# **ANIKA GUPTA**

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I'm a PhD student working at the intersection of data science and high-throughput biology through the lens of single cell genomics. I'm passionate about data-driven biomedical innovation through venture creation.

# **EDUCATION**

# **Harvard University**

Doctor of Philosophy, Bioinformatics and Integrative Genomics

2018 - present

# Massachusetts Institute of Technology

Bachelor of Science, Computer Science and Molecular Biology 2014 - 2018

# **Programming Languages**

Python (keras, scikit-learn, pandas, numpy, scipy), R, HTML, Unix/Linux, LaTex

# **Teaching Experience**

Applied Machine Learning

Deep Learning for Biomedical Data

#### **Select Courses**

# Computational:

- Machine Learning
- Design and Analysis of Algorithms
- Computational Genomics

#### Biomedical:

- Genetics
- Human Pathology (HMS)
- Concepts in Genome Analysis

#### **Biotech Entrepreneurship:**

- Strategic Decision Making in the Life Sciences (Sloan)
- Business of Biotech (RA Capital)

#### RESEARCH EXPERIENCE

#### Broad Institute of Harvard and MIT, PI: Eric Lander

Jan 2019 - Present

Inferring causal gene regulatory interactions from high-throughput, time stamped single cell transcriptomic data. Goal is to systematically identify cellular pathways without perturbing cells.

# Stanford University, PI: Dennis Wall

June 2017 - June 2018

Implemented coalitional game theory and unsupervised machine learning on the genomes of 4,610 individuals with autism spectrum disorder to map the combinatorial effect of genotype on ASD phenotypes.

# Broad Institute, Pls: Aviv Regev, Kasper Lage

Sep 2015 - June 2018

Detected cancer vulnerabilities through a statistical framework that targets protein interaction networks under purifying selection—those that are rarely mutated due to their key role in tumor proliferation—in 4,700 cancer genomes

#### Foundation Medicine, Cancer Genomics Team

May 2016 - May 2017

Characterized the therapeutically targetable gene alteration landscapes—driver mutations, tumor mutational burden, and checkpoint inhibitors—of lung cancers, through analysis of >20,000 patient tumors towards precision medicine.

#### Merck, Bioinformatics Team

May - Aug 2015

Analyzed gene expression and signaling pathway data for 416 genes to predict immunotherapy combination gene signatures and enable synergistic therapeutic delivery against melanoma.

## **PROJECTS**

#### The Data Pulse, Podcast Host

Jul 2020 - Present

I host a <u>podcast</u> at the intersection of data science & biomedical innovation, ranging from molecular to clinical and population scales, and spanning academia and industry. Season 1 has >10k downloads and >500 repeat listeners.

#### **5AM Ventures,** Fellow

Jul - Dec 2019

As one of two fellows, I guided strategic decisions in the venture creation arm. Designed the bioinformatics platform for an immuno-oncology company, outlined the translational biomarker strategy for a neurodegenerative disease company, and conducted scientific diligence in the regenerative medicine and RNA splicing domains for company builds.

# Undiagnosed Diseases Network, Case Analysis Team

Oct - Dec 2018

Standardized and automated a genomic analysis (variant classification) pipeline for the Brigham Genomic Medicine team's efforts to uncover the genetic causes of four previously intractable, rare patient disease cases.

#### Flagship Pioneering, VentureLabs Intern

Jan - May 2017

Built quantitative models to enable key strategic decisions that could maximize value creation for a mitochondrial therapy-based Series A biotech company build.

#### **LEADERSHIP**

#### Models, Inference, and Algorithms, Steering Committee

Aug 2020 - Present

Guide the dialogue on machine learning within the Broad Institute & broader community as a committee member, inviting researchers to share their latest work, with a focus on the theoretical underpinnings and a discussion-based forum to foster collaborations at the interface of machine learning and biomedicine.

#### MIT Biotechnology Group, Founder and Co-President

June 2015 - June 2017

Established the undergraduate chapter of MIT's first (now >1,000-member) biotech initiative as a liaison between students and the biotech industry. Organized pitch competitions, speaker panels, interactive workshops, mentorship programs, due diligence groups, and interactive symposiums to foster student entrepreneurship within the biotech industry.

# **PUBLICATIONS**

- Horn H, Fagre C, **Gupta A**, Tsafou K, Fornelos N, Neal JT, Lage K (2020). Using protein interaction networks to identify cancer dependencies from tumor genome data. *bioRxiv*.
- Sun M\*, **Gupta A**\*, Varma M, Paskov K, Jung J, Stockham N, Wall D (2019). Coalitional game theory facilitates identification of noncoding variants associated with autism. *Journal of Biomedical Informatics Insights*.
- Frampton GM, Hartmaier R, Sokol E, **Gupta A**, Greenbowe J, Roels S, Gay L, Stephens PJ (2018). Novel CDH1 mutations in breast invasive lobular carcinoma. *Cancer Research*. Volume 79, pp. 2363.
- **Gupta A\***, Sun M\*, Paskov K, Stockham N, Jung J, Wall D (2018). Coalitional game theory as a promising approach to identify candidate autism genes. *Pac Symp Biocomputing*. pp. 436-447.
- **Gupta A\***, Horn H\*, Razaz P, Kim A, Lawrence M, Getz G, Lage K (2017). Detecting cancer vulnerabilities through gene networks under purifying selection in 4,700 cancer genomes. *bioRxiv*

#### **CONFERENCE PRESENTATIONS**

- **Gupta A\***, Siraj L\*, Jones TR, Bloemendal A, Subramanian V, Lander ES (2019). Systematically learning cellular programs from single-cell transcriptional and chromatin accessibility data. 33<sup>rd</sup> Conference on Neural Information Processing Systems: Learning Meaningful Representations for Life workshop. Vancouver, CA.
- **Gupta A\***, Siraj L\*, Jones TR, Bloemendal A, Subramanian V, Lander ES (2019). Systematically learning biological pathway signatures from single cell gene expression data. 3<sup>rd</sup> Annual Women in Data Science Conference. Cambridge, MA.
- **Gupta A**, Horn H, Razaz P, Kim A, Lawrence M, Getz G, Lage K (2018). Detecting cancer vulnerabilities through gene networks under purifying selection. *American Society of Human Genetics Annual Meeting*. San Diego, CA.
- **Gupta A\***, Sun M\*, Paskov K, Stockham N, Jung J, Wall D (2018). Identifying candidate autism genes via coalitional game theory. *American Medical Informatics Association Informatics Summit.* San Francisco, CA.
- **Gupta A\***, Sun M\*, Paskov K, Stockham N, Jung J, Wall D (2018). Coalitional game theory as a promising approach to identify candidate autism genes. 23<sup>rd</sup> Annual Pacific Symposium on Biocomputing. Big Island, HI.
- Frampton G, Hartmaier R, Sokol E, **Gupta A**, Greenbow J, Roels S, Gay L, Stephens P (2018). Novel CDH1 mutations in breast invasive lobular carcinoma. *American Association for Cancer Research Annual Meeting*. Chicago, IL.
- Frampton G, **Gupta A**, Connelly C, Fabrizio D, et al (2017). Hybrid-capture based comprehensive genomic profiling of lung adenocarcinoma identifies patients who may benefit from targeted therapies as well as immunotherapies using tumor mutational Burden (TMB), a new predictive biomarker of response to immune checkpoint inhibitors. *Laboratory Investigation*.
- **Gupta A**, Chalmers Z, Connelly C, Frampton G, Chmielecki J, Ali S, Suh J, Schrock A, Ross J, Stephens P, Miller V (2016). The druggable mutation landscape of lung cancer. *IASLC 17th World Conference on Lung Cancer.* Vienna, Austria.
- **Gupta A**, Horn H, Lawrence M, Getz G, Lage K (2015). Identifying and targeting gene networks under purifying selection. 11th Annual Broad Institute Symposium. Cambridge, MA.