Albert Tian Chen

Interdisciplinary researcher with 5+ years of statistics, computational biology, and data visualization experience, as well as hands-on experience with protein engineering and proteomics. Excited to learn and work at the intersection of data and biology.

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RESEARCH EXPERIENCE

Vector Engineering Lab
Broad Institute of MIT and Harvard
https://vector.engineering

Senior Computational Associate	5/2021 – Present
Associate Computational Biologist	5/2020 – 5/2021
Bioinformatics Co-op	5/2019 – 12/2019

▸ Author on 2 papers (lead author on 1), author for 2 more manuscripts in preparation. Key contributor of data analysis, figure creation, and manuscript writing for our lab's projects in adeno-associated virus (AAV) capsid engineering for gene therapy in the central nervous system.

▸ Initiated, organized, and led a Capstone project with six Northeastern University students. Generated and helped students analyze single-cell transcriptome sequencing (scRNA-seq) data of AAV-producing cells, aiming to identify genes affecting AAV production. Currently validating gene hits with siRNA knockdowns, and exploring dynamics of AAV production, using fluorescent imaging, fluorescence-activated cell sorting (FACS), qPCR, and bulk RNAseq.

▸ Created COVID CG (https://covidcg.org), a tool for visualizing, filtering, and downloading mutations in over 4,000,000+ SARS-CoV-2 genomes. COVID CG has been visited 50,000+ times by users from over 180 countries. Fielded questions from news outlets and helped scientists from international government agencies analyze data from our site. Assisted in securing funding from AstraZeneca. Hired and now manage a contractor and an employee to develop and maintain the site.

▸ Building internal tools for automated, reproducible, and user-friendly processing/analysis of next-generation sequencing (NGS) data. Developing a centralized database and analysis engine for querying and analyzing 20 TB+ of AAV library screening data.

Slavov Lab, Northeastern University (https://slavovlab.net)   *Research Assistant*   7/2016 – 5/2019

▸ Lead author on 2 papers, DART-ID (https://dart-id.slavovlab.net), a Bayesian framework for increasing peptide identification rates in single cell mass spectrometry proteomics data, and DO-MS (https://do-ms.slavovlab.net), a modular, extensible, and automated data analysis/QC platform for rationally optimizing mass spectrometry experiments.

▸ Awarded $8000 in university fellowships support P-SCoPE (Single cell phosphoproteomics by mass spectrometry), a modification of the Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) method (https://scope2.slavovlab.net). Designed and ran LC/MS proteomics experiments, from cell culture to instrument operation. Analyzed data and optimized sample prep and mass spectrometer instrument parameters.

▸ Organized and ran weekly programming office hours for students and RAs in the lab. Tutored 2 RAs in programming basics, data analysis, and data visualization.

Waters Corporation, Separations R&D   *Chemistry Co-op*   7/2017 – 12/2017

▸ Prototyped high-throughput LC/MS workflow that doubled throughput to 4800 samples/day, through hardware/firmware modifications to existing instrumentation, low-level C++ data processing code, and an online data visualization dashboard.

EDUCATION

Northeastern University, *College of Engineering*   2015 – 2020
Bachelor of Science in Bioengineering   3.73 / 4.0 GPA (3.91 / 4.0 Major GPA)

PUBLICATIONS

Krolak T, Chan KY, Kaplan L, Huang Q, Wu J, Kozareva V, Tobey IG, Beddow T, Zheng Q, **Chen AT**, Ryvkin D, Gu C, Deverman BE. A High-Efficiency AAV for Endothelial Cell Transduction Throughout the Central Nervous System. (*under revision*)

Chen AT, Altschuler K, Zhan SH, Chan AY, Deverman BE. COVID-19 CG: Tracking SARS-CoV-2 mutations by locations and dates of interest. *eLife* (2021) https://doi.org/10.7554/eLife.63409
Website: https://covidcg.org

Chen AT, Franks A, Slavov N. DART-ID increases single-cell proteome coverage. *PLOS Computational Biology* (2019) https://doi.org/10.1371/journal.pcbi.1007082
Website: https://dart-id.slavovlab.net

Huffman RG*, **Chen AT***, Specht H*, Slavov N. DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. *Journal of Proteome Research* (2019) https://doi.org/10.1021/acs.jproteome.9b00039
*Contributed equally
Website: https://do-ms.slavovlab.net

IN PREPARATION

Elzahraa-Eid F, Chan KY, **Chen AT**, Huang Q, Tobey IG, Zheng Q, Pacouret S, Chan AY, Deverman BE. Systematic multi-trait AAV capsid engineering

- ▸ Engineering AAV capsids with multiple characteristics of interest is challenging because of the vast sequence space, rarity of enhanced variants, and potential incompatibility between desired traits. For example, a capsid with increased tropism may suffer from low production yields, a lack of target cell specificity, or poor translation across species.
- ▸ Leveraged deep learning, unbiased synthetic AAV capsid libraries, and quantitative screening to create an atlas of sequence-to-function maps.
- ▸ This atlas can be harnessed to predict AAV capsids, across the extensive sequence space, which exhibit high production fitness alongside multiple traits relevant to gene therapy.

AWARDS / FELLOWSHIPS

2021	Broad Institute Spot Award, Student/Employee Recognition Program
2020	NSF Graduate Research Fellowships Program (GRFP), Honorable Mention
2019	Summer Scholars Independent Research Fellowship, Northeastern University ($5000)
2018	Advanced Research/Creative Endeavor Award, Northeastern University ($3000)
2018	ASBMB Active Site Poster / Travel Award Winner
2018	Bioengineering Research Achievement Award, Northeastern University
2015–2020	Dean's List, Dean's Merit Scholarship

PRESENTATION HIGHLIGHTS

Presentation	**Chen AT**, Altschuler K, Favela D, Zhan SH, Chan AY, Deverman BE. COVID CG: SARS-CoV-2 mutation tracking and genomic data visualization. Presented at PyData Boston April 2021 (Virtual - Online) Video: https://www.youtube.com/watch?v=G744eRCdAYo
Oral Abstract	**Chen AT**, Altschuler K, Zhan SH, Chan AY, Deverman BE. COVID-19 CG: Tracking SARS-CoV-2 by Mutation, Location, and Date of Interest. Presented at ASGCT COVID-19 Symposium, September 2020 (Online).
Poster	**Chen AT**, Chan YA, Deverman BE, Elzahraa-Eid F. Clustif: Motif-based clustering of short peptides for protein engineering applications. Presented at 15th annual Broad Retreat (Broad Institute of MIT and Harvard), December 2019, Boston MA PDF: https://atchen.me/images/clustif_poster_v10.pdf

Presentation	**Chen AT**, Franks A & Slavov N. DART-ID Increases Single-Cell Proteome Coverage. Presented at Single Cell Proteomics (SCP) Conference, June 2019, Boston MA Video: https://www.youtube.com/watch?v=IWeasIXs5F0 Slides: https://atchen.me/images/DART_SCP_v3.pptx
Poster	**Chen AT**, Franks A & Slavov N. DART-ID Increases Single-Cell Proteome Coverage. Presented at Experimental Biology (EB) as part of ASBMB, April 2019, Orlando FL PDF: https://atchen.me/images/DART_poster_v6.pdf

TECHNICAL SKILLS

Programming

Advanced	Python, R, Vega, JavaScript, HTML/CSS
Proficient	MATLAB, LaTEX, SQL, PL/pgSQL, bash

Software / Libraries

Python	multiprocessing, numpy, scipy, pandas, scikit-learn, matplotlib, snakemake, networkx
R	dplyr/tidyverse ecosystem, ggplot, shiny, LIGER, Seurat
Sequencing	bcl2fastq, fastqc, bowtie2, STAR, kallisto, samtools, pysam, IGV, cellranger
JavaScript	node.js, React, MobX, Vega, Webpack
HPC	Slurm, UGE, Google Cloud (Compute Engine, Storage, SQL, Run, Functions)
Other	git, Linux, Docker, STAN, PostgreSQL, PyMOL, SnapGene, MaxQuant, Adobe Photoshop, Adobe Illustrator

Laboratory

Mammalian cell culture (suspension and adherent), Vector assembly + cloning, Transfection, PCR, FACS (Sony SH800z, MA900), Illumina NGS sample prep, Bulk RNAseq, Single cell RNAseq (10X), Proteomics sample prep, LC/MS operation + maintenance

Hands-On

Shop and hand tools, Basic bench electronic equipment, Computer building and repair

OTHER EXPERIENCE

Journal of Medical Insight (https://jomi.com)   *Lead Web Developer*   6/2014 – 9/2016

- ▸ In 3 months and with no prior web development experience, created journal website for viewing instructional surgical videos and managing article content.
- ▸ Assisted in filming live surgeries with video team.

Bikeway Source, Bedford MA   *Sales Associate / Bike Mechanic*   8/2012 – 6/2014

- ▸ Performed bike repair, facility construction, sales, and customer service.

RELEVANT COURSEWORK

Biology

Molecular Engineering, Cellular Engineering, Tissue Engineering, Genetics and Molecular Biology

Chemistry

Organic Chemistry 1 & 2, Biochemistry

Math / Statistics

Supervised Machine Learning (Audited), Unsupervised Machine Learning (Audited), Dynamic Modeling in Systems Biology, Differential Equations, Statistics (MIT OCW 18.05), Linear Algebra (MIT OCW 18.06)

Physics

Physics 1 & 2, Statics and Dynamics, Transport and Fluids, Circuits and Signal Processing