

Harim Chun

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EDUCATION

Korea University College of Medicine
Master of Science in Biomedical Sciences
Department of Biomedical Sciences

Seoul, Korea
Mar. 2021 – Aug. 2024 (expected)

University of Mississippi
Exchange Student, Biology

University, Mississippi, U.S.A.
Jan. 2019 – May 2019

Soongsil University
Undergraduate Student
Bachelor of Science, School of systems Biomedical Science

Seoul, Korea
Mar. 2015 – Feb. 2021

GPA AND ENGLISH SCORE

Undergraduate GPA: 4.11 / 4.5, Percentage equivalent: 94.0 / 100
Graduate GPA: 4.21 / 4.5, Percentage equivalent: 96.7 / 100
TOEIC: 875 (out of 990)
TEPS: 343 (out of 600)

RESEARCH EXPERIENCE

Choi Lab (Human Genetics and Genomics Lab)
Korea University
Undergraduate Research Intern (Advisor: Jungmin Choi, Ph.D.)
Graduate Student (Advisor: Jungmin Choi, Ph.D.)

Seoul, Korea
Jul. 2020 – Feb. 2021
Mar. 2021 – Aug. 2024 (expected)

- Discovering the heterogeneous tumor microenvironment of gastric cancer patients using scRNA-seq data
- Transcriptional heterogeneity in hematopoietic stem cell niche with scRNA-seq data
- Identifying the pseudogene-derived lncRNA biomarker responsible for the tumor progression and poor prognosis in liver cancer with bulk RNA-seq data
- Identification of biomarkers responsible for the metachronous gastric cancer progression with WES and bulk RNA-seq data
- Discovery of biomarkers affecting the response to the immune check inhibitors by the network analysis using scRNA-seq and scATAC-seq data
- Altered post-transcriptional modification at 3'-end in Yeast with bulk RNA-seq data
- Constructing pipeline for the alignment and variant calling of Whole genome sequencing data for the drug resistance inference and the construction of the phylogenetic tree

Insilicogen, INC.
Internship

Yongin, Korea
Jul. 2019 – Aug. 2019

- A personalized fruit or vegetable drinks service referring to the personal genomic data (Prototype, via Neo4J)

- Genomic, Transcriptomic data analysis utilizing QIAGEN CLC genomic workbench

Post-genome informatics lab

Soongsil University

Research Intern (Advisor: Sangsoo Kim, Ph.D.)

Seoul, Korea

Aug. 2019 – Jul. 2020

Personal Projects during the Undergraduate Course

- Identifying expression quantitative trait loci for pro-inflammatory response triggered by *TIFA* with genome-wide association study (Practice of Biostatistics)
- Drug repositioning and virtual screening against the calcium-dependent protein kinase 1 (*CDPK1*) with SMINA (Computational Molecular Biology and Lab)
- In silico analysis of gene expression and binding affinity to predict the susceptibility to covid-19 of pan-cancer patients (Undergraduate Thesis)

RESEARCH INTEREST

My research interests include investigating the mechanisms of cancer and other diseases through the analysis of omics data (genomic, transcriptomic, epigenomic, and proteomic) and the application of machine learning techniques.

RELEVANT SKILLS

Programming Languages

R, Python

Computing Skills

Hadoop, Apache Spark, Unix, Google Cloud Platform, AWS, Kakao cloud

Rosalind

Rank: 147 / 454 (Korea), 29 XP

Data analysis

- **Bulk NGS Data Analysis**
 - Genomic data analysis
 - Sequence alignment (BWA-MEM)
 - Detection of somatic and germline variants (GATK HaplotypeCaller, Mutect2)
 - Variant effect prediction (VEP, SnpEff, ANNOVAR)
 - Inferring phylogenetic tree (vcf2phyliip, iTOL)
 - Transcriptome analysis
 - Sequence alignment and transcriptome quantification (Hisat, Salmon, HTSeq)
 - Batch effect correction (ComBat-seq, Limma, SVA)
 - Differentially expressed gene analysis (DEseq2)
 - Non-coding transcriptome analysis
 - Deconvolution of bulk RNA-seq data (CIBERSORTx)
 - Pathway analysis (Gene Ontology, PANTHER, Enrichr, g:Profiler, clusterProfiler)
 - Geneset Enrichment Analysis (GSEA)
 - Ingenuity Pathway Analysis (IPA)
 - Transcription factor analysis (DoRothEA, decoupleR)
- **Single cell data Analysis**
 - Single cell RNA-seq data analysis
 - Batch effect correction (Harmony, fastMNN, BBKNN)
 - Cluster identification and dimensional reduction with PCA, tSNE, and UMAP (Seurat)
 - Cell type annotation and abundance analysis (miloR)
 - Differential gene expression analysis (MAST)
 - Pseudotime analysis (Monocle3)
 - Single-cell transcription factor analysis (DoRothEA, collecTRI, decoupleR)
 - Single cell browser (cellxgene, Rshiny)

- **Downstream Analysis**
 - Co-expression based Gene Network analysis (WGCNA, hdWGCNA)
 - Causal Gene regulatory network analysis (TENET, FigR)
 - Network visualization (Cytoscape)
 - Pattern analysis (Self-organizing map and Mfuzz)

Computational molecular biology

- Molecular dynamics (MD) simulation (NAMD, VMD)
- Molecular docking (Smina, DUDE, pubchem, ZINC)

TEACHING

KSBI-BIML 2024 , Korea Society for Bioinformatics	Seoul, Korea <i>Feb. 2024</i>
Single cell Multiomics	
KSBI-BIML 2023 , Korea Society for Bioinformatics	Seoul, Korea <i>Feb. 2023</i>
Spatial Transcriptome with R programming	
The 19th KOGO Winter Workshop , Korea Genome Organization	Seoul, Korea <i>Feb. 2023</i>
Spatial Transcriptome with R programming	
Training of Digital Healthcare Professionals , Korea University, INNOPOLIS	Seoul, Korea <i>Oct. 2022</i>
NGS Data Analysis Pipeline – GATK best practice workflow	
CoRE (Collaboration Real Energy) Tutoring , Soongsil University	Seoul, Korea <i>Sep. 2019 - Dec. 2019</i>
Taught Hadoop File System and PySpark to students who took <i>Distributed Big data Computing</i> class for the whole semester	

AWARDS AND HONORS

Excellence Poster Award	The 20 th KOGO Winter Symposium, 2024
Identification of molecular biomarkers for response to immune checkpoint inhibitors	
Semester Honor Scholarship	Soongsil University, 2020
CoRE Tutoring Best Tutor Award	Center for Innovative Teaching and Learning, Soongsil University, Korea, 2020
Semester Honor Scholarship	Soongsil University, 2016

CONFERENCE PRESENTATIONS

Identification of molecular biomarkers for response to immune checkpoint inhibitors	The 20 th KOGO Winter Symposium
Poster presentation	Hongcheon, Korea, <i>Feb. 2024</i>
Ctk1 regulates replicative lifespan by controlling the expression of ribosomal proteins	The 19 th KOGO Winter Symposium
Poster presentation	Hongcheon, Korea, <i>Feb. 2023</i>

PUBLICATIONS

Ctk1 regulates replicative lifespan by controlling the expression of ribosomal proteins. *in preparation*

Development and Validation of Predictive Markers for Metachronous Gastric Cancer Development in Patients with Early Gastric Cancer Treated with Endoscopic Submucosal Dissection. *in preparation*

Miao R, **Chun H**, Gomes A. C, Choi J, & Pereira J. Competition between hematopoietic stem and progenitor cells controls hematopoietic stem cell compartment size. *Nat Communications*. 2022.

Lee J*, Hwang JH*, **Chun H***, Woo W, Oh S, Choi J^, Kim LK^. PLEKHA8P1 Promotes Tumor Progression and Indicates Poor Prognosis of Liver Cancer. *Int. J. Mol. Sci.* 2021, 22, 7614

*: co-first Author