



Ronald J. Nowling

Assistant Professor, Electrical Engineering and Computer Science

Education

- Doctor of Philosophy, Computer Science & Engineering, University of Notre Dame, 2016
- MS, Computer Science & Engineering, University of Notre Dame, 2015
- BS, Computer Science/Mathematics, Eckerd College, 2010

Years of Service on this Faculty: 3

Date of Original Appointment: September, 2018

Advancement in Rank/Position

- Assistant Professor, September, 2018

Other Teaching Experience

- Adjunct Instructor, Marquette University, 2017–2018
- Teaching Assistant, University of Notre Dame, 2011–2013

Industrial / Research Experience

- Data Science Engineer, AdRoll, Inc., 2016–2018
- Software Engineer, Red Hat, Inc., 2014–2016
- Research Assistant, University of Notre Dame, 2010–2016

Funding

NSF: **CRII: III: RUI: Association Testing and Inversion Detection without Reference Genomes**, PI, \$174,231, 09/2020 – 08/2022

NSF REU Supplement, PI, \$12,600, 06/2021 – 08/2021.

CTSI Pilot Grant: **Hearing Patient's Voice: Contextual Phenotyping of Patient Narratives and Clinical Data using ML & NLP**, co-PI, \$50,000 (\$10,000 subcontract to MSOE), 07/2020 – 06/2021

Societies

- Council on Undergraduate Research, 2021 –
- Sigma Xi Scientific Research Honors Society, 2010 –
- Society for the Study of Evolution, 2021 –
- Society for Molecular Biology & Evolution, 2021 –

Professional Service

- Co-organizer, Big Data Wisconsin Conference, 2016 – 2017
- Co-organizer, Milwaukee Big Data Meetup, 2016 – 2018

Honors and Awards

- Sigma Xi Membership / Promotion Nomination (Full – 2020, Associate – 2010)
- GAANN Fellowship, 2012-2014
- OpenMM Visiting Scholar, 2012
- University of Notre Dame Kaneb Center Outstanding Graduate TA Award, 2012

Publications

* authors contributed equally † MSOE student

RJ Nowling, SK Behura, MS Halfon, SJ Emrich, and M Duman-Scheel. "PeakMatcher facilitates updated *Aedes aegypti* embryonic *cis*-regulatory element map." *Hereditas* 158, Article number: 7 (2021). Arthropod Genomics thematic series.

RJ Nowling, KS Manke[†], and SJ Emrich. "Detecting Inversions with PCA in the Presence of Population Structure." *PLoS One*. 2020.

RJ Nowling, J Bukowy, SD McGarry, AS Nencka, O Blasko, J Urbain, A Lowman, A Barrington, A Banerjee, KA Iczkowski, and PS LaViolette. “Classification Before Segmentation: Improved U-Net Prostate Segmentation.” *Proceedings of the 2019 IEEE-EMBS International Conference on Biomedical and Health Informatics (IEEE BHI 2019)*.

RJ Nowling and S Emrich. “Adjusted Likelihood-Ratio Test for Variants with Unknown Genotypes.” *Journal of Bioinformatics and Computational Biology (JBCB)*, 16(5): 2018. (Invited Paper)

RJ Nowling and S Emrich, “Detecting Chromosomal Inversions from Dense SNPs by Combination PCA and Association Tests.” *Proceedings of the 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, 2018.

RJ Nowling and S Emrich. “Adjusted Likelihood-Ratio Test for Variants with Unknown Genotypes.” *Proceedings of the 10th Annual Conference on Bioinformatics and Computational Biology (BICOB)*, 2018.

RJ Nowling and S Emrich. “Stable Feature Ranking with Logistic Regression Ensembles.” *Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine (IEEE BIBM)*, 2017.

RJ Nowling and J Vyas. “A domain-driven, generative data model for BigPetStore.” *Proceedings of the 4th IEEE International Conference on Big Data and Cloud Computing (BDCloud)*, 2014.

JC Sweet, **RJ Nowling**, TM Cickovski, CR Sweet, VS Pande, and JA Izaguirre. “Long Timestep Molecular Dynamics on the Graphical Processing Unit.” *Journal of Chemical Theory and Computation*, 9(8):3267– 3281, 2013.

RJ Nowling^{*}, JL Abrudan^{*}, DA Shoue, B Abdul-Wahid, M Wadsworth, G Stayback, FH Collins, MA McDowell, and JA Izaguirre. “Identification of Novel Arthropod Vector GPCRs.” *Parasites & Vectors*, 6:150, 2013.

HJC Ellis, G Weatherby, **RJ Nowling**, J Vyas, M Fenwick, and MR Gryk. “A Software Architecture for NMR Spectral Data Translation.” *CISE*, 15(1):76-83, 2013.

RJ Nowling and TM Cickovski. “Prototype to Release: Software Engineering for Scientific Software.” *Biomedical Computation Review*, Fall 2012.

RJ Nowling, J Vyas, G Weatherby, MW Fenwick, HJC Ellis, and MR Gryk. “CONNJUR Spectrum Translator: An open-source application for reformatting NMR spectral data.” *J Bio NMR*, 50:83-89, 2011.

RJ Nowling and H Mauch. “Priority Encoding Scheme for Solving Permutation and Constraint Problems with Genetic Algorithms and Simulated Annealing.” *Proceedings of the 8th International Conference on Information Technology - New Generations*, 2011.

HJC Ellis, J Vyas, **RJ Nowling**, TO Martyn and MR Gryk. “Iterative Development of an Application to Support Nuclear Magnetic Resonance Data Analysis of Proteins.” *Proceedings of the 8th International Conference on Information Technology - New Generations*, 2011.

J Vyas*, **RJ Nowling***, T Meusberger, D Sargeant, K Kadaveru, MR Gryk, V Kundeti, S Rajasekaran, and MR Schiller. “MimoSA: a system for minimotif annotation.” *BMC Bioinformatics*, 11:328, 2010.

J Vyas, **RJ Nowling**, MW Maciejewski, S Rajasekaran, MR Gryk, and MR Schiller. “A proposed syntax for Minimotif Semantics, version 1.” *BMC Genomics*, 10:360, 2009.

Presentations Given

RJ Nowling, RR Geromel[†], and BS Halligan[†]. Filtering STARR-Seq Peaks for Enhancers with Sequence Models. Poster presentation at the 11th Annual ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics, September 2020, Virtual.

RJ Nowling, CR Beal, SJ Emrich, SK Behura, MS Halfon, and M Duman-Scheel. PeakMatcher: Matching Peaks Across Genome Assemblies. Poster presentation at the 11th Annual ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics, September 2020, Virtual.

M Aleck[†] and **RJ Nowling**. Exploring Mechanisms of Molecular Evolution and Their Representations in PCA. Poster Presentation at the 43rd Annual IEEE Computer Software and Applications Conference (COMPSAC) 2019, Milwaukee, WI.

KS Manke[†], SJ Emrich, and **RJ Nowling**. Detecting and Localizing Inversions with SNPs. Poster Presentation at the 12th Annual Arthropod Genomics Symposium (2019), Manhattan, KS.

RJ Nowling, Jenica L. Abrudan, Scott Emrich. Populations Genetics without Population Labels. Poster Presentation at the 11th Annual Arthropod Genomics Symposium (2018), Urbana-Champaign, IL.

RJ Nowling and Scott Emrich, Feature Ranking as an Alternative to FST. Poster Presentation at the 10th Annual Arthropod Genomics Symposium (2017), Notre Dame, IN.

RJ Nowling. Real-World Lessons in Machine Learning Applied to Spam Classification. Milwaukee Big Data Meetup (May 2017), Milwaukee, WI, USA.

RJ Nowling. Insights into Customer Behavior from Clickstream Data. Spark Summit East (February 2016), New York City, NY, USA.

RJ Nowling. BigTop Bazaar: Simulating Customer Dynamics Driven by Booth Preferences at a Conference. Poster Presentation at the 2015 Annual Conference of the Great Lakes Section of the Society for Industrial and Applied Math (2015), Grand Rapids, MI.

RJ Nowling. Synthetic Data Generation for Realistic Analytics Examples and Testing. Apache: Big Data Europe (October 2015), Budapest, Hungary.

RJ Nowling, M Wadsworth, JL Abrudan, DA Shoue, B Abdul-Wahid, GM Stayback, FH Collins, MA McDowell, and JA Izaguirre. Identifying GPCRs in the Genome of the Sand Fly *P. papatasi* using Ensemble*. Poster Presentation at the 7th Annual Arthropod Genomics Symposium (2013), Notre Dame, IN.

RJ Nowling, CR Sweet, and JA Izaguirre. Extending Long Timestep Molecular Dynamics (LTMD) to Explicit Solvent. Poster Presentation at the Midwest Theoretical Chemistry Conference (2013), Urbana-Champaign, IL.

RJ Nowling, JL Abrudan, DA Shoue, B Abdul-Wahid, M Wadsworth, GM Stayback, FH Collins, MA McDowell, and JA Izaguirre. Evaluation and Development of GPCR Classifiers for Vectors. Poster Presentation at the Second Annual Eck Institute for Global Health Research Retreat (2013), Notre Dame, IN.