Sung Rye Park

Senior Bioinformatics Scientist

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Professional summary

Senior Bioinformatics Scientist with over 6 years of hands-on experience in various NGS data analysis and a strong publication record, including a co-first authorship in Nature Immunology (2024) for CD8+ Memory T cell fate. Proficient in the integration of comprehensive multi-omic datasets, encompassing transcriptomic, genomic, epigenomic, and clinical data, to drive research and development in immuno-oncology. At Dana Farber Cancer Institute, played a pivotal role in analyzing complex drug combination testing datasets and provided critical bioinformatics consultation. Passionate about applying a blend of technical proficiency and biological insights to enhance team success, particularly within innovative personalized cancer therapy programs.

GitHub Page for online resume & work samples

https://sung2021.github.io

Work Experience

Senior Bioinformatics scientist, 2022-current

Informatics & Analytics Department, Dana Farber Cancer Institute, Massachusetts

Bioinformatics analysis lead, Belfer Research Laboratory Thoracic Oncology team

- Managed and analyzed combinatorial immunotherapy trials leveraging scRNA-seq and scTCR-seq, targeting DGK inhibitor efficacy in combination with Nivolumab for SCLC treatments, using patient-derived cells in a collaborative study with BMS.
- Coordinated bioinformatic analyses for the DS-1062 and Pembrolizumab test, integrating scRNA-seq data to inform therapeutic strategies. Regularly reported results to Daiichi-Sankyo, advising on analysis applications and connecting experimental outcomes to transcriptomic data insights.
- 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.
- 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.
- Executed scRNA-seq analysis for TAK-676 and PD-1 blockade in SCLC, differentiating immune responses between patient groups. Crafted custom annotation methods for robust data interpretation, shared at the 2024 AACR conference. Takeda collaboration.
- Investigated the impact of NK cell augmentation on SCLC treatment with TAK-676, applying machine learning to discern NK cell ID in tumor immunity. Takeda collaboration.
- Analyzed immune cell trafficking within 3D microphysiological systems using scRNA-seq and RNA-seq for a collaborative study between BMS and Harvard. Currently co-authoring a manuscript set for 2024 submission, with a significant contribution to the bioinformatics analyses and data visualization in the paper.

- Identified target gene candidates for treatment-resistant NSCLC through PDX models, conducting gene network analysis and extensive correlation tests linked to oncogenic mutations.

Bioinformatics analysis lead, Massachusetts General Hospital Laboratory (Jain Lab)

- Performed integrative analysis of anti-CD47 therapy efficacy in PTCL-resistant mouse models, using the ITK-SYK system. Applied scRNA-seq to detail transcriptomic alterations during serial treatments and correlated findings with RNA-seq and ATAC-seq data from sorted tumor cells, aiding in the identification of promising therapeutic gene targets (several candidate genes testing in process)
- 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.
- Proficiently conducted broad-spectrum analyses encompassing RNA-seq, ATAC-seq, and whole-exome sequencing (WES), synthesizing genomic and transcriptomic data to uncover critical biological insights.

Postdoctoral Fellow, 2021-2022
Center for Discovery & Innovation, Hackensack Meridian Health, New Jersey
- Led bioinformatics efforts to redefine central memory CD8+ T cell fates by targeting the transcriptional cofactor Tle3, with findings published in Nature Immunology (2024). Formulated primary hypotheses and executed most of the data analyses.
- Led bioinformatics research to dissect the influences of chronic infection versus protein immunization on CD4+ Tfh cell development, highlighting the modulation by Icos. Developed and implemented a tailored CITE-seq pipeline for in-depth cellular analysis.
- Provided bioinformatics consulting and collaborated on a range of in-lab and external projects, contributing to interdisciplinary research endeavors with outcomes published in respected journals (e.g. PNAS 2302785120)
- Developed and maintained a robust in-house pipeline for next-generation sequencing (NGS) data analysis, streamlining processes and ensuring data integrity throughout various research phases.

Postdoctoral Fellow, 2020-2021
Cold Spring Harbor Laboratory, New York
- 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, 2018-2020
University of Michigan, Michigan
- Engaged in the setup and optimization of various NGS platforms within the lab, including DROP-seq, Seq-well, BD-Rhapsody, Slide-Seq, 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, probe design.

Skills

Technical Skills (Programming)
- Proficient in a wide array of NGS data pipelines and bioinformatics analyses including scRNA-seq, TCR-seq, CITE-Seq, ATAC-seq, bulk RNA-seq, as well as integrative approaches with TCGA and CCLE for genomic and epigenomic studies.
- Proficient in Linux, with advanced programming skills in Python and R, and skilled use of bioinformatics tools including Cellranger, Salmon, and a suite of sequence alignment and analysis utilities.
- Well-versed in peak calling, genomic visualization, and analysis using open-source platforms such as Seurat, scanpy, and the USCC Genome Browser.
- Expertise in pathway and network analysis to elucidate complex biological pathways, and statistical analysis for robust genomic data interpretation.
- Familiarity with high-performance computing environments and adept at managing in-lab NGS pipelines, ensuring quality and reproducibility through SOPs and in-house wikidocs.
- Skilled in data visualization and presentation, utilizing tools like ggplot2, Shiny, and Rmarkdown, to effectively communicate complex data to diverse audiences

Working knowledge in research and wet lab experience
- Expertise in immunology, oncology, and molecular biology with practical experience in public dataset analysis
- Developed and maintained specialized assay platforms including Drop-seq, Seq-well, and Seq-scope.
- Proficient in NGS library generation, particularly with single cell 10X genomics and RNA-seq.
- Experienced mentor to junior bioinformaticians, enhancing team skills and project outcomes. Hands-on laboratory skills in flow cytometry, qPCR, Western blot, and DNA/RNA techniques.

Project Management skills
- Autonomous work style, efficiently conducting research with minimal oversight.
- Guiding and mentoring interns in bioinformatics practices and project work.
- Consulting with collaborators to identify and apply novel bioinformatics analysis methods.
- Managing documentation and workflow sharing across collaborative platforms.
- Keeping meticulous records of both raw and processed data storage.

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

Publications (listed by recent date)

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)

Concurrent activation of growth factor and nutrient arms of mTORC1 induces oxidative liver injury. Cell Discovery volume 5, Article number: 60 (2019) Chun-Seok Cho, Allison Ho, Sim Namkoong, **Sung-Rye Park,** Shuangcheng Wu, Boyoung Kim, Amanda James, Bondong Gu, Ian A. Semple, Mohamed A. Tohamy, Sumeet Solanki, Uhn-Soo Cho, Joel K. Greenson, Yatrik Shah, Myungjin Kim, Jun Hee Lee. (https://doi.org/10.1152/ajpendo.00391.2020)

Transcriptome and epigenome analyses of vernalization in Arabidopsis thaliana. Yanpeng Xi, **Sung-Rye Park**, Dong-Hwan Kim, Eun-Deok Kim, Sibum Sung. (Plant Journal, 2020 May, https://doi.org/10.1111/tpj.14817)

Poster and Presentation

Multiomics analysis of impact of CD8+ and other cell populations in STING agonist treated ex vivo mesothelioma samples (AACR Annual Meeting 2024, San Diego, CA) Elena Ivanova, **Sung R. Park**, Ari P. Zlota, Nathaniel Spicer, Minh Ha, Sophie Kivlehan, Iliana Gjeci1, Simona Innocenti, Lauren Zasadil, Patrick Lizotte, Michael Y. Tolstorukov, Kai Ding, Adnan O. Abu-Yousif, Jeffrey Raizer, Vicky A. Appleman, Raphael Bueno, David A. Barbie, Cloud P. Paweletz.

Robust filtering of empty droplets in scRNA-seq experiments (poster). ASHG meeting 2019, Houston, Texas. Jingyue Xi, **Sung Rye Park**, Jun Hee Lee, Hyun Min Kang.

High fat diet alters zonation profile and fatty acid metabolism in hepatocytes at single cell resolution (presentation). Single-cell genomics in obesity and diabetes research club 2020 Feb, Ann Arbor, Michigan **Sung Rye Park.**