

VICTORIA CHEUNG

victoriakcheung@gmail.com

LinkedIn@[victoriacheung](#)

GitHub@[vic-cheung](#)

website: vic-cheung.github.io

PROFESSIONAL SUMMARY

Computational Biology | Data Science | Bioinformatics

Interdisciplinary computational biologist with expertise in multimodal biological data analysis, machine learning models, and bioinformatics tools. Experienced in high-throughput NGS data processing, predictive modeling using EHR data, and the integration of multi-omic datasets. Proficient in Python, R, and MATLAB for statistical analysis and data visualization. Passionate about transforming healthcare through computational solutions and advancing scientific discoveries. Proven leadership in cross-functional collaborations and mentoring teams.

EDUCATION

University of California, San Francisco (UCSF) – PhD in Genetics with a concentration in Systems Neuroscience

University of California, San Diego (UCSD) – Bachelor of Science in Microbiology

Genentech Discovery Program, L.E.A.D Supply Chain

Cold Spring Harbor Laboratory, Vision: Linking Circuits, Perception, and Behavior, Hemsley Scholar

TECHNICAL SKILLS

- **Data Analysis & Visualization:** Python, R, MATLAB, SQL (PostgreSQL)
- **Cloud Computing:** GCP, AWS, Azure
- **NGS Data Processing:** RNA-Seq, Whole Genome Sequencing (WGS), Methylation Sequencing
- **Multimomics Analysis:** Transcriptomics, Proteomics, Genomics, Fragmentomics, Methylomics
- **Tools:** Linux (bash, zsh), Histology/Immunohistochemistry, Fiji, Zen, PCR/qPCR
- **Virtual Environments:** Conda, Poetry
- **Additional Skills:** Arduino, Onshape, Cura, eMachineShop, CAD software, Animal Research, Image Processing

CAREER EXPERIENCE

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

- Applied bioinformatics and computational biology techniques to analyze high-throughput multi-omic datasets (genomic, transcriptomic, epigenetic) for liquid biopsy and cancer diagnostics.
- Developed and implemented computational tools and algorithms for analyzing complex data from various NGS platforms, including RNA-Seq, Whole Genome Sequencing (WGS), targeted sequencing, and methyl sequencing. Utilized existing bioinformatics tools (e.g., SAMtools, BedTools, fgsea, ScanPy) alongside custom scripting in Python and Bash to uncover insights and drive innovation in diagnostic solutions.
- 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 enhance the efficiency of NGS data processing, reducing the alignment and data aggregation time for scRNAseq from 8 days to half a day. Ensured the reproducibility and scalability of bioinformatics analyses.
- Led cross-functional collaborations with molecular and cancer biologists, computational researchers, and external partners to design, analyze, and interpret molecular experiments. Key contributions included building classifiers for early-stage cancer detection and identifying predictive biomarkers for treatment response.
- Conducted analyses of raw NGS data (FASTQ and BAM files) single-cell RNA-seq/bulk RNA-seq
- Applied machine learning and statistical methods to integrate multi-omic data, characterize cancer signatures, and monitor disease progression.
- Prepared detailed reports and presentations for stakeholders, including abstracts and posters presented at major conferences such as AACR and ASH. Communicated complex scientific findings effectively to both technical and non-technical audiences.
- Mentored junior scientists and facilitated knowledge sharing within the team through technical support, leading journal club discussions, and fostering a collaborative research environment.
- Identified and developed collaborations with key opinion leaders (KOLs) to leverage Freenome's platform as well as develop new computational tools.
- **Key Projects and Achievements:**
 - **Multi-Omic Data Integration:** Led the integration of multimomic data (fragmentomics, methylomics, and proteomics) for the development of early fusion and late fusion models for partnership work (computational lead). This work contributed to identifying novel cancer biomarkers and monitoring longitudinal disease progression.
 - **Partnership with ADCT:** 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 ([ASH 2022 abstract](#), [poster](#) 2nd author, [AACR 2023 abstract](#) co-first author)

- [Partnership with Siemens Healthineers](#): Modeled plasma DNA methylation, proteomics, and fragmentomics data to build classifiers for early-stage breast cancer detection.
- Fragmentomics Model Validation: Served as the computational lead on a project that validated Freenome's fragmentomics model
 - Manuscript currently in preparation as 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)
- Machine Learning in Liquid Biopsy: Applied machine learning models to detect colorectal cancer disease burden as well as perform longitudinal monitoring on patients through deep methylation sequencing of plasma, validated with imaging data ([AACR 2024 abstract](#), [poster](#) co-first author)

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

- Characterized gene signatures for T cell signaling pathways in cancer models, optimizing for biomarker discovery.
- Built a data processing pipeline using Scanpy, Numpy, Pandas, scikit-learn, SciPy for statistical analyses and Matplotlib/Seaborn visualization of single-cell RNA-Seq data.
- Performed statistical analyses on different drug treatment populations: gene set enrichment analysis, differential gene expression analysis.
- Applied supervised batch correction and unsupervised clustering (UMAP, topic modeling) to analyze scRNA-seq data.

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

- **Project 1:** Developed [VECTORseq](#), a high-throughput single-cell sequencing method for neurons, preserving connectivity information.
 - Developed a data processing pipeline using Python after genome alignment using Cellranger (10x Genomics) on an AWS EC2 instance.
 - Applied unsupervised ML techniques (t-SNE/UMAP clustering) to correlate molecular identities with neuronal function and behavioral output, using nearest neighbors algorithms to adjust for batch differences.
 - Enhanced neuron survivability yield by 100x through optimized brain dissociation techniques based on data-driven outcomes from clustering analyses.
 - Collaborated with the Chan-Zuckerberg Biohub (Spyros Darmanis Group)
- **Project 2:** Designed an audition-based behavioral paradigm to investigate sensorimotor integration in 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.
 - Explored sensory input representation and behavioral command transformation using custom analyses software for behavioral and fiber photometry data. Used CAD software to design and 3D print custom behavioral apparatuses.
 - Conducted neural activity recordings via calcium-based imaging and fiber photometry, applying signal processing techniques (e.g., noise filtering, event detection) to analyze neuronal dynamics.
 - Improved surgical protocols for delivery of viruses and optogenetic tools, increasing survival rates by 20%.
 - Validated optogenetic and fiber photometry experiments through electrophysiology recordings.

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

- Developed a predictive clinical tool to assess Acute Kidney Injury (AKI) in hospitalized patients, improving care management and reducing hospital stays.
- Queried and processed data from the MIMIC-III database using PostgreSQL and Python (Pandas), generating over 3 million rows of data and 70 unique features from 25 tables of data and 46,000 patients. Features included lab tests, demographic information, thousands of diagnoses, and other clinical documentation. Analyses were performed on an AWS EC2 instance.
- Applied supervised machine learning models (scikit-learn, XGBoost) to forecast AKI, achieving a predictive accuracy of ~91%.
- Published work in *Towards Data Science*: [Predicting Acute Kidney Injury in Hospitalized Patients Using Machine Learning](#)

ADDITIONAL 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 (S RTP) | UCSF @ David R. Copenhagen Lab | JUN 2014 – SEP 2014Area 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.

PUBLICATIONS

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- Herault, A, et al., **Cheung, V.** "NKG2D-bispecific enhances NK and CD8+ T cell antitumor immunity." *Cancer Immunology, Immunotherapy* 73.10 (2024): 1-16. [DOI](#)
- Tang, A.D.*, Gupte, R.*, **Cheung, V.***, Qing, T.*, et al "Noninvasive longitudinal monitoring of residual disease in chemotherapy-treated colorectal cancer patients." *Cancer Research* 84(6): 6258. [DOI](#)
- Leff, E.*, Tseng, A.*, **Cheung, V.**, et al. "Inference of gene expression using fragmentation patterns from targeted high-depth sequencing of cell-free DNA." *Cancer Research*, 84(6_Supplement), 2024, 4788. [DOI](#)
- Vallania, F.*, **Cheung, V.***, Tripathi, A., et al. "Discovery of plasma protein biomarkers associated with overall survival in R/R DLBCL patients treated with loncastuximab tesirine." *Cancer Research*, 83(7_Supplement), 2023, 5387. [DOI](#)
- Vallania, F., **Cheung, V.**, Zamba, MD., Liu, J., Pasupathy, A., et al. "Identification of Predictive Biomarkers for Response of R/R DLBCL Patients Treated with Loncastuximab Tesirine Using Low Pass Whole-Genome Sequencing (WGS)." *Blood*, 140(Supplement 1), 2022, 3551-3552. [DOI](#)
- Cheung, V.**, Chung, P., Feinberg, E.H. "Transcriptional profiling of mouse projection neurons with VECTORseq." *STAR Protocols*, 3(3), 2022, 101625. [DOI](#)
- Cheung, V.**, Chung, P., Bjorn, M., Shvareva, V.A., Lopez, Y.C., Feinberg, E.H. "Virally Encoded Connectivity Transgenic Overlay RNA sequencing (VECTORseq) defines projection neurons involved in sensorimotor integration." *Cell Reports*, 37(12), 2021, 110131. [DOI](#)
- Cheung, V.** "Predicting Acute Kidney Injury in Hospitalized Patients Using Machine Learning." *Towards Data Science*. Medium, 20 Jun. 2020. [Web](#)
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Cheung, V., Mullins, O., Nguyen, P., Huberman, A.D. "Extreme binocular plasticity and dynamic strategy implementation supports vision-dependent prey capture in cuttlefish." Proceedings of the SACNAS National Conference, 2014, p. 1159.

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	S RTP 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)

MENTORSHIP & DIVERSITY INITIATIVES

Mentor | [UCSF First Generation Mentor](#) | OCT 2022 — OCT 2024

- 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:
 - Received mentorship from prior two cohorts as part of the incoming cohort
 - Provided mentorship to the next two cohorts while progressing through the program

HONORS AND 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](#)