**Anasuya Dighe, PhD**

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A dedicated bioinformatician specializing in biological sciences with extensive experience in Next-Generation Sequencing (NGS) algorithm design, multi-omics analysis and pipeline optimization. Excels at developing and maintaining state-of-the-art computational methods including Bulk RNASeq, Whole Genome Sequencing (WGS), SingleCell RNASeq (scRNASeq) and SingleNucleus RNASeq (snRNASeq) pipelines across multiple projects in inter-disciplinary environments. Collaborated with a team of cancer biologists and biomedical engineers towards setting up custom analytical bioinformatics tools. Proven track record in the field of computational biology evidenced by research articles in high-impact scientific journals.

**Specialization** Computational Biology | Cancer Systems Biology | Coding: R and Python |

 Algorithm & Pipeline Design | Data Science | High Performance Computing

**Experience**

***Associate Research Scientist***

Yale Center of Molecular and Cellular Oncology (CMCO), Yale University, Connecticut, USA (May 2024 – till date)

* Generated end-to-end pipelines using single-cell proteogenomic tools to probe tumor microenvironment and identify cell populations determining response or resistance to immune checkpoint inhibitors.

***Associate Research Scientist***

Biomedical Engineering, Yale University, Connecticut, USA

(July 2023 – May 2024)

* Generated pipelines for analyzing single cell RNASeq data towards understanding macrophage polarization in tumor microenvironment using scRNASeq and CITE-Seq methods
* Designed study to integrate scRNAseq and CITEseq results using Multi-Omics Integration protocols
* Built customized user interfaces for understanding results in an interactive fashion

***Post-Doctoral Research Associate***

Systems Biology Institute, Yale University, Connecticut, USA

(November 2018 – June 2023)

* Worked as principal bioinformatician on projects in Cancer Systems Biology lab to mine large-scale transcriptomic datasets to understand evolutionary link between cancer metastasis and architecture of mammalian placenta
* Planned, generated, implemented, and maintained end-to-end bioinformatics pipelines for NGS analysis workflows (including bulk RNASeq, WGS, scRNASeq, snRNASeq) using R, Seurat and scanPY to create custom-analytical bioinformatics tools
* Conceptualized and formulated workflow to integrate bulk RNASeq data from 10+ mammalian species and perform quality control, alignment, differential gene expression profiles and create customized data visualizations
* Programmed computational pipelines to identify novel genetic variants using variant calling methods like GATK, FreeBayes
* Automated current in-house RNASeq and scRNASeq pipelines to reduce runtime by 50%
* Collaborated with High Performance Computing (HPC) core to build computing platforms and programming environments. Standardized these platforms for problem-specific computational pipelines
* Mentored two graduate students to guide them with lab computational workflows
* Presented research as talks and posters at Yale Cancer Systems Biology Symposium (2019-22)
* Authored papers in high-impact journals like *iScience,* *PNAS*, *Science Advances* and *Annual Reviews*

**UGC-NET Senior Research Fellow (2012-2017)**

*Indian Institute of Science, Bangalore, India*

* Implemented graph theory principles and network biology to study protein-drug interactions
* Investigated effects of drug binding on proteins by performing large-scale GPU-based Molecular Dynamics (MD) simulations of drug-protein complexes.
* Formalized, implemented and bench-marked a metric to score binding site similarity based on network architecture of binding site
* Initiated and published an in-depth study of drug-binding sites in G-Protein Coupled Receptors (GPCRs) to reveal network similarities in their architecture and identify major players of signal transduction

**Junior Research Fellow (2010-2012)**

*Indian Institute of Science, Bangalore, India*

* Computationally mined and curated a dataset of 65000 protein-drug interactions investigate structural similarity within drug binding sites
* Bench-marked an in-house algorithm and compared its performance to other programs and modified existing algorithm to implement parallel computing to accelerate compute time

**Additional Experience**

*Savitribai Phule Pune University, Pune, India || Masters dissertation (2008-10)*

* Constructed bioinformatics approaches to investigate sequence and structural properties of hemoglobin in insects (*Chironomidae* species)
* Computationally designed a homology model for insect hemoglobin based on sequence alignment findings

**Education**

2010-2017 PhD, Computational Biology, Indian Institute of Science (IISc),

Bangalore, India

2008-2010 Master of Science (MSc) Bioinformatics, Savitribai Phule Pune University,

Pune, India

2005-2008 Bachelor of Science (BSc) Biotechnology, Abasaheb Garware College,

Pune, India

**Technical Skills**

* Bioinformatics
	+ Sequence analysis: BLAST suite, ClustalW, MUSCLE, MUSTANG
	+ Next-Generation Sequencing (NGS) data analysis
	+ Quality control (FastQC, SAMtools, Trimmomatic, BEDtools, PICARD)
	+ Reference-based read alignment (Bowtie2, BWA-mem, HISAT, STAR, TopHat)
	+ Single Cell RNASeq Analysis: CellRanger, Seurat, Scanpy
	+ Variant discovery and genotyping (Freebayes, VEP, GATK, vcffilter, bcftools)
	+ Quantification & Differential Expression (kallisto, DESeq2)
	+ Visualization tools: IGV genome browser, ggplot
	+ Galaxy pipelines

* Computational (Technical)
	+ Programming languages: R, Python, Shell, Sed, Awk, Perl/Bioperl, C, C++, Java
	+ CRAN repositories, Bioconductor, R Markdown, Jupyter for reproducible research
	+ Database: mySQL
	+ Web: HTML, JavaScript
	+ Operating System: Linux/Unix, MacOS, Windows
	+ Version control: Git and Github
	+ Cloud computing: AWS Cloud
	+ Virtual Machines: Docker

**Publications**

Research Articles

1. Xu, W., Birch, G., Meliki, A., Moritz, V., Bharadwaj, M., Schindler, N. R., Labaki, C., Saliby, R. M., Dinh, K., Horst, J. T., Sun, M., Kashima, S., Hugaboom, M., **Dighe, A**., Machaalani, M., Lee, G.-S. M., Hurwitz, M., McGregor, B. A., Hirsch, M. S., ... Braun, D. A. (2025). Progressive natural killer cell dysfunction in advanced-stage clear-cell renal cell carcinoma and association with clinical outcomes. *ESMO Open*, 10(2), 104105.
2. **Dighe A.,** Maziarz J., Ibrahim-Hashim A, Gatenby R.A, Levchenko A., Wagner G. (2024) Experimental and Phylogenetic Evidence for Correlated Gene Expression Evolution in Endometrial and Skin Fibroblasts *iScience (27),108593*
3. Suhail, Y., Maziarz, J. D., Novin, A., **Dighe, A**., Afzal, J., Wagner, G., & Kshitiz (2022). Tracing the cis-regulatory changes underlying the endometrial control of placental invasion. *Proceedings of the National Academy of Sciences of the United States of America,* 119(6), e2111256119.
4. Ba, Q., Hei, Y., **Dighe, A.,** Li, W., Maziarz, J., Pak, I., Wang, S., Wagner, G. P., & Liu, Y. (2022). Proteotype coevolution and quantitative diversity across 11 mammalian species. *Science advances,* 8(36), eabn0756.
5. Ma, X., **Dighe, A.,** Maziarz, J., Neumann, E., Erkenbrack, E., Hei, Y. Y., Liu, Y., Suhail, Y., Kshitiz, Pak, I., Levchenko, A., & Wagner, G. P. (2022). Evolution of higher mesenchymal CD44 expression in the human lineage: A gene linked to cancer malignancy*. Evolution, medicine, and public health,* 10(1), 447–462.
6. Wagner G.P., Kshitiz, **Dighe, A.,** Levchenko, A. (2022) The Coevolution of Placentation and Cancer *Annual Review of Animal Biosciences* Vol. 10:259-279
7. Gadiyaram, V., **Dighe, A.** & Vishveshwara, S. (2019) Identification of crucial elements for network integrity: a perturbation approach through graph spectral method. *Int J Adv Eng Sci Appl Math* 11, 91–104

Book chapters

1. Gadiyaram V., **Dighe A.,** Ghosh S., Vishveshwara S. (2021) Network Re-Wiring During Allostery and Protein-Protein Interactions: A Graph Spectral Approach. In: Di Paola L., Giuliani A. (eds) *Allostery. Methods in Molecular Biology,* vol 2253. Humana, New York, NY.

Conference Proceedings

1. **Dighe A.,** Chandra N., Vishveshwara S., Ananthasuresh GK (2015) Dissecting Ligand Binding Sites: A Layer at a Time *Biophys J.* 108(2):1,pp.216a
2. Vishveshwara,S., **Dighe,A.,** Gadiyaram. V. (2019) Graph Spectral Properties of the Sidechain Networks of Protein Structures: Implications to Allostery and Structure Comparison *Biophys J.* 116 (3), 463a-464a

**References**

1. David Braun

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2. Günter Wagner

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