Sung Rye Park

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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

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 lead : David Barbie, Cloud Paweletz

- Analyzed scRNA transcriptome from TROP2-high cells, incorporating the immune environment, and cancer-cell enriched tissue RNA-seq in two distinct NSCLC patient cohorts (responders and non-responders) undergoing treatment with Dxd and DS-1062a. The study compared DS-1062a treatment to standalone Dxd therapy to better understand the enhancements in DS-1062a application through transcriptomic changes.
  Method: Data were analyzed 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)
- 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 using barcodes. Clonotypes were selected based on gene profile, abundance, and association with and were further subset and analyzed for CAR-T cell therapy design. (BMS)
- Conducted scRNA-seq 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. We used traditional and customized annotations to categorize cells for focused analysis.
  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)

- Conducted an integrative analysis with the ITK-SYK system to evaluate anti-CD47 therapy efficacy in PTCL models.
  Method: Utilized a multiomic approach, including scRNA-seq, to identify uniquely responding macrophages, bulk T-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

- 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.

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, BioGRID, 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
Highly motivated and Quick learner Known for rapid adaptation to the project and teams
Effective Team player

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)

Sublethal whole-body irradiation induces permanent loss and dysfunction in pathgen-specific circulating memory CD8T cell populations. (PNAS, July 2023) Mohammad Heidarian, Iassac J Jensen, Shravan Kumar Kannan, Lecia L Pewe, Mariah Hassert, **Sung Rye Park**, Hai-Hui Xue, John Harty, Vladimir Badovinac. (https://doi.org/10.1073/pnas.2302785120)

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)

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)

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) effects in mouse PBMCs and the tumor immune environment, 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
- Identified target gene candidates for treatment-resistant NSCLC through PDX models, conducting gene network analysis and extensive correlation tests linked to oncogenic mutations. (2023)
- 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, 2020).
- Holistic characterization of single Hepatocyte transcriptome responses to high fat diet (American Journal of Physiology, 2020)
- Multifaceted technical support in flow cytometry, immunoblotting, qPCR.