

Yaseswini Neelamraju

yaseswini.1404@gmail.com; yn9w@virginia.edu

A bioinformatics scientist with 5 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 contribute to translational research.

EDUCATION

2018 – Present	Ph.D. Candidate Department of Biochemistry and Molecular Genetics University of Virginia, Charlottesville Major: Bioinformatics Thesis: Identifying molecular signatures associated with aging in hematological malignancies
2011 – 2013	Masters 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	Bachelors of Technology, Biotechnology Department of Biotechnology Sreenidhi Institute of Science and Technology, Jawaharlal Nehru Technological University, India

PROFESSIONAL EXPERIENCE

Jun-Aug,2022	Summer Intern in Predictive Sciences Bristol-Myers Squibb, Cambridge, MA <ul style="list-style-type: none">• Worked on reproducing and applying an existing tumor microenvironment (TME) subtype method to pancreatic cancer data from TCGA• Modified the existing TME subtype classification approach to improve the accuracy• Developed a 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 TET2 knock down zebrafish developing myelodysplastic syndrome (MDS)
2013 – 2015	Research Scholar Indiana University-Purdue University, Indiana, USA

- 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

TEACHING ASSISTANTSHIP

2021 – 2022	University of Virginia Currently mentoring an undergraduate student in learning basics of computational biology. <ul style="list-style-type: none"> • Basic programming in R • Survival analysis
Spring, 2017	University of Virginia Teaching assistant for workshops on <ul style="list-style-type: none"> • Introduction to R • Advanced data manipulation in R • Visualization in R using ggplot2
2014	Indiana University Purdue University <ul style="list-style-type: none"> • 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
Next generation sequencing data analysis	Microarray data analysis Genome Visualization – UCSC genome browser, IGV Bulk-RNAseq: FastQC, STAR, HISAT, Salmon, Kallisto , TopHat , Bowtie, Differential gene expression analysis (DESeq2), Gene co-expression networks (WGCNA) , Deconvolution analysis methods for bulkRNAseq - CIBERSORT RNA-splicing: rMATS DNA methylation (Bisulphite sequencing): MethyKit, MethylSig, Integrative analysis with gene expression data ChIP-seq : MACS , Differential peak analysis using DESeq2
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 using igraph R package

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 . Experience working in conda environment
Version Control	GitHub, R markdown
Workflow Management	Nextflow (Beginner)
Web development	HTML, CSS, RShiny, GitHub Pages

PUBLICATIONS

1. **Yaseswini Neelamraju**, Evisa Gjini, Sagar Chhangawala, Hao Fan, Shuning He, Chang-Bin Jing, Ashley T Nguyen, Subhash Prajapati, Caroline Sheridan, Yariv Houvras, Ari Melnick, A. Thomas Look, Francine Garrett-Bakelman. "Depletion of tet2 results in age-dependent changes in DNA methylation and gene expression in a zebrafish model of myelodysplastic syndrome". (*Accepted for publication in Frontiers in Hematology*)
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.

PRESENTATIONS

- | | |
|-------------|--|
| 2023 | “A pro-inflammatory gene signature characterizes a better risk aged AML patient group in ECOG-ACRIN Cancer Research Group's clinical trial E3999” – Lightning talk and poster presentation
<i>FASEB, The Hematologic Malignancies Conference, FASEB, August 2023</i> |
| 2021 | “Identifying molecular determinants of sex associated outcomes in acute myeloid leukemia patients over the age of 60” – Poster presentation
<i>Biochemistry and Molecular Genetics Department Retreat, October 2021</i> |
| 2021 | “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)” – poster presentation
<i>FASEB, The Hematologic Malignancies Conference, FASEB, July 2021 (Virtual conference)</i> |
| 2021 | “An integrative classifier identifies as sex-associated outcome risk in AML patients older than sixty years of age” – Oral presentation
<i>Biomedical data science research club, April 2021</i> |
| 2019 | “Sex based differences in clinical outcomes of Acute Myeloid Leukemia patients over the age of 60”
<i>Biochemistry and Molecular Genetics Department Retreat, October 2019</i> |
| 2017 | “AMLs with high methylation in GADD45A promoter exhibit distinct molecular profiles associated with poor outcome” – oral presentation
<i>1st Annual Commonwealth of Virginia Cancer Research Conference 2017, Charlottesville</i> |
| 2015 | “Mutational landscape of RNA Binding Proteins in human cancer” – poster presentation
<i>Systems Biology: Global regulation of Gene Expression Meeting, 2015, Cold Spring Harbor Laboratory.</i> |
| 2014 | “The human RBPome: from genes and proteins to human disease” – poster presentation
<i>Rustbelt RNA Meeting, 2014, Pittsburg, PA</i> |

CONFERENCES AND WORKSHOPS

- | | |
|-------------|---|
| 2023 | FASEB, The Hematologic Malignancies Conference |
| 2023 | Bio Hackathon organized by St Jude's Children's Research Hospital |
| 2021 | FASEB, The Hematologic Malignancies Conference |
| 2020 | Biomedical Data Science (Virtual conference) – CSHL |
| 2016 | EpiWorkshop 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 |
| 2015 | Systems Biology: Global regulation of Gene Expression, Cold Spring Harbor Laboratory |

2014 Rustbelt RNA Meeting

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 during 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 Bachelors in Biotechnology for the years 2007 - 2010.

ACADEMIC VOLUNTEER ACTIVITIES

2022 Participated in the Skill2Give event organized by Bristol-Myers Squibb (BMS)

2021 – Current 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

WEBSITE

LinkedIn: [Yaseswini Neelamraju | LinkedIn](#)

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

HOBBIES

Hiking and trail walking with my dog; gardening; cooking; photography and learning all things creative!