**Harim Chun**

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# Education

**Korea University College of Medicine** **Seoul, Korea**

*Graduate Student* Mar. 2021 – Present

Department of Biomedical Sciences

**University of Mississippi University, Mississippi, U.S.A.**

*Exchange Student, Biology* Jan. 2019 – May 2019

**Soongsil University** **Seoul, Korea**

*Undergraduate Student* Mar. 2015 – Feb. 2021

Bachelor of Science, School of systems Biomedical Science

# Research Experience

**Choi Lab (Human Genetics and Genomics Lab) Seoul, Korea**

Korea University

*Undergraduate Research Intern (Advisor: Jungmin Choi, Ph.D.)* Jul. 2020 – Feb. 2021

* 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. Yongin, Korea**

*Internship* 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 Seoul, Korea**

Soongsil University Aug. 2019 – Jul. 2020

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

**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, decoupleR)
* **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 UniversitySeoul, Korea

*Tutor* 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