**CURRICULUM VITAE**

**University of Pittsburgh**

**School of Medicine**

**BIOGRAPHICAL**

|  |  |
| --- | --- |
| Name: Hatice Ülkü Osmanbeyoğlu | Business Address: 5051 Centre Ave, Pittsburgh, PA 15213 |
| Email: osmanbeyogluhu@pitt.edu | Business Phone: 412-623-7789 |
| Website: https://www.osmanbeyoglulab.com/ |  |

**EDUCATION and TRAINING**

**UNDERGRADUATE**

|  |  |  |  |
| --- | --- | --- | --- |
| 2002-2004 | Northeastern University, Boston, MA | BS2004  | Computer Engineering |
| 2000-2002 | Bogazici University, Istanbul,Turkey |  | Chemical Engineering |

**GRADUATE**

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| --- | --- | --- | --- |
| 2009-2012 | University of Pittsburgh School of Medicine, Pittsburgh, PA | PhD2012 | Biomedical Informatics |
| 2006-2009 | University of Pittsburgh,Pittsburgh, PA | MS2009 | Bioengineering |
| 2005-2006 | Carnegie Mellon University,Pittsburgh, PA | MS2006 | Electrical and Computer Engineering |

**POSTGRADUATE**

|  |  |  |  |
| --- | --- | --- | --- |
| 2013-2018 | Memorial Sloan Kettering Cancer Center, New York, NY | Postdoctoral Fellow | Advisor: Christina Leslie |
| 2015 | Memorial Sloan Kettering Cancer Center, New York, NY | Course attendee | Optimizing the Practice of Mentoring: how to be an effective research mentor |
| 2016 | Memorial Sloan Kettering Cancer Center, New York, NY | Course attendee | Leadership for Scientists |
| Aug. 2017 | The Jackson Laboratory, Bar Harbor ME | Course attendee | 26th Annual Short Course on Experimental Models of Human Cancer |
| Nov. 2018 | Cold Spring Harbor Laboratory Cold Spring Harbor, NY  | Course attendee | Scientific Writing Retreat |
| 2020 | University of Pittsburgh,Pittsburgh, PA | Course attendee | Leadership Academy for Early Career Faculty |
| 2021 | Memorial Sloan Kettering Cancer Center, New York, NY | Course attendee |  MSK Immuno-oncology for the Translational Researcher Short Course (ITRSC) |
| 2022 | University of Utah,Salt Lake City, UT | Course attendee | Cancer-Related Health Disparities Research, Mentoring, and Leadership |
| 2023 | The University of Texas MD Anderson Cancer Center, Houston, TX | Workshopattendee | Virtual Scientific Communication Advances Research Excellence (SCOARE) Workshop |

**APPOINTMENTS and POSITIONS**

|  |  |  |
| --- | --- | --- |
| 2018 – preset | University of Pittsburgh & UPMC Hillman Cancer Center Department of Biomedical Informatics | Assistant Professor |
| 2019 – present | University of Pittsburgh & Department of Bioengineering | Assistant Professor(secondary) |
| 2020 – present | University of Pittsburgh & Department of Biostatistics | Assistant Professor(secondary) |
| 2021 – present | University of Pittsburgh & Intelligent Systems Program |  Assistant Professor(secondary) |

**MEMBERSHIP in PROFESSIONAL and SCIENTIFIC SOCIETIES**

2012 – present Member, International Society for Computational Biology

2017 – present Member, American Association for Cancer Research

**HONORS**

|  |  |
| --- | --- |
| Dean’s List, Northeastern University | 2002-2004 |
| Outstanding Junior Award, Northeastern University | 2003 |
| Sears B. Condit Award, Northeastern University |  2004  |
| Winner, Northeastern University Capstone Design Group Competition | 2004 |
| Doctoral Comprehensive Exam passed with High Honors | 2011 |
| Finalist, Best Trainee Paper Award, University of Pittsburgh | 2012 |
| NSF Travel Award to the Research in Computational Molecular Biology Conference | 2012 |
| Travel Award to the Machine Learning Summer School in Santa Cruz, CA | 2012 |
| Travel Award to the Workshop for Women in Machine Learning, Lake Tahoe, NV | 2012 |
| Finalist, Best Performer in Phase 2 of DREAM7 Challenge, Breast Cancer Prognosis | 2012 |
| Intelligent Systems for Molecular Biology (ISMB) Conference Travel Fellowship | 2014 |
| NIH/NCI K99/R00 Pathway to Independence Award | 2016 |
| Memorial Sloan Kettering Postdoctoral Research Award | 2017 |
| NCI Scholarship for Experimental Models of Human Cancer Course at The Jackson Laboratory | 2017 |
| EMBL Corporate Partnership Fellowship for Cancer Genomics conference  | 2017 |
| Hillman Early-Career Fellow for Innovation Cancer ResearchNCI Early Investigator Advancement Program (EIAP) Scholar  | 20192022 |

**PUBLICATIONS**

1. ORIGINAL PEER REVIEWED ARTICLES:

1. **Osmanbeyoglu HU**, Hur TB, Kim HK. (2009) Thin alumina nanoporous membranes for similar size biomolecule separation. Journal of Membrane Science, 343, 1-6.
	* 5th top cited paper, 136 citations
2. **Osmanbeyoglu HU**, Wehner JA, Carbonell JG, Ganapathiraju MK. Active machine learning for transmembrane helix prediction. BMC Bioinformatics. 2010;11 Suppl 1:S58. Epub 2010/03/05. doi: 10.1186/1471-2105-11-S1-S58. PubMed PMID: 20122233; PMCID: PMC3009531.
3. **Osmanbeyoglu HU**, Ganapathiraju MK. N-gram analysis of 970 microbial organisms reveals presence of biological language models. BMC Bioinformatics. 2011;12:12. Epub 2011/01/12. doi: 10.1186/1471-2105-12-12. PubMed PMID: 21219653; PMCID: PMC3027111.
4. Kohle-Ersher A, Chatterjee P, **Osmanbeyoglu HU**, Hochheiser H, Bartos C. Evaluating the barriers to point-of-care documentation for nursing staff. Comput Inform Nurs. 2012;30(3):126-33. Epub 2011/10/26. doi: 10.1097/NCN.0b013e3182343f14. PubMed PMID: 22024972.
5. **Osmanbeyoglu HU**, Hartmaier RJ, Oesterreich S, Lu X. Improving ChIP-seq peak-calling for functional co-regulator binding by integrating multiple sources of biological information. BMC Genomics. 2012;13 Suppl 1:S1. Epub 2012/03/06. doi: 10.1186/1471-2164-13-S1-S1. PubMed PMID: 22369349; PMCID: PMC3439677.
6. **Osmanbeyoglu HU**, Lu KN, Oesterreich S, Day RS, Benos PV, Coronnello C, Lu X. Estrogen represses gene expression through reconfiguring chromatin structures. Nucleic Acids Res. 2013;41(17):8061-71. Epub 2013/07/04. doi: 10.1093/nar/gkt586. PubMed PMID: 23821662; PMCID: PMC3783169.
7. **Osmanbeyoglu HU**, Pelossof R, Bromberg JF, Leslie CS. Linking signaling pathways to transcriptional programs in breast cancer. Genome Res. 2014;24(11):1869-80. Epub 2014/09/04. doi: 10.1101/gr.173039.114. PubMed PMID: 25183703; PMCID: PMC4216927.
8. Feng Y, van der Veeken J, Shugay M, Putintseva EV, **Osmanbeyoglu HU**, Dikiy S, Hoyos BE, Moltedo B, Hemmers S, Treuting P, Leslie CS, Chudakov DM, Rudensky AY. A mechanism for expansion of regulatory T-cell repertoire and its role in self-tolerance. Nature. 2015;528(7580):132-6. Epub 2015/11/26. doi: 10.1038/nature16141. PubMed PMID: 26605529; PMCID: PMC4862833.
	* 4th top cited paper, 161 citations
9. Watters RJ, Hartmaier RJ, **Osmanbeyoglu HU**, Gillihan RM, Rae JM, Liao L, Chen K, Li W, Lu X, Oesterreich S. Steroid receptor coactivator-1 can regulate osteoblastogenesis independently of estrogen. Mol Cell Endocrinol. 2017;448:21-7. Epub 2017/03/14. doi: 10.1016/j.mce.2017.03.005. PubMed PMID: 28286232.
10. Nargund AM, Pham CG, Dong Y, Wang PI, **Osmanbeyoglu HU**, Xie Y, Aras O, Han S, Oyama T, Takeda S, Ray CE, Dong Z, Berge M, Hakimi AA, Monetta S, Lekaye CL, Koutcher JA, Leslie CS, Creighton CJ, Weinhold N, Lee W, Tickoo SK, Wang Z, Cheng EH, Hsieh JJ (2017) The SWI/SNF Protein PBMR1 Restrains VHL Loss-Driven Clear Cell Kidney Cancer, Cell Reports18, 2893-2906.
	* 3rd top cited paper, 169 citations
11. Toska E, **Osmanbeyoglu HU**, Castel P, Chan C, Hendrickson RC, Elkabets M, Dickler MN, Scaltriti M, Leslie CS, Armstrong SA, Baselga J. PI3K pathway regulates ER-dependent transcription in breast cancer through the epigenetic regulator KMT2D. Science. 2017;355(6331):1324-30. Epub 2017/03/25. doi: 10.1126/science.aah6893. PubMed PMID: 28336670; PMCID: PMC5485411.
	* 2nd top cited paper, 238 citations
12. Luo CT, **Osmanbeyoglu HU**, Do MH, Bivona MR, Toure A, Kang D, Xie Y, Leslie CS, Li MO. Ets transcription factor GABP controls T cell homeostasis and immunity. Nat Commun. 2017;8(1):1062. Epub 2017/10/21. doi: 10.1038/s41467-017-01020-6. PubMed PMID: 29051483; PMCID: PMC5648787.
13. **Osmanbeyoglu HU**, Toska E, Chan C, Baselga J, Leslie CS. Pancancer modelling predicts the context-specific impact of somatic mutations on transcriptional programs. Nat Commun. 2017;8:14249. Epub 2017/02/01. doi: 10.1038/ncomms14249. PubMed PMID: 28139702; PMCID: PMC5290314.
14. Korkut A, Zaidi S, Kanchi RS, Rao S, Gough NR, Schultz A, Li X, Lorenzi PL, Berger AC, Robertson G, Kwong LN, Datto M, Roszik J, Ling S, Ravikumar V, Manyam G, Rao A, Shelley S, Liu Y, Ju Z, Hansel D, de Velasco G, Pennathur A, Andersen JB, O'Rourke CJ, Ohshiro K, Jogunoori W, Nguyen BN, Li S, **Osmanbeyoglu HU**, Ajani JA, Mani SA, Houseman A, Wiznerowicz M, Chen J, Gu S, Ma W, Zhang J, Tong P, Cherniack AD, Deng C, Resar L, Cancer Genome Atlas Research N, Weinstein JN, Mishra L, Akbani R. A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-beta Superfamily. Cell Syst. 2018;7(4):422-37 e7. Epub 2018/10/01. doi: 10.1016/j.cels.2018.08.010. PubMed PMID: 30268436; PMCID: PMC6370347.
15. Hmeljak J, Sanchez-Vega F, Hoadley KA, Shih J, Stewart C, Heiman D, Tarpey P, Danilova L, Drill E, Gibb EA, Bowlby R, Kanchi R, **Osmanbeyoglu HU**, Sekido Y, Takeshita J, Newton Y, Graim K, Gupta M, Gay CM, Diao L, Gibbs DL, Thorsson V, Iype L, Kantheti H, Severson DT, Ravegnini G, Desmeules P, Jungbluth AA, Travis WD, Dacic S, Chirieac LR, Galateau-Salle F, Fujimoto J, Husain AN, Silveira HC, Rusch VW, Rintoul RC, Pass H, Kindler H, Zauderer MG, Kwiatkowski DJ, Bueno R, Tsao AS, Creaney J, Lichtenberg T, Leraas K, Bowen J, Network TR, Felau I, Zenklusen JC, Akbani R, Cherniack AD, Byers LA, Noble MS, Fletcher JA, Robertson AG, Shen R, Aburatani H, Robinson BW, Campbell P, Ladanyi M. Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discov. 2018;8(12):1548-65. Epub 2018/10/17. doi: 10.1158/2159-8290.CD-18-0804. PubMed PMID: 30322867; PMCID: PMC6310008.
	* Top cited paper, 457 citations
16. Moiseeva TN, Qian C, Sugitani N, **Osmanbeyoglu HU**, Bakkenist CJ. WEE1 kinase inhibitor AZD1775 induces CDK1 kinase-dependent origin firing in unperturbed G1- and S-phase cells. Proc Natl Acad Sci U S A. 2019;116(48):23891-3. Epub 2019/11/13. doi: 10.1073/pnas.1915108116. PubMed PMID: 31712441.
17. **Osmanbeyoglu HU**#, Shimizu F, Rynne-Vidal A, Alonso-Curbelo D, Chen HA, Wen HY, Yeung TL, Jelinic P, Razavi P, Lowe SW, Mok SC, Chiosis G, Levine DA, Leslie CS#. Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancers. Nat Commun. 2019;10(1):4369. Epub 2019/09/27. doi: 10.1038/s41467-019-12291-6. PubMed PMID: 31554806; PMCID: PMC6761109. (**#=co-corresponding authors)**
18. Moiseeva TN, Yin Y, Calderon MJ, Qian C, Schamus-Haynes S, Sugitani N, **Osmanbeyoglu HU**, Rothenberg E, Watkins SC, Bakkenist CJ. An ATR and CHK1 kinase signaling mechanism that limits origin firing during unperturbed DNA replication. Proc Natl Acad Sci U S A. 2019;116(27):13374-83. Epub 2019/06/19. doi: 10.1073/pnas.1903418116. PubMed PMID: 31209037; PMCID: PMC6613105.
19. Tanaka K, Yu HA, Yang S, Han S, Selcuklu SD, Kim K, Ramani S, Ganesan YT, Moyer A, Sinha S, Xie Y, Ishizawa K, **Osmanbeyoglu HU**, Lyu Y, Roper N, Guha U, Rudin CM, Kris MG, Hsieh JJ, Cheng EH. Targeting Aurora B kinase prevents and overcomes resistance to EGFR inhibitors in lung cancer by enhancing BIM- and PUMA-mediated apoptosis. Cancer Cell. 2021;39(9):1245-61 e6. Epub 2021/08/14. doi: 10.1016/j.ccell.2021.07.006. PubMed PMID: 34388376; PMCID: PMC8440494.
20. Vyas A, Harbison RA, Faden DL, Kubik M, Palmer D, Zhang Q, **Osmanbeyoglu HU**, Kiselyov K, Mendez E, Duvvuri U. Recurrent Human Papillomavirus-Related Head and Neck Cancer Undergoes Metabolic Reprogramming and Is Driven by Oxidative Phosphorylation. Clin Cancer Res. 2021. Epub 2021/08/20. doi: 10.1158/1078-0432.CCR-20-4789. PubMed PMID: 34407971.
21. Ma X, Somasundaram A, Qi Z, Hartman DJ, Singh H**, Osmanbeyoglu HU**. SPaRTAN, a computational framework for linking cell-surface receptors to transcriptional regulators. Nucleic Acids Res. 2021;49(17):9633-47. Epub 2021/09/10. doi: 10.1093/nar/gkab745. PubMed PMID: 34500467; PMCID: PMC8464045.
22. Cascio S, Chandler C, Zhang L, Sinno S, Gao B, Onkar S, Bruno TC, Vignali DAA, Mahdi H, **Osmanbeyoglu HU**, Vlad AM, Coffman LG, Buckanovich RJ. Cancer-associated MSC drive tumor immune exclusion and resistance to immunotherapy, which can be overcome by Hedgehog inhibition. Sci Adv.2021;7(46):eabi5790. Epub 2021/11/13. doi: 10.1126/sciadv.abi5790. PubMed PMID: 34767446; PMCID: PMC8589308.
23. Lee S, **Osmanbeyoglu HU**. Chromatin accessibility landscape and active transcription factors in primary human invasive lobular and ductal breast carcinomas. Breast Cancer Res. 2022;24(1):54. Epub 2022/07/30. doi: 10.1186/s13058-022-01550-y. PubMed PMID: 35906698; PMCID: PMC9338552.
24. Sugitani N, Vendetti FP, Cipriano AJ, Pandya P, Deppas JJ, Moiseeva TN, Schamus-Haynes S, Wang Y, Palmer D, **Osmanbeyoglu HU**, Bostwick A, Snyder NW, Gong YN, Aird KM, Delgoffe GM, Beumer JH, Bakkenist CJ. Thymidine rescues ATR kinase inhibitor-induced deoxyuridine contamination in genomic DNA, cell death, and interferon-alpha/beta expression. Cell Rep. 2022;40(12):111371. Epub 2022/09/22. doi: 10.1016/j.celrep.2022.111371. PubMed PMID: 36130512; PMCID: PMC9646445.
25. Tao Y\*, Ma X\*, Palmer D, Schwartz R, Lu X, **Osmanbeyoglu HU**. Interpretable deep learning for chromatin-informed inference of transcriptional programs driven by somatic alterations across cancers. Nucleic Acids Res. 2022. Epub 2022/10/17. doi: 10.1093/nar/gkac881. PubMed PMID: 36243974.
26. **Osmanbeyoglu HU#**, Palmer D, Sagan A, Sementino E, Becich MJ, Testa JR. Isolated BAP1 Genomic Alteration in Malignant Pleural Mesothelioma Predicts Distinct Immunogenicity with Implications for Immunotherapeutic Response. Cancers (Basel). 2022;14. (#corresponding author)
27. Onkar S, Cui J, Zou J, Cardello C, Cillo AR, Uddin MR, Sagan A, Joy M, **Osmanbeyoglu HU**, Pogue-Geile KL, McAuliffe PF, Lucas PC, Tseng GC, Lee AV, Bruno TC, Oesterreich S, Vignali DAA. Immune landscape in invasive ductal and lobular breast cancer reveals a divergent macrophage-driven microenvironment. Nature Cancer. 2023. doi: 10.1038/s43018-023-00527-w.
28. Ramjattun K\*, Ma X\*, Singh H, Gao SJ, **Osmanbeyoglu HU**. COVID-19db linkage maps of cell surface proteins and transcription factors in immune cells. J Med Virol. 2023;95(6):e28887. Epub 2023/06/21. doi: 10.1002/jmv.28887. PubMed PMID: 37341527.
29. Gau D, Daoud A, Allen A, Joy M, Sagan A, Lee S, Lucas PC, Duensing S, Boone D, **Osmanbeyoglu HU**, Roy P. Vascular endothelial profilin-1 drives a protumorigenic tumor microenvironment and tumor progression in renal cancer. J Biol Chem. 2023;299(8):105044. Epub 2023/07/15. doi: 10.1016/j.jbc.2023.105044. PubMed PMID: 37451478.
30. Bibee KP, Kulkarni L, Lee s, Ho J, **Osmanbeyoglu HU**, Ferri RL, Zandberg DP. Genomic and transcriptomic analysis of cutaneous squamous cell carcinoma arising in immunocompetent and immunosuppressed patients. Oral Oncology, Volume 148,2024,106582, ISSN 1368-8375, <https://doi.org/10.1016/j.oraloncology.2023.106582>.
31. Zhang L\*, Cascio S\*, Mellors JW, Buckanovich RJ, **Osmanbeyoglu HU**. Single-cell analysis reveals the stromal dynamics and tumor-specific characteristics in the microenvironment of ovarian cancer. Communications Biology (Accepted)

**Peer Reviewed Conference Proceedings:**

1. **Osmanbeyoglu HU**, Ganapathiraju MK. Rapid deployment of viral-human interactome prediction for new viruses. Proc of the American Medical Informatics Association Summit onTranslational Bioinformatics*.*  March 7-11, 2011, San Francisco, CA, USA

**UNDER REVIEW**

1. Ma X, Lembersky D, Kim ES, Bruno TC, Testa JR, **Osmanbeyoglu HU**. Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment. bioRxiv 2023.09.06.556559; doi: https://doi.org/10.1101/2023.09.06.556559

2. Sinno S, Bai S, Gomes-Jourdan N, Coronnello C, Zhang L, **Osmanbeyoglu HU**, Haider M, Buckanovich RJ, Cascio S. Egfl6 promotes ovarian cancer progression by enhancing the immunosuppressive functions of tumor-associated myeloid cells

3. Park R, Pathak H, Al-Bzour A, Dai J, Phadnis M, Al-Rajabi R, Kasi A, Baranda J, Sun W, Williamson S, Chiu YC, **Osmanbeyoglu HU**, Madan R, Abushukair H, Mulvaney K, Godwin A , Saeed A. Clinical and Biomarker Results from A Phase II Trial of Combined Cabozantinib and Durvalumab in Patients with Chemotherapy-refractory Colorectal Cancer (CRC): CAMILLA CRC Cohort

2. OTHER PEER REVIEWED PUBLICATIONS

1. Nargund AM, **Osmanbeyoglu HU**, Cheng EH, Hsieh JJ. SWI/SNF tumor suppressor gene PBRM1/BAF180 in human clear cell kidney cancer. Mol Cell Oncol. 2017;4(4):e1342747. Epub 2017/09/05. doi: 10.1080/23723556.2017.1342747. PubMed PMID: 28868352; PMCID: PMC5540208.

3. OTHER NON-PEER REVIEWED PUBLICATIONS

Chalancon G, Kosloff M, **Osmanbeyoglu HU**, Saraswathi S. PLoS Computational Biology conference postcards from ISMB 2010. **PLoS Comput Biol**. 2010;6(11):e1002000. Epub 2010/11/19. doi: 10.1371/journal.pcbi.1002000. PubMed PMID: 21085638; PMCID: PMC2978693.

4. BOOKS, BOOK CHAPTERS AND MONOGRAPHS

1. Iyer A, **Osmanbeyoglu HU**, Leslie CS. Computational methods to dissect gene regulatory networks in cancer. Current Opinion in Systems Biology2017*,* **2**:115-122*.*
2. Sagan A, Ma X, Ramjattun K, **Osmanbeyoglu HU**. Linking Expression of Cell-Surface Receptors with Transcription Factors by Computational Analysis of Paired Single-Cell Proteomes and Transcriptomes. Methods Mol Biol 2023, 2660:149-169.

**PROFESSIONAL ACTIVITIES**

**TEACHING**

**Graduate Student Teaching:**

2007: Teaching Assistant, BIOENG2520 Molecular Biology and Biophysics 1,

Department of Bioengineering, University of Pittsburgh (one semester)

2011: Teaching Assistant, BIOINF 2051 Foundations of Bioinformatics, Department of Biomedical

 Informatics, University of Pittsburgh (one semester)

2015: Teaching Assistant, Introduction to R and Bioconductor,

Memorial Sloan Kettering Cancer Center (one semester)

2016-2017: Co-instructor, Quantitative and Computational Biology,

Memorial Sloan Kettering Cancer Center (one semester)

2019: Guest lecturer, Institute of Systems Biology (ISB) Summer Course, Seattle, WA, USA. (One session)

2021: Guest lecturer, COBB 2110. Foundations of Computational Biology. Department of Biomedical Informatics, University of Pittsburgh (One session)

2021: Guest lecturer, BIOINF 2134. Publication and Presentation in Biomedical Informatics. Department of Biomedical Informatics, University of Pittsburgh (One session)

2022: Guest lecturer, BIOINF 2134. Publication and Presentation in Biomedical Informatics. Department of Biomedical Informatics, University of Pittsburgh (One session)

2023: Guest lecturer, BIOINF 2134. Publication and Presentation in Biomedical Informatics. Department of Biomedical Informatics, University of Pittsburgh (One session)

**Undergraduate Student Teaching:**

2008: Teaching Assistant, BIOENG1330 Biomedical Imaging, Department of Bioengineering,

University of Pittsburgh (one semester)

2021: Guest lecturer, Bioinformatics, guest lecture at University of Victoria (One session)

**Mentoring**

**Postdoctoral Fellow**

Feb 2020 – Feb 2021: Linan Zhang, PhD, Post-Doctoral Scholar in Biomedical Informatics

(Next position: Assistant Professor, Ningbo University)

Honored with the best poster award at the 2023 GIW ISCB-Asia

Aug 2021 – Feb 2023: April Sagan, PhD, NLM Post-Doctoral Scholar in Biomedical Informatics

(Next position: Bioinformatics Scientist at Grail)

Aug 2021 – June 2023: Sanghoon Lee, PhD, Post-Doctoral Scholar in Biomedical Informatics

Awarded - Hillman Postdoctoral Fellowship for Innovative Cancer Research

(Next position: Postdoctoral Associate at UPMC HCC)

July 2023 – present: Elena Kim, PhD, NLM Post-Doctoral Scholar in Biomedical Informatics

 Honored with a poster award at the 2023 Center for Systems Immunology Retreat.

Sept 2023 – present: Parham Hadikhani, PhD, Post-Doctoral Scholar in Biomedical Informatics

**Medical Student**

June 2022– present: Maneka Puligandla, University of Pittsburgh

Awarded - 2022 Hillman Medical Student Fellows for Innovative Cancer Research

July 2022– April 2023: David Lembersky, University of Pittsburgh

Sept 2023: Liu Tianhao, Tsinghua University Medical Student Rotation

**Graduate Student**

Ph.D. thesis supervisor:

May 2022 – present: Koushul Ramjattun (expected 2025) in Biomedical Informatics

Honored with the Best Student Paper 1st Place award at the 2023 Biomedical Informatics Training Program Retreat

Rotation supervisor:

Sept 2019: Smitha Edakalavan, University of Pittsburgh SOM, Department of Biomedical Informatics

Oct 2020: Alexander R Hummels, University of Pittsburgh SOM, Joint Carnegie-Mellon Pitt Computational Biology (CPCB) program

Sept 2020: Mostofa Rafid Uddin, University of Pittsburgh SOM, CPCB program

Sept 2021: Koushul Ramjattun, University of Pittsburgh SOM, Department of Biomedical Informatics

Oct 2021: Israel Omar Dilan-Pantojas, University of Pittsburgh SOM, Department of Biomedical Informatics

Sept 2021: Sonish Sivarajkumar, University of Pittsburgh SCI, Intelligent Systems Program (ISP) program

Sept 2022: Prosper Chukwuemeka, University of Pittsburgh SOM, Integrative Systems Biology program

Sept 2023: Alyson Wang, University of Pittsburgh SOM, CPCB program

Master’s level Research supervisor:

Apr 2019 – Aug 2019: Chen'ao Qian, University of Pittsburgh, Masters in Biostatistics (next position: Bioinformatician at Penn Medicine, University of Pennsylvania Health System)

July 2019 – Nov 2019: Hanzhong Zheng, University of Pittsburgh, PhD candidate in Computer Science

Aug 2020 – Oct 2020: Yingjin Zhang, University of Pittsburgh, PhD candidate in Biostatistics

July 2021 – Aug 2021: Elizabeth Chiyka, University of Pittsburgh, Masters in Genome Bioinformatics

 (Next position: Biostatistician at ACESO)

July 2021 – Jan 2022: Devin Dikec, University of Pittsburgh, Masters in Genome Bioinformatics

(Next position: Bioinformatician in the Cruchaga lab at Washington University in St. Louis)

Sept 2023 – present: Arjun Singh, University of Pittsburgh, Masters in the Computational Biomedicine

and Biotechnology (CoBB) (Directed study mentor)

**Undergraduate Student**

June – Aug 2019: Louis Gil, University of Puerto Rico Rio Piedras, iBRIC summer program

(Next position: Bioinformatics Analyst Allegheny Health Network)

June – Dec 2019: Melanie Chin, University of Pittsburgh, Undergraduate Computer Biology

(Next position: Graduate student at Northeastern University)

Sept 2019 – Sept 2021: Drake Palmer, University of Pittsburgh, Undergraduate Computer Biology

Sept 2019 – April 2020: Boyan Zhang, University of Pittsburgh, Undergraduate Bioengineering

Sept 2019 – April 2020: Ibrahim Albaba, University of Pittsburgh, Undergraduate Information Science

 (Next position: Data Scientist at CLS Health)

May 2020 – Dec 2020: Ronak Khamar, University of Pittsburgh, Undergraduate Computer Biology

Sept 2020 – Dec 2020: Aaron Fairchild, University of Pittsburgh, Undergraduate Computer Biology

June – August 2022: Yash Patel, Vassar College, Poughkeepsie, New York,

Hillman academy summer program

Jan 2023 – Aug 2023: Ambar Gautam, University of Pittsburgh, BS candidate Computer Biology

Jan 2023 – May 2023: Vinisha Sant, University of Pittsburgh, BS candidate Computer Biology

June 2023 – Aug 2023: Matthew Lu, University of Pittsburgh, BS candidate Computer Science

**High school Student**

Jun 2021 – Aug 2021: Research Supervisor, Michelle Orioha, High School Student, Hillman Summer Academy (Next position: Undergraduate student at Case Western Reserve University)

Jun 2022 – Aug 2022: Research Supervisor, Hillary Boyzo, High School Student, Hillman Summer Academy (Next position: Undergraduate student at Case Western Reserve University)

**Teaching-related service:**

Graduate student committees:

2020 – 2021: Hanzhong Zheng, Chang laboratory, Department of Computer Science, University of Pittsburgh

2022 – present: Han Zhang, Lu & Chen laboratory, Department of Biomedical Informatics, University of Pittsburgh

Other teaching-related service:

2020, Member, Admissions Committee, Biomedical Informatics Graduate Program

2021, Member, Admissions Committee, Biomedical Informatics Graduate Program

2022, Member, Admissions Committee, Joint Carnegie-Mellon Pitt Computational Biology (CPCB) program

2023, Member, Admissions Committee, Biomedical Informatics Graduate Program

**RESEARCH**

**Current Grant Support**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| NIH / NIGMSR35GM1412820 | Computational methods for delineating cell context-specific regulatory programs | PI%516.12 months | 09/15/2022-08/31/2027 | Direct:$1,250,000Indirect:$671,420 |
| NIH / NCIR01CA276279 | The Role of EGFL6 in Ovarian Tumor Immunity | Co-I%50.6 months | 06/07/2023 – 05/31/2028 | Direct:$64,661 Indirect: $34,374 |
| NIH / NCIR01CA278100 | Evaluating unique aspects of quiescent ovarian cancer cell biology for therapeutic targets | Co-I%30.36 months | 07/15/2023 –06/30/2028 | Direct:$27,820Indirect: $16,413 |

**Pending Grant Support**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| NIH / NCIR01 | Mechanistic insights into immune suppression and novel therapeutic opportunities in renal cancer | Co-I%50.6 months | 07/01/2025-06/30/2027 | Direct: $38,590Indirect: $10,150 |
| NIH / NCIR01 | Integrative framework for surface protein imputation for spatial biology of cancer  | PI%202.4 months | 07/01/2024-06/30/2026 | Direct: $275,000Indirect: $162,250 |
| Chan Zuckerberg InitiativeDI3-0000000161 | Enhancing the Utility of Spatial Transcriptomics through Protein Imputation | PI%202.4 months | 08/01/2024-01/31/2026 | Direct: $173,912Indirect: $26,088 |

**Completed Grant Support**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| NIH / NCIK99CA207871 | Algorithms to link signaling pathways with transcriptional programs for precision medicine | PI%10010 months  | 2016-2018 | Direct: $249,822Indirect: $19,986 |
| INNOVATION IN CANCER INFORMATICS (ICI) | Integrative computational framework for linking cell surface proteins todownstream transcriptional programs in cells | PI%101.2 months | 05/01/2019 - 05/30/2022 | Direct:$200,000Indirect:$24,000 |
| OCRA Renewal | Targeting Tumor Desmoplasia to Enhance Immunotherapy | Co-I%70.84 months | 01/01/2022-12/31/2022 | Direct: $12,007  Indirect:$1,201 |
| NIH / NIGMSR35GM1412820(Supplement) | Computational methods for delineating cell context-specific regulatory programs | PI%00 months | 05/01/2023-07/31/2023 | Direct:$7,250Indirect$4,278 |
| NIH / NCIR00CA207871 | Algorithms to link signaling pathways with transcriptional programs for precision medicine. | PI%759 months  | 12/01/2018-11/30/2023(NCE) | Direct: $477,315Indirect: $269,682 |
| NIH / NCIR01CA218026 | The Function of EGFL6 in Ovarian Cancer Cell Biology, Tumor Initiation, and Therapy | Co-I%50.6 months  | 12/01/2021 - 11/30/2023 | Direct $16,321Indirect$9,221 |

**Journal refereeing**

IEEE/ACM Transactions on Computational Biology and Bioinformatics x1

Bioinformatics x2

BMC Supplements x1

BMC Bioinformatics x1

Clinical Colorectal Cancer x5

PLOS Computational Biology x5

PLOS ONE x1

Oncology Research x4

Clinical and Translational Medicine x2

Nature Communications x2

Nature x1

Cell Reports Methods x1

iScience x2

Genome Research x1

Science Advances x1

Frontiers in Immunology x1

Journal of Medical Virology x2

**Editorships**

Guest Editor for PLOS Computational Biology, 2022 - present

Review Editor in Frontiers in Immunology - Cancer Immunity and Immunotherapy, 2022 – present

Review Editor in Frontiers in Oncology - Cancer Epidemiology and Prevention, 2023 - present

**Grant reviewing**

2021 Nov, Ad-hoc reviewer for the Peer Reviewed Cancer Research Program (PRCRP)

 Mesothelioma panel

2022 June, Ad-hoc reviewer for NIH Genomics, Computational Biology and Technologies (GCAT) Study

 Section

2023 Feb, Ad-hoc reviewer for NIH Maximizing Investigators’ Research Award (MRAA) Study Section

2023 Oct, Mail reviewer for NIH Therapeutic Immune Regulation (TIR) Study Section

**LIST of CURRENT RESEARCH INTERESTS**

* Computational omics
* Cancer genomics
* Systems biology and immunology
* Epigenetics
* Spatial biology
* Applied machine learning

**INVITED SEMINARS AND LECTURESHIPS**

**Local Presentations**

1. Nov 2016: Sloan Kettering Postdoctoral Symposium, New York, NY, USA: Modeling the impact of somatic alterations on signaling pathways and transcriptional programs in human cancers
2. Mar 2019: University of Pittsburgh Department of Biomedical Informatics seminar series, Pittsburgh PA: Predictive gene regulatory models for precision medicine
3. Sept 2019: University of Pittsburgh Women’s Cancer Research Center seminar series, Pittsburgh PA: Predictive gene regulatory models for precision medicine
4. Sept 2019: University of Pittsburgh Department of Bioengineering seminar series, Pittsburgh PA: Predictive gene regulatory models for precision medicine
5. Oct 2019: UPMC Hillman Cancer Center Basic & Translational Research Seminar Series, Pittsburgh PA: Linking Signaling and Transcriptional Programs for Precision Cancer Therapy
6. Oct 2019: Computational Medicine Conference, University of Pittsburgh's Clinical and Translational Science Institute and the Institute for Precision Medicine, Pittsburgh PA: Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancers
7. Nov 2019: Joint CMU-Pitt Ph.D Program in Computational Biology seminar series, Pittsburgh PA: Systems biology approaches to dissect regulatory pathways in cancer
8. Jan 2020: CSB/IMM Workshop, University of Pittsburgh, Pittsburgh PA: Systems biology approaches to dissect regulatory pathways.
9. Jan 2020: Joint CMU-Pitt Ph.D Program in Recruitment Event, Pittsburgh PA: Systems biology approaches to dissect regulatory pathways in cancer
10. Oct 2020: National Mesothelioma Virtual Bank Annual Virtual Meeting, Pittsburgh PA: Decoding regulatory landscape in malignant mesotheliomas
11. Feb 2021: Intelligent Systems Program (ISP) Artificial Intelligence (AI) Forum, Pittsburgh PA: Decoding regulatory landscape in malignant mesotheliomas
12. Oct 2021: UPMC Hillman Cancer Center Basic & Translational Research Seminar Series, Pittsburgh PA: Computational Methods for Elucidating Transcriptional Programs using Multi-omics Datasets
13. Feb 2022:Center for Systems ImmunologySeminar Series, Pittsburgh, PA: Isolated BAP1 loss predicts a distinct immunogenic subtype of malignant pleural mesothelioma with implications for immunotherapy response
14. Mar 2022:UPMC Hillman Cancer Center Basic Cancer Immunology and Immunotherapy Program Seminar Series, Pittsburgh, PA: Isolated BAP1 loss predicts a distinct immunogenic subtype of malignant pleural mesothelioma with implications for immunotherapy response
15. Oct 2022:National Mesothelioma Virtual Bank Annual Virtual Meeting, Pittsburgh PA: Isolated BAP1 loss predicts a distinct immunogenic subtype of malignant pleural mesothelioma with implications for immunotherapy response
16. Nov 2022:The Spatial Omics and Computational Imaging in Human Diseases Symposium (SPCIG), Pittsburgh PA: Spatially resolved analysis of breast cancer tumor immune microenvironment
17. June 2023: The Cancer Therapeutics Program (CTP) Seminar Series, Pittsburgh PA: Integrative Omics Approaches for Cancer Research
18. Oct 2023: The Cancer Biology Program Seminar Series, Pittsburgh PA: Computational Omics for Cancer Research
19. Oct 2023: National Mesothelioma Virtual Bank Annual Virtual Meeting, Pittsburgh PA: Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment

**Local Presentations by Trainees**

1. Oct 2021: Dr. Sanghoon Lee, postdoctoral fellow; Annual UPMC Hillman Cancer Center, Pittsburgh PA: Chromatin accessibility landscape in primary human invasive lobular and ductal breast carcinomas (poster presentation)

2. Oct 2021: Dr. April Sagan, postdoctoral fellow; Annual UPMC Hillman Cancer Center, Pittsburgh PA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs (poster presentation)

3. Jan. 2022: Dr. Sanghoon Lee, postdoctoral fellow; University of Pittsburgh Department of Biomedical Informatics seminar series, Pittsburgh PA: Chromatin accessibility landscape in primary human invasive lobular and ductal breast carcinomas

4. Jan. 2022: Dr. April Sagan, postdoctoral fellow; University of Pittsburgh Department of Biomedical Informatics seminar series, Pittsburgh PA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs

5. Mar 2022: Dr. Sanghoon Lee, postdoctoral fellow; UPMC Hillman Cancer Center Cancer Biology Program Seminar Series, Pittsburgh PA: Chromatin accessibility landscape in primary human invasive lobular and ductal breast carcinomas

6. May 2022: Dr. April Sagan, postdoctoral fellow; The Fifteenth Postdoctoral Data & Dine Symposium Pittsburgh PA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs (poster presentation)

7. May 2022: Dr. Sanghoon Lee, postdoctoral fellow; The Fifteenth Postdoctoral Data & Dine Symposium, Pittsburgh PA: Decoding the regulatory landscape in macrophage-rich ER-positive breast cancer (poster presentation)

9. Sept 2022: Dr. April Sagan, postdoctoral fellow; Center for Systems Immunology (CSI) Annual Retreat, Pittsburgh PA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs (poster presentation)

10. Sept 2022: Dr. Sanghoon Lee, postdoctoral fellow; Center for Systems Immunology (CSI) Annual Retreat, Pittsburgh PA: Decoding the regulatory landscape in macrophage-rich ER-positive breast cancer (poster presentation)

11. Oct 2022: Dr. April Sagan, postdoctoral fellow; UPMC Hillman Cancer Center Annual Retreat, Pittsburgh PA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs (poster presentation)

12. Oct 2022: Dr. Sanghoon Lee, postdoctoral fellow; UPMC Hillman Cancer Center Annual Retreat, Pittsburgh PA: Decoding the regulatory landscape in macrophage-rich ER-positive breast cancer (poster presentation)

13. Oct 2022: Dr. April Sagan, postdoctoral fellow; Center for Systems ImmunologySeminar Series, Pittsburgh, USA: STAN, a computational framework for inferring spatially informed transcription factor activity networks

13. Sept 2023: Dr. Elena Kim, postdoctoral fellow; Center for Systems ImmunologySeminar Series, Pittsburgh, USA: Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment

14. Sept 2023: Dr. Elena Kim, postdoctoral fellow; UPMC Hillman Cancer Center Annual Retreat, Pittsburgh, USA: Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment

15. Sept 2023: Dr. Elena Kim, postdoctoral fellow; BGSA Symposium, Pittsburgh, USA: Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment

16. Oct 2023: Koushul Ramjattun, graduate student; Center for Systems ImmunologySeminar Series,

Pittsburgh, USA: Spatially-informed Protein Imputation using Constrained Embeddings from Shared

latent Spaces

**Regional Presentations**

 Oct 2021: Great Lakes Breast Cancer Symposium (Virtual): Predictive gene regulatory models

**National Presentations**

1. Nov 2012: National Center for Biotechnology Information, MD, USA: Information integration approaches for investigating estrogen receptor mediated transcription
2. Dec 2012: Memorial Sloan Kettering Cancer Center*,* New York, NY, USA: Information integration approaches for investigating estrogen receptor mediated transcription
3. Dec 2012: Harvard Medical School, Boston, MA, USA: Information integration approaches for investigating estrogen receptor mediated transcription
4. Mar 2015: ENCODE Consortium Meeting, Cold Spring Harbor, USA: Inferring the impact of genetic aberrations on transcriptional programs in prostate cancer
5. May 2016: Stony Brook University, Stony Brook, NY, USA: Integrative Computational Modeling Across Tumors Reveals Context Specific Impact of Mutations
6. Feb 2017: University of Southern California, Los Angles, LA, USA: Predictive gene regulatory models for precision medicine
7. Feb 2017: North Carolina at Chapel Hill, Chapel Hill, NC, USA: Predictive gene regulatory models for precision medicine
8. Feb 2017: Carnegie Mellon University, Pittsburgh, PA, USA: Predictive gene regulatory models for precision medicine
9. Mar 2017: Icahn School of Medicine at Mount Sinai, NY, USA: Predictive gene regulatory models for precision medicine
10. Mar 2017: University of California Riverside, Riverside, CA, USA: Predictive gene regulatory models for precision medicine
11. Mar 2017: University of Illinois at Chicago, Chicago, IL, USA: Predictive gene regulatory models for precision medicine
12. Sept 2017: Rutgers Cancer Institute of New Jersey, NJ, USA: Predictive gene regulatory models for precision medicine
13. Oct 2017: Weill Cornell Medicine, New York, NY, USA: Predictive gene regulatory models for precision medicine
14. Jan 2018: New York University, NY, USA: Predictive gene regulatory models for precision medicine
15. Jan 2018: University of Washington, Saint Louis, MO, USA: Predictive gene regulatory models for precision medicine
16. Jan 2018: Cold Spring Harbor Laboratory, NY, USA: Predictive gene regulatory models for precision medicine
17. Feb 2018: Johns Hopkins University, Baltimore, MD, USA: Predictive gene regulatory models for precision medicine
18. Feb 2018: University of Wisconsin Madison, WI, USA: Predictive gene regulatory models for precision medicine
19. Mar 2018: Columbia University, NY, USA: Predictive gene regulatory models for precision medicine
20. Mar 2018: Brown University, RI, USA: Predictive gene regulatory models for precision medicine
21. Apr 2018: Johns Hopkins University, Baltimore, MD, USA: Predictive gene regulatory models for precision medicine
22. May 2018: Dartmouth College, Hanover, NH, USA: Predictive gene regulatory models for precision medicine
23. July 2018: University of Pittsburgh, Pittsburgh, PA, USA: Predictive gene regulatory models for precision medicine
24. Sept 2019: Toyota Technological Institute at Chicago, Chicago, IL, USA: Predictive gene regulatory models for precision medicine
25. Nov 2020: Johns Hopkins University, Baltimore, MD, USA (Virtual): Predictive cell-specific gene regulatory models
26. Feb 2023: Stony Brook Cancer Center, Stony Brook, NY, USA (Virtual):  Integrative Omics Approaches for Cancer Research
27. March 2023: NCI Spring School on Algorithmic Cancer Biology, Bethesda, MD: Interpretable deep learning for chromatin-informed inference of transcriptional programs driven by somatic alterations across cancers (selected lightning talk)
28. Sept 2023: MLxMed (Machine Learning in Medicine) virtual seminar series: Machine learning for single-cell regulatory program inference
29. Sept 2023: Toyota Technological Institute at Chicago, Chicago, IL, USA: Computational methods for delineating cell context-specific regulatory programs
30. Sept 2023: Rutgers University, New Jersey, NJ, USA: Machine learning for single-cell regulatory program inference
31. Oct 2023: University of Michigan – Ann Harbor, MI, USA: Machine learning for single-cell regulatory program inference
32. Oct 2023: Brown University, RI, USA: Machine learning for single-cell regulatory program inference

**International Presentations**

1. July 2008: 16th International Conference on Mechanics in Medicine and Biology, Pittsburgh, PA, USA: Thin Nanoporous Membranes for Biomolecule Separation
2. Nov 2013: RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2013, Toronto, Ontario, Canada: Linking signaling pathways to transcriptional response in breast cancer.
3. July 2014: **Intelligent Systems for Molecular Biology (ISMB) Conference**, Boston, USA: Linking signaling pathways to transcriptional response in breast cancer.
4. Apr 2015: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB), Warsaw, Poland: Linking signaling pathways to transcriptional response in breast cancer.
5. Feb 2016: Computational Cancer Biology Workshop, Berkeley, CA, USA: Modeling the impact of genomic aberrations on transcriptional programs across human cancers.
6. Apr 2016: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB), Los Angeles, CA, USA: Modeling the impact of genomic aberrations on transcriptional programs across human cancers.
7. June 2016: EMBL-EBI, Hinxton, United Kingdom: Integrative Computational Modeling Across Tumors Reveals Context Specific Impact of Mutations
8. June 2016: ICML Workshop on Computational Biology, New York, NY: Integrative computational modeling across tumors reveals context specific impact of mutations.
9. July 2016: **Intelligent Systems for Molecular Biology (ISMB) Conference**, Orlando, Florida, USA: Integrative computational modeling across tumors reveals context specific impact of mutations.
10. Nov 2016: RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges & Cytoscape Workshop 2016, Phoenix, Arizona, USA: Modeling the impact of somatic alterations on signaling pathways and transcriptional programs in human cancers.
11. Aug 2017: ACM-BCB, Boston, MA, USA: Pancancer modeling predicts the context-specific impact of somatic mutations on transcriptional programs.
12. Feb 2018: University of Oslo, Centre for Molecular Medicine Norway, Oslo, Norway: Predictive gene regulatory models for precision medicine
13. Apr 2018: IRIC – University of Montreal, Montreal, Canada: Predictive gene regulatory models for precision medicine
14. July 2018: **Intelligent Systems for Molecular Biology (ISMB) Conference**, Chicago, USA: Inferring transcriptional regulatory programs in gynecologic cancers.
15. Dec 2018: RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2018, New York, New York, USA: Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancer
16. Dec 2018: Sabanci University, Istanbul, Turkey: Predictive gene regulatory models for precision medicine
17. May 2019: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB), Washington, DC, USA: Chromatin-informed inference of transcriptional programs in gynecologic and basal breast cancers
18. Nov 2019: RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2019, New York, New York, USA: Integrative computational framework for linking signaling and transcriptional programs in single cells.
19. Nov 2019: Women in Computational Biology, Virginia, VA, USA: Integrative computational framework for linking signaling and transcriptional programs in single cells.
20. March 2020: Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY, USA: Integrative computational framework for linking signaling and transcriptional programs in single cells. Online due to covid-19.
21. Nov 2020: Systems Approaches to Cancer Biology (Virtual): SPaRTAN, a computational framework for linking surface proteins to transcriptional regulators.
22. May 2022: Women in Data Science Istanbul (Virtual): Interpretable Deep Learning and Cancer Genomics
23. May 2022: The 26th Annual International Conference on Research in Computational Molecular Biology (RECOMB), La Jolla, USA: SPaRTAN, a computational framework for linking surface proteins to transcriptional regulators.
24. May 2022: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB) 2022, La Jolla, USA: Interpretable deep learning for chromatin-informed inference of transcriptional programs driven by somatic alterations across cancers.
25. April 2023: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB) 2023, Istanbul, Turkey: Interpretable deep learning for chromatin-informed inference of transcriptional programs driven by somatic alterations across cancers.
26. April 2023: The RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-CCB) 2023, Istanbul, Turkey: STAN, a computational framework for inferring spatially informed transcription factor activity networks.
27. July 2023: I**ntelligent Systems for Molecular Biology (ISMB)/European Conference on Computational Biology (ECCB)**, Lyon, France: STAN, a computational framework for inferring spatially informed transcription factor activity networks.

**International Presentations by Trainees**

1. July 2022: Dr. April Sagan, postdoctoral fellow; **Intelligent Systems for Molecular Biology (ISMB) Conference**, Madison, Wisconsin, USA: Utilizing spatial transcriptomics data to identify cell context-specific regulatory programs (poster presentation)
2. Nov 2022: Dr. April Sagan, postdoctoral fellow; RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges 2022, Las Vegas, Nevada, USA: STAN, a computational framework for inferring spatially informed transcription factor activity networks (selected talk)
3. July 2023: Koushul Ramjattun, graduate student; I**ntelligent Systems for Molecular Biology (ISMB)/European Conference on Computational Biology (ECCB)**, Lyon, France: COVID-19db linkage maps of cell surface proteins and transcription factors in immune cells (poster presentation).
4. Nov 2023: Linan Zhang, postdoctoral fellow; 2023 Genome Informatics Workshop/International Society for Computational Biology-Asia(GIW ISCB-Asia), Singapore: Single-cell analysis reveals the stromal dynamics and tumor-specific characteristics in the microenvironment of ovarian cancer

**SERVICE**

**University and Medical School Service**

2019, Poster Judge, UPMC Hillman Cancer Center Retreat

2019, Poster Judge, joint retreat of Immunology and Computational and Systems Biology Department

2020, Poster Judge, joint retreat of Immunology and Computational and Systems Biology Department

2022, Poster Judge, UPMC Hillman Cancer Center Retreat

2023, Member of search committee for the Center for Systems Immunology (CSI)/Tumor

 Microenvironment Center (TMC) Faculty Position

2023, Poster Judge, UPMC Hillman Cancer Center Retreat

**Diversity, Equity, and Inclusion Activities**

2019 – 2021**,** Women’s Task Force, Pittsburgh, PA, USA

2023, Member of admission committee for of UPMC Hillman Cancer Center Summer Academy-Cancer

 Biology Site

**Local/Community Service Activities**

2012, Judge, Intel’s International Science & Engineering Fair, Pittsburgh, PA, USA

**Regional Service**

2012, Judge, Pittsburgh Regional Science Fair (PSEF), Pittsburgh, PA, USA

**National Service**

2013-2014, Representative, NCI’s Integrative Cancer Biology Program’s Early-Stage Investigators Steering Committee Meeting

**International Service**

2017, Referee, Women in Machine Learning Workshop

2017, Member, Program Committee, Workshop on Computation Biology, Sydney, Australia

2019, Member, Program committee of ISMB/ECCB2019, Basel, Switzerland

2020, Member, Program Committee, ISMB, Montreal, Canada (Virtual)

2020, Member, Program committee of RECOMB-RSG (Virtual)

2020, Member, Program committee of ISMB (Virtual)

2021, Member, Program Committee, ISMB/ECCB (Virtual)

2021, Co-chair**,** ICHI 2021 Special Session on COVID-19

2022, Member, Program committee of ISMB, Madison, Wisconsin

2022, Member, Program Committee (Highlights track), RECOMB, La Jolla

2022, Member, Program Committee, RSGDREAM, Las Vegas

2023, Member, Program Committee, ISMB/ECCB, Lyon, France

2023, Member, Program Committee, RSGDREAM, Los Angeles

2024, Co-organizer**,** the Great Lakes Bioinformatics Conference (GLBIO) Special Session on

 Computational approaches for spatial omics, Pittsburgh