

Harim Chun

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EDUCATION

Korea University College of Medicine

Graduate Student

Department of Biomedical Sciences

Seoul, Korea

Mar. 2021 – Present

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

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 – Present

- Discovering the heterogeneous tumor microenvironment of gastric cancer patients using Single-cell RNA-sequencing
- Transcriptional heterogeneity in hematopoietic stem cell niche with Single-cell RNA-sequencing data
- Identifying the pseudogene-derived lncRNA biomarker responsible for the tumor progression and poor prognosis in liver cancer with transcriptomic data
- Identification of biomarkers responsible for the metachronous gastric cancer progression
- Discovery of master regulator affecting the resistance to the immunotherapy by the network analysis
- Altered post-transcriptional modification at 3'-end in Yeast
- 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)

GPA AND ENGLISH SCORE

Undergraduate GPA: 4.11 / 4.5, Percentage equivalent: 94.0 / 100

Graduate GPA: 4.27 / 4.5, Percentage equivalent: 97.4 / 100

TOEIC: 875 (out of 990)

RESEARCH INTEREST

Interested in unraveling the mechanisms of cancer or disease using omics data including WES, Bulk RNA-sequencing, and Single cell RNA-sequencing data by utilizing various methodologies.

Making a platform or pipeline for the automated analysis.

RELEVANT SKILLS

Software language Python, R

Computing Skills Hadoop, Apache Spark (python based), Unix, Google Cloud Platform, AWS

Rosalind Rank: 89 / 330 (Korea), 29 XP

Sequencing data analysis

- **Bulk NGS Data Analysis**
 - Pipeline for the analysis
 - Bash-based
 - Rscript-based
 - 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 (vcf2phylip, 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)
 - Geneset Enrichment Analysis (GSEA)
 - Ingenuity Pathway Analysis (IPA)
 - Transcription factor analysis (DoRothEA, decouplerR)
- **Single cell data Analysis**
 - Single cell RNA-seq data analysis
 - Batch effect correction (Harmony, fastMNN)
 - Cluster identification and dimensional reduction with PCA, tSNE, and UMAP (Seurat)
 - Cell type annotation and abundance analysis (miloR)

- Differential gene expression analysis (Seurat, MAST)
 - Pseudotime analysis (Monocle3)
 - Single-cell transcription factor analysis (DoRothEA, decoupleR)
 - Single cell browser (cellxgene, Rshiny)
- **Downstream Analysis**
 - Co-expression based Gene Network analysis (WGCNA)
 - Causal Gene network analysis (TENET)
 - Network visualization (Cytoscape)
 - Pattern analysis (especially gene expression, Self-organizing map and Mfuzz)

Computational molecular biology

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

TEACHING

CoRE (Collaboration Real Energy) Tutoring, Soongsil University
Tutor

Seoul, Korea
 Sep. 2019 - Dec. 2019

Taught Hadoop File System and PySpark to students who took *Distributed Big data Computing* class for the whole semester
 Taught python programming to students who are not accustomed to the python programming

AWARDS AND HONORS

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

PUBLICATIONS

Identification of biomarkers responsible for the metachronous gastric cancer progression. *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