Ananthan Nambiar

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Academic Background

Institution	Discipline	Recognitions	Graduation
University of Illinois at Urbana-Champaign	Ph.D. Bioengineering (CGPA: 4.0) Focusing on computational and systems biology.		2024
Reed College, Portland	B.A. Computer Science (CGPA: 3.7) With coursework in deep learning, statistics and numerical analysis.	Commendation for Excellence in Scholarship (2016/17, 2017/18, 2018/19)	2019

Research Experience

Research Area	Period
Machine Learning for Cancer Drug Response **Supervised by Sergei Maslov (UIUC).** Studying interpretable machine learning models that can be used to understand cancer biology in addition to predicting drug response. I am using existing techniques for interpreting random forests as well as developing new ones specifically for tasks relevant to cancer drug response.	August 2019 - present
Machine Learning for Proteomics **Supervised by Mark Hopkins (Reed), Anna Ritz (Reed) and Sergei Maslov (UIUC).** Using deep learning to predict protein families and missing edges in sparse protein-protein interaction networks. Focus was on treating protein sequences as a language and adapting ideas from natural language processing to identify higher level properties.	August 2018 – present
Machine Learning and Computational Social Science **Supervised by Norman Packard (Daptics) and Mark Bedau (Reed).** Studied open-ended evolution of a real non-biological system using patent records. I also worked on an Intelligence Advanced Research Projects Activity (IARPA) funded project on predicting technological progress.	May 2018 – August 2019, Summer 2020
Computational Biophysics **Supervised by Sanjay Jain (Delhi U. & Santa Fe Inst.).** Studied the controllability of genetic regulatory networks of bacteria, focusing on *E. coli*. I focused on the target controllability of functional classes of genes to understand the relationship between the controllability of a class and its function.	Summer 2017

Papers and Conferences

N. Packard, N. Gigliotti, **A. Nambiar**, T. Janssen and M. Bedau. An Evolving Classification for Forecasting Technology. Paper in preparation.

A. Nambiar, T. Janssen, J. McCaull, M. Bedau. A Consensus of Document Embeddings Shows Dropping Product Diversity in US Public Firms. Paper under peer-review.

A. Nambiar, M. Heflin, S. Liu, S. Maslov, M. Hopkins and A. Ritz. Transforming the Language of Life: Transformer Neural Networks for Protein Prediction Tasks. In Proceedings of *ACM-BCB'20: 11th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics,* September 2020.

A. Nambiar, M. Hopkins and A. Ritz. Computing the Language of Life: NLP Approaches to Feature Extraction for Protein Family Classification. Poster presentation at *ISMB/ECCB'19: 27th Conference on Intelligent Systems for Molecular Biology and the 18th European Conference on Computational Biology*, July 2019.

M. Bedau, N. Gigliotti, T. Janssen, A. Kosik, **A. Nambiar** and N. Packard. Open-ended Technological Innovation. *Artificial Life,* 25 (1). 2019.

M. Bedau, N. Gigliotti, T. Janssen, A. Kosik, **A. Nambiar** and N. Packard. Detecting the On-going Emergence of Technological Innovations. Oral presentation at *ALIFE'18: The 2018 Conference of Artificial Life – Workshop on Open-Ended Evolution*, July 2018.

A. Nambiar. Controllability of Functional Classes in the Genetic Regulatory Network of *E. coli*. Poster presentation at *SIAMAN'18: 2018 SIAM Annual Meeting*, July 2018.

	Students Supervised	
<u>Name</u>	<u>Topic</u>	<u>Year</u>
Maeve Heflin (UIUC '22)	Unsupervised learning to study properties of proteins from vector embeddings	2019/20
Simon Liu (UIUC '23)	Transformer networks for embedding amino acid sequences	2019/20

	External Talks
Google Developer Students Club, University of Malaya	Presented on **Linking the Language of Life**. I shared about developing a deep learning model that is applicable for protein characterization tasks including protein family classification and protein-protein interaction prediction.
Pacific Northwest Quantitative Biology Symposium	Presented on **The Controllability of the Genetic Regulatory Network of *E. coli***. Discussed controllability of networks, structural controllability and how the low controllability of the genetic regulatory network of *E. coli* can provide biological insight.
St. Stephen's College Feynman Club Colloquium	Presented on **Analysing the Presence of Terrorist Organisations on Social Media**. Discussed sentiment analysis, scale-free networks and robustness of networks in this context.

	Grants Offered	
<u>Grant</u>	<u>Detail(s)</u>	<u>Year</u>
Google Research Credits	To study the use of transfer learning for protein feature embedding.	2020
Reed Opportunity Grant	To study the use of machine learning to predict protein functions.	2019
Reed Opportunity Fellowship & Summer Experience Award	To study the effect of semi-synchronous updating on homeostasis in Boolean networks. Chose not to accept.	2018
Reed Student Opportunity Subsidy	To study genetic regulation in bacterial cells.	2017

	Outreach	
<u>Program</u>	<u>Description</u>	<u>Years</u>
Reed College Science Outreach	As a **Lead Instructor**, I led several teams of Reed students whose duties include in-class teaching at a Portland public schools, guiding the students through science projects and teaching them safety in the lab.	2015 - 2017
SMKWM After School Science	I **taught Biology, Chemistry, Physics, Additional Mathematics and ICT** to students from underprivileged backgrounds and were unable to afford tutoring	2013 - 2014

	Other Activities
ACM International Programming Contest 2016	Participated in the Pacific Northwest regional competition as part of the team, Algogriffins 2. Personally solved 2 problems. The team collectively solved 4 problems.

	Skills
Programming Languages	Proficient: Python, Wolfram, C Familiar with: Standard ML, Go, R, x86 assembly
Computer Skills	Gephi, Logisim, NetworkX, PyOpenGL, SQLite, Scikit-Learn, Gensim, PyTorch