Sanghoon Lee

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Summary

During the post-doctoral training, I will grow my career prospects in cancer systems immunology, capabilities to become a competent post-doc, and fulfill the ultimate aim of the Hillman Post-doctoral Fellowship, which is the application of K99 grant and thereby transition to becoming an independent researcher.

Skills

- Integrative bioinformatics
- Machine Learning and Deep Learning
- Biostatistics
- WGS, WXS, and RNAseq analysis pipelines
- Solid skills in R, Perl, and Shell
- Solid skills in High Performance Computing
- Experienced with genomic data sources such as NCBI GEO, SRA, and dbGaP, GDC, ICGC, EGA, COSMIC, CCLE, GDSC, GTEx, Metabric.

Educational Background

08/2017 – 05/2021 Pittsburgh, PA	**Ph.D in Biomedical Informatics, University of Pittsburgh**
08/2015 – 07/2017 Pittsburgh, PA	**M.S. in Biomedical Informatics, University of Pittsburgh** Courses taken: Bioinformatics, Statistics in Bioinformatics, Probabilistic Methods in AI, Algorithm Implementation
08/2008 – 04/2012 Salt Lake City, UT	**M.S. in Biomedical Informatics, University of Utah** Courses taken: Statistics for Biomedical Informatics, Programming in Genomics – Unix/Linux, Shell Script and Perl, Database Fundamentals
03/2000 – 02/2002 Seoul, South Korea	**M.S. in Biochemistry and Molecular Biology, Seoul National University** Courses taken: Biochemistry, Genomics

Research Experience

05/2017 – Present Pittsburgh, PA **Graduate Student**	**Integral multi-omics modeling to predict breast cancer patient response to HER2-targeted therapy** - Research Mentor: Xiaosong Wang, M.D., Ph.D, University of Pittsburgh - As the main topic of my thesis project, I have performed novel integral genomic signature modeling (iGenSig) to predict patient response to HER2 targeted therapy based on multi-omics data from breast cancer clinical trials. I successfully applied the iGenSig model to three clinical trial datasets and showed that the model retains resilience against simulated errors in genomic features (Manuscript in preparation, first author).

Landscape analysis of adjacent gene rearrangements reveals BCL2L14-ETV6 gene fusions in more aggressive triple-negative breast cancer

- Research Mentor: Xiaosong Wang, M.D., Ph.D, University of Pittsburgh
- I performed landscape studies of adjacent gene rearrangements (AGRs) based on WGS data for 215 breast tumors. This revealed multiple cryptic AGRs, including BCL2L14-ETV6, that are specific to triple negative breast cancer (TNBC). BCL2L14-ETV6 is enriched in more aggressive TNBC tumors with necrotic and mesenchymal characteristics, and promote epithelial mesenchymal transition and paclitaxel resistance. (PNAS, first author).

Concept Signature Enrichment Analysis: a novel pathway enrichment analysis method for interpreting complex pathway alterations and for single cell sequencing datasets

- Research Mentor: Xiaosong Wang, M.D., Ph.D, University of Pittsburgh
- I participated in the development of a novel pathway enrichment analysis method called concept signature enrichment analysis (CSEA), examined its application to interpret complex pathway changes during change of cell states using single cell transcriptome sequencing (scRNAseq), and compared CSEA with other pathway enrichment methods under simulated noise in scRNAseq (Briefings in Bioinformatics, co-first author).

08/2015 – 04/2017
Pittsburgh, PA

Graduate Student

An algorithm for direct causal learning of influences on patient outcomes,
- Research Mentor: Xia Jiang, Ph.D, University of Pittsburgh
- Developed Direct Causal Learner (DCL) algorithm to learn the direct causal influences of a target such as a disease outcome.

Modeling miRNA-mRNA interactions that cause phenotypic abnormality in breast cancer patients
- Research Mentor: Xia Jiang, Ph.D, University of Pittsburgh
- Developed Multiple Beam Search (MBS) algorithm to learn miRNA and mRNA expression profile data using a Bayesian Network, and identified miRNA-mRNA interactions that probabilistically affect breast cancer pathogenesis.

10/2012 – 04/2015
Salt Lake City, UT

Lab Technician

Identification of master regulators that regulate White or Brown Adipose Tissue (WAT or BAT) differentiation
- Research Mentor: Claudio Villanueva, Ph.D, University of Utah
- Analyzed transcriptomic data of WAT and BAT and examined enriched gene signatures.
- Constructed WAT- and BAT-specific gene regulatory network and identified master regulators that control the enriched gene signatures.

11/2011 – 01/2013
Salt Lake City, UT

Research Volunteer

Robust meta-analysis shows that glioma transcriptional subtyping complements traditional approaches
- Research Mentor: Steve Piccolo, Ph.D and Kristina Allen-Brady, Ph.D, University of Utah
- Applied quality control, normalization, and batch adjustment algorithms to the transcriptomic data of 1,000 glioma samples.
- Applied machine learning algorithms to find stable transcriptional clusters that have a better correlation with survival time and chemo/radio therapy response.

01/2010 – 12/2011
VA Health Center
Salt Lake City, UT

**Research
Coordinator**

**Center for Health Information and Research (CHIR) Information Extraction
Methods and Ejection Fraction**
- Research Mentor: Qing Zheng, Ph.D, University of Utah
- Coordinated and monitored IRB and R&D approval among multiple research institutes.
- Applied natural language process (NLP) annotation tools to clinical free texts for mining clinical concepts.

01/2009 – 04/2012
Salt Lake City, UT

Graduate Student

Structuring Genomic variant data for the electronic health record (EHR)
- Research Mentor: Bruce Bray, M.D., Ph.D and Karen Eilbeck, Ph.D, University of Utah
- Developed an automatic software tool to annotate genomic variant data in text and designed Genome Variation Format (GVF) based one XML file format.
- Standardized genomic variant data using Sequence Ontology (SO) and integrated them to HL7 CDA Genetic Test Report Template.

08/2007 – 05/2008
Seoul, South Korea

Research Assistant

**Discover prostate cancer mechanism by analyzing transcriptomic data of
monoterpene-treated prostate cancer cells**
- Research Mentor: Ju-Hong Jeon, Ph.D, Seoul National University
- Applied reverse engineering to transcriptomic data to generate prostate cancer-specific global transcriptional network using ARACNe (Algorithm for the Reconstruction of Accurate Cellular Networks) algorithm.
- Performed Master Regulator Analysis (MRA) to identify master regulators of signature genes

Teaching Experience

03/2020
Pittsburgh, PA

Lecture for graduate students in the course, Foundations of Biomedical Informatics
Biomedical Informatics, University of Pittsburgh
- Main Instructor: Madhavi Ganapathiraju, Ph.D
- Lectured on Genomic expression data analysis.

01/2019 – 04/2019
Pittsburgh, PA

Teaching Assistant, Translational Informatics
Biomedical Informatics, University of Pittsburgh
- Main Instructor: Madhavi Ganapathiraju, Ph.D
- Lectured RNA-seq data analysis and R coding.
- Provided hands-on practice for Gene Set Enrichment Analysis (GSEA).

08/2017 – 12/2017
Pittsburgh, PA

Teaching Assistant, Foundations of Bioinformatics
Biomedical Informatics, University of Pittsburgh
- Main Instructor: Xinghua Lu, M.D., Ph.D
- Lectured microarray data analysis and machine learning application.
- Created and graded assignments, mid-term, and final exams

Leadership & Mentoring

07/2020 – 08/2020 Pittsburgh, PA	**Mentor for a high school student, Oscar Heller** Biomedical Informatics, University of Pittsburgh • Internship program: Computer Science, Biology, and Biomedical Informatics Innovation (CoSBBI) • Project: Detecting somatic mutations in Her2-positive breast cancer patients to predict drug response
07/2019 – 08/2019 Pittsburgh, PA	**Mentor for a graduate student, Tanika Simoneaux** Biomedical Informatics, University of Pittsburgh • Internship program: Internship in Biomedical Research, Informatics, and Computer Science (iBRIC) • Project: Landscape analysis of intergenic gene rearrangements
07/2018 – 08/2018 Pittsburgh, PA	**Mentor for an undergraduate student, Sebastian Cruz** Biomedical Informatics, University of Pittsburgh • Internship program: Computer Science, Biology, and Biomedical Informatics Innovation (CoSBBI) • Project: Detecting cancer-causal structural aberrations affecting aromatase inhibitor-resistance in luminal breast cancer patients

Honors & Awards

08/2020 Pittsburgh, PA	**The 2nd Best publication of the year in the Department of Biomedical Informatics**, University of Pittsburgh • 1st author publication in PNAS
08/2018 Pittsburgh, PA	**The 2nd Best publication of the year in the department of Biomedical Informatics**, University of Pittsburgh • 1st author publication in PLoS ONE

Reviewer of Journal

• Student reviewer: AMIA 2020 and 2021 Annual Symposium

Peer Reviewed Publications, First Author

In reverse chronological orders. * co-first author

8. **Sanghoon Lee**, Jung Nyeo Chun, Hae-Jeung Lee, Hyun Ho Park, Insuk So, Ju-Hong Jeon and Eun-Jung Park. Transcriptome Analysis of the Anti-TGFβ Effect of Schisandra chinensis Fruit Extract and Schisandrin B in A7r5 Vascular Smooth Muscle. Life, 2021 Feb.

7. **Sanghoon Lee**, Yiheng Hu, Suet Kee Loo, Ying Tan, Rohit Bhargava, Michael T. Lewis, and Xiao-Song Wang. Landscape analysis of adjacent gene rearrangements reveals BCL2L14-ETV6 gene fusions in more aggressive

triple-negative breast cancer. **PNAS**, 2020; 117(18):9912-9921

6. Xu Chi, Maureen A Sartor, **Sanghoon Lee*,** Meenakshi Anurag, Snehal Patil, Pelle Hall, Matthew Wexler, and Xiao-Song Wang. Universal Concept Signature Analysis: Genome-Wide Quantification of New Biological and Pathological Functions of Genes and Pathways. **Briefings In Bioinformatics**, 2020; 25;21(5):1717-1732

5. **Sanghoon Lee*** and Xia Jiang.Modeling miRNA-mRNA interactions that cause phenotypic abnormality in breast cancer patients. **PLoS ONE**, 2017;12(8)

4. **Sanghoon Lee*,** Y. R. Park, Su-HWa Kim, Eun-Jung Park, Min Ji Kang, Insuk So, Jung Nyeo Chun and Ju-Hong Jeon. Geraniol suppresses prostate cancer growth through down-regulation of E2F8. **Cancer medicine**, 2016; 5(10), 2899-2908.

3. **Sanghoon Lee*,** Stephen R Piccolo, and Kristina Allen-Brady. Robust meta-analysis shows that glioma transcriptional subtyping complements traditional approaches. **Cellular Oncology**, 2014; 37(5), 317-329.

2. **Sanghoon Lee,** Jung Nyeo Chun, Su-Hwa Kim, Insuk So, and Ju-HongJeon. Icilin inhibits E2F1-mediated cell cycle regulatory programs in prostate cancer. **Biochemical and Biophysical Research Communications**, 2013; 441(4), 1005-1010.

1. Su-Hwa Kim*, **Sanghoon Lee*,** Stephen R.Piccolo, Kristina Allen-Bradye, Eun-Jung Park, Jung Nyeo Chun, Tae Woo Kim, Nam-Hyuk Cho, In-Gyu Kim, Insuk So, and Ju-Hong Jeon. Menthol induces cell-cycle arrest in PC-3 cells by down-regulating G2/M genes, including polo-like kinase 1. **Biochemical and Biophysical Research Communications**, 2012; 422(3), 436-441.

Peer Reviewed Publications, Co-author

16. Xian Wang, Jamunarani Veeraraghavan, Chia-Chia Liu, Xixi Cao, Lanfang Qin, Jin-Ah Kim, Ying Tan, Suet Kee Loo, Yiheng Hu, Ling Lin, **Sanghoon Lee**, Martin J. Shea, Tamika Mitchell, Shunqiang Li, Matthew J. Ellis, Susan G. Hilsenbeck, Rachel Schiff and Xiao-Song Wang. Therapeutic targeting of nemo-like kinase in primary and acquired endocrine-resistant breast cancer. **Clinical Cancer Research**, 2021, Feb.

15. Chia-Chia Liu, Jamunarani Veeraraghavan, Ying Tan, Jin-Ah Kim, Xian Wang, Suet Kee Loo, **Sanghoon Lee,** Yiheng Hu and Xiao-Song Wang. A novel neoplastic fusion transcript, RAD51AP1-DYRK4, confers sensitivity to the MEK inhibitor trametinib in aggressive breast cancers. **Clinical Cancer Research**, 2021, Feb.

14. Vanja Panic, Stephanie Pearson, James Banks, Trevor S Tippetts, Jesse N Velasco-Silva, **Sanghoon Lee,** Judith Simcox, Gisela Geoghegan, Claire L Bensard, Tyler van Ry, Will L Holland, Scott A Summers, James Cox, Gregory S Ducker, Jared Rutter, Claudio J Villanueva. Mitochondrial pyruvate carrier is required for optimal brown fat thermogenesis. **eLife**, 2020; 9, e52558

13. Li Li, Ling Lin, Jamunarani Veeraraghavan, Yiheng Hu, Xian Wang, **Sanghoon Lee**, Ying Tan, Rachel Schiff, and Xiao-Song Wang. Therapeutic role of recurrent ESR1CCDC170 gene fusions in breast cancer endocrine resistance. **Breast Cancer Research**, 2020; 22 (1), 1-15

12. Soonbum Park, Jin-Muk Lim, Jung Nyeo Chun, **Sanghoon Lee**, Tae Min Kim, Dong-Wan Kim, Sang-Yeob Kim, Dong-Jun Bae, Sang-Mun Bae, Insuk So, Hong-Gee Kim, Ji-Yeob Choi, Ju-Hong Jeon. Altered expression of fucosylation pathway genes is associated with poor prognosis and tumor metastasis in non-small cell lung cancer. **International Journal of Oncology**, 2020; 56(2), 559-567.

11. Stephanie Pearson, Anne Loft, Prashant Rajbhandari, Judith Simcox, **Sanghoon Lee**, Peter Tontonoz, Susanne Mandrup and Claudio J. Villanueva. Loss of TLE3 Promotes Mitochondrial Program in Beige Adipocytes and Improves Glucose Metabolism.
Gene & Development, 2019; 33(13-14):747-762.

10. Jung Nyeo Chun, Soonbum Park, **Sanghoon Lee**, Jae-Kyung Kim, Eun-Jung Park, MinJi Kang, Hye Kyung Kim, Jong Kwan Park, Insuk So, and Ju-Hong Jeon. Schisandrol B and schisandrin B inhibit TGFβ1-mediated NF-κB activation via a Smad-independent mechanism. **Oncotarget**, 2018; 9(3), 3121-3130

9. Judith Simcox, Gisela Geoghegan, John Alan Maschek, Claire L.Bensard, Marzia Pasquali, Ren Miao, **Sanghoon Lee**, Lei Jiang, Ian Huck, Erin E.Kershaw, Anthony J.Donato, Udayan Apte, Nicola Longo, Jared Rutter, Renate Schreiber, Rudolf Zechner, JamesCox, and Claudio J.Villanueva. Global Analysis of Plasma Lipids Identifies Liver Derived Acylcarnitines as a Fuel Source for Brown Fat Thermogenesis. **Cell Metabolism**, 2017; 26, 509–522.

8. Chandra Rathnam, **Sanghoon Lee**, and Xia Jiang. An algorithm for direct causal learning of influences on patient outcomes. **Artificial Intelligence in Medicine**, 2017; 75, 1-15.

7. Soonbum Park, **Sanghoon Lee**, Eun-Jung Park, MinJi Kang, Insuk So, Ju-Hong Jeon, Jung Nyeo Chun TGFβ1 induces stress fiber formation through upregulation of TRPC6 in vascular smooth muscle cells. **Biochemical and Biophysical Research Communications**, 2017; 483(1), 129–134

6. Wonjun Yang, Aerin Yoon, **Sanghoon Lee**, Jungwon Han, and Junho Chung. Next-generation sequencing enables the discovery of more diverse positive clones from a phage-displayed antibody library. **Experimental & Molecular Medicine**, 2017; 49, e308.

5. Sung Chul Kam, **Sanghoon Lee**, Ju Hong Jeon, Insuk So, Mee Ree Chae, Jong Kwan Park, and Sung Won Lee. Gene expression profile comparison in the penile tissue of diabetes and cavernous nerve injury-induced erectile dysfunction rat model. **Investigative and Clinical Urology**, 2016; 57(4), 286-297.

4. Byung Joo Kim, Sung-Young Kim, **Sanghoon Lee**, Ju-Hong Jeon, Hirofumi Matsui, Young Kyu Kwon, Seon Jeong Kim, and Insuk So. The role of transient receptor potential channel blockers in human gastric cancer cell viability. **Canadian Journal of Physiology and Pharmacology**, 2012; 90(2), 175-186.

3. Su-Hwa Kim, Eun-Jung Park, Chae Ryun Lee, Jung Nyeo Chun, Nam-Hyuk Cho, In-Gyu Kim, **Sanghoon Lee,** Tae Woo Kim, Hyun Ho Park, Insuk So, and Ju-Hong Jeon. Geraniol induces cooperative interaction of apoptosis and autophagy to elicit cell death in PC-3 prostate cancer cells. **Int J Oncol**, 2012; 40(5), 1683-1690

2. Stéphane M. Meystre, **Sanghoon Lee**, and Raphaël Chevrier. Common data model for natural language processing based on two existing standard information models: CDA+GrAF. **Journal of Biomedical Informatics**, 2011; 45(4), 703-710.

1. Su-Hwa Kim, Hyun Cheol Bae, Eun-Jung Park, Chae Ryun Lee, Byung-Joo Kim, **Sanghoon Lee,** Hyun Ho Park, Sung-Joon Kim, Insuk So, Tae Woo Kim, and Ju-Hong Jeon. Geraniol inhibits prostate cancer growth by targeting cell cycle and apoptosis pathways. **Biochemical and Biophysical Research Communications**, 2011; 407(1), 129-134.

Manuscripts under Review or Preparation

1. Xiaosong Wang, **Sanghoon Lee**, Gong Tang, Yue Wang. An integral genomic signature approach for tailored cancer targeted therapy using genome-wide sequencing data. Under Revision in **Nature Communications.**

2. **Sanghoon Lee,** Yihung Hu, Xiaosong Wang. Integral genomic signature modeling to predict the response to HER2 targeted therapy in HER2-positive patients. In preparation.

3. Yumin Wang, Boya Gao, Luyuan Zhang, Siang Boon Koh, Haibo Yang, Xiaolan Zhu, **Sanghoon Lee,** Jian Ouyang, Lee Zou, Leif W. Ellisen, Xiao-Song Wang, Li Lan. Overexpression of the Meiotic Protein SYCP2 in Breast Cancer Promotes Homologous Recombination and Endows Broad Resistance to DNA Repair-Targeting Drugs. In preparation.

4. **Sanghoon Lee**, Young Sik Kim, Soonbum Park, Eun-Jung Park, Da Young Lee, Hyun-Ho Park, Insuk So, Jung Nyeo Chun, and Ju-Hong Jeon. Cyclosporin A suppresses E2F8 expression in prostate cancer in a MELK-dependent manner. Under Review in **International Journal of Oncology**.