

TIN NGUYEN

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Computer Science and Engineering
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RESEARCH INTERESTS

- **Machine learning:** unsupervised and supervised learning, statistical modeling, neural networks and deep learning, big data analytics
- **Bioinformatics:** gene networks, pathway analysis, cancer subtyping, single-cell genomics, multi-omics integration, meta-analysis

EDUCATION

- PhD, Computer Science, Wayne State University** Detroit, Michigan
– Advisor: Professor Sorin Draghici Aug 2011 - May 2017
– Dissertation: “*Horizontal and vertical integration of bio-molecular data*”
- MS & BS, Computer Science, Eotvos Lorand University** Budapest, Hungary
– Major: graph theory, information systems, and calculus Feb 2008

PROFESSIONAL APPOINTMENT

Assistant Professor (*July 2017 – present*), Department of Computer Science and Engineering, University of Nevada, Reno, Nevada

Bioinformatics Scientist (*Feb 2017 – Jun 2017*), Progenity Inc., Ann Arbor, Michigan

Graduate Research Assistant (*Aug 2011 – Dec 2016*), Computer Science Department, Wayne State University, Detroit, Michigan

GRANT AWARDS AND APPLICATIONS

Awarded

- National Aeronautics and Space Administration – PI** \$100,000 Aug 2019 - Jul 2020
– Multi-cohort, Pathway-level Analysis of Spaceflight Disorders
- Nevada Space Grant Consortium – co-PI** \$50,000 Aug 2018 - Jul 2019
– Robotics and Big Data Curriculum for Undergraduate and Graduate Students of UNR College of Engineering

Pending

- National Science Foundation – co-PI** (pending) \$1,761,000 Feb 2020
– Collaborative Research: URoL: Epigenetics 2: Understanding the epigenetic mechanisms associated with ticks' adaptability to different hosts and pathogens
– PI: Monika Gulia-Nuss, University of Nevada, Reno

Nevada Space Grant Consortium – PI (pending)	\$50,000	Feb 2020
– Machine Learning and Applied Data Analytics Curriculum Development for UNR College of Engineering		
National Science Foundation – UNR co-PI (pending)	\$5,831,000	Jan 2020
– RII Track-2 FEC: EPSCoR Research Infrastructure Improvement Program		
– PI: Xiaogang Ma, University of Idaho		
National Science Foundation – UNR co-PI (pending)	\$6,000,000	Aug 2020
– RII Track-2 FEC: Harnessing multi-modal data to understand the effects of disasters on survivors from genome to phenome		
– PI: Qing Wu, University of Nevada, Las Vegas		
National Institute of Health – PI (pending)	\$1,084,000	Nov 2019
– Novel and integrative approaches for cancer subtype identification and systems-level characterization		
National Science Foundation – PI (pending)	\$500,000	Nov 2019
– FET: III: Small: Innovative Approaches for Bias Correction and Systems-level Analysis in Integrated Multi-omics Data		
National Science Foundation – co-PI (pending)	\$600,000	Nov 2019
– Elements: The ThYme database and identifying representative amino acid sequences that originate thioester-active enzyme families		
– PI: David Cantu, University of Nevada, Reno		

Declined

National Aeronautics and Space Administration – PI	\$981,000	Oct 2019
– Novel Methods for Spaceflight Disorder Characterization and Drug Repurposing		
– Ranked competitive (ranked among top proposals but not selected)		
National Science Foundation – co-PI (declined)	\$600,000	Apr 2019
– Elements: The ThYme database and identifying representative amino acid sequences that originate thioester-active enzyme families		
– PI: David Cantu, University of Nevada, Reno		
– Ranked competitive		
National Science Foundation – PI (declined)	\$175,000	Aug 2018
– CRII: SCH: Meta-analysis in integrated genomic data for molecular subtype identification		
– Ranked competitive		
National Institute of Health – PI (declined)	\$424,000	Jun 2018
– R15 Novel Methods for Multi-cohort Analysis and Disease Subtyping		
– Ranked competitive (Impact score 28, marginally missed the NIH NCI payline of 25)		
National Science Foundation – PI (declined)	\$175,000	Aug 2019
– CRII: SCH: Cross-cohort Clustering in Integrated Genomic Data for Molecular Subtype Identification		
National Institute of Health – PI (declined)	\$2,412,000	Jun 2019
– R01 Integrated, multi-cohort approaches for disease subtyping and drug repurposing		
National Institute of Health – PI (declined)	\$426,000	Feb 2019

- R15 Novel Methods for Multi-cohort Analysis and Disease Subtyping
- National Science Foundation – UNR co-PI** (declined) \$5,998,000 Jan 2019
- RII Track-2 FEC: Leveraging Big Data to Improve Prediction of Tick-Borne Disease Patterns and Dynamics.
- PI: Xiaogang Ma, University of Idaho
- National Science Foundation – co-PI** (declined) \$44,000 Sep 2018
- Symposium on Mathematical and Computational Oncology
- PI: George Bebis, University of Nevada, Reno
- National Science Foundation – UNR co-PI** (declined) \$2,460,000 Jan 2018
- RII Track-2 FEC: Genomes to Phenomes: Environmentally Driven Evolution from Dry to Fleshy Fruit and the Ripening Syndrome.
- PI: Joe Song, New Mexico State University

PUBLICATIONS

Journal Articles

- J.1. Hung Nguyen, Sangam Shrestha, Sorin Draghici, and **Tin Nguyen**. PINSPlus: a tool for tumor subtype discovery in integrated genomic data. **Bioinformatics**, 35(16):2843-2846, 2019. *Impact factor 4.531*.
- J.2. Tuan-Minh Nguyen, Adib Shafi, **Tin Nguyen**, and Sorin Draghici. Identifying significantly impacted pathways: a comprehensive review and assessment. **Genome Biology**, 20(1):203, 2019. *Impact factor 14.028*.
- J.3. Michael Menden, Dennis Wang, Yuanfang Guan, Michael Mason, Bence Szalai, Krishna Bulusu, Thomas Yu, Jaewoo Kang, Minji Jeon, Russ Wolfinger, **Tin Nguyen**, Mikhail Zaslavskiy, DREAM Consortium, In Sock Jang, Zara Ghazoui, Mehmet Ahsen, Robert Vogel, Elias Neto, Thea Norman, Eric Tang, Mathew Garnett, Giovanni Veroli, Steve Fawell, Gustavo Stolovitzky, Justin Guinney, Jonathan Dry, Julio Saez-Rodriguez. Community assessment of cancer drug combination screens identifies strategies for synergy prediction. **Nature Communication**, 10:2674, 2019. *Impact factor 11.878*.
- J.4. Adib Shafi, **Tin Nguyen**, Azam Peyvandipour, and Sorin Draghici. GSMA: an approach to identify robust global and test Gene Signatures using Meta-Analysis. **Bioinformatics**, DOI: 10.1093/bioinformatics/btz561, 2019. *Impact factor 4.531*.
- J.5. Hung Nguyen, Sangam Shrestha, Duc Tran, Adib Shafi, Sorin Draghici, and **Tin Nguyen**. A comprehensive survey tools and software for active subnetwork identification. **Frontiers in Genetics**, 10:155, 2019. *Impact factor 3.517*.
- J.6. Adib Shafi, **Tin Nguyen**, Azam Peyvandipour, Hung Nguyen, and Sorin Draghici. A multi-cohort and multi-omics meta-analysis framework to identify network-based gene signatures. **Frontiers in Genetics**, 10:150, 2019. *Impact factor 3.517*.
- J.7. Edward Cruz, Hung Nguyen, **Tin Nguyen**, and Ian Wallace. Functional analysis tools for post-translational modification: a post-translational modification database for analysis of proteins and metabolic pathways. **The Plant Journal**, DOI: 10.1111/tpj.14372, 2019. *Impact factor 5.726*.

- J.8. John Stansfield, Duc Tran, **Tin Nguyen**, and Mikhail Dozmorov. R Tutorial: detection of differentially interacting chromatin regions from multiple Hi-C datasets. **Current Protocols in Bioinformatics**, 66(1):e76, 2019. *Impact factor 9.625*.
- J.9. Alfred Schissler, Hung Nguyen, **Tin Nguyen**, Juli Petereit, and Vincent Gardeux. Statistical Software. **Wiley StatsRef: Statistics Reference Online**, DOI: 10.1002/9781118445112.stat00527.pub2
- J.10. **Tin Nguyen**, Cristina Mitrea, and Sorin Draghici. Network-based approaches for pathway level analysis. **Current Protocols in Bioinformatics**, 61(1):8.25.1-8.25.24, 2018. *Impact factor 9.625*.
- J.11. **Tin Nguyen**, Rebecca Tagett, Diana Diaz, and Sorin Draghici. A novel method for data integration and disease subtyping. **Genome Research**, 27(12):2025-2039, 2017. *Impact factor 9.944*.
- J.12. **Tin Nguyen**, Cristina Mitrea, Rebecca Tagett, and Sorin Draghici. DANUBE: Data-driven meta-ANalysis using UnBiased Empirical distributions – applied to biological pathway analysis. **Proceedings of the IEEE**, 105(3):496-515, 2017. *Impact factor 10.694*.
- J.13. Adib Shafi, Cristina Mitrea, **Tin Nguyen**, and Sorin Draghici. A survey of the approaches for identifying differential methylation using bisulfite sequencing data. **Briefings in Bioinformatics**. DOI: 10.1093/bib/bbx013, 2017. *Impact factor 9.101*.
- J.14. **Tin Nguyen**, Rebecca Tagett, Michele Donato, Cristina Mitrea, and Sorin Draghici. A novel bi-level meta-analysis approach: applied to biological pathway analysis. **Bioinformatics**, 32(3):409-416, 2016. *Impact factor 5.4*.
- J.15. **Tin Nguyen**, Diana Diaz, Rebecca Tagett, and Sorin Draghici. Overcoming the matched-sample bottleneck: an orthogonal approach to integrate omic data. **Scientific Reports**, 6:29251, 2016. *Impact factor 4.011*.

Peer-Reviewed Conferences Proceedings

- C.1. Suzan Arslanturk, **Tin Nguyen**, and Sorin Draghici. Integrated Cancer Subtyping using Heterogeneous Genome-Scale Molecular Datasets. In *Pacific Symposium on Biocomputing*, volume 25, pages 551-562, 2020.
- C.2. Bang Tran, Duc Tran, Hung Nguyen, Nam Sy Vo, and **Tin Nguyen**. RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing. In *Proceedings of the 11th IEEE International Conference on Knowledge and Systems Engineering*, pages 1-9, 2019.
- C.3. Hung Nguyen, Sushil Louis, and **Tin Nguyen**. MGKA: A genetic algorithm-based clustering technique for genomic data. In *Proceedings of the 2019 IEEE Congress on Evolutionary Computation*, pages 103-110, 2019.
- C.4. Yan Yan, **Tin Nguyen**, Bobby Bryant, and Frederick Harris Jr. Robust Fuzzy Cluster Ensemble on Cancer Gene Expression Data. In *Proceedings of the 11th International Conference on Bioinformatics and Computational Biology*, 60:120-128, 2019.
- C.5. Brian Marks, Nina Hees, Hung Nguyen, and **Tin Nguyen**. MIA: A Multi-cohort Integrated Analysis for biomarker identification. In *Proceedings of the 9th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics*, pages 360-365. ACM, 2018.

- C.6. **Tin Nguyen**, Diana Diaz, and Sorin Draghici. TOMAS: A novel TOpology-aware Meta-Analysis approach applied to System biology. In *Proceedings of the 7th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics*, pages 13-22. ACM, 2016.
- C.7. **Tin Nguyen** and Dongxiao Zhu. Markovbin: An algorithm to cluster metagenomic reads using a mixture modeling of hierarchical distributions. In *Proceedings of the 4th International Conference on Bioinformatics, Computational Biology and Biomedical Informatics*, page 115. ACM, 2013.
- C.8. **Tin Nguyen**, Nan Deng, Guorong Xu, Zhansheng Duan, and Dongxiao Zhu. iQuant: A fast yet accurate GUI tool for transcript quantification. In *Proceedings of the 2011 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pages 1048-1050. IEEE, 2011.
- C.9. **Tin Nguyen**, Zhiyu Zhao, and Dongxiao Zhu. SPATA: A highly accurate GUI tool for de novo transcriptome assembly. In *Proceedings of the 2011 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pages 1051-1053. IEEE, 2011.
- C.10. Diana Diaz, Michele Donato, **Tin Nguyen**, and Sorin Draghici. MicroRNA-augmented pathways (mirAP) and their applications to pathway analysis and disease subtyping. In *Pacific Symposium on Biocomputing*, volume 22, pages 390-401, 2016.
- C.11. Diana Diaz, **Tin Nguyen**, and Sorin Draghici. A systems biology approach for unsupervised clustering of high-dimensional data. In *International Workshop on Machine Learning, Optimization and Big Data*, pages 193–203. Springer, 2016.
- C.12. Thair Judeh, **Tin Nguyen**, and Dongxiao Zhu. QSEA for fuzzy subgraph querying of KEGG pathways. In *Proceedings of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine*, pages 474-481. ACM, 2012.
- C.13. Zhiyu Zhao, **Tin Nguyen**, Nan Deng, Kristen Johnson, and Dongxiao Zhu. SPATA: a seeding and patching algorithm for de novo transcriptome assembly. In *Proceedings of the 2011 IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW)*, pages 26-33. IEEE, 2011.

Submitted and Pending

- Hung Nguyen, Duc Tran, Bang Tran, Bahadir Pehlivan, and **Tin Nguyen**. A comprehensive survey of regulatory network inference methods using single-cell RNA sequencing data. **Briefings in Bioinformatics** (major revision).
- Bang Tran, Duc Tran, Hung Nguyen, and **Tin Nguyen**. scISR: Single-cell imputation using subspace regression. **Nucleic Acids Research** (major revision).
- Jovan Tanevski, Thin Nguyen, Buu Truong, Nikolaos Karaikos, Mehmet Eren Ahsen, Xinyu Zhang, Chang Shu, Ying Hu, Hoang VV Pham, Xiaomei Li, Thuc Duy Le, Adi Tarca, Gaurav Bhatti, Roberto Romero, Nestoras Karathanasis, Phillipe Loher, Yang Chen, Zhengqing Ouyang, Disheng Mao, Yuping Zhang, Maryam Zand, Jianhua Ruan, Christoph Hafemeister, Peng Qiu, Duc Tran, **Tin Nguyen**, Attila Gabor, Thomas Yu, Enrico Glaab, Roland Krause, Peter Banda, Gustavo Stolovitzky, Nikolaus Rajewsky, Julio Saez-Rodriguez, Pablo Meyer.

Predicting cellular position in the Drosophila embryo from single-cell transcriptomics data. **Cell Systems** (major revision).

- Duc Tran, Hung Nguyen, Bang Tran, Carlo La Vecchia, Hung Luu, and **Tin Nguyen**. Fast and precise single-cell data analysis using hierarchical autoencoder. **Nature Communications** (under review).
- Duc Tran, Hung Nguyen, George Bebis, Hung Luu, and **Tin Nguyen**. A novel method for cancer subtyping and risk prediction using consensus factor analysis. **Frontiers in Oncology** (under review).

PATENTS AND DISCLOSURES

- Sorin Draghici and **Tin Nguyen**. PINS: A Perturbation Clustering Approach for Data Integration and Disease Subtyping. US patent number 10529451, 2020.
- Sorin Draghici and **Tin Nguyen**. Orthogonal approach to integrate independent omic data. US patent application number 1609975, 2019.

AWARDS AND HONORS

- **Best paper award** in 11th IEEE International Conference on Knowledge and Systems Engineering (KSE 2019)
- **Second place** in the DREAM Single Cell Signaling in Breast Cancer Challenge, 2019.
- **Second place** in the DREAM Single-Cell Transcriptomics Challenge, 2018.
- **Second place** in the AstraZeneca-Sanger Drug Combination DREAM Challenge, 2016.
- **Ralph H. Kummeler Award** for Distinguished Achievement in Research, among all graduate students in all departments of the College of Engineering, Wayne State University, 2016
- **Outstanding Research Assistant**, Computer Science, Wayne State University, 2016
- **Graduated with honors** (M.Sc. and B.Sc.), Eotvos Lorand University, Hungary
- **6-year scholarship** from the Minister of Education (M.Sc. and B.Sc.), Hungary
- **4th prize** in the National Olympiad in Physics, Vietnam
- **1st prize** in Saigon Olympiad in Physics, Vietnam

TEACHING

University of Nevada, Reno

- Developed three new bioinformatics courses: CS 461/661, CS 491/691, and CS 792
- CS 461/661 Statistical Methods in Bioinformatics (Fall 2020)
- CS 791 Advanced Topics in Bioinformatics (Spring 2019, 2020)
- CS 491/691 Introduction to Bioinformatics (Fall 2017, 2018, 2019)

- CS 493 Directed Study (Spring 2018, 2019, 2020)
- BCH 793, CS 793 Independent Study (Spring 2018, 2019, 2020)

Wayne State University

- CSC 3110 Algorithm Design and Analysis (Spring/Summer 2016)

ACADEMIC ADVISING

PhD students

- Bang Tran (Fall 2018 – present)
 - Expected Graduation May 2022
- Duc Tran (Fall 2018 – present)
 - Expected Graduation May 2022
- Hung Nguyen (Fall 2017 – present)
 - Expected Graduation May 2022

Master students

- Alena Lee (Fall 2017 – Summer 2018)
 - MS in Biotechnology, UNR
 - Graduated in August 2018
- Sangam Shrestha (Spring 2018 – Fall 2019)
 - MS in Computer Science and Engineering, UNR
 - Graduated in December 2019

Undergraduate students

- Nicholas Manson (Fall 2019 – present)
- Brian Marks (Fall 2017 – present)
- Nina Hees (Fall 2017 – Fall 2018)
- Dalton Navalta (Fall 2017 – Fall 2018)
- Adam Montano (Fall 2017 – Fall 2018)
- Joshua Pike (Fall 2017 – Fall 2018)

UNIVERSITY SERVICE

Department

- Member, CSE Graduate Committee, 2017 – present
- Member, Colloquium Committee, 2017 – present
- CSE Representative, Nevada Bound, 2017 – present
- Undergraduate Academic Advisor

College & University

- Judge, Graduate Student Association Poster Symposium, Fall 2017
- Judge, Graduate Student Association Paper Competition, Spring 2018
- CSE Representative, Engineering Reception, Spring 2018

PROFESSIONAL SERVICE AND TRAINING

- **Program Committee** of ISMCO 2020, BICOB 2020, BICOB 2019, and SEDE 2019.
- **Bioinformatics Session Chair** of KSE 2019
- **Local Arrangement Chair** of ISMCO 2019
- **Member of the Board of Trustees** of Coral Academy of Science (2018 -), K-12 Charter School, Reno, NV
- **Vice president** (2015 – 2016), ACM-W student chapter, Wayne State University
- **Member, Engineering Student Faculty Board** (2015 – 2016), ACM and ACM-W student chapter, Wayne State University
- **Reviewer**
 - Journals: Bioinformatics, Briefings in Bioinformatics, Nature Scientific Reports, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Cancer Research, Nucleic Acids Research, PLoS ONE, Journal of Computational Biology, Balkan Journal of Medical Genetics
 - Conferences: BICOB 2020, BICOB 2019, KSE 2019, SEDE 2019, ISMCO 2019, ICIT 2017, BIBM 2012
- **NSF I-Corps program** (*Winter 2015*): an intensive training program to help researchers transform research ideas and technical innovations into commercializable and marketable opportunities. Through extensive customer engagement, researchers are able to validate the sustainability of their start-up business.

REFERENCES

Sorin Draghici, PhD

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