

# Fong Shun (April) Lo

## *Curriculum Vitae*

aprillo@uw.edu; aprilfslo@gmail.com

(734) 355-5618      Seattle, WA

aprilpamyl.com

## EDUCATION

**Ph.D. in Genome Sciences with certificate in Advanced Data Science.** *University of Washington, School of Medicine, Seattle, WA.* Sep 2016 – June 2022

**B.S. Biomedical Engineering and Applied Mathematics & Statistics with Honors.** *The Johns Hopkins University, Whiting School of Engineering, Baltimore, MD.* 3.62 GPA. Sep 2012 – May 2016.

## EXPERIENCE

**Doctoral Candidate**, advised by Dr. Alice Berger, Jun 2017 – Present

Human Biology Division, *Fred Hutchinson Cancer Research Center, Seattle, WA*

- **Dissertation: Oncogene-driven post-transcriptional regulation in lung adenocarcinoma**
- *Major research interests:* Analyzing whole transcriptomes and proteomes of genetically perturbed cells to understand the post-transcriptional effects of oncogenes in lung adenocarcinoma
- Developed, tested, and maintained bioinformatic pipelines to process and analyze high-throughput RNA-seq data involving >300 human cell lines to study differential expression and alternative splicing

**Undergraduate Researcher**, Big Data to Knowledge (BD2K) Summer Program, advised by Dr. Peter Kharchenko, Jun 2015 – Aug 2015

Department of Biomedical Informatics, *Harvard Medical School, Boston, MA*

- Processing and statistical analysis of single-cell mass cytometry protein data

**Undergraduate Researcher**, advised by Dr. Rachel Karchin, Feb 2014 – May 2015

Institute for Computational Medicine, *Johns Hopkins University, Baltimore, Maryland*

- Applied GATK methods and pipelines to perform quality control and call somatic variants for multi-region whole genome and whole exome NGS data of human and mouse tumors (*Niknafs et al., 2019*)

**Informatics Intern**, *iOmics, Massachusetts Biomedical Initiative, Worcester, MA*, Jul 2013 – Jun 2014

- Integrated and processed data from biomedical and clinical data sources including NCBI Gene, Gencode, and Wiki Pathways

**High School Research Intern**, advised by Dr. Sharon Cantor, Jun 2011 – Aug 2011

Department of Cancer Biology, *University of Massachusetts Medical School, Worcester, MA*

- Validation of genetic screen investigating cisplatin resistance in ovarian cancer cells

## PUBLICATIONS

**Lo A**, Holmes K, Kamlapurkar S, Mundt F, Moorthi S, Fung I, ..., Berger AH. Multiomic characterization of oncogenic signaling mediated by wild-type and mutant RIT1. *Sci Signal*. 2021.

Ursu O, Neal JT, Shea E, ..., **Lo A**, ..., Berger AH, Regev A, Boehm JS. Massively parallel phenotyping of variant impact in cancer with Perturb-seq reveals a shift in the spectrum of cell states induced by somatic mutations. *Nat Biotech*. 2021.

Vichas A, Riley AK, Nkinsi NT, Kamlapurkar S, Parrish PCR, **Lo A**, ..., Berger AH. Integrative oncogene-dependency mapping identifies RIT1 vulnerabilities and synergies in lung cancer. *Nat Commun*. 2021.

Thornton AM, Fang L, **Lo A**, ..., Berger AH, Giannakis M, Brooks AN. eVIP2: Expression-based variant impact phenotyping to predict the function of gene variants. *PLoS Comput Biol*. 2021.

Niknafs N, Zhong Y, Moral JA, Zhang L, Shao MX, **Lo A**, ..., Karchin R. Characterization of genetic subclonal evolution in pancreatic cancer mouse models. *Nat Commun*. 2019.

## TEACHING, MENTORING, AND OUTREACH

**Women in Genome Sciences**, 2016 – present

- Board Member, Communications and Events, 2017 - 2021

**Mentor**, *Issaquah High School Intern*, 2021 - present

**Facilitator**, *Girls Who Code*, Fred Hutch Chapter, 2018 – present

**Teacher**, *Coding for Cancer*, Fred Hutch, 2021

**Teacher**, *Genome Hackers*, 2017 - 2020

**Teaching Assistant**, *Bioinformatic Workflows*, University of Washington, Mar 2020 – May 2020

- Helped develop and teach a graduate course on developing computational pipelines for data analyses

**Teaching Assistant**, *Fund. of Genetics and Genomics*, University of Washington, Jun 2019 - Aug 2019

- Led discussion sections and office hours on core genetics concepts

**Teaching Assistant**, *Systems Bioengineering II*, The Johns Hopkins University, Jan 2016 - May 2016

- Led discussion sections on topics in computational neuroscience, integrating lectures from

**Teaching Assistant**, *Intro to Scientific Computing*, The Johns Hopkins University, Jan 2015 - May 2015

- Taught and graded assignments for Intro programming in Python and MATLAB

## POSTER PRESENTATIONS

*Dysregulation of alternative mRNA splicing by oncogenic KRAS in lung adenocarcinoma*

AACR 2022 Annual Meeting, New Orleans, LA, Apr 2022

*A large-scale RNA-seq screen to identify regulators of alternative splicing in cancer*

AACR 2019 Annual Meeting, Atlanta, GA, Apr 2019

*Investigating dysregulation of RNA splicing by oncogenic signaling pathways*

SLU Collaborative Seminar, Topics in Computational Biology, Seattle, WA, Oct 2018

*Using support vector machines to classify cells in single-cell RNA-Seq*

NHGRI Research Training & Career Development Annual Meeting, St. Louis, MO, Apr 2017

## FELLOWSHIPS AND AWARDS

**NSF IGERT in Big Data and Data Science Fellowship**, Sep 2017 – Sep 2019

**NIH/NHGRI Pre-doctoral T32 Training Grant Predoctoral Trainee**, Sep 2016 – Sep 2017

**Design Team**, *Aezon, Qualcomm Tricorder XPRIZE Finalist*, Baltimore, MD, Feb 2013 – Jun 2016

- Performed medical device research and design including disease diagnosis assay development

## PROFESSIONAL ORGANIZATIONS

**American Association of Cancer Research (AACR)**, 2019 – present

**Women in Biology (WiB)**, *Seattle chapter*, 2021 - present

## PROGRAMMING SKILLS

**Daily** R, bash

**Weekly** Snakemake, Python, Git

**As needed** Java, C, C++, LATEX, JavaScript

## LANGUAGES

**Expert** English, Chinese (Cantonese)

**Fluent** Chinese (Mandarin)

## REFERENCES

**A. Berger** ahberger@fredhutch.org

**D. Macpherson** dmacpher@fredhutch.org

**C. Trapnell** coletrap@uw.edu

**R. Bradley** rbradley@fredhutch.org