetic Variants in Ciliopathy Genes Increase Risk of Ritodrine-induced Cardiac and Pulmonary Side Effects.** Heewon Seo[†], Eun Jin Kwont, Young-Ah You, Yoomi Park, Byung Joo Min, Kyunghun Yoo, Han Sung Hwang, Ju Han Kim*, and Young Ju Kim* *BMC Med Genomics* 2018;11(1):4
- **APEX1 Polymorphism and Mercaptopurine-related Early Onset Neutropenia in Pediatric Acute Lymphoblastic Leukemia.** Hyery Kim[†], Heewon Seo[†], Yoomi Park, Byung Joo Min, Myung Eui Seo, Kyung Duk Park, Hee Young Shin, Ju Han Kim*, and Hyoung Jin Kang* *Cancer Res Treat* 2018;50(3):823-834
- **Idiopathic Hypereosinophilia Is Clonal Disorder? Clonality Identified by Targeted Sequencing.** Jee-Soo Leet, Heewon Seo, Kyongok Im, Si Nae Park, Sung-Min Kim, Jung-Ah Kim, Seon Young Kim, Joon-hee Lee, Sunghoon Kwon, Miyoung Kim, Insong Koh, Seungwoo Hwang, Heung-Woo Park, Ju Han Kim, and Dong Soon Lee* *PLoS One* 2017;12(10):e0185602
- **Evaluation of Exome Variants using the Ion Proton Platform to Sequence Error-Prone Regions.** Heewon Seo[†], Yoomi Park[†], Byung Joo Min, Myung Eui Seo, and Ju Han Kim* *PLoS One* 2017;12(7):e0181304
- **Posttranslational control of T-cell development by the ESCRT protein CHMP5.** Stanley Adoro[†], Kwang H Park, Sarah E Bettigole, Raphael Lis, Hee Rae Shin, Heewon Seo, Ju Han Kim, Klaus-Peter Knobloch, Jae-Hyuck Shim*, Laurie H Glimcher* *Nat Immunol* 2017;18(7):780-790
- **Disease Markers of Pediatric Idiopathic Nephrotic Syndrome and Markers of Steroid-responsiveness: Whole-transcriptome Sequencing of Peripheral Mononuclear Cells.** Hee Gyung Kang[†], Heewon Seo[†], Jae Hyun Lim, Jong Il Kim, Kyoung Hee Han, Hey Won Park, Ja Wook Koo, Kee Hyuck Kim, Ju Han Kim*, Hae Il Cheong, and Il-Soo Ha* *J Int Med Res* 2017;45(3):948-963
- **Gastrointestinal Tuberculosis is not Associated with Proton Pump Inhibitors: A Retrospective Cohort Study.** Kyoung Sup Hong[†], Seung Joo Kang, Jong Kyoung Choi, Ju Han Kim, Heewon Seo, Suehyun Lee, Jae-Woo Jung, Hye-Ryun Kang, Sang-Heon Cho, and Joo Sung Kim* *World J Gastroenterol* 2013;19(2):258-264
- **Development of Korean Rare Disease Knowledge Base.** Heewon Seo[†], Dokyoon Kim, Jong-Hee Chae, Hee Gyung Kang, Buyng Chan Lim, Hae Il Cheong, and Ju Han Kim* *Healthc Inform Res* 2012;18(04):272-278

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ABSTRACTS/POSTERS

- **Targeting Pancreatic Cancer Organoids with Dual BET and CBP/P300 Inhibitor NEO2734.** Nikolina Radulovich, Laura Tramblyn, Heewon Seo, Benjamin Haibe-Kains, Mathieu Lupien, Francis Giles, and Ming-Sound Tsao *AACR Pancreas* 2019
- **Pharmacogenomics of Gemcitabine in Pancreatic Cancer Cell Lines.** Heewon Seo and Benjamin Haibe-Kains, *BioC* 2018
- **Discovery of Donor Genotype Associated with Long-Term Survival of Patients with Hematopoietic Stem Cell Transplantation in Refractory Acute Myeloid Leukemia.** Chan-Young Ock, Heewon Seo, Dae-Yoon Kim, Inho Kim, Sung-Soo Yoon, Ju Han Kim and Youngil Koh *Blood* 2017
- **Analysis of Genetic Variants Related to the Hepatic Veno-Occlusive Disease in Pediatric Patients Receiving HSCT with Targeted Dose Busulfan Based Conditioning.** Jung Yoon Choi, Heewon Seo, Yoomi Park, ByungJoo Min, Hyery Kim, Kyung Taek Hong, Che Ry Hong, Sang Hoon Song, Kyung-Sang Yu, In-Jin Jang, Kyung Duk Park, Hee Young Shin, Ju Han Kim and Hyoung Jin Kang *Blood* 2017
- **Staring inside of Idiopathic Hypereosinophilia: Identification of Clonality Using Targeted Exome Sequencing.** Jee-Soo Lee, Heewon Seo, Kyongok Im, Si Nae Park, Jung-Ah Kim, Seon Young Kim, Joon-hee Lee, Sunghoon Kwon, Insong Koh, Seungwoo Hwang, Heung-Woo Park, Hye-Ryun Kang, Ju Han Kim, Miyoung Kim and Dong Soon Lee *Blood* 2016
- **Clonal Changes Detected By Target Capture Sequencing and Molecular Cytogenetic Study in Patients with Aplastic Anemia.** Heesue Park, Heewon Seo, Si Nae Park, Kyoungok Im, Jung Ah Kim, Sang Mee Hwang, Ju Han Kim and Dong Soon Lee *Blood* 2015

TEACHING EXPERIENCE

- **Rare and Common Disease Variant Analysis using Next-generation Sequence** Feb 2017
The 12th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea
- **Exome Sequencing Analysis in Clinical Research** Feb 2014 - Feb 2017
From 6th to 12th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea
- **NGS Platforms and Applications** Aug 2013 - Feb 2017
From 5th to 12th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea
- **Advanced Methods and Algorithms for Genetic and Genomic data Analysis** Aug 2016
The 11th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea
- **Advanced R Graphics** Mar 2013 - Mar 2016
From 5th to 12th R for Bioinformatics and Biomedicine Workshop, Seoul National University, Seoul, Korea
- **The 1000 Genomes Project and Human Genome Diversity** Feb 2015 - Feb 2016
From 8th to 10th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea

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TEACHING EXPERIENCE (Cont'd)

- **RNA-Seq Expression Profile Analysis** *Aug 2012 - Feb 2016*
From 3rd to 10th Genome Data Analysis (GDA) Workshop, Seoul National University, Seoul, Korea
- **Introduction to Linux for Genome Data Analysis** *May 2014 - Nov 2014*
Course: Certified Scientist in BioMedical Informatics (**CSBMI**), Seoul National University, Seoul, Korea

SOFTWARE

- **SYNERGxDB** (<http://SYNERGxDB.ca/>) is a web-based database that provides the largest integrated database in drug combination screenings and molecular profiles to discover effective combinations and predictive biomarkers.
- **CaReAI** [kæri:əl] (Capturing Read Alignments, <https://github.com/lootpiz/CaReAI>) is a high-performance alignment capturing tool for visualizing the read-alignment status of nucleotide sequences and obtaining read-level data for evaluating variant calls and detecting technical biases.
- **VVA** (Variant Visualization and Annotation, <https://github.com/lootpiz/VVA>) is a gene- and variant-centred visualization tool to be used for exome sequencing data analysis and is optimized for displaying the overall distribution of variants in a gene at a glance.
- **KRDK** (Korean Rare Disease Knowledge base, <http://www.snubi.org/software/raredisease/>) is a web-based, research oriented data repository that provides comprehensive information for rare disease research: disease review, clinics, directory, mutation database, patient registry, and biobank.

PROGRAMMING LANGUAGE SKILLS

- High-level languages: C/C++
- Scripting languages: R, Python, HTML, PHP, and javascript (Node)
- Structured query languages (SQL): MySQL, MariaDB, and MongoDB (NoSQL)

REFERENCES

- **Benjamin Haibe-Kains, PhD**, benjamin.haibe.kains@utoronto.ca
Senior Scientist,
Princess Margaret Cancer Centre, University Health Network, Toronto, Canada
- **Ju Han Kim, MD, PhD, MS**, juhan@snu.ac.kr
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Seoul National University College of Medicine, Seoul, Korea