

Yaseswini Neelamraju , PhD

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Bioinformatics scientist with 10 years of professional experience in analyzing next-generation DNA and RNA sequencing data primarily from human subjects diagnosed with cancer. I am committed to developing and applying computational tools to new and/or existing genomic data and contributing to translational research.

WORK EXPERIENCE

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| Jan2024 – Present | Research Scientist, Bioinformatics & Computational Biology
University of Virginia, Charlottesville, VA |
| Jun-Aug,2022 | Summer Intern in Predictive Sciences
Bristol-Myers Squibb, Cambridge, MA <ul style="list-style-type: none">• Reproduced and applied an existing tumor microenvironment (TME) subtype method to pancreatic cancer data from TCGA• Modified the existing TME subtype classification approach for pan-cancer data• Developed an R shiny application implementing existing and improved TME classification method on tumor data |
| 2017 – 2018 | Bioinformatics Analyst
University of Virginia, Charlottesville, USA <ul style="list-style-type: none">• Identified DNA methylation and transcriptional changes in patients diagnosed and relapsed with acute myeloid leukemia (AML)• Contributed to three peer-reviewed manuscripts through collaborative research. |
| 2015 – 2017 | Bioinformatics Analyst
Weill Cornell Medicine, New York, USA <ul style="list-style-type: none">• Identified DNA methylation and transcriptional changes in patients diagnosed and relapsed with acute myeloid leukemia (AML)• Identified DNA methylation changes contributing to age-related changes in <i>TET2</i> knock down zebrafish developing myelodysplastic syndrome (MDS) |
| 2013 – 2015 | Bioinformatician
Indiana University-Purdue University, Indiana, USA <ul style="list-style-type: none">• Analyzed and identified mutational landscape of RNA binding proteins across 6000 cancer genomics constituting 26 cancer types from TCGA consortium• Identified splicing alternations contributing to endocrine resistance in breast cancer cell lines in collaborative research with IU School of Medicine.• Curated RNA binding proteins and their known functional characteristics identified in humans to construct a database useful for researchers in the field |

EDUCATION

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| 2018 – 2023 | Doctor of Philosophy
Department of Biochemistry and Molecular Genetics
University of Virginia, Charlottesville
Major: Bioinformatics
Thesis: Identifying molecular signatures associated with aging in myeloid malignancies |
| 2011 – 2013 | Master's in Technology, Bioinformatics
Department of Biotechnology and Bioinformatics
University of Hyderabad, India |

Thesis: Integrating disease-gene and protein-protein interactions to identify candidate genes for Psoriasis using network theory.

2007 – 2011

Bachelor of Technology, Biotechnology

Department of Biotechnology

Sreenidhi Institute of Science and Technology,

Jawaharlal Nehru Technological University, India

MENTORSHIP

2022 -- Present

University of Virginia

Co-mentor for BME capstone undergraduate students in developing prognostic models based on DNA methylation and gene expression data generated from patients diagnosed with AML

TEACHING ASSISTANTSHIP

2021 – 2022

University of Virginia

Mentored an undergraduate student in learning the basics of computational biology.

- Basic programming in R
- Survival analysis

Spring, 2017

University of Virginia

Teaching assistant for workshops on

- Introduction to R
- Advanced data manipulation in R
- Visualization in R using ggplot2

2014

Indiana University Purdue University

- Analysis of microarray array using R

SKILLS

- Experience working with human clinical trial data
- Experience working on high-performance computing systems
- I have experience working with large genetic, genomic, and clinical datasets identified from TCGA, DepMap, Beat-AML, ENCODE, NCBI GEO, cBioPortal
- Experience in integrative analysis using multiple genomic datasets and clinical information
- Excellent oral and written communicable skills
- Excellent molecular biology background.

Sequence analysis	Sequence alignment tools (DNA and protein): BLAST, BLAT, ClustalW
NGS data	DNA methylation (Bisulphite sequencing) Bulk & single-cell RNA sequencing ChIP-sequencing ATAC-sequencing
Data analysis tools	Microarray data analysis Genome Visualization – UCSC genome browser, IGV

	Methylkit , MethylSig , MACS , Differential peak analysis using DESeq2 FastQC, STAR, HISAT, Salmon, Kallisto , TopHat , Bowtie, Differential gene expression analysis (DESeq2), Gene co-expression networks (WGCNA), Deconvolution analysis methods for bulkRNAseq – CIBERSORT, Single-cell RNAsequencing , Splicing analysis using rMATS
Functional genomics	Gene set enrichment analysis (GSEA), single sample Gene set enrichment analysis (ssGSEA) , Gene set variation analysis (GSVA) , Ingenuity Pathway analysis (IPA), EnrichR , GProfileR , GREAT (Genomic Regions Enrichment of Annotations Tool) , Transcription factor binding analysis (HOMER ,MEME suite of tools).
Systems biology	Network analysis
Biostatistics	Application of statistical tests to genomic data, Survival analysis, Cox proportional hazards model, Correlation
Machine Learning	Principal Component analysis, K-means clustering, Hierarchical clustering, Linear models, Logistic regression, Generalized linear regression methods, principal component regression (PCR), partial least squares regression (PLS), Xtreme Gradient Boosting (XGBoost)
Operating Systems	Linux, Mac OS and Windows
Scripting/Programming Languages	C (beginner), Perl, R, Python
Version Control	GitHub, R markdown
Workflow Management	Nextflow
Web development	HTML, CSS

PUBLICATIONS

* Authors contributed equally

1. **Neelamraju Y.***, E. Gjini, S. Chhangawala, H. Fan, S. He, C. B. Jing, A. T. Nguyen, S. Prajapati, C. Sheridan, Y. Houvras, A. Melnick, A. T. Look and F. E. Garrett-Bakelman (2023). "Depletion of tet2 results in age-dependent changes in DNA methylation and gene expression in a zebrafish model of myelodysplastic syndrome." Front Hematol 2.
2. Rapaport, F.*, K. Seier*, **Y. Neelamraju***, D. Hassane, T. Baslan, D. T. Gildea, S. Haddox, T. Lee, H. M. Murdock, C. Sheridan, A. Thurmond, L. Wang, M. Carroll, L. D. Cripe, H. Fernandez, C. E. Mason, E. Paietta, G. J. Roboz, Z. Sun, M. S. Tallman, Y. Zhang, M. Gonen, R. Levine, A. M. Melnick, M. Kleppe and F. E. Garrett-Bakelman (2022). "Integrative analysis identifies an older female-linked AML patient group with better risk in ECOG-ACRIN Cancer Research Group's clinical trial E3999." Blood Cancer J 12(9): 137.
3. Barreyro, L., A. M. Sampson, C. Ishikawa, K. M. Hueneman, K. Choi, M. A. Pujato, S. Chutipongtanate, et al. "Blocking Ube2n Abrogates Oncogenic Immune Signaling in Acute Myeloid Leukemia." Sci Transl Med 14, no. 635 (Mar 9 2022): eabb7695.
4. Rapaport F, **Neelamraju Y**, Baslan T, Hassane D, Gruszczynska A, Robert de Massy M, et al. Genomic and evolutionary portraits of disease relapse in acute myeloid leukemia. Leukemia. 2021.
5. Olson TL, Cheon H, Xing JC, Olson KC, Paila U, Hamele CE, et al. Frequent somatic TET2 mutations in chronic NK-LGL leukemia with distinct patterns of cytopenias. Blood. 2021;138(8):662-73.
6. Abshiru NA, Sikora JW, Camarillo JM, Morris JA, Compton PD, Lee T, et al. Targeted detection and quantitation of histone modifications from 1,000 cells. PLoS One. 2020;15(10):e0240829.

7. Gokmen-Polar Y, **Neelamraju Y**, Goswami CP, Gu Y, Gu X, Nallamotheu G, et al. Splicing factor ESRP1 controls ER-positive breast cancer by altering metabolic pathways. *EMBO Rep.* 2019;20(2).
8. **Neelamraju Y**, Gonzalez-Perez A, Bhat-Nakshatri P, Nakshatri H, Janga SC. Mutational landscape of RNA-binding proteins in human cancers. *RNA Biol.* 2018;15(1):115-29.
9. Nishtala S, **Neelamraju Y**, Janga SC. Dissecting the expression relationships between RNA-binding proteins and their cognate targets in eukaryotic post-transcriptional regulatory networks. *Sci Rep.* 2016; 6:25711.
10. **Neelamraju Y**, Hashemikhabir S, Janga SC. The human RBPome: from genes and proteins to human disease. *J Proteomics.* 2015;127(Pt A):61-70.
11. Hashemikhabir S, **Neelamraju Y**, Janga SC. Database of RNA binding protein expression and disease dynamics (READ DB). Database (Oxford). 2015;2015: bav072.
12. Gokmen-Polar Y, Vladislav IT, **Neelamraju Y**, Janga SC, Badve S. Prognostic impact of HOTAIR expression is restricted to ER-negative breast cancers. *Sci Rep.* 2015; 5:8765.
13. Gokmen-Polar Y, **Neelamraju Y**, Goswami CP, Gu X, Nallamotheu G, Janga SC, et al. Expression levels of SF3B3 correlate with prognosis and endocrine resistance in estrogen receptor-positive breast cancer. *Mod Pathol.* 2015;28(5):677-85.
14. Chaturvedi P, **Neelamraju Y**, Arif W, Kalsotra A, Janga SC. Uncovering RNA binding proteins associated with age and gender during liver maturation. *Sci Rep.* 2015; 5:9512.

CONFERENCE PRESENTATIONS

POSTER

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| 2023 | 65th ASH Annual Meeting and Exposition
“A pro-inflammatory gene signature characterizes a better risk aged AML patient group in ECOG-ACRIN Cancer Research Group's clinical trial E3999”

FASEB, The Hematologic Malignancies Conference, FASEB, August 2023
“A pro-inflammatory gene signature characterizes a better risk aged AML patient group in ECOG-ACRIN Cancer Research Group's clinical trial E3999” – also selected for lightning talk |
| 2021 | FASEB, The Hematologic Malignancies Conference, FASEB, July 2021 (Virtual conference)
“An integrative analysis identifies a female-linked group that associates with better risk for AML patients older than sixty years of age in a clinical trial of the ECOG-ACRIN Cancer Research Group (E3999)” |
| 2015 | Cold Spring Harbor Meeting. Systems Biology: Global regulation of Gene Expression
“Mutational landscape of RNA Binding Proteins in human cancer” |
| 2014 | Rustbelt RNA Meeting, 2014, Pittsburg, PA
“The human RBPome: from genes and proteins to human disease” – poster presentation |

ORAL

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| 2017 | 1st Annual Commonwealth of Virginia Cancer Research Conference 2017, Charlottesville
“AMLs with high methylation in GADD45A promoter exhibit distinct molecular profiles associated with poor outcome” |
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HACKATHONS

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- 2023** Bio Hackathon organized by St Jude's Children's Research Hospital
- Developed shiny modules to visualize DNA methylation data

CONFERENCES & WORKSHOP ATTENDANCE

- 2020** Biomedical Data Science (Virtual conference) – CSHL
- 2016** Epi workshop jointly organized by Weill Cornell Medicine, Hospital for Special Surgery and New York City College of Technology
- 2015** Advances in Genome Science, NYC Illumina User Group Meeting 2015.
- 2015** Great Lakes Bioinformatics Conference

HONORS, AWARDS, AND SCHOLARSHIP

- 2023** UVA's Cancer Center trainee travel award to attend the hematologic malignancies conference organized by FASEB
- 2015** Stipend award to attend the Cold Spring Laboratory Meeting on "Systems Biology: Global regulation of Gene Expression" held in Puerto Rico from 28th Jan,15 - 01st Feb,15)
- 2011** SNIST-ISTE Gold medal for securing first rank amongst the students of B.Tech Biotechnology Class of 2011.
- 2007-2010** Academic excellence awards while pursuing Bachelor in Biotechnology for the years 2007 - 2010.

VOLUNTEER ACTIVITIES

- 2024 - Present** Member, website development team for the Women-in-bioinformatics (Boston chapter)
- 2022** Participated in the Skill2Give event organized by Bristol-Myers Squibb (BMS)
- 2021 – 2023** Co-organizer of CPHG (Center for Public Health Genomics) computing club.
- 2022** BMG recruitment, UVA student host for 1 weekend
- 2019 – 2020** BMG recruitment, UVA, *student* host for 1-2 weekends per year
- 2019-2020** Volunteer Coordinator at Society for the Promotion of Indian Classical Music and Culture Amongst Youth (SPICMACAY), UVA Chapter
- 2019** Participated in the data hackathon organized by the UVA Biomedical Data Sciences Training Program
- 2017-2018** Volunteer at Society for the Promotion of Indian Classical Music and Culture Amongst Youth (SPICMACAY), UVA Chapter

WEBSITES

LinkedIn: [Yaseswini Neelamraju | LinkedIn](#)

Google Scholar: <https://scholar.google.com/citations?user=wzrrprAAAAAJ>

GitHub: <https://github.com/Yaseswini>