# **Augustine George Chemparathy**

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#### **EDUCATION**

# Stanford University, Stanford, CA

Sep 2015-Present

- BS, Computer Science and Bioengineering, Phi Beta Kappa, with Distinction
- MS, Management Science and Engineering, Health Systems Modeling and Policy track
- Relevant coursework: Deep Learning (CS 230); Systems Biology (BioE 101); Healthcare Operations Management (MS&E 263); Health Policy Modeling (MS&E 292)

#### **EXPERIENCE**

## Qi Lab, Stanford Bioengineering, Computational Biology Research Assistant September 2019-Present

- Used bioinformatic tools to search bacterial and archaeal genomes for novel DNA-cutting enzymes. These enzymes can provide an alternative to CRISPR-Cas for use in gene therapies.
- Developed a bioinformatic method to target a broad spectrum of RNA viruses with a minimal set of Cas13d guides. Created the website crispr-pacman.stanford.edu to make antiviral crRNA sets available to the research community.

## Systems Utilization Research for Stanford Medicine (SURF) student

March 2018-Present

Designed and evaluated a electronic health record dashboard at Stanford Children's Hospital to increase
adherence to the central line-associated bloodstream infection (CLABSI) prevention bundle. In the 15
months after the dashboard was deployed, adherence to the entire CLABSI bundle across the hospital
increased from 25% to 44%.

# Dror Lab, Stanford Computer Science, Computational Biology Intern

June 2017-January 2020

- Developed a data analysis tool to gather insights from noncovalent interaction data from molecular dynamics (MD) simulations. Available at getcontacts.github.io.
- Optimized ComBind, a software package for ranking ligand docking poses. Used ligands that do not bind to an enzyme in order to improve pose ranking for ligands that bind to the enzyme.

## Arbor Biotechnologies, Computational Biology Intern

June 2019-September 2019

• Identified novel CRISPR/Cas proteins using Arbor's metagenomic database. Developed a machine learning model to predict which computational hits were most likely to function as biologically active CRISPR effectors.

#### **ACTIVITIES**

## **Volunteer Organizer**

July 2018-Present

I organize Stanford students to cook and serve breakfast at the Palo Alto Opportunity Center, a transitional shelter for the homeless in the Palo Alto community.

## Co-President, Stanford Students in Biodesign (SSB)

May 2017-June 2019

Coordinate recruitment, activities, and club organization for Stanford's largest undergraduate organization for interdisciplinary biosciences.

## Writing Tutor, Stanford Hume Center for Writing And Speaking

Sept 2016-June 2019

Assist undergraduate and graduate students at Stanford with all stages of the writing process for conference publications, theses, term papers, applications, and other academic writing pieces.

**Teaching Assistant, Linear Dynamical Systems (EE 263), Stanford University**Sept 2017-Dec 2017 Held office hours, wrote midterm problems, and graded exams for 135 students in Stanford's highest-enrollment electrical engineering course.

#### **HONORS AND AWARDS**

• Phi Beta Kappa 2019

2017
2015
2015

## **PUBLICATIONS**

- Chemparathy, A., Seneviratne, M., Ward, A., Mirchandani, S., Li, R., Mathew, R., Wood, M., Shin, A., Donnelly, L., Scheinker, D., Lee, G. (2021). Development and implementation of a real-time bundle adherence dashboard for central line associated bloodstream infections. Upcoming publication in Pediatric Quality and Safety.
- Lin, X.\*, Liu, Y.\*, Chemparathy, A.\*, La Russa, M., Qi, Lei S. (2021). A comprehensive analysis and resource to use CRISPR-Cas13 for broad-spectrum targeting of RNA viruses. Cell Reports Medicine. (\*these authors contributed equally)
- Abbott, T., Dhamdhere, G., Liu, Y., Lin, X., Goudy, L., Zeng, L., Chemparathy, A., Chmura, S., Heaton, N., Debs, R., Pande, T., Endy, D., La Russa, M., Lewis, D., Qi, Lei S. (2020). Development of CRISPR as an antiviral strategy to combat SARS-CoV-2 and influenza. Cell.
- Lin, X., Chemparathy, A., La Russa, M., Daley, T., Qi, Lei S. (2020). Computational Methods for Analysis of Large-Scale CRISPR Screens. Annual Review of Biomedical Data Science.
- Paggi, J., Belk, J., Hollingsworth, A., Villaneuva, N., Powers, A., Clark, M., Chemparathy, A., Tynan, J., Lau, T., Sunahara, R., Dror, R. (2020). Leveraging non-structural data to predict structures of proteinligand complexes. bioRxiv.
- Venkatakrishnan, AJ, Fonseca, R., Ma, A., Hollingsworth, S., **Chemparathy, A.**, Hilger, D., Kooistra, A., Ahmari, R., Madan Babu, M., Kobilka, B., Dror, R. (2019). Uncovering patterns of atomic interactions in static and dynamic structures of proteins. bioRxiv.