

## Neil Thomas

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EDUCATION	<b>University of California, Berkeley</b> <b>PhD Student, Computer Science</b> <ul style="list-style-type: none"><li>My research focuses on developing machine learning methods for learning meaningful representations of proteins, with the aim of enabling applications in protein design, functional annotation, homology detection, and structure prediction.</li></ul>	2017 - Present
	University of California, Berkeley BS, Engineering Mathematics & Statistics, <i>High Honors</i>	2011 - 2015
	Independent University of Moscow, Russia Study-abroad program: <i>Math in Moscow</i>	Spring 2014
SELECTED COURSEWORK	Organic Chemistry, Microbial Ecology, Statistical Mechanics, Convex Optimization	
PUBLICATIONS	Nicholas Bhattacharya*, <b>Neil Thomas*</b> , Roshan Rao, Justas Dauparas, Peter K. Koo, David Baker, Yun S. Song, Sergey Ovchinnikov “Interpreting Potts and Transformer Protein Models Through the Lens of Simplified Attention” <i>Pacific Symposium on Biocomputing (2022)</i>	
	Lucy Colwell, <b>Neil Thomas</b> “Minding the gaps: The importance of navigating holes in protein fitness landscapes” <i>Cell Systems (2021)</i>	
	Samantha Petti, Nicholas Bhattacharya, Roshan Rao, Justas Dauparas, <b>Neil Thomas</b> , Juannan Zhou, Alexander M. Rush, Peter K. Koo, Sergey Ovchinnikov “End-to-end learning of multiple sequence alignments with differentiable Smith-Waterman” <i>bioRxiv (2021)</i>	
	Roshan Rao*, Nicholas Bhattacharya*, <b>Neil Thomas*</b> , Yan Duan, Xi Chen, John Canny, Pieter Abbeel, Yun S. Song “Evaluating Protein Transfer Learning with TAPE” <i>Advances in Neural Information Processing Systems 32 (NeurIPS 2019)</i> . Selected as <b>Spotlight Talk</b> . (2.4% of submissions)	
WORK EXPERIENCE	<i>Research Intern</i> Google, Remote <ul style="list-style-type: none"><li>Developed open source codebase for benchmarking protein sequence design on synthetic fitness landscapes. <a href="https://github.com/google-research/slip">https://github.com/google-research/slip</a></li></ul>	Aug 2021 - Dec 2021
	<i>AI Resident</i> X (formerly Google X), Remote <ul style="list-style-type: none"><li>Part of an early-stage protein engineering project at the intersection of machine learning and high-throughput experimental characterization. Working to facilitate a shift towards a bioeconomy, low carbon growth and advances in human health.</li></ul>	March 2021 - Aug 2021
	<i>Software Engineer</i> 23andMe, Mountain View, CA <ul style="list-style-type: none"><li>Implemented IBD (Identity by Descent) pipeline in Apache Spark to take advantage of data locality and parallelism. Relieved backlog of customer processing.</li><li>Automated imputation pipeline using Minimac3 and Luigi. Imputed over 1 million individuals on custom reference panel with improved accuracy.</li><li>Deployed to AWS to scale computation pipelines to handle massive customer demand.</li><li>Built haplotype phasing application using modified BEAGLE algorithm. Wrote Python wrappers for extracting and deploying legacy research C++ code.</li><li>Responsible for collaborative project planning - distilling input from multiple teams.</li></ul>	Aug 2015 - June 2017

Interviewed candidates. Mentored and onboarded new engineers.

<b>TEACHING</b>	<i>Graduate Student Instructor</i> Summer 2022 Introduction to Artificial Intelligence (CS 188), UC Berkeley <ul style="list-style-type: none"><li>• Topics include: Search, Games, Graphical models, HMMs, RL, Machine Learning</li><li>• Led 2 weekly discussion sections.</li></ul>
	<i>Graduate Student Instructor</i> Fall 2020 Mathematical Statistics (STAT 135), UC Berkeley <ul style="list-style-type: none"><li>• Core upper division course for statistics majors. Topics include: parameter estimation, hypothesis testing, linear regression.</li><li>• Led 3 weekly discussion sections, totalling 40 students.</li></ul>
<b>AWARDS</b>	<i>NIH Genomics Training Grant</i> 2018 - 2020 <i>Best Lightning Talk</i> - UC Berkeley Computational Biology Retreat 2019 <i>Winner</i> - 23andMe Hackathon 2016 <ul style="list-style-type: none"><li>• Part of a 5-person team that, in 1.5 days, built an interactive way to explore 23andMe genetic reports using the human body.</li></ul>
	<i>Honorable Mention</i> (top 40%) - COMAP Mathematical Contest in Modeling 2015 <ul style="list-style-type: none"><li>• <b>Neil Thomas</b>, Lukas Whaley-Mayda, Miles Rusch. “Leveraging the Criticality of Outbreaks to Eradicate Ebola.” February 2015. Simulated vaccine effect on an Ebola outbreak using site-percolation model.</li></ul>
<b>LEADERSHIP &amp; SERVICE</b>	<i>Board Representative</i> , Berkeley Student Cooperative Aug 2020 - March 2021 Member of executive board of \$14M/year nonprofit that provides affordable housing to students. Crafted policy and planned budget as part of Capital and Finance Committee.
	<i>Network Manager</i> , The Convent, Berkeley Student Cooperative Jan 2018 - Aug 2022 Manage IT infrastructure for 25-person dwelling.
	<i>Organizer</i> , Protein ML Reading Group Nov 2019 - Dec 2020 Weekly online reading group focused on machine learning for biology. Facilitated discussion and recruited speakers.
<b>LANGUAGES</b>	Python, R, Java
<b>TOOLS</b>	AWS, Ansible, Apache Spark, Azure, Git, Jenkins, JIRA, L <sup>A</sup> T <sub>E</sub> X, MySQL, Packer, PyMol, PyTorch, Tensorflow, Vagrant
<b>FOREIGN LANGUAGES</b>	Russian, <i>Fluent</i>
<b>HOBBIES</b>	Ultimate Frisbee, Piano, Cycling, Hiking, Rap, Improv, Dunking <sup>†</sup> <sup>†</sup> - <i>in progress</i>