

**SIDHANT PUNTAMBEKAR**  
**Computer Scientist | Computational Biologist**

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## Education

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### **Computer Science Undergraduate, Computational Biology Minor, Molecular Biology Minor**

**University of Colorado Boulder**, August 2019 - present

- University of Colorado Esteemed Scholar. **Overall GPA: 3.958, Major GPA: 4.000**

### **International Baccalaureate Diploma, High School Diploma**

**Fairview High School**, Boulder, CO, August 2015 - May 2019

- Advanced Placement Honors with Distinction

## Work Experience

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### **Biomedical Informatics Research Intern, Sunyaev Lab**

**Harvard Medical School**, Boston, MA, May 2021 - present

- Biomedical Informatics Research Intern at Harvard Medical School working in the computational genomics lab of Dr. Shamil Sunyaev.
- Analyzing the Broad Institute's Genome Aggregation Database (gnomAD) dataset to better quantify and understand the mutational constraint on missense and loss of function genomic variants using a fine-scale mutation map.
- Modelled mutational spectrum using machine learning techniques (logistic regressions) on a training set of over 125,000 synonymous genome and exome sequences.
- Built a classifier to predict which genes are most likely to succumb to debilitating loss of function mutations.

### **Tech Team Director, HackCU**

**University of Colorado Boulder**, Boulder, CO, May 2020 - Present

- Developed the new HackCU hub website ([hackcu.org](http://hackcu.org)) utilizing full stack development tools and continuous integration (CI/CD) as part of the technology/software development team.
- Migrating HackCU website over to Next.js framework to integrate backend, database, and content management system calls.
- Hosted workshops during hackathons on bioinformatics and recruited new contributors to HackCU Development team.

### **Bioinformatics Research Intern, RNA Bioscience Initiative**

**University of Colorado Anschutz Medical School**, Denver, CO, May 2020 - May 2021

- Primary author on research paper published in Public Library Of Sciences Biology journal (May, 2021) regarding the problem of single cell RNA-sequencing metadata submission in gene expression databases (NCBI GEO).
- Developed R Shiny web application for the clustifyr R library in order to facilitate analysis of scRNA-seq data.
- Conducted a meta-analysis of scRNA-seq data sets from NCBI Gene Expression Omnibus and Tabula Muris (mouse scRNA-seq atlas) utilizing principal component analysis, graph based clustering, and uniform manifold approximation and projection.

### **Learning Assistant, CSCI 1300**

**University of Colorado Boulder**, Boulder, CO, January 2020 - May 2020

- Assisted students in learning course material for CSCI 1300: Starting Computing by holding weekly office hours, conducting recitation periods, and participating in crafting lesson plans.

### **Research Intern**

**The National Center for Atmospheric Research (NCAR)**, Boulder, CO, June 2018 - January 2019

- Researched landfalling tropical cyclones along the US eastern coastline to improve computational forecasting models using statistical analysis and data visualization from Extended Best Track Hurricane data set.
- Presented research at 99th American Meteorological Society conference in Phoenix, Arizona.

## Skills & Interests

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**Languages:** Python, Java, C/C++, R, HTML5, CSS, JavaScript, TypeScript, SQL, MATLAB, Scala

**Testing Tools:** Mocha, Chai, Jest, Cypress

**Continuous Integration Tools:** TravisCI, CircleCI, Jenkins

**Production Tools:** Google Cloud Platform, AWS, Git, Heroku, Docker/Kubernetes, NPM, Surge

**JavaScript Technologies:** ReactJS, NodeJS, ExpressJS, PassportJS, Bootstrap

**Databases:** MongoDB, MySQL, PostgreSQL

**Operating Systems:** Mac OS X, Linux (Ubuntu, CentOS), Windows