

Shankara K. Anand

LINKS:     

Last updated: March 13, 2023

ABOUT	I am a rising fourth year medical student at Boston University School of Medicine passionate about hematology/oncology and applying ML/AI to clinical practice. I have a masters from Stanford where I completed coursework in machine & deep learning and 4+ years of experience as a computational biology researcher at the Broad Institute of MIT & Harvard. My expertise includes single-cell genomics, multi-omic integration, and structural proteomics with an emphasis on algorithmic development.	
EDUCATION	M.D. Candidate , Boston University, <i>Boston, MA</i>	(exp.) 2024
	M.S. Biomedical Informatics , Stanford University, <i>Stanford, CA</i>	2019
	B.S. Chemical Engineering , Stanford University, <i>Stanford, CA</i>	2017
RESEARCH	Associate Computational Biologist , Broad Institute of MIT & Harvard Aug. 2018 - Present Supervised by Dr. Gad Getz & the Genotype Tissue Expression Experiment (GTEx) <ul style="list-style-type: none">• Led computational direction of pan-cancer, proteogenomic study (CPTAC)• Mapped a single-nucleus, cross-tissue, transcriptome atlas of the human body (GTEx)• Risk stratified Smoldering Multiple Myeloma patients with genomics (advised by Dr. Irene Ghobrial) Researcher , Stanford Dept. of Bioengineering Jan. - June 2018 Supervised by Dr. Possu Huang <ul style="list-style-type: none">• Designed <i>de novo</i>, end-to-end (computational to wet-lab) proteins using Rosetta software• Predicted ligand binding sites of proteins using deep learning frameworks (GitHub) Scientific Intern , Novartis Summer 2017 Computer Aided Drug Discovery Team <ul style="list-style-type: none">• Developed machine learning framework for detecting pKa of in-house compounds• Published work in <i>Journal of Chemical Information & Modeling</i> Research Intern , Genentech Summer 2016 Early Stage Pharmaceutical Development <ul style="list-style-type: none">• Built computational pipeline for running large molecular dynamics simulations to investigate surfactant structure and antibody degradation	
LEADERSHIP	Student Leader , BUSM Genetics Interest Group	April 2021 - March 2022
	Student Leader , BUSM in.Vision Tech x Medicine Group	April 2021 - March 2022
	STEM Tutor , Stanford Academic Resource Center	Summer 2017
	Dance Captain , Stanford Basmati Raas (Indian Dance)	Sept. 2013 - June 2018
	Resident Assistant , 2x years at Stanford Residential Education	Sept. 2015 - June 2017
	Program Coordinator , Stanford LGBT Community Resource Center	Sept. 2015 - June 2017
VOLUNTEER	Child Life Volunteer , Boston Children's Hospital Oncology (<i>150 hrs</i>)	Oct. 2018 - Feb. 2020
	Fundraising Coordinator & Volunteer , Stanford Camp Kesem (<i>650 hrs</i>)	April 2016 - July 2018
	Reading Tutor , Stanford Ravenswood Reads (<i>120 hrs</i>)	Spring 2016
AWARDS	American Association of Cancer Research: Scholar in Training Award	2023
	American Society of Hematology: Abstract Achievement Award	2021
	Stanford Achievement Award , awarded to 10% of graduating class	2017
	Genentech Outstanding Student Award , selected Junior in Chemical Engineering	2016

SKILLS	<p>Advanced: Python, R, PyTorch, TensorFlow, git</p> <p>Basic: Matlab, L^AT_EX</p>
SOFTWARE	<p>Signature Analyzer: a fast, GPU enabled implementation of bayesian non-negative matrix factorization for extracting mutational and genomic expression signatures (GitHub).</p> <p>CLUMPS-PTM: an algorithm for identifying 3D clusters of post-translational modifications (GitHub).</p> <p>CLUMPS-2: an algorithm for identifying 3D clusters of somatic mutations (GitHub).</p> <p>Mudi: python utilities for single-cell RNA-sequencing analyses (GitHub).</p> <p>SITEFINDER: using deep learning to identify ligand site binding in proteins (Stanford CS231n) (GitHub).</p>
PUBLICATIONS	<p>Pre-Prints</p> <p>[1] Rouhana, J. M., Wang, J., Eraslan, G., Anand, S., Hamel, A. R., Cole, B. et al. ECLIPSER: identifying causal cell types and genes for complex traits through single cell enrichment of e/sQTL-mapped genes in GWAS loci. bioRxiv (2021). doi: 10.1101/2021.11.24.469720</p> <p>Peer-Reviewed Publications</p> <p>† indicates co-first authorship ‡ indicates co-second authorship</p> <p>[1] Boiarsky, R., Haradhvala, N. J., Alberge, J. B., Sklavenitis-Pistofidis, R., Mouhieddine, T. H., Zavidij, O. et al. Single Cell Characterization of Myeloma and its Precursor Conditions Reveals Transcriptional Signatures of Early Tumorigenesis. Nature Communications, 13, 7040 (2022). doi: 10.1038/s41467-022-33944-z</p> <p>[2] Sklavenitis-Pistofidis, R., Aranha, M. P., Redd, R. A., Baginska, J., Haradhvala, N. J., Hallisey, M., et al. Immune biomarkers of response to immunotherapy in patients with high-risk smoldering myeloma. Cancer Cell, 40(11), 1358-1373 (2022). doi: 10.1016/j.ccell.2022.10.017</p> <p>[3] Yaron, T. M., Heaton, B. E., Levy, T. M., Johnson, J. L., Jordan, T. X., Cohen, B. M. et al. Host protein kinases required for SARS-CoV-2 nucleocapsid phosphorylation and viral replication. Science Signaling, 15(757) (2022). doi: 10.1126/scisignal.abm0808</p> <p>[4] Roh, W., Geffen, Y., Cha, H., Miller, M., Anand, S., Kim, J. et al. High-resolution profiling of lung adenocarcinoma identifies expression subtypes with specific biomarkers and clinically relevant vulnerabilities. Cancer Research (2022). doi: 10.1158/0008-5472.CAN-22-0432</p> <p>[5] Knisbacher, B. A., Lin, Z., Hahn, C. K., Nadeu, F., Duran-Ferrer, M., Stevenson, K. E. et al. The CLL-1100 project: towards complete genomic characterization and improved prognostics for CLL. Nature Genetics, 1-11 (2022). doi: 10.1038/s41588-022-01140-w</p> <p>[6] Bustoros, M.[†], Anand, S.[†], Sklavenitis-Pistofidis, R. et al. Genetic subtypes of smoldering multiple myeloma are associated with distinct pathogenic phenotypes and clinical outcomes. Nature Communications, 13, 3449 (2022). doi: 10.1038/s41467-022-30694-w (GitHub)</p> <p>[7] Eraslan, G.[†], Drokhyansky, E.[†], Anand, S.[‡], Fiskin, E.[‡], Subramanian, A.[‡], Sylper, M.[‡], Wang, J.[‡] et al. Single-nucleus cross-tissue molecular reference maps toward understanding disease gene function. Science, 376(6594) (2022). doi: 10.1126/science.abl4290</p> <p>[8] Beauchamp, E. M., Leventhal, M., Bernard, E., Hoppe, E. R., Todisco, G., Creignou, M. et al. ZBTB33 is mutated in clonal hematopoiesis and myelodysplastic syndromes and impacts RNA splicing. Blood Cancer Discovery, 2(5), 500-517 (2021). doi: 10.1158/2643-3230.BCD-20-0224</p> <p>[9] Satpathy, S., Krug, K., Beltran, P. M. J., Savage, S. R., Petralia, F., Kumar-Sinha, C. et al. A proteogenomic portrait of lung squamous cell carcinoma. Cell, 184(16), 4348-4371 (2021). doi: 10.1016/j.cell.2021.07.016</p> <p>[10] de Goede, O. M., Nachun, D. C., Ferraro, N. M., Gloudemans, M. J., Rao, A. S., Smail, C. et al. Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell,</p>

- 184(10), 2633-2648 (2021). doi: [10.1016/j.cell.2021.03.050](https://doi.org/10.1016/j.cell.2021.03.050)
- [11] Jiang, L., Wang, M., Lin, S., Jian, R., Li, X., Chan, J. et al. A quantitative proteome map of the human body. **Cell**, 183(1), 269-283 (2020). doi: [10.1016/j.cell.2020.08.036](https://doi.org/10.1016/j.cell.2020.08.036)
 - [12] Ferraro, N. M., Strober, B. J., Einson, J., Abell, N. S., Aguet, F., Barbeira, A. N. et al. Transcriptional signatures across human tissues identify functional rare genetic variation. **Science**, 369(6509) (2020). doi: [10.1126/science.aaz5900](https://doi.org/10.1126/science.aaz5900)
 - [13] GTEx Consortium. The GTEx Consortium atlas of genetic regulatory effects across human tissues. **Science**, 369(6509), 1318-1330 (2020). doi: [10.1126/science.aaz1776](https://doi.org/10.1126/science.aaz1776)
 - [14] Bustoros, M., Sklavenitis-Pistofidis, R., Park, J., Redd, R., Zhitomirsky, B., Dunford, A. J. et al. Genomic profiling of smoldering multiple myeloma identifies patients at a high risk of disease progression. **Journal of Clinical Oncology**, 38(21), 2380 (2020). doi: [10.1200/JCO.20.00437](https://doi.org/10.1200/JCO.20.00437)
 - [15] Taylor-Weiner, A., Aguet, F., Haradhvala, N. J., Gosai, S., **Anand, S.**, Kim, J. et al. Scaling computational genomics to millions of individuals with GPUs. **Genome Biology**, 20(1), 1-5 (2019). doi: [10.1186/s13059-019-1836-7](https://doi.org/10.1186/s13059-019-1836-7)
 - [16] Lu, Y., **Anand, S.**, Shirley, W., Gedeck, P., Kelley, B. P., Skolnik, S. et al. Prediction of pK_a using machine learning methods with rooted topological torsion fingerprints: application to aliphatic amines. **Journal of Chemical Information and Modeling**, 59(11), 4706-4719 (2019). doi: [10.1021/acs.jcim.9b00498](https://doi.org/10.1021/acs.jcim.9b00498)
 - [17] **Anand, S.**, Kalesinskas, L., Smail, C., & Tanigawa, Y. SNPs2ChIP: Latent Factors of ChIP-seq to infer functions of non-coding SNPs. **Proceedings of the Pacific Symposium** (pp. 184-195) (2018). doi: [10.1142/9789813279827_0017](https://doi.org/10.1142/9789813279827_0017)

PRESENTATION Talks

- [1] Roh, W., Geffen, Y., Miller, M., **Anand, S.**, Kim, J., Heiman, D. et al. Identification and proteogenomic characterization of novel lung adenocarcinoma subtypes with therapeutic relevance. **American Association of Cancer Research (AACR)**, 82(12_Supplement), 2151-2151 (2022). doi: [10.1158/1538-7445.AM2022-2151](https://doi.org/10.1158/1538-7445.AM2022-2151)
- [2] Kubler, K., Nardone, A., **Anand, S.**, Gorvich, D., Droog, M., Hermida-Prado, F. et al. Abstract GS2-09: Tamoxifen instigates uterine cancer development by activating PI3K signaling and supersedes PIK3CA driver mutations. **San Antonio Breast Cancer Symposium (SABCS)**, 82(4_Supplement) (2021). doi: [10.1158/1538-7445.SABCS21-GS2-09](https://doi.org/10.1158/1538-7445.SABCS21-GS2-09)
- [3] Sklavenitis-Pistofidis, R., Dutta, A. K., Ujwary, S., Redd, R. A., Savell, A., Fléchon, L. et al. Single-Cell RNA-Sequencing Identifies Immune Biomarkers of Response to Immunotherapy in Patients with High-Risk Smoldering Myeloma. **American Society of Hematology (ASH)**, 138, 330 (2021). doi: [10.1182/blood-2021-147623](https://doi.org/10.1182/blood-2021-147623)
- [4] **Anand, S.**[†], Bustoros, M.[†], Sklavenitis-Pistofidis, R., Redd, R. A., Boyle, E. M., Tai, Y. T. et al. Genomic Profiling of Smoldering Multiple Myeloma Classifies Molecular Groups with Distinct Pathogenic Phenotypes and Clinical Outcomes. **American Society of Hematology (ASH)**, 138, 723 (2021).
- [5] **Anand, S.** "Genomic profiling of smoldering myeloma identifies high- and low- risk patients | ASH 2021." **The Video Journal of Hematological Oncology**, Dec. 12, 2021. Interviews: [Part 1](#). [Part 2](#).
- [6] Geffen, Y.[†], **Anand, S.**[†], Akiyama, Y.[†], Yaron, T. M., Kerelsky, A., Johnson, J. L., ... & Oncogenic Drivers and Pathways Group, Clinical Proteomic Tumor Analysis Consortium (CPTAC). Patterns and regulation of post translational modifications in cancer. **American Association of Cancer Research (AACR)**, 81(13_Supplement), 16-16. doi: [10.1158/1538-7445.AM2021-16](https://doi.org/10.1158/1538-7445.AM2021-16)

Posters & Abstracts

- [1] **Anand, S.**, Geffen, Y., Akiyama, Y., Aguet, F., Getz, G. *CLUMPS-PTM: Spatial Clustering of Post-Translational Modifications Across Cancer Types*. **American Association of Cancer Research (AACR)** (2023, *upcoming*).
- [2] Boiarsky, R., Haradhvala, N., Sklavenitis-Pistofidis, R., Mouhieddine, T. H., Alberge, J. B., Zavidij, O. et al. Single Cell Characterization of Myeloma and its Precursor Conditions Reveals Transcriptional Signatures of Early Tumorigenesis. **American Society of Hematology (ASH)**, 138, 2219 (2021). doi: [10.1182/blood-2021-150889](https://doi.org/10.1182/blood-2021-150889)
- [3] Akiyama, Y., Geffen, Y., **Anand, S.**, Yaron, T., Johnson, J. L., Huntsman, E. et al. Pan-cancer proteogenomic analysis reveals functional mechanisms underlying DNA repair deficiencies. **American Association of Cancer Research (AACR)**, 82(12_Supplement), 794-794 (2022). doi: [10.1158/1538-7445.AM2022-794](https://doi.org/10.1158/1538-7445.AM2022-794)
- [4] **Anand, S.**, Bustoros, M., Aguet, F., Sklavenitis-Pistofidis, R., Redd, R., Zhitomirsky, B. et al. Genomic profiling of smoldering multiple myeloma classifies distinct molecular groups. **American Association of Cancer Research (AACR)**, 81(13_Supplement), 2240-2240 (2021). doi: [10.1158/1538-7445.AM2021-2240](https://doi.org/10.1158/1538-7445.AM2021-2240)
- [5] **Anand, S.**, Aguet, F., Taylor-Weiner, A., et al. Signature Analyzer: scaling Bayesian NMF to millions of individuals with GPUs. **Broad Institute of MIT & Harvard Retreat**, (2019). [GitHub](#).

INTERESTS

Rass/Garba (Indian) dance: 5+ years of dancing and choreographing at cultural events (ex. Stanford Holi), national competitions, and family weddings.

Music: 15+ years of classical violin training, performed with Stanford Symphony Orchestra, chamber music groups, and musical theater pit orchestras; also enjoy guitar & ukulele.

Dogs: my wife and I have a 3 year old Mudi dog, Hazel, that we do trick training, frisbee catching, and agility with. She comes with us back-country skiing and watches over us when we climb outdoors.

Ski Mountaineering: ask me about the glacier we climbed up and skied down in the Selkirk Mountains of British Columbia, Canada!

Rock Climbing: we love indoor & outdoor lead climbing + finding new routes along the Pacific Coast.

Running: causal runner; completed a half-marathon and hoping to work-up to a full marathon soon!