CARMELLE CATAMURA

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Education

Ph.D. Computational Biology. University of California, Berkeley   2020-present
B.S. Biomolecular Engineering and Bioinformatics. University of California Santa Cruz   2016-2020

Skills

- Proficient Python programming (pandas, numpy, scikit-learn) with 8+ years of experience; extensive experience in R and Bash shell scripting; working knowledge of C, C++, Java and SQL
- Developing reproducible pipelines for large-scale and ad hoc data analysis (conda, Jupyter notebooks, git, github)
- Working with large-scale genomic, transcriptomic, and epigenomic data and databases (UCSC Genome Browser, Ensembl, GENCODE, GEO/SRA.)
- Next Generation Sequencing (NGS) analysis including bulk and single-cell RNA-seq analysis.
- Retraining deep learning architectures (SpliceAI) and applying machine learning methods to biological data

Publications

- **Designing de novo splicing with deep learning for allele-specific suppression of disease genes.** Catamura, et al. *Manuscript in progress, submitting to Nature Biotechnology (2025).*
- **Genome-wide, bidirectional CRISPR screens identify mucins as critical host factors modulating SARS-CoV-2 infection.** Biering SB, Sarnik SA, Wang E, et al. *NatGenet* 54, 1078–1089 (2022). https://doi.org/10.1038/s41588-022-01131-x

Patents

- **Composition and methods for treating Huntington's disease.** University of California, Berkeley. Liana Lareau, Fyodor Urnov, Carmelle Catamura. Patent Application No. PCT/US2023/068738.

- **Composition and methods for reducing RNA levels.** University of California, Berkeley. Liana Lareau, Fyodor Urnov, Carmelle Catamura. Patent Application No. PCT/US2023/068732.

Teaching Experience

Teaching Assistant, Computational Functional Genomics (BIOENG 149/249)   2023 Fall
Instructor/Coordinator/Curriculum developer, CCB Python Bootcamp   2023-present

Research Experience

Supervisor: Dr. Liana Lareau. University of California, Berkeley   2020-present
Supervisor: Dr. Angela Brooks. University of California, Santa Cruz   2017-2020
Supervisor: Dr. Valerie Arboleda. University of California, Los Angeles   2019

Research Projects

Designing de novo splicing with deep learning for allele-specific splicing editing in Huntington's disease
Lareau Lab, University of California Berkeley (2021-present)

- Developed a deep learning-guided framework to design allele-specific CRISPR base edits that introduce novel splice sites and trigger mRNA decay
- Demonstrated efficacy of the approach in targeting Huntington's disease
- Co-inventor on patent

Exploring the use of 10x single-cell RNA-seq data for isoform detection
Lareau Lab, University of California Berkeley (2021)
- Evaluated the feasibility of detecting alternative splicing isoforms from 3'-biased 10x single-cell RNA-seq data
- Assessed limitations of partial transcript coverage for isoform-level resolution

Genomic Mining for CRISPR-associated integrases
Hsu Lab, University of California Berkeley (2020)
- Built a computational pipeline to mine large public genomic datasets for novel CRISPR-associated integrases, aimed at overcoming limitations of existing CRISPR-based genome editing approaches

Age-associated splicing signatures
Sudmant Lab, University of California Berkeley (2020)
- Analyzed bulk RNA-seq data from mouse heart and lung tissue to identify age-associated splicing patterns
- Developed a multi-stage analysis pipeline including alignment, junction extraction, and differential splicing analysis
- Evaluated competing hypotheses on whether age-related splicing changes reflect regulation or loss of splicing fidelity

Mutually exclusive splicing analysis (MESA)
Brooks Lab, University of California Santa Cruz (2019-2020)
- Extended the MESA splicing analysis tool to detect retained introns
- Benchmarked performance against existing splicing tools (JuncBASE, MAJIQ, JUM) on RNA-seq data from drug-treated HeLa cells

Detection and Evaluation of Intron Events
Brooks Lab and Jurica Lab, University of California Santa Cruz (2019-2020)
- Developed methods to identify aberrant splicing events across cancer cell lines
- Integrated splicing profiles with pharmacological response data from CCLE and GDSC
- Identified associations between aberrant splicing and sensitivity to kinase-targeting drugs

Analysis of Epigenetic Dysregulation in KAT6A Mutant Patients
Arboleda Lab, University of California Los Angeles (2019)
- Analyzed epigenomic data from patient-derived fibroblasts to study downstream effects of *KAT6A* mutations
- Developed a similarity-based method to construct combinatorial histone features and identify overlaps with differentially methylated regions

Aberrant Splicing as Biomarkers in Cancer Cell Lines Sensitized to Drugs that Target Splicing Regulators
Brooks Lab, University of California Santa Cruz (2018-2019)
- Analyzed RNA-seq data from HeLa cells treated with spliceosome inhibitors across multiple dosages and assessed dose-dependent effects of spliceosome inhibition on splicing fidelity
- Compared performance of four splicing analysis pipelines to evaluate detection of intron retention events

Mutant KRAS associated Alternative Splicing
Brooks Lab, University of California Santa Cruz (2018-2019)
- Analyzed alternative splicing patterns associated with oncogenic *KRAS* mutations in lung adenocarcinoma (LUAD) patient data
- Developed downstream analysis and visualization tools for JuncBASE to compare splicing profiles across mutation status

Other Projects
Low-cost Electrocardiograph
Supervised by Dr. Kevin Karplus (2017)
- Built a low-cost electrocardiograph using a microcontroller and PteroDAQ, an open-source data-acquisition system. This project was done as a part of a freshman design course.

Fellowships
Bakar Fellows Program, Innovation Fellow	2024-present
NIH-IMSD (Initiative for Maximizing Diversity) Fellow	2019-2020
Computational Sciences REU at UCLA (Award number: 1758002)	2019
Koret Undergraduate Research Scholar	2019

Awards
UC Berkeley Computational and Genomic Biology Retreat Best Talk 2nd place	2024
UC Berkeley Computational and Genomic Biology Retreat Best Poster 2nd place	2021
Bruins in Genomics Best Poster	2019
SACNAS 2019 Outstanding Presentation of Research	2019
Chan Zuckerberg Initiative Travel Scholarship	2019

Oral Presentations
American Society of Human Genetics. 2023. Washington D.C., USA.
Bay Area RNA Club. 2023. San Francisco, USA.
Genetics, Genomics, Evolution and Development Retreat. 2024. Berkeley, USA.
Computational and Genomic Biology Retreat. 2024. Santa Cruz, USA.
Computational and Genomic Biology Retreat. 2022. Santa Cruz, USA.

Poster Presentations
Intelligent Systems for Molecular Biology, 2024. Montreal, Canada. (Awarded Best Poster iRNA track)
American Society of Human Genetics. 2024. Denver, USA.
Center for Computational Biology Annual Computational and Genomic Biology Retreat. 2021, 2022. Berkeley, USA. (Awarded Best Poster 2021)
Bay Area RNA Club Annual Meeting. 2023. San Francisco, USA.
SACNAS National Diversity in STEM Conference. 2019. Honolulu, USA. (Awarded Best Poster)
Koret Scholars Undergraduate Research Slam. 2019. Santa Cruz, USA.
22nd Annual Undergraduate Poster Symposium Division of Physical and Biological Sciences Jack Baskin School of Engineering. 2019. Santa Cruz, USA.
Bruins in Genomics Summer Research Program Symposium. 2019. Los Angeles, USA.

Mentorship and Outreach
Christopher Zavala, Undergraduate Research Mentee	2024-present
Computational Biology CSU Outreach initiative	2024-present
TAYO Mentorship Program. University of California Berkeley	2024
Mentorship Program, Center for Computational Biology	2022-2024
POWER Bay Area Mentorship Program	2020-2022