AVINASH RAMU

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Education

2016–Present	**PhD student., Human and Statistical Genetics** Washington University in St. Louis, St. Louis, MO Advised by **Barak Cohen**
2011	**M.S., Electrical Engineering**, University of Florida, Gainesville, FL
2005–2009	**B.Tech., Electronics and Communication Engineering**, National Institute of Technology, India

Selected Publications

Rockweiler, N. B., **Ramu, A.**, Nagirnaja, L., Wong, W. H., Noordam, M. J., Drubin, C. W., Huang, N., Miller, B., Todres, E. Z., Vigh-Conrad, K. A., Zito, A., Small, K. S., Ardlie, K. G., Cohen, B. A., & Conrad, D. F. (2023). The origins and functional effects of postzygotic mutations throughout the human life span. Science, 380(6641), eabn7113. https://doi.org/10.1126/science.abn7113

Cotto, K. C., Feng, Y.-Y., **Ramu, A.**, Richters, M., Freshour, S. L., Skidmore, Z. L., Xia, H., McMichael, J. F., Kunisaki, J., Campbell, K. M., Chen, T. H.-P., Rozycki, E. B., Adkins, D., Devarakonda, S., Sankararaman, S., Lin, Y., Chapman, W. C., Maher, C. A., Arora, V., . . . Griffith, M. (2023). Integrated analysis of genomic and transcriptomic data for the discovery of splice-associated variants in cancer. Nature Communications, 14(1), 1589. https://doi.org/10.1038/s41467-023-37266-6

Huang, H., Pan, J., Spielberg, D. R., Hanchard, N. A., Scott, D. A., Burrage, L. C., Dai, H., Murdock, D., Rosenfeld, J. A., Mohammad, A., Huang, T., Lindsey, A. G., Kim, H., Chen, J., **Ramu, A.**, Morrison, S. A., Dawson, Z. D., Hu, A. Z., Tycksen, E., . . . Schedl, T. (2022). A dominant negative variant of RAB5B disrupts maturation of surfactant protein B and surfactant protein C. Proceedings of the National Academy of Sciences of the United States of America, 119(6), e2105228119. https://doi.org/10.1073/pnas.2105228119

Ramu, A. & Cohen, B. Transcription factor fluctuations underlie cell-to-cell variability in a signaling pathway response. *bioRxiv* (2022) doi:10.1101/2022.11.30.518555.

Hong, C. K.[*], **Ramu, A.**[*], Zhao, S.[*] & Cohen, B. A. Effect of genomic and cellular environments on gene expression noise. *bioRxiv* (2022) doi:10.1101/2022.08.31.506082.

Laisk, T. et al. The genetic architecture of sporadic and multiple consecutive miscarriage. *Nature Communications* 11, 5980 (2020).

Ramu, A., Noordam, M. J., Schwartz, R. S., Wuster, A., Hurles, M. E., Cartwright, R. A. & Conrad, D. F. DeNovoGear: de novo indel and point mutation discovery and phasing. *Nat. Methods* 10, 985–987 (2013).

Lopes, A. M. et al. Human spermatogenic failure purges deleterious mutation load from the autosomes and both sex chromosomes, including the gene DMRT1. *PLoS Genet.* 9, e1003349 (2013).

Ramu, A., Kahveci, T. & Burleigh, J. G. A scalable method for identifying frequent subtrees in sets of large phylogenetic trees. *BMC Bioinformatics* 13, 256 (2012).

Employment History

Summer 2021   **Computational Biology Intern,**
Adaptive Biotechnologies, Seattle
Role - Developed machine learning models to understand antigen recognition by T-cell receptors.

2013–2016   **Bioinformaticist,**
The McDonnell Genome Institute (Obi and Malachi Griffith lab),
Washington University in St. Louis School of Medicine
Role - Analyzed rare-cancer patient genomes and designed computational analysis infrastructure.

2011–2013   **Bioinformaticist,**
Don Conrad Lab (Human Genetics focus), Department of Genetics,
Washington University in St. Louis School of Medicine
Role - Developed statistical models to identify de-novo and somatic mutations and to study underlying mutational processes. Performed GWAS studies for 2 complex traits (miscarriage and spermatogenesis).

Professional Activities

Tech Leadership Fellow, Launchcode, St. Louis.

Reviewer for Nature Methods, PLOS Computational Biology, GigaScience.

Leadership Committee, Student Advisory Committee, Washington University in St. Louis.

Honors

July 2019   Scholarship to attend Center for the Physics of Living Cells (UIUC) summer school.

July 2017   Travel award to attend *Summer Institute in Statistical Genetics*, University of Washington, Seattle.