

Nam D. Nguyen

PHD CANDIDATE IN COMPUTER SCIENCE · MACHINE LEARNING RESEARCHER · BIOINFORMATICIAN · SOFTWARE ENGINEER

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Summary

I focus on the tasks of machine learning on graphs and manifolds with applications currently on understanding molecular mechanisms and improving genotype-phenotype predictions in complex biological systems. With my expertise in Python/PyTorch and years of experience of software engineering, I also desire to develop large-scale data analytic and scalable machine learning systems for real-world applications.

Research Interests

Machine Learning Multiview Learning, Manifold Learning, Geometric Deep Learning, Interpretable Learning, Statistical Learning Theory
Network Science Link Prediction, Network Diffusion, Network Embedding, Network Curvatures, Social & Biological Network Analysis
Bioinformatics Single-cell Multiomics, Gene Expression & Regulation, Precision Medicine, Computational Genomics

Education

Stony Brook University

PH.D. IN COMPUTER SCIENCE

Stony Brook, NY, USA

Aug. 2016 - Exp. Aug. 2021

- Thesis Proposal: “Interpretable Multiview Learning for Understanding Functional Multiomics”
- Committee members: Drs. Daifeng Wang (advisor), Fusheng Wang (committee chair), Steven Skiena
- GPA: 3.84/4.00
- Relevant coursework: Machine Learning & Convex Optimization, Data Science, Analysis of Algorithm, Translational Bioinformatics

Hanoi University of Science and Technology

B.ENG. IN COMPUTER SCIENCE

Hanoi, Vietnam

Aug. 2005 - Aug. 2010

- Thesis Title: “Integrating Security into Software Engineering, Using Security Patterns and SecureUML”
- GPA: 3.16/4.00

Experience

Daifeng Wang Laboratory, Waisman Center, University of Wisconsin-Madison

RESEARCH FELLOW

Madison, WI, USA

Sep. 2019 – Current

- Design machine learning algorithms for problems in functional genomics, cancers, & brain disorders
- Implement these algorithms, resulting in their high empirical performance, & maintain them as Python/R packages on GitHub
- Formulate a theoretical framework for multiview learning, MV-ERM, to unify & analyze state-of-the-art multiview learning algorithms
- Solve the trade-off between parametric & nonlinear manifold alignment by designing a variant of stochastic gradient descent on a Riemannian space to train a pair of deep neural nets
- Survey state-of-the-art quantum machine learning algorithms for potential applications in genomics
- Collect & analyze single-cell (scRNA-Seq) data to identify the genetic risk of variation associated with neuropsychiatric symptoms

Daifeng Wang Laboratory, Stony Brook University

RESEARCH ASSISTANT

Stony Brook, NY, USA

May 2017 - Aug 2019

- Designed, implemented, & deployed algorithms using manifold alignment to reveal functional links between gene networks
- Explored the capabilities of manifold alignment in the settings of multiview learning
- Designed & implemented computational pipelines to analyze RNA-Seq data for bladder cancer research
- Led a team in 2 prediction competitions on Kaggle (top 22%) & a project of training the machine to distinguish good from poor singing.

Department of Biology, Brookhaven National Laboratory

RESEARCH ASSISTANT

Brookhaven, NY, USA

May 2017 - May 2018

- Developed computational pipeline to collect & analyze RNA-Seq data of algae for the project “Large-Scale Comparative Regulatory Network Analysis in Photosynthetic Organisms”

Software Engineering Lab., Pohang University of Science and Technology (POSTECH)

RESEARCHER & SOFTWARE ENGINEER

Pohang, S. Korea

Mar. 2011 - May 2013

- Researched feature-oriented product line engineering & model checking
- Specified & implemented a set of rules to automatically verify consistency between a feature model & other requirements models
- Investigated the complex network structures (e.g., small world, scale-free) & formulated a set of software metrics for large-scale software systems

Graphics & Virtual Reality Lab., Vietnam Academy of Science and Technology

RESEARCH INTERN

Hanoi, Vietnam

Jun. 2007 - Aug. 2007

- Surveyed & applied the wavelet transform to image denoising & compression; implemented a prototype in MATLAB

Publications

*equal contribution

JOURNALS

Nguyen, N. D., Jin, T., & Wang, D. (2020). *Varmole: A biologically drop-connect deep neural network model for prioritizing disease risk variants and genes*. *Bioinformatics*, , btaa866

Jin*, T., **Nguyen***, N. D., Talos, F., & Wang, D. (2020). *ECMarker: Interpretable machine learning model identifies gene expression biomarkers predicting clinical outcomes and reveals molecular mechanisms of human disease in early stages*. *Bioinformatics*, , btaa935

Nguyen, N. D., & Wang, D. (2020). *Multiview learning for understanding functional multiomics*. *PLOS Computational Biology*, **16**(4), e1007677.

Nguyen, N. D., Blaby, I. K., & Wang, D. (2019). *ManiNetCluster: A novel manifold learning approach to reveal the functional links between gene networks*. *BMC Genomics*, **20**(12), 1–14.

CONFERENCE TALKS & PRESENTATIONS

Nguyen, N. D., Jin, T., & Wang, D. (2020). *Varmole: A biologically drop-connect deep neural network model for prioritizing disease risk variants and genes*. *The 13th annual RECOMB/ISCB conference on regulatory & systems genomics with DREAM challenges (RSGDREAM)*.

Nguyen, N. D., & Wang, D. (2020). *Multiview learning for understanding functional multiomics*. *The 28th conference on intelligent systems for molecular biology (ISMB)*.

Nguyen, N. D., Blaby, I., & Wang, D. (2019). *ManiNetCluster: A novel manifold learning approach to reveal the functional links between gene networks*. *The international conference on intelligent biology and medicine (ICIBM)*. Columbus, OH, USA. (selected as one of the best papers)

Nguyen, N. D., Blaby, I., & Wang, D. (2018). *A manifold learning based approach to reveal the functional linkages across multiple gene networks*. *Proceedings of the 2018 ACM international conference on bioinformatics, computational biology, and health informatics (ACM-BCB)*, 514–514. Washington, D.C., USA. (award paper)

MANUSCRIPTS IN PREPARATION

Nguyen, N. D., & Wang, D. (2021). *Deep Manifold Alignment for Regularized Learning to Reveal Functional Multiomics of Genotyp-Phenotype Interactions*. *In Preparation*.

Honors & Awards

2019	NSF (US National Science Foundation) Travel Award , ICIBM 2019	Columbus, OH, USA
2018	Best Poster Award , ACM-BCB 2018	USA
2016-17	VEF Doctoral Fellowship , The US National Academy of Sciences	USA
2011-12	POSTECH Research Scholarship , National Research Foundation of Korea	S. Korea
2010	Scholarship for Excellent Students , Ministry of Education and Training of Vietnam	Vietnam

Teaching & Services

2018	Mentor , Computer Science and Informatics Summer Research Experience Program	Stony Brook Univ.
2018	Guest Lecturer , BMI511 - Translational Bioinformatics	Stony Brook Univ.
2017	Teaching Assistant , CSE114 - Introduction to Object-Oriented Programming	Stony Brook Univ.
2016	Teaching Assistant , CSE101 - Computer Science Principles	Stony Brook Univ.
2018-19	Student Member , International Society for Computational Biology (ISCB)	
2011	Organizing Volunteer , 12th International Conference on Software Reuse (ICSR 2011)	Pohang, S. Korea

Skills & Certifications

Programming	Python/PyTorch, R (5-year experience); MATLAB (3-year experience); C++, Java (2-year experience)
DevOps & Reproducible Report	Bash, AWK, Vim, Git, LaTeX, Markdown & RMarkdown, Jupyter Notebook
Software Engineering	Object-Oriented Analysis & Design, UML, Design Patterns (4-year experience); EMF (1-year experience)
Bioinformatics	Next-generation Sequencing Analysis (RNA-Seq), Differential Gene Expression Analysis, WGCNA
Mathematics	Linear Algebra, Probability & Statistics, Multivariate Calculus, Convex Optimization
Coursera Certificates	Social Network Analysis; Game Theory; Model Thinking
IBM Certified	Solution Designer - Object-Oriented Analysis & Design; Application Developer; Database Associate

References

Daifeng Wang, PhD	Assistant Professor; University of Wisconsin-Madison; Email: daifeng.wang@wisc.edu
Flaminia Talos, MD, PhD	Assistant Professor; Stony Brook University; Email: Flaminia.Talos@stonybrookmedicine.edu