

Philippe Chlenski

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EDUCATION

Columbia University

PhD Computer Science | GPA 4.00 | Advisor: Itsik Pe'er

New York, NY

Aug 2020–Present

Relevant coursework: Machine Learning, Deep Learning and Neural Networks, Causal Inference, Computational Genomics, Introduction to Database Systems, Analysis of Algorithms.

Yale University

BA Mathematics & Philosophy | GPA 3.85 | cum laude with distinction

New Haven, CT

Aug 2015–May 2018

Deep Springs College

AA Liberal Arts | GPA 3.76

Deep Springs, CA

Jul 2012–Jun 2014

RESEARCH EXPERIENCE

Columbia University

NSF Graduate Research Fellow

New York, NY

Sep 2020–Present

- Developed and analyzed bioinformatics tools to study temporal dynamics in the microbiome using single metagenomic samples in the context of sparse, noisy, or otherwise irregular clinical data.
- Built a synthetic data engine for study design and interpretable testing of causal inference frameworks.
- Built inference systems to relate longitudinal multi-omics data, microbial dynamics, and disease states.
- Plan and supervise end-to-end student research projects in computational biology.

Argonne National Laboratory

Comparative Genomics Researcher

Chicago, IL

Oct 2018–Sep 2020

- Improved speed, accuracy, and quality control of RASTtk genome annotation pipeline with machine learning tools built in Python with Scikit-Learn, Keras, and TensorFlow.
- Developed pipeline for AI-based strain discovery and data analysis in synthetic biology.
- Contributed extensively to three grant applications, two of which have been funded.

PUBLICATIONS AND TALKS

First author: Chlenski, Hsu, and Pe'er. MiSDEED: a synthetic multi-omics engine for microbiome power analysis and study design. [doi: 10.1101/2021.08.09.455682](https://doi.org/10.1101/2021.08.09.455682) [Under review]

Second author: Joseph *et al.* Accurate and robust inference of microbial growth dynamics from metagenomic sequencing. [doi: 10.1101/2021.02.02.429365](https://doi.org/10.1101/2021.02.02.429365) [Under review]

Second+corresponding author: Parrello *et al.* Extraction of near-complete genomes from metagenomic samples. *PLOS ONE*. 2021. [doi: 10.1371/journal.pone.0250092](https://doi.org/10.1371/journal.pone.0250092)

Author: Davis *et al.* The PATRIC Bioinformatics Resource Center: Expanding data and analysis capabilities. *Nucleic Acids Research*. 2020. [doi: 10.1093/nar/gkz943](https://doi.org/10.1093/nar/gkz943)

Corresponding author: Parrello *et al.* A machine learning-based service for estimating quality of genomes using PATRIC. *BMC Bioinformatics*. 2019. [doi: 10.1186/s12859-019-3068-y](https://doi.org/10.1186/s12859-019-3068-y)

Poster: Peak-to-trough ratio analysis reveals novel associations with microbial dynamics in liver transplant patients. *Biology of Genomes*. May 2021.

Talk: Annotate a genome in PATRIC using RASTtk. *PATRIC workshop*. April 2019.

In preparation: Fonstein *et al.* Organism engineering by computational biology: production of threonine in *E. coli*.

WORK EXPERIENCE

Yale University

Student Technology Coordinator

New Haven, CT

Dec 2015–Aug 2018

- Managed and trained 3 technicians to provide primary IT support to over 900 students.

Head Transfer Counselor

May 2016–May 2017

- Managed a team of 16 counselors to orient and mentor new transfer students.

SKILLS

Programming: Python, Perl, Bash, SQL, HTML/CSS.

Tools and frameworks: Tensorflow, Scikit, NumPy, Biopython, Git, Linux, bioinformatics, high-performance computing.

Spoken languages: Russian (native), English (fluent), French (conversational).