Curriculum Vitae

Harim Chun

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EDUCATION

The Catholic University of Korea Ph.D., Department of Biomedical Sciences (expected)

Korea University College of Medicine M.S., Department of Biomedical Sciences

University of Mississippi Exchange Student, Biology

Soongsil University

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

RESEARCH INTEREST

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

Seoul, Korea Mar. 2025 –

Seoul, Korea *Mar. 2021 – Aug. 2024*

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

> **Seoul, Korea** *Mar. 2015 – Fed. 2021*

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

Graduate GPA (M.S.): 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) TEPS: 343 (out of 600)

RESEARCH EXPERIENCE

PathFinderLabSeoul, KoreaThe Catholic University of Korea College of Medicine and Korea University Anam HospitalMar. 2025 –Graduate Student (Advisor: Sung Hak Lee, M.D., Ph.D.)Mar. 2025 –Research AssociateSep. 2024 – Feb. 2025

Cancer Genomics

Spatial Transcriptomics

Choi Lab (Human Genetics and Genomics Lab)	Seoul, Korea
Korea University	
Graduate Student (Advisor: Jungmin Choi, Ph.D.)	Mar. 2021 – Aug. 2024
Undergraduate Research Intern (Advisor: Jungmin Choi, Ph.D.)	Jul. 2020–Feb. 2021

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

- 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

- o 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

o 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 ctk1∆ 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 ctk1∆ at 3'UTR.
- In ctk1∆ 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.
- o 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.)

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

Programming Languages Computing Skills	R, Python 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)
 - \circ 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

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

Seoul, Korea

Aug. 2019 – Jul. 2020

Computational molecular biology

- 0 Molecular dynamics (MD) simulation (NAMD, VMD)
- Molecular docking (Smina, DUDE, pubchem, ZINC) 0

TEACHING

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 19th 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
NGS Data Analysis Pipeline – GATK best practice workflow	0.00.2022
CoRE (Collaboration Real Energy) Tutoring, Soongsil University	Seoul, Korea

CoRE (Collaboration Real Energy) Tutoring, Soongsil University

Taught Hadoop File System and PySpark to students who took Distributed Big data Computing class for the whole semester

AWARDS AND HONORS

Excellence Poster Award	The 20th 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

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

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

PUBLICATIONS

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

Kim B*, Chun H*, Lee J, Park M, Kwak Y, Kim JM, Kim SG, Ryu JK, Choi J, Cho SJ. Predictive biomarkers for metachronous gastric cancer development after endoscopic resection of early gastric cancer. Cancer Medicine. 2024.

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.

Sep. 2019 - Dec. 2019

Lee J*, Hwang JH*, <u>Chun H*</u>, 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