# Albert T. Chen

Address: 1 Terrace St. A1, Boston MA 02120
Phone: 339-927-0113
Email: chen.alb@husky.neu.edu
Portfolio: http://halfgrain.com/
Github: https://github.com/blahoink

Student researcher looking to apply an interdisciplinary skillset of statistics, data science, and data visualization in the field of systems and single cell biology

Available full-time July 2019 – December 2019

## TECHNICAL SKILLS

*Programming:*

Python, MATLAB, R, LaTEX, JavaScript, C/C++

*Software/Libraries:*

numpy, pandas, STAN, shiny, dplyr, ggplot, Photoshop, Illustrator

*Laboratory:*

Mammalian, Bacterial Cell Culture, Proteomics Sample Prep, LC/MS operation + maintenance

*Hands-On:*

Shop and Hand Tools, Basic Bench Electronic Equipment, Computer Building and Repair

## COURSEWORK

Supervised and Unsupervised Machine Learning, Cellular Engineering, Molecular Engineering, Dynamic Modeling in Systems Biology, Statistics, Bayesian Methods, Differential Equations and Linear Algebra, Circuits and Signal Processing, Genetics, Organic Chemistry, Biochemistry, Statics and Dynamics, Transport and Fluids

## ADDITIONAL INFO

*Interests:*

Video game development, creating fake album cover art, bicycle touring, pick-up soccer, cooking greasy food, eating greasy food, weightlifting

**References available upon request**

## EDUCATION

**Northeastern University**, *College of Engineering*, Boston, MA          *9/2015 – Present*
Candidate for Bachelor of Science in Bioengineering          *Expected 2020*

*Honors:*
- 3.7 / 4.0 GPA | 3.8 / 4.0 Major Courses GPA
- Dean's List, Dean's Merit Scholarship
- Bioengineering Department Research Achievement Award (2018)
- ASBMB Active Site 2018 Poster/Travel Award Winner
- Advanced Research/Creative Endeavor Award ($2900)

## WORK/RESEARCH EXPERIENCE

**Slavov Laboratory, NEU**, *Research Assistant*, Boston MA          *7/2016 – Present*
- First author on *DART-ID* project (under review, PLOS Comp Bio), which increases peptide identification rates using statistical models that combine evidence from retention time and spectral data.
  Preprint: https://www.biorxiv.org/content/early/2018/08/23/399121
- Develop DO-MS, a modular, extensible, and automated analysis and visualization platform (under review, Journal of Proteome Research).
  Preprint: https://www.biorxiv.org/content/early/2019/01/06/512152
- Design, prepare, and run LC/MS single cell proteomics experiments with Single Cell Proteomics by Mass Spectrometry (SCoPE-MS) method
- Implement computational workflows on proteomics data, for troubleshooting, optimizing methods, and drawing biological conclusions

**Waters Corporation**, *R&D – Chemistry Intern*, Milford MA          *7/2017 – 12/2017*
- Designed and carried out LC/MS experiments characterizing viability and hardware effects of experimental high-throughput workflow
- Implemented efficient low-level data processing software in C++ and Armadillo for high-throughput workflows
- Performed maintenance, repairs, and modifications on Acquity LC instruments and Waters mass spectrometry instruments
- Created application to dynamically link various mass spectrometry analysis tools
- Presented results in weekly lab meetings and to upper-level management

**Journal of Medical Insight**, *Lead Web Developer*, Boston MA          *6/2014 – 9/2016*
- Lead development of websites: http://old.jomi.com and https://jomi.com
- Assisted in filming live surgeries with video team

## OTHER EXPERIENCE

**Bevy**, *Co-Founder and Developer*, Boston MA          *5/2015 – 6/2016*
- Developed concept into website, iOS and Android apps, in under 8 months
- Managed 30-hour workweeks while maintaining a high GPA

**826 Boston**, *Tutor*, Boston MA          *2/2016 – 5/2016*
- Tutored grammar and essay composition at the O'Bryant High School

**Bikeway Source**, *Sales Associate/Bike Mechanic*, Bedford MA          *8/2012 – 6/2014*
- Performed sales, customer service, inventory management, and bike repair