

Curriculum Vitae

Jennifer Lu

July 2020

Position:	Ph.D. Candidate Steven Salzberg Lab	Address: Johns Hopkins University Wyman Park Building, Room S220
Institution:	Johns Hopkins University	3100 Wyman Park Drive
Email:	jennifer.lu717@gmail.com	Baltimore, MD, 21205, USA
Phone:	240-449-7437	
Website:	http://ccb.jhu.edu/people/jennifer.lu/	
Github Page:	http://github.com/jenniferlu717/	

EDUCATION

08/2015 - Present

Ph.D. Candidate in the Department of Biomedical Engineering, Johns Hopkins University, Baltimore, MD. Thesis Advisor: Professor Steven Salzberg, Expected Degree Completion: Dec 2020

09/2011 - 12/2014

Bachelors of Science in Chemical and Biomolecular Engineering from Johns Hopkins University, Baltimore, MD. GPA 3.87/4.00. Minor in Computer Science

RESEARCH EXPERIENCE

08/2015 – Present

Ph.D. Researcher in the Center for Computational Biology, Steven Salzberg, Johns Hopkins University, Baltimore, MD.

- Researched next-generation sequencing for diagnosing infections in human corneal and brain samples.
- Designed open-source software for analysis of DNA sequencing reads.
- Analyzed microbial DNA sequence complexities, similarities, and contamination.
- Long-read sequencing using Oxford Nanopore MinION and GridION technologies.
- Studied plant and water DNA extraction and sequencing.

08/2014 — 04/2015

Student Researcher for Dr. Rebecca Schulman's Nanotechnology Lab at Johns Hopkins University, Baltimore, MD.

- Generated DNA-origami structures.
- Assessed the kinetics of dimer formation between DNA-origami structures.

05/2012 — 08/2012

Student Intern for the Laboratory of Receptor Biology and Gene Expression at the NIH, NCI, Bethesda, MD.

- Researched Chromosome Conformation Capture experiments and the experimental biases present in Hi-C experiments.
- Developed programs in Perl and R to analyze Hi-C data.

05/2014 — 12/2014

Student Intern for Dr. Navin Varadarajan's Single Cell Lab, at the University of Houston, Houston, TX.

- Developed a Python interface for processing microscopy data from single-cell assays while quantifying intercellular interactions.
- Employed the MySQL database system to store microscopy data for future analysis.

PUBLICATIONS

SUBMITTED PREPRINTS

J. Lu, S. L. Salzberg “Ultrafast and accurate 16S microbial community analysis using Kraken 2.” *bioRxiv*, 2020.03.27.012047, <https://doi.org/10.1101/2020.03.27.012047> (Submitted for publication).

J. Lu, S. L. Salzberg “SkewIT: Skew Index Test for detecting mis-assembled bacterial genomes.” *bioRxiv*, 2020.02.27.968214 <https://doi.org/10.1101/2020.02.27.968214>. (Submitted for publication).

FIRST AUTHORED, PEER-REVIEWED PUBLICATIONS

J. Lu, S. L. Salzberg (2018). “Removing contaminants from databases of draft genomes.” *PLoS Comput Biol*, 14(6): e1006277. <https://doi.org/10.1371/journal.pcbi.1006277>

J. Lu, F. P. Breitwieser, P. Thielen, S. L. Salzberg, (2017). “Bracken: estimating species abundance in metagenomics data.” *PeerJ Computer Science*, 3:e104 <https://doi.org/10.7717/peerj-cs.104>

CO-AUTHORED, PEER-REVIEWED PUBLICATIONS

D.E. Wood, **J. Lu**, B. Langmead (2019). “Improved metagenomic analysis with Kraken 2.” *Genome Biol*, 20 (257). <https://doi.org/10.1186/s13059-019-1891-0>

Z. Li, F. P. Breitwieser, **J. Lu**, A. S. Jun, S. L. Salzberg, C. G. Eberhart. (2018). “Identifying corneal infections in formalin fixed specimens using next generation sequencing.” *Investigative Ophthalmology & Visual Science (IOVS)*. <https://doi.org/10.1167/iovs.17-21617>.

F.P. Breitwieser, **J. Lu**, S.L. Salzberg, (2017). “A review of methods and databases for metagenomic classification and assembly.” *Briefings in Bioinformatics*, bbx120 <https://doi.org/10.1093/bib/bbx120>

J. Fern, **J. Lu**, R. Schulman (2016). ”The Energy Landscape for the Self-Assembly of a Two-Dimensional DNA Origami Complex” *ACS nano*, 10 (2), 1836-1844

A. Merouane, N. Rey-Villamizar, Y. Lu, I. Liadi, G. Romain, **J. Lu**, H. Singh, L. J. N. Cooper, N. Varadarajan, B. Roysam (2015). ”Automated profiling of individual cell–cell interactions from high-throughput time-lapse imaging microscopy in nanowell grids (TIMING)” *Bioinformatics* 31 (19), 3189-3197

PRESENTATIONS

- | | |
|---------|---|
| 2019/09 | “Bioinformatics of Kraken 2 and the Loch Ness Monster.” Presented at the Microbiome Meeting, Johns Hopkins University, Baltimore, MD |
| 2018/04 | “Removing Contaminants from Metagenomic Databases.” Presented at the BME PhD Student Seminar Series, Johns Hopkins University, Baltimore, MD |
| 2017/12 | “Don’t Feed the Kraken.” Virtual Lab Talk in the Microbial Bioinformatics Slack |
| 2017/05 | “Computational Challenges in Sequenced-Based Medical Diagnoses.” Presented at the Lectures in Computational Biophysics Seminar, Johns Hopkins University, Baltimore, MD |
| 2017/01 | “Bracken: Bayesian Reestimation of Abundance with KrakEN” Presented at the Joint Biostats-Genomics Lab Meeting, Johns Hopkins University, Baltimore, MD. |

POSTERS

- 2019/11 **J. Lu**, S.L. Salzberg. “Identifying Mis-assembled Bacterial Genomes using GC Skew”. Presented at the Genome Informatics, Cold Spring Harbor Laboratory, NY.
- 2019/11 **J. Lu**, S.L. Salzberg. “Fast and accurate 16S microbial community analysis using Kraken 2.” Presented at Genome Informatics, Cold Spring Harbor Laboratory, NY.
- 2018/11 **J. Lu**, F. P. Breitwieser, S.L. Salzberg. “Identifying and removing contamination from bacterial, archaeal, and eukaryotic genomes.” Presented at Biological Data Science, Cold Spring Harbor Laboratory, NY.
- 2018/11 D. E. Wood, **J. Lu**, B. Langmead. “Re-releasing the Kraken – Kraken 2.” Presented at Biological Data Science, Cold Spring Harbor Laboratory, NY
- 2017/05 **J. Lu**, F. P. Breitwieser, S.L. Salzberg. “Improving draft genomes of human pathogens for use in metagenomic studies”, Presented at Biology of Genomes, Cold Spring Harbor Laboratory, NY.
- 2014/07 **J. Lu**, N. Varadarajan, B. Roysam. (07/2014). “Bioinformatics of Single Cell Microscopy.” Presented at the University of Houston, Houston, TX.

SOFTWARE PACKAGES

Bracken (<https://github.com/jenniferlu717/Bracken/>)
Software package for abundance estimation with the Kraken
(<https://github.com/DerrickWood/kraken2/>) classification system.

KrakenTools (<https://github.com/jenniferlu717/KrakenTools/>)
Suite of programs for downstream analysis and visualization of Kraken, Kraken 2, KrakenUniq, and Bracken results.

SkewIT (<https://github.com/jenniferlu717/SkewIT>, <https://jenniferlu717.shinyapps.io/SkewIT/>)
Tools for analysis of GC Skew in bacterial genomes and ShinyApp for visualization of GC Skew in bacterial genomes. ShinyApp also provides visual analysis of GC Skew patterns in the NCBI Refseq bacterial library.

TEACHING EXPERIENCE

09/2017 — 12/2017

Teaching Assistant for Statistical Mechanics and Thermodynamics at Johns Hopkins University, Baltimore, MD. Class taught by Dr. Michael Beer. Taught small weekly section classes. Engaged students to help them understand statistical mechanics and thermodynamics and their application in biological systems.

02/2017 — 05/2017

Teaching Assistant for Introduction to Genomic Research at Johns Hopkins University, Baltimore, MD. Class taught by Dr. Steven Salzberg. Taught students about UNIX commands and using Python coding for genomic research analysis. Introduced students to genomic assembly, metagenomic sample analysis, DNA sequencing technology, and RNA-seq technology. Bioinformatics tools included: SPAdes, MUMmer, Kraken, Centrifuge, Bowtie, TopHat, HISAT, and StringTie.

09/2013 — 12/2013

Classroom Assistant for Immediate Programming at Johns Hopkins University, Baltimore, MD. Class taught by Dr. Yair Amir. Assisted students with the development of data structures and programs in the programming languages of C and C++, memory management and code development.

SKILLS AND QUALIFICATIONS

SOFTWARE ENGINEERING

Operating Systems	Linux/Unix, Microsoft Windows XP, 7-10, Mac OS X
Programming Languages	C, C++, Python, Perl, R, Java, MATLAB®, L ^A T _E X, HTML
Databases	MySQL

LABORATORY SKILLS

Spectrophotometry, PCR, microscopy
Oxford Nanopore DNA sequencing using the MinION/GriION
DNA extraction from plants, soil, and water

PEER-REVIEWED FOR JOURNALS

Briefings in Bioinformatics, Microbial Genomics, PeerJ

LANGUAGES

English (native), Chinese (conversational), Spanish (conversational)