

Vinhthuy Phan

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Research Interest

Bioinformatics with a focus on methods for analyzing sequencing data

(Recently) Computer Science Education with a focus on active learning platforms and pedagogies

Education

Ph.D. in Computer Science, Stony Brook University, 2003

M.S. in Computer Science, Stony Brook University, 2001

B.S. in Mathematics and Computer Science, Brandeis University, 1998

Professional Experience

Associate Chair, The University of Memphis, 2016–present

Associate Professor, The University of Memphis, 2010–present

Assistant Professor, The University of Memphis 2003–2010

Research Assistant, Electronic Design Automation Group, IBM, 2002

Honors & Awards

Pat Burlison Professorship Award, College of Arts and Sciences, University of Memphis, 2018

GAANN Fellowship, Stony Brook University, 1998-2001

Graduated Summa Cum Laude, Brandeis University, 1998

Best Paper Award, Graduate Student Conference, Stony Brook University, 2001

Funding

External Funding

Analysis of Gene Expression Data using Transitive Directed Graphs, funded by NSF-CCF, \$280,000, 2013-2017. *Synopsis: developed methods for the detection of patterns of genetic response to drug treatments.*

A Microarray Analysis Software for Comparisons and Extrapolations Relevant to Toxicology, funded by the Center of Alternatives to Animal Testing (CAAT), John Hopkins University, \$50,000, 2009-2012. *Synopsis: developed software to visualize patterns of gene response to chemicals.*

Internal Funding

TigerCrew, Strengthening Communities, \$19,000, 2016-2018. *Synopsis: worked with undergraduate students, CodeCrew (a non-profit organization) and the Public Library of Memphis to teach high school students to create video games.*

Faculty Research Grant, \$6,000, 2004. *Synopsis: worked on software to visualize different modes of protein motion.*

Outreach

Learning Circles Project, National Center for Women & Information Technology (2018-present) *In this on-going effort, I helped secure a \$10,000 award for the department to recruit and retain female students.*

Data Science Workshop (2016-present). *Trained local professionals. Helped promote department's profile.*

Creative Game Design Summer Camp (2012-present). *Attract high school students to university and COMP major*

Praxis Exam Prep (2018). *Sponsored by Google, worked with CodeCrew to help teachers obtain certifications to teach computer science courses in high schools.*

TigerCrew (2016-2018). *See Internal Funding.*

Programming Challenge (2005-2009). *Worked with Linda Sherrell & Sajjan Shiva, who were supported by the NSF, to recruit high school students to the major.*

Professional Service

Ph.D. Advisees

Nam Sy Vo (graduated 2016, Senior Bioinformatician at the University of Chicago)

Sujoy Roy (co-Advised, graduated 2012, Research Assistant Professor in Ramin Homayouni's Group)

Quang Tran (expected graduation 2020)

Diem-Trang Pham (expected graduation 2021)

Eric Hicks (expected graduation 2022)

Notable M.S. Advisees / Student Co-authors

Nick Furlotte (Senior Scientist at 23andMe)

Shanshan Gao (Software Engineer at Google)

Sunder Tatta (Senior Technical Staff at AT&T)

Allen Thomas (Software Engineer III, St. Jude's Children Research Hospital)

Nhu-Quynh Tran (Staff Scientist, St. Jude's Children Research Hospital)

Jim Greer (Manager, Operations Technology Innovation at FedEx)

National and International Funding Review Panel

NSF CCF Interdisciplinary projects (2009)

NSF Reviewer (2009, 2015)

NAFOSTED (Vietnamese National Foundation for Science and Technology Development), 2010, 2015, 2016

Journal and Conference Service

Organizing Committee Member: Thirteen International Conference on DNA Computing (2007)

Program Committee Member: IEEE International Conference on Bioinformatics and Biomedicine (2010-2018), International Joint Conference on Neural Network (2010), IEEE International Conference on Bioinformatics and BioEngineering (2007), International Symposium on Computational Models for Life Sciences (2007)

Reviewer: SIGCSE (2018), ITiCSE (2018), Bioinformatics (2010, 2012), BMC Bioinformatics (2009), PLoSOne (2010-2013), Journal of Computational Biology (2009), IEEE International Conference on Bioinformatics & Biomedicine (2009), International Symposium on Bioinformatics Research and Applications (2008), IEEE International Conference on Bioinformatics and BioEngineering (2007), International Symposium on Computational Models for Life Sciences (2007), Journal of Natural Computing (2004), Journal of Computational Biology (2001).

The University of Memphis

Undergraduate Coordinator (2011-present). *Managed UG matters including ABET accreditation, curriculum assessment and development.*

Associate Chair (2016-present). *Helped Chair to manage various important activities including instructor hiring, teaching evaluation, course scheduling and various outreach efforts.*

ACM Chapter Advisor (2004-2014) *Helped create the first ACM chapter, and more importantly, sustain a critical mass of student interest in extra-curricular activities so that they can self-run and self-organize as they do today.*

Peer-reviewed Publications

Notation: [J]: journal article; [JC]: journal article originated from selected conference articles that were subjected to additional rounds of review; [C]: conference article.

- [J] Vinhthuy Phan, Diem-Trang Pham, Caroline Melton, Adam Ramsey, Bernie Daigle Jr., and Jennifer Mandel, 2019, "icHET: Interactive Visualization of Cytoplasmic Heteroplasmy", *Bioinformatics*, accepted for publication. (**h5-index: 110**)
- [C] Shanshan Gao, Quang Tran, and Vinhthuy Phan, 2019, "Understand Effective Coverage by Mapped Reads using Genome Repeat Complexity". In Proceedings of 11th International Conference on Bioinformatics and Computational Biology (Vol. 60, pages 65-73).
- [J] Nam Vo and Vinhthuy Phan, 2018, "Leveraging known genomic variants to improve detection of variants, especially close-by Indels". *Bioinformatics*, bty183, <https://doi.org/10.1093/bioinformatics/bty183>. (**h5-index: 110**)

- [C] Vinhthuy Phan and Eric Hicks, 2018, "Code4Brownies: An Active Learning Solution for Teaching Programming and Problem Solving in the Classroom". In Proceedings of 23rd Annual ACM Conference on Innovation and Technology in Computer Science Education (ITiCSE), pages 153-158. ([h5-index: 20](#))
- [JC] Quang Tran, Diem-Trang Pham and Vinhthuy Phan, 2017, "Using 16S rRNA gene as marker to detect unknown bacteria in microbial communities", *BMC Bioinformatics*, 18(Suppl 14):499. ([h5-index: 61](#))
- [JC] Diem-Trang Pham, Shanshan Gao, Vinhthuy Phan, 2017, "An accurate and fast alignment-free method for profiling microbial communities", *Journal of Bioinformatics and Computational Biology*, Vol. 15, No. 3 1740001. DOI: <http://dx.doi.org/10.1142/S0219720017400017> ([h5-index: 16](#))
- [JC] Quang Tran, Shanshan Gao and Vinhthuy Phan, 2016, "Analysis of optimal alignments unfolds aligners's bias in existing variant profiles", *BMC Bioinformatics*, 17(Suppl 13):349. ([h5-index: 61](#))
- [C] Quang Tran, Shanshan Gao, Vinhthuy Phan, 2016, "Repeat complexity of genomes as a means to predict the performance of short-read aligners", *Proceedings of the 8th International Conference on Bioinformatics and Computational Biology* (BiCOB 2016), pages 135-142.
- [JC] Vinhthuy Phan, Shanshan Gao, Quang Tran and Nam Sy Vo, 2015, "How genome complexity can explain the hardness of aligning reads to genomes". *BMC Bioinformatics*, 16(Suppl 17):S3. ([h5-index: 61](#))
- [JC] Nam Sy Vo, Quang Tran, Nibal Niraula, Vinhthuy Phan, 2014, "RandAL: a randomized approach to aligning DNA sequences to reference genomes", *BMC Genomics*, 15(Suppl 5):S2 doi:10.1186/1471-2164-15-S5-S2. ([h5-index: 80](#))
- [JC] Nam Sy Vo, Vinhthuy Phan, 2014, "Exploiting dependencies of pairwise comparison outcomes to predict patterns of gene response". *BMC Bioinformatics*, 15(Suppl 11):S2 doi:10.1186/1471-2105-15-S11-S2. ([h5-index: 61](#))
- [J] Nam Sy Vo, Thomas Sutter, Vinhthuy Phan, 2013, "mDAG: A web tool for analyzing, visualizing, and interpreting response patterns in gene expression data with multiple treatments", *Advances in Bioscience and Biotechnology*, 4(6): 706-709. ([h5-index: 17](#))
- [C] Vinhthuy Phan, Nam Sy Vo, Thomas Sutter, 2013, "Inferring Directed-graph Patterns of Gene Responses to Treatments", *Proceedings of the 5th International Conference on Bioinformatics and Computational Biology*, 7-12.
- [C] Nam S. Vo, Vinhthuy Phan and Thomas Sutter, 2012, "Predicting Possible Directed-graph Patterns of Gene Expressions in Studies Involving Multiple Treatments", *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 579-581.
- [C] Nam S. Vo and Vinhthuy Phan, 2012, "Pattern Analysis: a Web-based Tool for Analyzing Response Patterns in Low-replication, Many-treatment Gene Expression Data". *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, 539-541.
- [J] Sujoy Roy, Kevin Heinrich, Vinhthuy Phan, Michael Berry, Ramin Homanyouni, 2011, "Latent Semantic Indexing of PubMed abstract for identification of transcription factor candidates from microarray derived gene sets", *BMC Bioinformatics*, 12(Suppl 10):S19 ([h5-index: 61](#))
- [J] Vinhthuy Phan, Nam Sy Vo, Thomas Sutter, 2011, "mDAG: a web-based tool for analyzing microarray data with multiple treatments", *BMC Bioinformatics*, 12(Suppl 7):A7. ([h5-index: 61](#))
- [J] Max Garzon, K. Bobba, Andrew Neel, Vinhthuy Phan, 2010, "DNA-Based Indexing", *International Journal of Nanotechnology and Molecular Computation*, 2(3):25-45.

- [J] Vinhthuy Phan, Allen Thomas, Kriangsiri Malasri, Carie Sutter, 2010, "Stability of RNA Structural Motifs and Its Influence on Editing Efficiency by Adenosine Deaminases", *International Journal of Bioinformatics Research and Application*, Vol. 6, No. 1, p21-36. (**h5-index: 9**)
- [J] Vinhthuy Phan, Sudip Saha, A. Pandey, Tit-Yee Wong. 2010, "Synthetic Gene Design with a Large Number of Hidden Stop Codons", *International Journal of Data Mining and Bioinformatics*, Vol. 4, No. 4, p377-394. (**h5-index: 12**)
- [J] Vinhthuy Phan, Max Garzon. "On Codeword Design in Metric DNA Spaces", 2009, *Journal of Natural Computing*, 8(3):571-588.
- [J] Nhu-Quynh Tran, L. Xu, Vinhthuy Phan, S. Goodwin, M. Rahman, V. Jin, C.H. Sutter, B. Roebuck, T. Kensler, E.O. George, Thomas Sutter, 2009, "Chemical Genomics of Cancer Chemopreventive Dithiolethiones", *Carcinogenesis*, 30(3):480-486. (**h5-index: 64**)
- [C] Max Garzon, Tit-Yee Wong, Vinhthuy Phan, 2009. "DNA Chips for Species identification and Biological Phylogenies", *15th International Conference on DNA Computing and Molecular Programming*, Vol. 5877, p55-66.
- [J] Vinhthuy Phan, Nick Furlotte, 2008, "Motif Tool Manager: a web-based framework for motif discovery", *Bioinformatics*, 24(24):2930-2931. (**h5-index: 110**)
- [J] Vinhthuy Phan, E.O. George, Nhu-Quynh Tran, S. Goodwin, S. Boddreddigari, Thomas Sutter, 2009, "Analyzing Microarray Data with Transitive Directed Acyclic Graphs", *Journal of Bioinformatics and Computational Biology*, 7(1):135-156. (**h5-index: 16**)
- [J] Vinhthuy Phan and Max H. Garzon. 2009. "On codeword design in metric DNA spaces". *Journal of Natural Computing*, Vol. 8, No. 3, 571-588. DOI=<http://dx.doi.org/10.1007/s11047-008-9088-6>
- [J] Max Garzon, Vinhthuy Phan, Andrew Neel, 2009, "Optimal DNA Codes for Computing and Self-Assembly", *International Journal of Nanotechnology and Molecular Computation*, (1):1 1-17.
- [C] Vinhthuy Phan, E.O. George, Nhu-Quynh Tran, Thomas Sutter, 2008, "Toward a Combinatorial Approach to the Sample Size Problem in Multiple-treatment Microarray Studies", *Proceedings of the 2008 International Conference on Bioinformatics and Computational Biology*, p175-181.
- [J] Vinhthuy Phan, Kriangsiri Malasri, 2008, "BioTDMS: a General-purpose System for Integrative Management of Bioinformatics Tools and Data", *International Journal of Computational Biology and Drug Design*, (1):2 174-184. (**h5-index: 9**)
- [C] Kiran Bobba, Andrew Neal, Max Garzon, Vinhthuy Phan, 2006, "Reason and Talking DNA: Can DNA understand English? Can we tell?", *The 12th International Meeting on DNA Computing*, Lecture Notes in Computer Science, 4287:337-349, Springer-Verlag.
- [C] Max Garzon, Vinhthuy Phan, Sujoy Roy, Andrew Neal, 2006, "In Search of Optimal Codes for DNA Computing", *12th International Meeting on DNA Computing*, Lecture Notes in Computer Science, 4287:143-156.
- [C] Max Garzon, Vinhthuy Phan, Kiran Bobba, R. Kontham, 2005, "Sensitivity and Capacity of Microarray Encodings", *11th International Meeting on DNA Computing*, Lecture Notes in Computer Science, 3892:81-95.
- [C] Vinhthuy Phan, Max Garzon, 2005, "The Capacity of DNA for Information Encoding", *10th International Meeting on DNA Computing*, Lecture Notes in Computer Science, 3384:281-292.

- [C] Vinhthuy Phan, S. Skiena, 2005, "An Improved Time-sensitive Metaheuristic Framework for Combinatorial Optimization", *3rd Workshop on Efficient and Experimental Algorithms*, Lecture Notes in Computer Science, 3059:432-445.
- [C] Vinhthuy Phan, Pavel Sumazin, Steve Skiena, 2003, "Model for Analyzing Black-box Optimization", *Workshop on Algorithms and Data Structures*, Lecture Notes in Computer Science, 2748:424-438.
- [C] Vinhthuy Phan, Pavel Sumazin, S. Skiena, 2002, "A Time-sensitive System for Black-box Optimization", *Algorithm Engineering and Experiments*, Lecture Notes in Computer Science, 2409:16-28.
- [C] Vinhthuy Phan, Steve Skiena, 2002, "Coloring Graphs with a General Heuristic Engine", *Computational Symposium on Graph Coloring and its Generalization*, pages 92-99.
- [C] Vinhthuy Phan, Maharaj Mukherjee, 2002, "Improved Line-End Fore-Shortening and Corner-Rounding Control in Optical Proximity Correction using Radius of Curvature Method", *Proceedings of SPIE, Optical Microlithography XV*, 4691:1082- 1090.
- [J] Vinhthuy Phan, Steve Skiena, 2001, "Dealing with Errors in Interactive Sequencing by Hybridization", *Bioinformatics*, (17):10 862-70. (**h5-index: 110**)

Teaching Experience

Graduate: Data Mining, Algorithms, Bioinformatics Algorithms, Advanced Algorithms.

Undergraduate: Algorithms, Programming Languages, Data Science, CS2.