

# 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

### 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

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## RESEARCH EXPERIENCE

### Columbia University

NSF Graduate Research Fellow

New York, NY  
Sep 2020–Present

- Analyze and develop bioinformatics tools to infer temporal dynamics in the microbiome from single metagenomic samples in the context of clinical data.
- Relate longitudinal multi-omics data, microbial dynamics, and disease states.
- Build synthetic data for interpretable testing of AI-based causal inference frameworks.
- 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.

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## PUBLICATIONS

**Corresponding author:** Parrello *et al.* Extraction of near-complete genomes from metagenomic samples: a new service in PATRIC. *PLOS ONE*. 2021. [doi.org/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.org/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.org/10.1186/s12859-019-3068-y](https://doi.org/10.1186/s12859-019-3068-y)

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

**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.

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## 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.

Lazarus Summer Intern

May 2016–Aug 2016

- Provided data analysis, IT support, and programming assistance for the Yale Farm.