Philippe Chlenski

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EDUCATION

Columbia University   New York, NY
PhD Computer Science | GPA 4.00 | Advisor: Itsik Pe'er   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   New Haven, CT
BA Mathematics & Philosophy | GPA 3.85 | cum laude with distinction   Aug 2015–May 2018

Deep Springs College   Deep Springs, CA
AA Liberal Arts | GPA 3.76   Jul 2012–Jun 2014

RESEARCH EXPERIENCE

Columbia University   New York, NY
NSF Graduate Research Fellow   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.
- Planned and supervised 8 end-to-end student research projects in computational biology.

Argonne National Laboratory   Chicago, IL
Comparative Genomics Researcher   Oct 2018–Sep 2020
- Improved speed, accuracy, and quality control of RASTtk genome annotation pipeline with 4 novel 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 3 grant applications, 2 of which have been funded.

PUBLICATIONS AND TALKS

- **Chlenski**, Hsu, and Pe'er. MiSDEED: a synthetic multi-omics engine for microbiome power analysis and study design. *Bioinformatics*.   **[Under review]** doi: 10.1101/2021.08.09.455682
- Joseph, **Chlenski**, Korem, and Pe'er. Accurate and robust inference of microbial growth dynamics from metagenomic sequencing. *Genome research.*   **[Under review]** doi: 10.1101/2021.02.02.429365
- Parrello, Butler, **Chlenski**, Pusch, and Overbeek. Supervised extraction of near-complete genomes from metagenomic samples: a new service in PATRIC. *PLOS ONE.* 2021.   doi: 10.1371/journal.pone.0250092
- Davis *et al*. The PATRIC Bioinformatics Resource Center: Expanding data and analysis capabilities. *Nucleic Acids Research.* 2020.   doi: 10.1093/nar/gkz943
- Parrello, Butler, **Chlenski**, *et al*. A machine learning-based service for estimating quality of genomes using PATRIC. *BMC Bioinformatics.* 2019.   doi: 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   New Haven, CT
Student Technology Coordinator   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).