Curriculum Vitae
Jennifer Lu

Position:	Staff Scientist	**Address:**	
	Steven Salzberg Lab	Johns Hopkins University	
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EDUCATION

08/2015 - 11/2020
Ph.D. in Biomedical Engineering, Johns Hopkins University, Baltimore, MD. Doctoral Thesis:
'SkewIT, Bracken, and Kraken: Methods for analyzing a complex, but invisible world.' Thesis Advisor:
Professor Steven Salzberg

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

07/2022 – Present
Staff Scientist in the Center for Computational Biology, Steven Salzberg, Johns Hopkins University, Baltimore, MD.
- Identified protein mutations in clinically isolated microbes.
- Evaluated the genome-based phylogeny of clinically isolated microbes.

11/2020 – 07/2022
Post-Doctoral Fellow 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.
- Developed tools, resources, and protocols for metagenomics sequencing data.

08/2015 – 11/2020
Ph.D. Researcher in the Center for Computational Biology, Steven Salzberg, Johns Hopkins University, Baltimore, MD.
- Designed open-source software for analysis of DNA sequencing reads.
- Performed 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.
- 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
- Employed the MySQL database system to store microscopy data for future analysis.

Publications

First Authored, Peer-Reviewed Publications

J. Lu, N. Rincon, D. E. Wood, F. P. Breitwieser, C. Pockrandt, B. Langmead, S. L. Salzberg, M. Steinegger. (*in press*) "Metagenome analysis using the Kraken software suite" In: *Nature Protocols*.

J. Lu, S. L. Salzberg "SkewIT: The Skew Index Test for large-scale GC Skew analysis of bacterial genomes." *PLoS Comput Biol*, 16(12): e1008439. https://doi.org/10.1371/journal.pcbi.1008439

J. Lu, S. L. Salzberg "Ultrafast and accurate 16S rRNA microbial community analysis using Kraken 2." *Microbiome* 8, 124 (2020). https://doi.org/10.1186/s40168-020-00900-2

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

A.S. Shifera, C. Pockrandt, N. Rincon, Y. Ge, **J. Lu**, A. Varabyou, et al. (2021) "Identification of microbial agents in tissue specimens of ocular and periocular sarcoidosis using a metagenomics approach" *F1000Research*, https://doi.org/10.12688/f1000research.55090.1

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

2021/11	"Bacteria or Cow? Bioinformatics Challenges for Metagenomics Medical Diagnoses." Presented at the 2021 International Online Symposium on Bioinformatics for Metagenomic Analysis, Hosted by Seoul National University, Steinegger Lab.
2021/10	"Metagenomic Diagnostics of Maya, a National Aquarium Dolphin." Presented at the Joint Biostats-Genomics Lab Meeting, Johns Hopkins University, Baltimore, MD
2021/04	"Computational Methods for Infectious Disease Diagnostics from Metagenomics Sequencing Data." Presented at the Microbiome Meeting, Johns Hopkins University, Baltimore, MD
2021/02	"Cancer Associated Pathogens." Presented at the Joint Biostats-Genomics Lab Meeting, Johns Hopkins University, Baltimore, MD
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.

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 and visualization of GC Skew in bacterial genomes. ShinyApp provides visual analysis of GC Skew patterns in the NCBI Refseq bacterial library.

Teaching Experience

03/2022
Guest Lecture for Genomic Data Science at Johns Hopkins University, Baltimore, MD.
Class taught by Dr. Stevern Salzberg. Explained the basics of DNA extraction and nanopore sequencing.

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®, LaTeX, HTML
Databases	MySQL

Laboratory Skills

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

Peer-Reviewed for Journals

Briefings in Bioinformatics, Microbial Genomics, PeerJ

Languages

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