

Aroon Chande

Computational Biologist & Bioinformatics Engineer

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I've spent ten-plus years working across clinical genomics, oncology, and drug development — from CDC pathogen surveillance and drug development at Seagen to clinical genomics at Color and the NIH All of Us program.

EXPERIENCE

Staff Bioinformatics Engineer

May 2022 – Present

Color Health · San Francisco, CA

- Co-own the computational infrastructure for the NIH *All of Us* return-of-results program, processing hereditary and pharmacogenetic variants for 200,000+ participants.
- Led a full refresh of the pharmacogenetics product line for oncology care — combining literature review and computational analysis to prioritize new genes and variants.
- Design and validate clinical genomics pipelines in close collaboration with lab, clinical, and product teams, turning sequencing data into reproducible, analysis-ready results for patient return-of-results.

Bioinformatics Scientist

Aug 2020 – May 2022

Seagen · Seattle, WA

- Built an R Shiny analysis platform enabling bench scientists to run ML-based clustering and differential gene expression analysis for drug development.
- Facilitated analysis of a 30,000+ patient harmonized tumor RNA-seq dataset spanning public (TCGA, GTEx, cBioPortal) and internal data.
- Served as lead developer and technical lead for an integrated platform supporting RNA-seq, proteomics, and IHC pathology annotation; supported design of new cancer cell lines and genome-wide editing screens.

Scientific Advisor

May 2016 – May 2022

Applied Bioinformatics Laboratory · Atlanta, GA

- Collaborated with CDC on biosecurity-focused pathogen surveillance software for efficient reconstruction of pathogen genes and genomes from environmental samples.
- Developed novel algorithms and high-performance platforms to simplify analysis of NGS data for detecting select agents (anthrax, Ebola, and other highly contagious viral diseases).

COVID-19 Pandemic Response

Mar – Aug 2020

Georgia Institute of Technology · Atlanta, GA

- Lead developer for the COVID-19 Event Risk Assessment Planning Tool — serving 50 million risk predictions to 8 million users.
- Lead developer of the MyTest platform for asymptomatic COVID-19 testing — the first campus-wide free testing program in the nation, facilitating over 250,000 tests.

EDUCATION

Ph.D. Bioinformatics

2020

Georgia Institute of Technology

- Human computational genetics — models for disease burden across Colombia and South America, focused on complex diseases such as type 2 diabetes and coronary artery disease.
- Visiting Scientist Fellowship, São Paulo Research Foundation (2018); Graduate Research Award (2017–2020).

M.S. Bioinformatics

2016

Georgia Institute of Technology

- Graduate Research Award (2015–2016).

B.S. Microbiology & B.S. Biology

2013 – 2015

University of Iowa

SKILLS

LANGUAGES Python · R · C++ · SQL · Bash · Terraform

CLOUD & INFRA AWS · Docker · Kubernetes · CI/CD
(GitHub Actions, CircleCI)

PIPELINES & WORKFLOWS Nextflow · WDL / Cromwell ·
Conda / Bioconda · ETL pipelines

FULL-STACK DEV Flask · Django · FastAPI · R Shiny ·
React

GENOMICS WGS · WES · RNA-seq · Microarray ·
Pharmacogenetics

VARIANT ANALYSIS GATK · samtools / bcftools · BWA /
minimap2 · VEP / SnpEff

DATA & ML ML clustering · Differential expression ·
Scientific computing

SELECTED PUBLICATIONS

The Impact of Ethnicity and Genetic Ancestry on Disease Prevalence and Risk in Colombia

Frontiers in Genetics (2021) · Chande AT, Nagar SD, Rishishwar L, Mariño-Ramírez L, Medina-Rivas MA, Valderrama-Aguirre A, et al.

Real-time, interactive website for US-county-level COVID-19 event risk assessment

Nature Human Behaviour (2020) · Chande AT, Lee S, Harris M, Nguyen Q, Beckett SJ, Hilley T, et al.

Ancestry effects on type 2 diabetes genetic risk inference in Hispanic/Latino populations.

BMC Medical Genetics (2020) · Chande AT, Rishishwar L, Conley AB, Valderrama-Aguirre A, Medina-Rivas MA, Jordan IK

The phenotypic consequences of genetic divergence between admixed Latin American populations: Antioquia and Chocó, Colombia

Genome Biology and Evolution (2020) · Chande AT, Rishishwar L, Ban D, Nagar SD, Conley AB, Rowell J, et al.

STing: accurate and ultrafast genomic profiling with exact sequence matches

Nucleic Acids Research (2019) · Espitia H, Chande AT, Nagar SD, Smith H., Jordan IK, Rishishwar L

Influence of genetic ancestry and socioeconomic status on type 2 diabetes in the diverse Colombian populations of Chocó and Antioquia

Scientific Reports (2017) · Chande AT, Rowell J, Rishishwar L, Conley AB, Norris ET, Valderrama-Aguirre A, et al.