Sung Rye Park

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Summary Experienced Senior Bioinformatics Scientist specializing in immunology, cancer biology, and therapeutic efficacy testing projects. Skilled in customized integrative analyses of diverse datasets and in managing multiple projects simultaneously with strong organizational skills. Distinguished for combining biological insights with computational methodologies. First author-publications in Nature Immunology and Cell Reports. Managed bioinformatics collaborations with pharmaceutical firms at Dana Farber Cancer Institute.

Professional Experience (selected)

Senior Bioinformatics scientist. Dana Farber Cancer Institute. Boston, MA 2022 – 2024

Informatics & Analytics, the Bioinformatics group
Research of the Belfer Center for Applied Cancer Science, Thoracic Oncology group
Team mentors: David Barbie, Cloud Paweletz

- **DS-1062a testing:** Analyzed scRNA-seq data from TROP2-high cells, incorporating the tumor immune environment, and cancer-cell enriched tissue RNA-seq in two distinct NSCLC patient cohorts (responders and non-responders) undergoing treatment with Dxd/IgG-Dxd and DS-1062a. The study compared DS-1062a efficacy to standalone Dxd therapy through comprehensive transcriptomic changes in tumor cells and related immune cells (NK and macrophage).
  Method: Analyzed data based on cohort types, immune cell types, and unique subsets. Comparisons of groups treated with DS-1062a/Dxd were conducted for canonical gene expressions, populations, pathway enrichment, customized scoring, clustering, and feature selections using lasso regression. scRNA-seq and RNA-seq data were linked through shared features using the pseudo-bulk RNA method. (Daiichi-Sankyo)
- **DGK inhibitor combinational therapy:** Analyzed scRNA-seq and scTCR-seq data from combinational therapy trials of a DGK inhibitor with Nivolumab in SCLC, utilizing patient-derived cells (pDOTs) in a collaboration with Bristol-Myers Squibb.
  Method: The integration of scTCR-seq with scRNA-seq. Clonotypes were selected based on gene profile, abundance, and association with selected cell populations and were further subset and analyzed for CAR-T cell therapy design. (BMS)
- **TAK-676 combinational therapy in addition to NK cell injection**: Conducted scRNA-seq analysis across six cohorts, analyzing transcriptomic changes from combinational treatments of TAK-676 and Pembrolizumab.
  Method: Rigorous data quality control involved customized filtering, integration, and normalization. Traditional and customized annotations were used to categorize cells for focused analysis. CD8T cells-specific analysis for activated immune response by TAK-676 with Pembro was conducted.
  Simultaneously, machine learning was used to segregate NK cells without external tags, distinguishing endogenous NK cells from therapeutic ones. This revealed their unique transcriptional profiles, informing their potential impact on therapy responses. (Takeda)

Massachusetts General Hospital Laboratory (Salvia Jain Lab)

- **Anti-CD47 therapy in PTCL model:** An integrative analysis using the unique ITK-SYK system was conducted to evaluate the efficacy of anti-CD47 therapy in PTCL models (tumor). scRNA-seq data from ITK-SYK PTCL mice were analyzed to determine the time-dependent effects of anti-CD47 therapy, at 2 hours and 2 weeks, on control and treatment-resistant phenotype mice. Initial findings, particularly focusing on macrophages and NK cell populations, informed a grant proposal submitted in 2024. Subsequent RNA-seq and ATAC-seq analyses of the same mouse samples were carried out to identify T-cell specific features and their genomic locations.
  Method: Utilized a multiomic approach, including scRNA-seq, to identify uniquely responding macrophages, bulk tumor-cell RNA-seq to validate driver genes, and ATAC-seq to investigate candidate associations in recognized loci. Plans were made to incorporate Cut&Tag data to further elucidate the epigenetic factors influencing therapy responses.

Postdoctoral Fellow. Hackensack Meridian Health. Netley, NJ 2021 – 2022

Center for Discovery & Innovation. Hai-Hui Xue laboratory

- **Novel Tle3 coactivator function analysis:** Led bioinformatics efforts to explore the novel role of the transcriptional cofactor Tle3 in redefining central memory CD8+ T cell fates. This pioneering research was published in Nature Immunology (2024). I developed the primary hypotheses and conducted the majority of the bioinformatic analyses.
  Method: Utilized scRNA-seq (CITE-seq) to uncover key features of Tle3 knockout (KO) and integrated RNA-seq, ATAC-seq, and Cut&Run data for Tle3, Runx3, and Tbet to investigate further connections under the novel roles of Tle3. The findings were validated through extensive mouse experiments, confirming the impactful insights derived from the computational studies.

Detailed recent work experience history (link)

Bioinformatics Skills

Programming language Proficient in R, Python, Linux, custom scripting
Linux based Samtools, GATK, BEDTools,VCFtools, CellRanger, BWA, Bowtie, STAR, MACS2, Salmon, DeepTools,MultiQC, bamtools, HISAT2, awk, VS Code
Bioconductor dplyr, tidyr, ggplot2, DESeq2, edgeR, Seurat, harmony, monocle, GenomicRanges, rtracker, Diffbind, Pheatmap, doubletFinder, cellchat, scater, Rsamtools, ChIPseeker, TCGAbiolinks, OragnismDbi, MethylKit, ClusterProfiler, enrichR, ssGSEA, BiocParallel, WGCNA, STRINGdb, pathview, corrplot, maftool
Public database TCGA, CCLE, GTEx, COSMIC, STRING, GEO, MsigDB.
Interactive Data visualization shiny (shinyapps.io), Rmarkdown, plotly, Flexdashboard, UCSC Genome browser
Cloud computing HPC(PBS,SLURM), DNANexus

Other Skills

Strong Project management Demonstrated ability to organize, manage, and track multiple complex projects simultaneously, with successful completion. **Frequently recognized by managers for effectively organizing and managing multiple complex projects, ensuring timely and successful completion**
Cross-Disciplinary Expertise Deep understanding of both biology and computational methodologies, enabling effective communication with diverse collaborators
Expertise in **immunology, oncology**, molecular biology, and practical experience in statistical analysis skills for bioinformatics research

Education

Ph.D. in Plant Biology. University of Texas at Austin, Austin, Texas	2010 - 2017
M.S. in Biology (Education). Seoul National University, Seoul, Korea	2007 - 2010
B.S. in Biology. Yonsei University, Seoul, Korea.	2005 - 2007

Publications (selected)

The transcriptional cofactor Tle3 reciprocally controls effector and central memory CD8+ T cell fates. (Nature Immunology, 2024. X.Zhao, W.Hu, **S.R.Park**, S.Zhu, S.S.Hu, C.Zang, W.Peng, Q.Shan ,H.H. Xue. *co-first (Zhao, W.Hu, Park and Zhu as co-first authors with equal contribution) (https://doi.org/10.1038/s41590-023-01720-w)

SiftCell: A robust framework to detect and isolate cell-containing droplets from single-cell RNA sequence reads. (Cell Systems, 2023) Jingyue Xi, **Sung Rye Park**, Jun Hee Lee and Hyun Min Kang. https://doi.org/10.1016/j.cels.2023.06.002)

Simultaneous loss of TSC1 and DEPDC5 in skeletal and cardiac muscles produces early-onset myopathy and cardiac dysfunction associated with oxidative damage and SQSTM1/p62 accumulation. (Autophagy, 2021) Chun-Seok Cho, Yongsung Kim, **Sung-Rye Park**, Boyoung Kim, Carol Davis, Irene Hwang, Susan V Brooks, Jun Hee Lee, Myungjin Kim. (https://doi.org/10.1080/15548627.2021.2016255)

Seq-Scope: Microscopic examination of spatial transcriptome using Seq-Scope. (Cell, 2021) Chun-Seok Cho, Jingyue Xi, Yichen Si, **Sung-Rye Park**, Jer-En Hsu, Myungjin Kim, Goo Jun, Hyun-Min Kang, Jun Hee Lee. (https://doi.org/10.1016/j.cell.2021.05.010)

Single cell transcriptome analysis of colon cancer cell response to 5-fluorouracil-induced DNA damage (Cell Reports, 2020) **Sung Rye Park,** Sim Namkoong, Zac Zezhi Zhang, Leon Friesen, Euisik Yoon, Chang H. Kim, Hojoong Kwak, Hyun Min Kang and Jun Hee Lee. (https://doi.org/10.1016/j.celrep.2020.108077) * first author

Holistic Characterization of Single Hepatocyte Transcriptome Responses to High Fat Diet (American Journal of Physiology-Endocrionlogy and Metabolism, 2020) **Sung Rye Park**, Chun-Seok Cho, Hyun Min Kang and Jun Hee Lee. (https://doi.org/10.1152/ajpendo.00391.2020) * first author

Professional Experience (continued)

Senior Bioinformatics scientist. Dana Farber Cancer Institute. Boston, MA 2022 – 2024

- Conducted validation studies for EZH2 inhibitor candidates using ChIP-seq methodologies at Janne lab, DFCI. Developed custom processes to achieve normalization of signal peaks across samples and established a systematic approach for comparative analysis. (2023)
- **Facilitated the evaluation of STING agonist (ADU-100).** Investigated ADU-100 effects in mouse PBMCs model regarding changes in the tumor immune environment and clonotype expansion, applying scRNA-seq and TCR-seq techniques. This study, in collaboration with BMS, is being prepared for resubmission to the journal Cancer Discovery in 2024. Method: The single cell transcriptome and single cell clonotypes in the tumor environment were analyzed and integrated (scTCR-seq with scRNA-seq). Clonotypes were selected based on gene profile, abundance, and association with selected cell type populations and were further subset and analyzed separately. Interesting cell types with positive clonotypes were intensively assessed for DEG, pathway enrichment analysis, and network analysis (CellChat).
- Identified target gene candidates for treatment-resistant NSCLC through PDX models, conducting gene network analysis and extensive correlation tests linked to oncogenic mutations. (2023)
- **TROP2 hi/lo group analysis in TNBC-TCGA.** Data analysis on TNBC-TCGA to investigate the association of known cell types (TNBC, Basal, HER2, Luminal A, Luminal B) within TROP2-hi/lo subgroups. Data preprocessing, filtering, and categorization were completed, setting the stage for in-depth analysis and further exploration. (2024).
- Supported the bioinformatics analysis for the resubmission of a manuscript detailing the KLRG1 depletion study in patients with mature T cell lymphoma, contributing to a publication in Clinical Cancer Research 2024.

Postdoctoral Fellow. Cold Spring Harbor Laboratory. Cold Spring Harbor, NY 2020 – 2021

Dr. Janowitz Laboratory

- Conducted bioinformatic analyses on the glucocorticoid response in cancer cell models, identifying key regulatory pathways and potential therapeutic targets.
- Investigated cachexia-inducing molecules, elucidating their mechanisms and impact on metabolism within cancer progression.

Postdoctoral Fellow. University of Michigan. Ann Arbor, MI 2018 – 2020

Dr. Jun Hee Lee laboratory, co-advisor: Dr. Hyun Min Kang

- Engaged in the setup and optimization of various NGS platforms within the lab, including DROP-seq, Seq-well, BD-Rhapsody, and Seq-Scope, contributing to developments published in Cell (2021).
- Conducted a single-cell transcriptome study on colon cancer cells to investigate responses to 5FU-induced DNA damage, with findings detailed in Cell Reports (first author paper, 2020).
- Holistic characterization of single Hepatocyte transcriptome responses to high fat diet (first author paper, American Journal of Physiology, 2020)
- Multifaceted technical support in flow cytometry, immunoblotting, qPCR.