

# Albert Tian Chen

Interdisciplinary student researcher with 3+ years of statistics, data science and visualization experience, as well as a coursework foundation in biology and the basic sciences. Attending graduate school to apply both wet and dry lab techniques towards studies of molecular biology and systems biology.

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## EDUCATION

**Northeastern University**, College of Engineering, Boston, MA

9/2015 – 05/2020

Candidate for Bachelor of Science in *Bioengineering*

- 3.7 / 4.0 GPA

## PUBLICATIONS

**Chen AT**, Franks A, Slavov N (2019) DART-ID increases single-cell proteome coverage. *PLOS Computational Biology* 15(7): e1007082. <https://doi.org/10.1371/journal.pcbi.1007082>  
Website: <https://dart-id.slavovlab.net/>

**Chen AT\***, Huffman RG\*, Specht H\*, Slavov N (2019) DO-MS: Data-Driven Optimization of Mass Spectrometry Methods. *Journal of Proteome Research* 18(6): 2493-2500.  
<https://doi.org/10.1021/acs.jproteome.9b00039>. \* Co-first authors  
Website: <https://do-ms.slavovlab.net/>

## RESEARCH EXPERIENCE

**Vector Engineering Team, Broad Institute of MIT and Harvard** ([Link](#))

Research Assistant, Cambridge MA

5/2019 – Present

- With [a Broad Shark Tank-winning team](#), accelerate discovery of promising recombinant adeno-associated viruses (AAV) for gene therapy in the central nervous system, by developing a novel computational method of identifying functional variants from large screens of randomized gene libraries
- Mine complex atomic interactions in AAV capsid proteins with PyMOL scripts, and visualize them in an interactive application built with Python and Bokeh
- Build a user-friendly and code-free data processing pipeline for next-generation sequencing data, and store/query results with PostgreSQL, using the Google Cloud Platform

**Slavov Laboratory, Northeastern University** ([Link](#))

Research Assistant, Boston MA

7/2016 – 05/2020

- First author on [DART-ID](#) project, a Bayesian framework for increasing peptide identification rates in mass-spec proteomics experiments, by incorporating peptide retention time as additional evidence.
- Co-first author on [DO-MS](#), a modular, extensible, and automated data analysis and visualization platform for rationally optimizing mass spectrometry methods
- Design and run LC/MS single cell proteomics experiments, from cell culture to instrument operation, with the Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) method (<http://scope2.slavovlab.net/>)

## **Waters Corporation, Separations R&D**

*Chemistry Co-op, Milford MA*

*7/2017 – 12/2017*

- Prototyped high-throughput LC/MS analysis workflow that doubled throughput to 4800 samples/day, through hardware and firmware modifications to existing instrumentation
- Implemented efficient low-level data processing software in C++ and Armadillo
- Performed maintenance, repairs, and installed custom modifications on Acquity LC instruments and Waters mass spectrometry instruments

## **AWARDS / FELLOWSHIPS**

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

## **TECHNICAL SKILLS**

### **Programming:**

*Advanced:* Python, R, JavaScript, HTML/CSS

*Proficient:* MATLAB, LaTeX, SQL, bash, C

### **Software / Libraries:**

numpy, pandas, bokeh, STAN, shiny, dplyr, matplotlib, ggplot, git, Google Cloud Platform (Compute Engine, Storage, SQL), Adobe Photoshop, Adobe Illustrator

### **Laboratory:**

Mammalian Cell Culture, 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 (JOMI), Lead Web Developer, Boston MA** *6/2014 – 9/2016*

- Led development of <http://old.jomi.com> with no prior web development experience, in 3 months
- Rebuilt site in Node.js, MongoDB, and React as <https://jomi.com> a year later, again in 3 months
- Assisted in filming live surgeries with video team

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

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

## PRESENTATIONS

Poster: **Chen AT**, Chan YA, Deverman BE, Elzahraa-Eid F. Clustif: Motif-based clustering of short peptides for protein engineering applications. Presented at 15<sup>th</sup> annual Broad Retreat (Broad Institute of MIT and Harvard), December 2019, Boston MA

PDF: [https://atchen.me/images/clustif\\_poster\\_v10.pdf](https://atchen.me/images/clustif_poster_v10.pdf)

Poster: **Chen AT**, Perlman DH, Emmott E, Huffman RG & Slavov N. P-SCOPE: Carrier-enabled low-input phosphoproteomics by mass spectrometry. Presented at American Society of Biochemistry and Molecular Biology (ASBMB) Active Site Northeast Regional Meeting, November 2019, Boston MA

PDF: [https://atchen.me/images/PSCOPE\\_poster\\_v2.pdf](https://atchen.me/images/PSCOPE_poster_v2.pdf)

Poster: **Chen AT**, Perlman DH, Emmott E, Huffman RG & Slavov N. P-SCOPE: Carrier-enabled low-input phosphoproteomics by mass spectrometry. Presented at Northeastern University Creative Endeavor and Research Experience Symposium (CERES), October 2019, Boston MA

PDF: [https://atchen.me/images/NUSPURF\\_Vertical\\_2019.pdf](https://atchen.me/images/NUSPURF_Vertical_2019.pdf)

Poster: **Chen AT**, Perlman DH, Emmott E, Huffman RG & Slavov N. P-SCOPE: Carrier-enabled low-input phosphoproteomics by mass spectrometry. Presented at Northeastern Bioengineering Research Symposium, June 2019, Boston MA

PDF: [https://atchen.me/images/PSCOPE\\_poster\\_v1.pdf](https://atchen.me/images/PSCOPE_poster_v1.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](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 the American Society of Biochemistry and Molecular Biology (ASBMB), April 2019, Orlando FL

PDF: [https://atchen.me/images/DART\\_poster\\_v6.pdf](https://atchen.me/images/DART_poster_v6.pdf)

Poster: **Chen AT**, Franks A & Slavov N. DART-ID Increases Single-Cell Proteome Coverage. Presented at Northeastern Research, Innovation, and Scholarship Expo (RISE), April 2019, Boston MA

PDF: [https://atchen.me/images/DART\\_RISE\\_Poster.pdf](https://atchen.me/images/DART_RISE_Poster.pdf)

Poster: **Chen AT**, Franks A & Slavov N. DART-ID Increases Proteome Coverage with Data-Driven Alignment of Retention Times. Presented at American Society of Biochemistry and Molecular Biology (ASBMB) Active Site Northeast Regional Meeting, November 2018, Boston MA

PDF: [https://atchen.me/images/dart\\_poster\\_v2\\_3.pdf](https://atchen.me/images/dart_poster_v2_3.pdf)

Poster: **Chen AT**, Franks A & Slavov N. DART-ID Data-Driven Alignment of Retention Times for Peptide Identification increases peptide coverage by 75%. Presented at Single Cell Proteomics (SCP) Conference, June 2018, Boston MA

PDF: [https://atchen.me/images/scp\\_poster\\_v6.pdf](https://atchen.me/images/scp_poster_v6.pdf)

## 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