Alison Tang

Curriculum Vitae

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Education

2016–2022 **Ph.D. Biomolecular Engineering and Bioinformatics**, *University of California*, Santa Cruz.

2012–2016 **B.A. Molecular and Cell Biology**, *University of California*, Berkeley.
Concentration in genetics, genomics, and development

Experience

Industry

2022–Present **Computational Biologist I, Translational Sciences**, *Freenome*, South San Francisco.

- Modeling multi-omics plasma data (including the DNA methylome and fragmentome) to build classifiers for early stage breast cancer detection in partnership with SIEMENS Healthineers
- Working with Freenome's machine learning models to detect colorectal cancer disease burden from deep methylation sequencing of plasma, performing longitudinal monitoring on patients in parallel with imaging

Academic

2016–2022 **Graduate Student Researcher**, *Department of Biomolecular Engineering*, Santa Cruz, Angela Brooks Lab.

- Interrogated the regulatory mechanisms involved in A-to-I RNA editing, RNA splicing, and lung adenocarcinoma progression. I knocked down ADAR in lung ADC cells and sequenced bulk RNA with R2C2 nanopore and Illumina sequencing. I developed computational methods to analyze the cis-effects of variants on splicing changes at a single molecule level
- Analyzed long nanopore cDNA sequencing of chronic lymphocytic leukemia patients with recurrent splicing factor *SF3B1* mutations to characterize mutant- and cancer-specific RNA isoforms. I developed FLAIR, a leading tool for analyzing long-read data that summarizes noisy long reads into high-confidence isoforms and also performs differential splicing and isoform analyses (github.com/BrooksLabUCSC/flair)
- As part of the Native RNA Consortium, I analyzed RNA isoforms in a nanopore direct RNA-Seq dataset and facilitated the discovery of allele-specific and RNA modification-bearing isoforms
- In collaboration with Dr. Ophir Klein's lab at UCSF, we are studying the regulatory effect of splicing factor SRSF1 expression on murine incisor development. I performed the computational leg of the project: detecting differential expression, alternative splicing, and binding motifs with Illumina RNA-Seq data

2015–2016 **Undergraduate Researcher**, *Integrated Biology Department*, Berkeley, Rasmus Nielsen Lab.

- Modeled inversion polymorphism F_{ST} and performed GO permutation analyses to investigate selective bias for SNPs with large divergence between subpopulations of *D. melanogaster* genomes with and without inversions using R and python
- Created visualizations of forward-time simulation data for studying the impact of inversions on recombination and fitness in R

2014–2016 **Undergraduate Researcher**, *Children's Hospital Oakland Research Institute*, Oakland, Dario Boffelli Lab.

- Studied the epithelial mesenchymal transition in breast cancer cell lines using CRISPR/Cas9 to knock out AID, followed by RNA-Seq and standard NGS differential expression workflows to study the role of AID in promoting EMT
- Studied the extent of epigenetic variation in isogenic mice through phenotypic differences from RNA-seq analysis using ANOVAs

Teaching, Mentoring, Outreach

2018-2021 **Research Mentor**, *Brooks Lab*, Santa Cruz.

I have guided two undergraduate students through introductory research projects to identify RNA modifications that perturb splicing in nanopore native RNA sequencing using bioinformatics tools, *ad hoc* python and R scripting, and statistical testing.

2019-2020 **Seminar Coordinator**, *Cancer Research Club*, Santa Cruz.

Recognizing the need for a less disjointed cancer community at UCSC, I started a cancer seminar on campus featuring two monthly speakers. I am responsible for finding speakers and promoting attendance through e-mails and flyers. I obtained $1000/quarter of funding from Startup Sandbox for the seminars.

2017 **Event Coordinator**, *Northern California Computational Biology Symposium*, Santa Cruz.

NCCB is a conference led by graduate students which I helped plan and create the website for.

2016 **Teaching Assistant**, *Biomolecular Engineering 160*, Santa Cruz.

Research Programming in the Life Sciences, in Python. Led labs and assisted students during labs, held office hours, gave two programming lectures, graded assignments.

Awards

2022 Darrell Long and Elaine Long Prize in Experimental Engineering for Ph.D. Dissertations

2020-2023 F-31 Ruth L. Kirschstein Predoctoral Individual National Research Service Award

2017-2018 T-32 Genome Sciences NIH Training Grant

Skills

Advanced PYTHON, R, Inkscape

Intermediate Java, C

Wet lab Molecular biology techniques to go from cell culture to nanopore sequencing, Western blotting

Publications

2023 Life Science Alliance. Cameron M. Soulette, Eva Hrabeta-Robinson, Carlos Arevalo, Colette Felton, **Alison D. Tang**, Maximillian G. Marin, Angela N. Brooks. *Nanopore sequencing reveals U2AF1 S34F-associated full-length isoforms.*

2022 Developmental Cell. Tingsheng Yu, Oscar Cazares, **Alison D. Tang**, Hyun-Yi Kim, Tomas Wald, Adya Verma, Qi Liu, Mary Helen Barcellos-Hoff, Stephen N. Floor, Han-Sung Jung, Angela N. Brooks, and Ophir D. Klein. *SRSF1 governs progenitor-specific alternative splicing to maintain adult epithelial tissue homeostasis and renewal.*

2020 Nature Communications. **Alison D. Tang**, Cameron M. Soulette, Marijke J. Van Baren, Kevyn Hart, Eva Hrabeta-Robinson, Catherine J. Wu, Angela N. Brooks. *Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia reveals downregulation of retained introns.*

2019 Nature Methods. Rachael E. Workman*, **Alison D. Tang***, Paul S. Tang*, Miten Jain*, John R. Tyson*, Roham Razaghi*, Philip C. Zuzarte, Timothy Gilpatrick,Joshua Quick, Norah Sadowski, Nadine Holmes, Jaqueline Goes de Jesus, Karen L. Jones, Cameron M. Soulette, Terrance P. Snutch, Nicholas Loman, Benedict Paten, Matthew Loose, Jared T. Simpson, Hugh E. Olsen, Angela N. Brooks, Mark Akeson, Winston Timp. *Nanopore native RNA sequencing of a human poly(A) transcriptome.*

2016 Molecular Biology and Evolution. Justin B. Lack, Jeremy D. Lange, **Alison D. Tang**, Russell B. Corbett-Detig, and John E. Pool. *A Thousand Fly Genomes: An Expanded Drosophila Genome Nexus.*

In review

2023 BioRxiv. **Alison D. Tang**, Eva Hrabeta-Robinson, Roger Volden, Chris Vollmers, Angela N. Brooks. *Detecting haplotype-specific transcript variation in long reads with FLAIR2.*

2022 BioRxiv. Colette Felton, **Alison D. Tang**, Binyamin Knisbacher, Catherine J. Wu, Angela N. Brooks. *Detection of alternative isoforms of gene fusions from long-read RNA-seq with FLAIR-fusion.*

2021 Nature Portfolio preprint. Francisco Pardo-Palacios, Fairlie Reese, Silvia Carbonell-Sala, Mark Diekhans, Cindy Liang, Dingjie Wang, Brian Williams, Matthew Adams, Amit Behera, Julien Lagarde, Haoran Li, Andrew Prjibelski, Gabriela Balderrama-Gutierrez, Muhammed Hasan Celik, Maite de Maria, Nancy Denslow, Natalia Garcida-Reyero, Stefan Goetz, Margaret Hunter, Jane Loveland, Carlos Menor, David Moraga, Jonathan Mudge, Hazki Takahashi, **Alison Tang**, Ingrid Youngworth, Piero Carninci, Roderic Guigo, Hagen Tilgner, Barbara Wold, Christopher Vollmers, Gloria Sheynkman, Adam Frankish, Kin Fai Au, Ana Conesa, Ali Mortazavi, Angela N. Brooks. *Systematic evaluation of long-read RNA-seq methods for transcript identification and quantification.*

Presentations

2021 CSHL Eukaryotic mRNA Processing Meeting. *Detecting haplotype-specific RNA variation in long reads.* Virtual. Poster Presentation.

2021 NHGRI Annual Meeting. *Detecting allele-specific isoform variation in long reads.* Virtual. Poster Presentation.

2020 Bay Area RNA Club. *Interrogating the role of ADAR1 in lung adenocarcinoma through identification of A-to-I editing in long reads.* Virtual. Poster Presentation.

2020 NHGRI Annual Meeting. *Full-length characterization of SF3B1 mutation in CLL reveals downregulation of intron retention.* Virtual. Poster Presentation.

2019 Nanopore Community Meeting. *Full-length transcript characterization of SF3B1 mutation in chronic lymphocytic leukemia.* New York, NY. Oral Presentation and Panelist.

2019 ENCODE Long-Read RNA-Seq Meeting. *FLAIR: Full-length alternative isoform analysis of RNA.* Barcelona, Spain. Oral Presentation.

2019 Workshop on Splicing Factor Mutations and RNA Biology in Cancer. *Full-length Alternative Isoform analysis of RNA (FLAIR) for nanopore reads.* New Haven, CT. Poster Presentation.

2018 Nanopore Community Meeting. *Full-Length Alternative Isoform analysis of RNA for noisy nanopore reads.* San Francisco, CA. Oral/Poster Presentation.

2018 RNA Society. *Full-length characterization of transcript isoforms to investigate cancer-associated mutations.* Berkeley, CA. Oral Presentation.

2018 AACR Annual Meeting. *Full-length characterization of transcript isoforms to investigate cancer-associated mutations.* Chicago, IL. Poster Presentation.

2018 NHGRI Annual Meeting. *Full-length characterization of transcript isoforms to investigate cancer-associated mutations.* Los Angeles, CA. Poster Presentation.

2017 PBSE Research Conference. *Differential isoform usage in SF3B1 mutated chronic lymphocytic leukemia using nanopore sequencing.* Santa Cruz, CA. Oral Presentation.