

## Curriculum Vitae

### Harim Chun

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#### EDUCATION

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**Korea University College of Medicine**

**Seoul, Korea**

M.S., Department of Biomedical Sciences

*Mar. 2021 – Aug. 2024 (expected)*

**University of Mississippi**

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

*Exchange Student, Biology*

*Jan. 2019 – May 2019*

**Soongsil University**

**Seoul, Korea**

B.S., School of systems Biomedical Science  
Interdisciplinary Major in Big Data Computing

*Mar. 2015 – Feb. 2021*

#### RESEARCH INTEREST

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##### Cancer Genomics

Investigating the genetic underpinnings of cancer to understand the mechanisms driving oncogenesis, with a special focus on the interaction between tumors and the immune system. This includes identifying genetic and molecular markers that predict response to immunotherapy, developing personalized immunotherapeutic strategies, and enhancing early diagnosis and treatment approaches to improve patient outcomes through precision oncology.

##### Single-cell Genomics

Exploring the genetic and transcriptomic landscape of individual cells to uncover cellular diversity, identify rare cell populations, and understand cell-type-specific roles in complex tissues. This approach reveals insights into tissue development, disease progression, and therapeutic responses, ultimately contributing to more precise and effective medical interventions.

##### Multi-Omics

Integrating various omics data (genomics, transcriptomics, epigenomics, proteomics) to achieve a comprehensive understanding of biological systems. This approach uncovers molecular mechanisms driving diseases, identifies biomarkers for diagnostics and prognostics, and develops personalized therapeutic strategies.

##### Bioinformatics

Developing and applying computational tools, methods, and pipelines to analyze and interpret complex biological data. This facilitates the discovery of new biological insights and advances the fields of genomics, transcriptomics, proteomics, and other high-throughput technologies through innovative data analysis approaches.

#### GPA AND ENGLISH SCORE

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Graduate GPA: 4.21 / 4.5, Percentage equivalent: 96.7 / 100

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

TOEIC: 875 (out of 990)

## RESEARCH EXPERIENCE

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### Choi Lab (Human Genetics and Genomics Lab)

Seoul, Korea

Korea University

Undergraduate Research Intern (Advisor: Jungmin Choi, Ph.D.)

Jul. 2020 – Feb. 2021

Graduate Student (Advisor: Jungmin Choi, Ph.D.)

Mar. 2021 – Aug. 2024 (expected)

#### ▪ Cancer Genomics

- Identifying the pseudogene-derived lncRNA biomarker responsible for the tumor progression and poor prognosis in liver cancer with bulk RNA-seq data

Collaborated with Prof. Lark Kyun Kim (Yonsei University College of Medicine)

Contributed to publication: Lee *et al.*, International journal of molecular sciences 2021

- Analyzed the transcriptomic data of the TCGA-LIHC (liver hepatocellular carcinoma) dataset, comprising 369 primary liver tumor tissues and 49 adjacent normal tissues.
- Identified 465 differentially expressed pseudogenes. Ten candidate pseudogenes showing significant associations with tumor grade, overall survival, and disease-free survival were ultimately identified.
- Among the 10 candidates differentially expressed pseudogenes, the upregulation of *PLEKHA8P1* and its parental gene *PLEKHA8* was observed in liver cancer and promote tumorigenesis in liver cancer.

- Identification of biomarkers responsible for the metachronous gastric cancer progression with WES and bulk RNA-seq data

Collaborated with Prof. Soo-jeong Cho (Seoul National University College of Medicine)

Contributed to publication: Kim *et al.*, Cancer Medicine 2024. *Submitted*

- Analyzed bulk RNA sequencing data from 23 control gastric cancer patients and 23 metachronous gastric cancer (mGC) patients, revealing transcriptomic heterogeneity.
- Identified 13 DEGs, with 9 upregulated and 4 downregulated in mGC. Selected 5 DEGs, including *KDF1*, which showed significantly higher expression in mGC.
- *CDK1* showed a strong correlation with new gastric carcinoma and *CREB5* expression increased with OLGA and OLGIM stages by the SOM (Self-Organizing Map) analysis.

#### ▪ Single-cell Genomics

- Transcriptional heterogeneity in hematopoietic stem cell niche with scRNA-seq data

Collaborated with Prof. Joao Pereira (Yale University School of Medicine)

Contributed to publication: Miao *et al.*, Nature Communications 2022

- Analyzed the transcriptional heterogeneity of non-hematopoietic bone marrow cells in Cxcr4 cKO and control mice using droplet-based scRNA-seq data.
- Conducted a differential abundance test, revealing no significant differences in cellular states between control and cKO datasets. Identified a small number of DEGs with no major biological pathways implicated in HSC regulation.
- Major regulators of HSC homeostasis, such as *Cxcl12*, *Kitl*, *Ptn*, *Vcam1*, and *Icam1*, were equally expressed in both samples. No differences in hematopoietic growth factors were detected.

#### ▪ Multi-Omics

- Discovery of biomarkers affecting the response to the immune check inhibitors by the network analysis using scRNA-seq and scATAC-seq data

Collaborated with Prof. Tae-woo Kim (Korea University College of Medicine)

- Exploring the multiple biological networks that potentially impact the outcomes of immune checkpoint inhibitors in Basal cell carcinoma patients at the single-cell level, utilizing data from scRNA-seq and scATAC-seq.
- Figured out the response associated GRNs. GRNs regulated by the CD4 CTL-M2, Th17-M1, Th17-M2, and Th1-M4 modules are associated with the non-response. And CD8 Tex-M2, CD4 CTL-M1, and Th1-M2 modules are associated with the response.
- Marker genes of each module were associated with the stress response, T cell activation, and T cell proliferation.

#### ▪ Bioinformatics

- Altered post-transcriptional modification at 3'-end in Yeast with bulk RNA-seq data

Collaborated with Prof. Hong-Yeoul Ryu (Kyungpook National University)

- Examined the significant differences in gene expression between *ctk1Δ* mutants and WT of *Saccharomyces cerevisiae* (Yeast).
- 2,066 DEGs at CDS and 164 DEGs which are exclusively significant at 3'UTR were discovered, and Ribosomal pathway is enriched in WT at CDS and in *ctk1Δ* at 3'UTR.
- In *ctk1Δ* mutants, ribosomal gene expression is reduced at the coding sequence (CDS), whereas aging-related genes show increased expression; moreover, ribosomal genes have elongated 3'UTRs, potentially impacting cytoplasmic translation.

- 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

Collaborated with Prof. Seung Heon Lee (Korea University Ansan Hospital)

- Set up the pipeline for the Mycobacterium Tuberculosis WGS data analysis to infer drug resistance.
- Implemented the GATK best practices for automated read alignment and variant calling pipelines.
- Drug resistance inference was subsequently performed based on the identified variants using this pipeline.

- Clustering and Representing GO BP Terms: An Unbiased Approach – Enrichmate

- Redundant GO BP terms are clustered by semantic similarity.
- Representative terms for each cluster are set using multiple approaches (under development)

#### **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)

## RELEVANT SKILLS

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### 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 (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, 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

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**KSBI-BIML 2024**, Korea Society for Bioinformatics

**Seoul, Korea**

*Feb. 2024*

Single cell Multiomics

**KSBI-BIML 2023**, Korea Society for Bioinformatics

**Seoul, Korea**

*Feb. 2023*

Spatial Transcriptome with R programming

The 19<sup>th</sup> KOGO Winter Workshop, Korea Genome Organization

Seoul, Korea

Feb. 2023

Spatial Transcriptome with R programming

Training of Digital Healthcare Professionals, Korea University, INNOPOLIS

Seoul, Korea

Oct. 2022

NGS Data Analysis Pipeline – GATK best practice workflow

CoRE (Collaboration Real Energy) Tutoring, Soongsil University

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

## AWARDS AND HONORS

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Excellence Poster Award

The 20<sup>th</sup> KOGO Winter Symposium, 2024

Brain Korea 21 (BK21) Scholarships

Korea Research Foundation, 2021-2022

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

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**Identification of molecular biomarkers for response to immune checkpoint inhibitors** The 20<sup>th</sup> KOGO Winter Symposium  
Poster presentation Hongcheon, Korea, Feb. 2024

**Ctk1 regulates replicative lifespan by controlling the expression of ribosomal proteins** The 19<sup>th</sup> KOGO Winter Symposium  
Poster presentation Hongcheon, Korea, Feb. 2023

## PUBLICATIONS

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*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. *Cancer Medicine*. 2024. *Submitted*

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