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### Research Interests\_

Machine Learning Multiview Learning, Geometric Deep Learning, Interpretable Learning, Theoretical Machine Learning

**Network Science** Link Prediction, Network Diffusion, Community Detection

**Bioinformatics** Single-cell Multiomics, Gene Expression & Regulation, Precision Medicine

# **Education**

**Stony Brook University** Stony Brook, NY, USA

Ph.D. IN COMPUTER SCIENCE • 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

### Hanoi University of Science and Technology

Hanoi, Vietnam

Aug. 2016 - Exp. Aug. 2021

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

# **Experience**

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

Madison, WI, USA

RESEARCH FELLOW

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 and nonlinear manifold alignment by designing a variant of stochastic gradient descent on a non-Euclidean space
- · 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, molecular mechanisms and neuropathological changes associated with neuropsychiatric symptoms in Alzheimer Disease

### **Daifeng Wang Laboratory, Stony Brook University**

Stony Brook, NY, USA

RESEARCH ASSISTANT

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
- Desgined & implemented computational pipelines to analyze RNA-Seq data for bladder cancer research
- Led a team in 2 prediction competitions on Kaggle (top 22%) and a project of training the machine to distinguished good from 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"

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

Pohang, S. Korea Mar. 2011 - May 2013

RESEARCHER & SOFTWARE ENGINEER

- Researched feature-oriented product line engineering & model checking
- · Specified & implemented a set of rules to automatically verify consistency between a feature model and 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

Hanoi Vietnam

RESEARCH INTERN Jun. 2007 - Aug. 2007

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

# **Publications**

\*equal contribution

### **JOURNALS**

NAM D. NGUYEN · RÉSUMÉ **DECEMBER 29, 2020** 

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.**, Jin, T., & Wang, D. (2020). *Varmole: A biologically drop-connect deep neural network model for prioritizing disease risk variants and genes. <i>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. <i>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).* 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 (ACM-BCB), 514–514. Washington, D.C., USA.

#### 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	USA
2018	Best Poster Award, ACM-BCB 2018	USA
2016-2017	VEF Doctoral Fellowship, The US National Academy of Sciences	USA
2011-2012 <b>POSTECH Research Scholarship,</b> National Research Foundation of Korea S. Korea		
2010	<b>Scholarship for Excellent Students,</b> Ministry of Education and Training of Vietnam	Vietnam

# Activities

### **TEACHING**

2018	Mentor, Computer Science and Informatics Summer Research Experience Program	Stony Brook Univ.
2018	Guest Lecturer, BMI511 - Translational Bioinformatics	Stony Brook Univ.
2017	<b>Teaching Assistant</b> , CSE114 - Introduction to Object-Oriented Programming	Stony Brook Univ.
2016	<b>Teaching Assistant,</b> CSE101 - Computer Science Principles	Stony Brook Univ.

### **SERVICES**

2018-2019	Student Member, International Society for Computational Biology (ISCB)	Global
2011	Organizing Volunteer, 12th International Conference on Software Reuse (ICSR 2011)	Pohang, S. Korea

## **Skills**

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
Software Engineering	Object-Oriented Analysis & Design, UML (3-year experience)
Bioinformatics	Next-generation Sequencing Analysis (RNA-Seq), Differential Gene Expression Analysis, WGCNA

# Certifications

<b>Coursera Certificates</b>	Social Network Analysis, Game Theory, Model Thinking
IBM Certified	Solution Designer - Object-Oriented Analysis & Design
IBM Certified	Application Developer - Rational Application Developer for WebShere Software V6.0
IBM Certified	Database Associate - DB2 Fundamentals