

VICTORIA CHEUNG

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SUMMARY

Interdisciplinary computational biologist with a proven track record of leveraging advanced algorithms and computational techniques to tackle complex biological problems. Proficient in analyzing multimodal large-scale biological data sets and utilizing EHR data to develop predictive models, and to identify novel patterns to drive breakthrough discoveries. Skilled in programming languages such as Python with a deep understanding of statistical analysis, machine learning, and data visualization. Experienced in collaborating with interdisciplinary teams to translate biological questions into computational solutions, leading to impactful research outcomes. Passionate about harnessing the power of computational biology to revolutionize healthcare and advance scientific understanding.

EDUCATION

(UCSF) University of California, San Francisco
(UCSD) University of California, San Diego
Genentech Discovery Program
Cold Spring Harbor Laboratory

PhD Genetics conc. Systems Neuroscience
BS Microbiology
Certification L.E.A.D Supply Chain
Vision: Linking Circuits, Perception, and Behavior

SKILLS

TECHNICAL:

Data Analysis (Python, R, MATLAB)	Adobe Creative Suite (Ai, Lr, Ps)	Animal Research/Surgery
Linux (bash, zsh)	Arduino	PCR/qPCR
Cloud compute (GCP, AWS)	CAD (Onshape, Cura, eMachineShop)	Microscopy
Experimental Design	Histology/Immunohistochemistry	Image Processing (FIJI, Zen)
SQL (PostgreSQL)	NGS	
Multiomics (transcriptomics, proteomics, genomics, fragmentomics, methylomics)		

DOMAIN KNOWLEDGE:

Biochemistry	Microbiology	Neuroscience/Systems Neuroscience
Genetics/Single-cell Omics	Molecular Biology	Physiology
Immuno-oncology		

CAREER EXPERIENCE

Computational Biologist, Translational Science | [Freenome](#) | APR 2022 — PRESENT

- Apply bioinformatics, data science, and computational methods (including machine learning techniques) to analyze multi-omic data to reveal, model, and interpret changes in both the cancer (pathways, gene activities, proteins) and the immune system (composition, activity, and repertoires) associated with clinical outcomes.
- Partner cross-functionally in the scientific planning and execution of collaborative projects, such as molecular and cancer biologists, computational biologists, medical affairs, commercial, business development.
- Developed 2 software packages for reproducible data analysis for the team.
 - (1) Freenome's internal fragmentomics modeling architecture to predict gene activation scores from cfDNA.
 - (2) Wrote distributed workflows (Flyte) to increase efficiency of scRNAseq alignment and data aggregation from a scale of running for 8 days to half a day.
- Worked with multiple omics data (scRNAseq, RNAseq, ATACseq, proteomic, methylation, and fragmentomic (cfDNA) data) as single analytes or in multimodal data integration (exploratory data analysis, unsupervised machine learning, supervised machine learning, early fusion, late fusion, feature engineering, feature selection) for the purpose of characterizing signatures in cancer, patterns of cancer progression, longitudinal monitoring of disease, as well as characterizing responders and non-responders to treatment.
- Computational Lead on an internal project that validates and characterizes features of Freenome's fragmentomics model
- Execute research projects, to model various biological changes resulting from diseases such as cancer, autoimmune disease, and infection with various business partners. Worked collaboratively on:
 - Modeling multi-omics plasma data (DNA methylation, proteomics, fragmentomics) to build classifiers for early stage breast cancer detection in partnership with SIEMENS Healthineers
 - Determining predictive biomarkers for response in R/R DLBCL and characterized responders vs non responders to treatment of Lonca using fragmentomic signatures from whole genome sequencing (WGS) as well as identifying predictive biomarkers for overall survival from plasma proteomics in partnership with ADCT ([ASH 2022 abstract](#), [poster](#) 2nd author, [AACR 2023 abstract](#) co-first author)

- Worked with Freenome's machine learning models to detect colorectal cancer disease burden from deep methylation sequencing of plasma, performing longitudinal monitoring on patients validated with imaging data ([AACR 2024 abstract, poster co-first author](#))
- LOD quantification of Freenome's computational fragmentomics approach. Successfully determined the minimum quantity of input mass required to obtain reliable and accurate readouts to establish analytical sensitivity. ([AACR 2024 abstract, poster 2nd author](#))
- Mentored other scientists on the team through technical support, infrastructure support, as well as leading journal club discussions.
- Identified and developed collaborations with key opinion leaders (KOLs) to leverage Freenome's platform as well as develop new computational tools.

Oncology Bioinformatics and Molecular Oncology PhD Intern | [Genentech](#) | SEP 2021 — APR 2022

- Characterized gene signature development and refinement for T cell signaling pathways in cancer models
 - Wrote a data processing pipeline utilizing Scanpy, Numpy, Pandas, scikit-learn, SciPy
 - Performed statistical analyses on different drug treatment populations: gene set enrichment analysis, differential gene expression analysis.
 - Utilized supervised batch correction techniques and unsupervised clustering algorithms (UMAP, topic modeling) to visualize and analyze single cell RNA seq data outputs.
- Wrote custom plotting functions using Matplotlib to better visualize the effect of drug treatments.

Graduate Researcher in Single-cell Omics, Systems Neuroscience | [UCSF @Evan Feinberg Lab](#) | JUL 2016 — SEP 2021

- **Project 1:** Developed a multiplexed, high-throughput, single-cell sequencing method for neurons that preserve connectivity information in addition to obtaining molecular identity (VECTORseq).
 - Wrote the data processing pipeline using Python after genome alignment using Cellranger (10x Genomics) on an AWS EC2 instance.
 - Used unsupervised machine learning techniques such as t-SNE/UMAP clustering to match molecular identities to cellular function and role in behavioral output.
 - Implemented nearest neighbors algorithms to account for batch differences when merging datasets.
 - Streamlined brain dissociation techniques and increased neuron survivability yield 100-fold based on data-driven outcomes from clustering analyses.
 - Validated clustering results of single-cell sequencing against the [2020 10x sequencing dataset from the Allen Atlas](#) and that the methodology was functional.
 - Evaluated range of highly variable genes expressed per cluster for the validation of cell identity.
 - Managed collaborations with the Chan-Zuckerberg Biohub (Spyros Darmanis Group, now @ Genentech)
- **Project 2:** Designed an audition-based behavioral paradigm to study sensorimotor integration in the context of mice.
 - Wrote custom software to support custom-built hardware using serial communication between MATLAB and an Arduino microprocessor, which increased productivity by 6-fold from the parallelization and automation of data acquisition, storage, and analysis.
 - Used this system in exploring how sensory input is represented in the brain and transformed into behavioral commands, using mice as the model organism.
 - Wrote custom analyses software to automate, refine, and interpret both raw behavioral data and fiber photometry signals. Used CAD software to design and 3D print custom behavioral apparatuses.
 - Refined surgical protocols to increase survival surgery success by 20%. Delivery of viruses, drugs, and organic dyes into the mouse brain.
 - Performed physiology recordings on brain slices to validate optogenetic and fiber photometry experiments.
 - Assembled fiber photometry and optogenetic manipulation equipment to record and perturb neuronal activity in the context of quantitative behavioral assays.

Data Scientist, Health Data Fellowship | [Insight Data Science](#) | MAY 2020 – JULY 2020

- Developed a predictive clinical calculator to assess Acute Kidney Injury in hospitalized patients, which would result in better management, care/medication dosing, injury prevention, and reduced hospital length of stay, thus freeing up occupied resources and minimizing financial costs to both patient and hospital.
- Utilized PostgreSQL querying to gather relevant data from the MIMIC-III database and manipulated the data with Python Pandas from 25 tables of data, 46,000 patients, thousands of diagnoses and lab tests, and clinical documentation--generating over 3 million rows of data and 70 unique features comprising lab tests and demographic information. Analyses were performed on an AWS EC2 instance.
- Used supervised machine learning in Python such as regression models from scikit-learn and XGBoost to forecast Acute Kidney Injury, with a predictive accuracy of ~91%.

- *Medium Article* in *Towards Data Science*: [Predicting Acute Kidney Injury in Hospitalized Patients Using Machine Learning](#)

OTHER EXPERIENCE

Genentech Discovery Program: L.E.A.D. Supply Chain | [Genentech certification](#) | JULY 2020 – AUG 2020

- Learned about the fundamentals of supply chain, how the supply chain spans a variety of roles throughout Genentech's delivery of therapies as well as its involvement in providing medication access to underserved communities and its drive towards sustainability.
- Participated as Operations Lead in a **supply chain simulation** where my team and I **placed second** overall.

Graduate Researcher | [UCSF @Guo Huang Lab](#) | APR 2016 – JUN 2016

Area of Research: Regenerative Potential of Cardiomyocytes

- Performed heart explants for cell culture and subsequent drug studies for the purpose of exploring organ regeneration and repair in neonatal mice—with an emphasis on the pathways that regulate resident stem cell activation and mature cell de-differentiation/proliferation.
 - Explored organ regeneration and development from an evolutionary standpoint across different species of animals *i.e.* naked mole rat, finch, rat, mouse, zebrafish.
- Utilized innovative and integrated approaches in engineering, single cell analysis, advanced imaging microscopy, drug delivery, and genome manipulation technology.

Graduate Researcher | [UCSF @Dengke Ma Lab](#) | SEP 2015 – DEC 2015

Area of Research: Homeostatic Response to Extreme Abiotic Factors

- Created a functional mutant line in *C. elegans* via cDNA microinjections and exposed the mutants to extreme abiotic environments via behavioral assays to understand cellular intrinsic tolerance of hypoxia/anoxia and hypothermia.
 - Utilized RNA-seq to identify genes implicated in cryopreservation/hypoxia-tolerance with therapeutic potential.
 - Obtained qualitative behavioral data on how animals sensed and responded to changes in internal states to elicit behavior and maintain homeostasis.

Undergraduate Research Fellow – UC LEADS & STARS | [UCSD @ Andrew D. Huberman Lab](#) | DEC 2012 – JUL 2015

Area of Research: BINOCULAR PLASTICITY & DYNAMIC STRATEGY IMPLEMENTATION IN CUTTLEFISH

- Developed a model of visual perception and prey capture using cuttlefish to study the neural circuit organization supporting flexible eye movements.
 - Underlying goal: provide insight into amblyopia (lazy eye)
- Optimized behavioral parameters and refined surgical techniques for the novel model organism.
 - Increased consistency between experiments for reproducibility.
- Optimized tracking and analysis of dynamical eye movements using multi-planar high-speed imaging and *Simi Motion* software.
 - Increased productivity and output by 40%
- 3D-reconstructed neuron structure for morphometric analysis using *Neurolucida*.

Research Fellow – UCSF Summer Research Training Program (SRTP) | [UCSF @ David R. Copenhagen Lab](#) | JUN 2014 – SEP 2014

Area of Research: EFFECTS OF LIGHT DEPENDENT Ca^{2+} SIGNALING DURING RETINAL DEVELOPMENT

- Explored the effects of light dependent Ca^{2+} waves in the developing mouse retina with a focus on the coupling of amacrine cells to melanopsin ganglion cells via gap junctions.
- Characterized appropriate transgenic lines and established baseline comparisons in adult retina to observe and document deviations from the developed animal to the developing animal.
 - Performed retinal dissections for cell coupling studies.

MENTORSHIP | DIVERSITY

Mentor | [UCSF First Generation Mentor](#) | OCT 2022 – PRESENT

- As a post-graduate of UCSF's PhD program, I volunteered to be a mentor for an incoming first year PhD student.
- Topics we cover: choosing a PI during rotations, career development, navigating higher education as a first-generation student

Mentor for Undergraduates | [UCSF @ Evan Feinberg Lab](#) | JUN 2016 – SEP 2021

- Trained and mentored 3 undergraduates on performing research tasks on how to: think independently, plan experiments, perform surgical protocols, and analyze data. Provided career/research advice.

Student Advisor | [UCSF Summer Research Training Program \(SRTP\)](#) | JUN 2019 – AUG 2019

- Developed curriculum to teach rising junior and senior undergraduates on: how to become a strong graduate school applicant, how to create compelling posters and presentations, how to write personal statements, how to read and dissect scientific papers

Student Teacher | [UCSF Science & Health Education Partnership \(SEP\)](#) | JAN 2016 — JUN 2016

- Created and developed a series of interactive and investigative lesson plans to teach freshman biology.
- Mentored URMs and socioeconomically disadvantaged students on different career paths in science.

Scholar | [UC LEADs \(University of California, Leadership Excellence through Advanced Degrees\)](#) | MAR 2013 — JUN 2015

- Mentorship program for underprivileged and socioeconomically disadvantaged undergraduates for success in graduate school to later assume positions of leadership in industry, government, public service, and academia following completion of a doctoral STEM degree
 - Two-way avenue:
 1. Received mentorship from prior two cohorts as part of the incoming cohort
 2. Provided mentorship to the next two cohorts while progressing through the program

CONFERENCES | TALKS

SCIENTIFIC:

2023	American Association for Cancer Research (AACR)	poster presentation, abstract link
2022	American Society Hematology (ASH)	poster presentation
2018	UCSF Tetrad	oral (15 min) presentation
2017	UCSF Tetrad	poster presentation
2015	UC LEADs Research Symposium	poster presentation
2014	SFN Annual Conference	poster presentation
2014	UCSF Summer Research Training Program Symposium	poster + oral (15 min) presentation
2014	UCSD Academic Enrichment Program	poster presentation (invited)
2014	SACNAS National Conference	poster presentation
2014	UCLEADs Annual Research Symposium	poster presentation
2013	UCSD Academic Enrichment Program	poster presentation (invited)
2013	SACNAS National Conference	poster presentation
2013	UCSD STARS Summer Research Conference	oral presentation (15 min)

DIVERSITY:

2022	SRTP Co-Curriculum: What Can You Do With a PhD?	panelist (1hr)
2019	Northern California Forum for Diversity in Graduate Education	panelist (1hr)
2018	Northern California Forum for Diversity in Graduate Education	panelist (1hr)

HONORS | AWARDS

2022	UCSF Diversity Graduation, Graduate Division Speaker
2017	Helmsley Scholar
2015	UC LEADs Symposium Presentation Award
2014	SACNAS National Research Conference Travel Scholarship
2013	UCSD STARS Scholarly Presentation Award
2013	SACNAS National Research Conference Travel Scholarship
2013	UCSD Provost Honors
2012	UCSD Provost Honors
2011	UCSD Provost Honors
2012	Kaiser Permanente Volunteer Award
2011	Kaiser Permanente Student Achievement Award

MEDIA PRESENCE

2019	UCSF Article: Students Who Are First in Their Family to Attend College Share Stories, Experiences
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PUBLICATIONS

Tang, A.D.* , Gupte, R.* , **Cheung, V.*** , Qing, T.* , Cauwels, A., Leff, E., Walter, K., Tabari, E., Lovejoy, A., Lin, C.H.J.; ; (2024) [Noninvasive longitudinal monitoring of residual disease in chemotherapy-treated colorectal cancer patients](#). Cancer Res (2024) 84 (6_Supplement): 6258. <https://doi.org/10.1158/1538-7445.AM2024-6258>

- Leff, E.*, Tseng, A.*, **Cheung, V.**, Tabari, T., Walter, K., Lovejoy, A., Lin, C.H.J.; (2024) [Inference of gene expression using fragmentation patterns from targeted high-depth sequencing of cell-free DNA](https://doi.org/10.1158/1538-7445.AM2024-4788). Cancer Res (2024) 84 (6_Supplement): 4788. <https://doi.org/10.1158/1538-7445.AM2024-4788>
- Vallania, F.*, **Cheung, V.***, Tripathi, A., Louie, M., Snyder, T., Lin, J., Havenith, K., Qin, Y., Pantano, S., Wuerthner, J., van Berkel P.H.; (2023) [Discovery of plasma protein biomarkers associated with overall survival in R/R DLBCL patients treated with loncastuximab tesirine](https://doi.org/10.1158/1538-7445.AM2023-5387). Cancer Res 1 April 2023; 83 (7_Supplement): 5387. <https://doi.org/10.1158/1538-7445.AM2023-5387>
- Vallania, F., **Cheung, V.**, Zamba, MD., Liu, J., Pasupathy, A., Donnell, H., Bailey, M., Louie, M., Lin, J., Havenith, K., Qin, Y., Pantano, S., Wuerthner, J., van Berkel, PH.; (2022) [Identification of Predictive Biomarkers for Response of R/R DLBCL Patients Treated with Loncastuximab Tesirine Using Low Pass Whole-Genome Sequencing \(WGS\)](https://doi.org/10.1182/blood-2022-168993). Blood 2022; 140 (Supplement 1): 3551–3552. doi: <https://doi.org/10.1182/blood-2022-168993>
- Cheung, V.**, Chung, P., and Feinberg, E.H. (2022) [Transcriptional profiling of mouse projection neurons with VECTORseq](https://doi.org/10.1016/j.xpro.2022.101625). STAR Protocols , 3(3):101625
- Cheung, V.**, Chung, P., Bjorn, M., Shvareva, V.A., Lopez, Y.C., and Feinberg, E.H. (2021) [Virally Encoded Connectivity Transgenic Overlay RNA sequencing \(VECTORseq\) defines projection neurons involved in sensorimotor integration](https://doi.org/10.1016/j.celrep.2021.110131). Cell Reports, 37(12):110131
- Cheung, V.** (2020) [“Predicting Acute Kidney Injury in Hospitalized Patients Using Machine Learning”](https://medium.com/@victoriacheung/predicting-acute-kidney-injury-in-hospitalized-patients-using-machine-learning-20jun2020) Towards Data Science. Medium, 20 Jun. 2020. Web.
- Cheung, V.**, Mullins, O., Nguyen, P., Huberman, AD. (2014) Extreme binocular plasticity and dynamic strategy implementation supports vision-dependent prey capture in cuttlefish. Proceedings of the SACNAS National Conference, ed G Miranda-Carboni (Society for the Advancement of Hispanics/Chicanos and Native Americans in Science, Santa Cruz, CA), p 1159.