

Nam D. Nguyen

PH.D. CANDIDATE IN COMPUTER SCIENCE

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Research Interests

- Machine Learning: Multiview Learning, Geometric Deep Learning, Interpretable Learning, Theoretical Machine Learning
- Network Science: Link Prediction, Network Diffusion
- Bioinformatics: Multiomics Intergration, Computational Genomics, Comparative Genomics

Education

Stony Brook University

Stony Brook, NY, USA

PH.D. IN COMPUTER SCIENCE

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
- Selected courses: Machine Learning & Convex Optimization (Dr. Francesco Orabona), Data Science (Dr. Steven Skiena), Analysis of Algorithm (Dr. Jie Gao)

Hanoi University of Science and Technology

Hanoi, Vietnam

B.ENG. IN COMPUTER SCIENCE

Aug. 2005 - Aug. 2010

- Thesis Title: "Integrating Security into Software Engineering, Using Security Patterns and SecureUML"
- GPA: 3.16/4.00
- Selected courses: Linear Algebra, Probability & Statistics, Numerical Methods, Digital Signal Processing, Artificial Intelligence, Software Design & Development

Research & Work Experience

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

Madison, WI, USA

RESEARCH FELLOW

Sep. 2019 - Current

- Lead research group in developing novel machine learning algorithms (and related tools—R and Python packages) to apply in functional genomics, brain disorders and cancers
- Formulate a theoretical framework for multiview learning, MV-ERM, to unify and analyze state-of-the-art multiview learning algorithms
- Author papers published in PLOS Computational Biology, Bioinformatics; presented at ISMB 2020 & RSG 2020, resulting in favorable feedback
- Collaborate with Icahn School of Medicine at Mount Sinai to collect & analyze single cell data (scRNA-Seq) to identify the genetic risk of variation, molecular mechanisms and neuropathological changes associated with neuropsychiatric symptoms in Alzheimer Disease (Project IDs: NIH/NIA R01AG067025, NIH/NCI R21CA237955)
- Solve the trade-off between parametric and nonlinear manifold alignment by designing a deep architecture, trained by a novel non-Euclidean gradient descent algorithms; implemented in PyTorch
- Survey state-of-the-art quantum machine learning methods for potential applications in genomics (e.g., to solve the inherent problem of "high dimension, low sample size", ubiquitous in genomic domains)

Daifeng Wang Laboratory, Stony Brook University

Stony Brook, NY, USA

RESEARCH ASSISTANT

May 2017 - Aug 2019

- Led research group in a research using manifold alignment to reveal functional links between gene networks; authored a related papers, published in BMC Genomics; presented at ACM-BCB 2018, RSGDREAM 2018, ICIBM 2019, resulting in favorable feedback and recommendation for inclusion in the next phase of the project
- Designed and implemented computational pipelines to analyze RNA-Seq data for the project "A new bladder cancer model based on tissue reprogramming and gene targeting" (ID: NIH/NCI R21CA237955)
- Led a team in 2 prediction competitions (on Kaggle), Zillow Prize & Online Dating Matchmaking (top 22%)
- Led the project "Automated Singing Evaluation" to train the machine to distinguished between good & poor singing

Department of Biology, Brookhaven National Laboratory

Brookhaven, NY, USA

RESEARCH ASSISTANT

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" (ID: DOE 0000250595)

Software Engineering Laboratory, Division of Information Technology Convergence Engineering, Pohang University of Science and Technology (POSTECH)

Pohang, S. Korea

RESEARCHER

Mar. 2011 - May 2013

- Researched Feature Oriented Product Line Software Engineering, Model Checking with Feature Transition Systems
- Specified & implemented a set of rules to automatically verify consistency between a feature model and other requirements
- Investigated the complex network structures (e.g., small world, scale-free) & formulated a set of software metrics for large-scale software systems; applied community detection for software refactoring; presented at ISITCE 2011

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

Hanoi, Vietnam

RESEARCH INTERN

Jun. 2007 - Aug. 2007

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

Publications

REFREED JOURNALS

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*. <https://doi.org/10.1093/bioinformatics/btaa935>

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*. <https://doi.org/10.1093/bioinformatics/btaa866>

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.

REFREED CONFERENCE ORAL AND POSTERS PRESENTATION

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)*. <https://doi.org/10.7490/f1000research.1118190.1>

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.

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*, 514–514. Washington DC, USA.

Awards and Honours

NSF Travel Award

USA

INTERNATIONAL CONFERENCE ON INTELLIGENT BIOLOGY AND MEDICINE (ICIBM)

2019

Best Poster Award

USA

THE 9TH ACM CONFERENCE ON BIOINFORMATICS, COMPUTATIONAL BIOLOGY, AND HEALTH INFORMATICS (ACM BCB)

2018

- for the poster “A Manifold Learning Approach to Reveal Functional Linkage Across Gene Networks”

VEF Doctoral Fellowship

USA

THE US NATIONAL ACADEMY OF SCIENCES

2016 - 2017

- awarded to top 30 Vietnamese students in STEM fields (cohort 2016)

Research Scholarship

S. Korea

NATIONAL RESEARCH FOUNDATION OF KOREA

2011 - 2012

Activities & Services

TEACHING

College of Engineering and Applied Sciences, Stony Brook University

Stony Brook, NY, USA

MENTOR FOR CSIRE (COMPUTER SCIENCE AND INFORMATICS SUMMER RESEARCH EXPERIENCE PROGRAM)

2018

- Designed and instructed high school students (with programming background) to conduct research on comparative network analysis, resulting on their final posters exhibited in Computer Science Department

Department of Biomedical Informatics, Stony Brook University

Stony Brook, NY, USA

GUEST LECTURER FOR BMI511 - TRANSLATIONAL BIOINFORMATICS

2018

- On state-of-the-art methods in machine learning & network analysis for genomic sciences

Department of Computer Science, Stony Brook University

Stony Brook, NY, USA

TEACHING ASSISTANT FOR CSE114 - INTRODUCTION TO OBJECT-ORIENTED PROGRAMMING

2017

- Hold office hours; handled recitation & exam review sections; graded & provided feedback on homework/quizzes/exams

Department of Computer Science, Stony Brook University

Stony Brook, NY, USA

TEACHING ASSISTANT FOR CSE101 - COMPUTER SCIENCE PRINCIPLES

2016

- Proctored exams; graded & provided feedback on homework/quizzes/exams ; assembled scores into official grade book

SERVICE

ISCB (International Society for Computational Biology)

Global

STUDENT MEMBER

2018 - 2019

12th International Conference on Software Reuse (ICSR 2011)

Pohang, S. Korea

ORGANIZING VOLUNTEER

2011

Related Professional Skills

TECHNICAL SKILLS

- Programming: Python, R, MATLAB (author and maintain packages on GitHub, 5 years experiences); C++, Java
- DevOps & Reproducible Report: Bash, AWK, Vim, Git, LaTeX, Markdown and RMarkdown
- Software Engineering: Object-Oriented Analysis & Design, UML, CASE Tools (deep understanding with certificates and 3 years experiences)
- Others: Gephi, Cytoscape, Inkscape

BIOINFORMATICS SKILLS

- Next-generation sequencing data analysis (RNA-Seq), Differential gene expression analysis, WGCNA, regulatory network analysis

Certifications

Coursera Certificates

Global

COURSERA

2014 - Present

- Social Network Analysis, Game Theory, Model Thinking

IBM Certificates

Global

IBM

2010 - Present

- Certified Solution Designer - Object-Oriented Analysis & Design
- Certified Application Developer - Rational Application Developer for WebSphere Software V6.0
- Certified Database Associate - DB2 Fundamentals