

CURRICULUM VITAE

SCOTT J. EMRICH

CURRENT ADDRESS

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EDUCATION

| | | | |
|------|-------|--|----------------------------|
| 2007 | Ph.D. | Bioinformatics and Computational Biology | Iowa State University |
| 2002 | B.S. | Biology and Computer Science | Loyola College in Maryland |

ACADEMIC EXPERIENCE

Academic Appointments

University of Tennessee - Knoxville

2019–present Adjunct Associate Professor, Dept of Ecology and Evolutionary Biology

2018–present Associate Professor, Dept. of Electrical Engineering and Computer Science

University of Notre Dame

2015–2017 Director of Bioinformatics appointed by Notre Dame VP for Research

2015–2017 Concurrent Associate Professor, Dept. of Biological Sciences

2014–2017 Research Associate Professor, Dept. of Computer Science and Engineering

8/2007–2014 Assistant Professor, Dept. of Computer Science and Engineering

Affiliations and Positions Held

University of Tennessee

2018–present Core faculty, Genome Science and Technology (GST) PhD

2019–present Core faculty, Bredesen Center for Interdisciplinary Research and Graduate Education
Data Science and Engineering PhD program

University of Notre Dame

2011-2017 Bioinformatics director, Notre Dame Genomics and Bioinformatics Core (GBC)

2011-2017 Member, Environmental Change Initiative
2008-2017 Member, Eck Institute for Global Health

International

Indian Institute of Technology (IIT), Bombay

Fall 2006 Visiting Scholar, Kanwal Rekhi School of Information Technology

BRIEF SUMMARY OF RESEARCH IMPACT AND EXTERNAL FUNDING SUCCESS

- Over 95 peer-reviewed publications. Full report available via Google Scholar
- \$43.37 million in awards as PI or co-PI during my first decade as faculty at Notre Dame (ND) including a new NIH P01 award in 2017 (Ferdig PI).
- Two new awards (as co-PI) since joining UT faculty in Jan 2018: Blum, Gwinn (UTIA) PIs
- 49th most cited UT-Knoxville tenured/tenure-track researcher per Google Scholar. Of these 46 are full professors or emeritus full professors, and twelve (26%) are full professors in EECS.

| Citation summary | All | Since 2015 | Funding role | Last year at ND (2017) | Details |
|------------------|------|------------|--------------|------------------------|------------------------|
| Citations | 9355 | 5830 | PI | \$2,198,944 direct | \$643,541 to SJE |
| h index | 31 | 25 | co-PI | \$215,000 direct | shared postdoc and PhD |
| i10 index | 57 | 45 | Impact | 5% of all ND awards | Same as 2016 |

HONORS AND AWARDS

2020 Best paper, International Conference on Bioinformatics and Computational Biology

2010 Invited and participated in 2010 Indo-American Frontiers of Engineering Symposium, National Academy of Engineering

2008 Iowa State University Zaffrano Prize for Graduate Research

2007 Iowa State University Research Excellence Award

2006 Electrical and Computer Engineering Research Excellence, Iowa State University

2006 *IEEE International Parallel and Distributed Processing Symposium (IPDPS) best paper*

REFEREED PUBLICATIONS

Journal *Graduate and Undergraduate students are underlined below, postdoctoral trainees in italics*

2020 Flanley, C.M, Ramalho-Ortigao, M., Coutinho-Abreu, I.V., Mukbel, R., Hanafi, H.A., El-Hossary, S.S., Fawaz, E.Y., Hoel, D.F., Bray, A.W., Stayback, G., Shoue, D.A., Kamhawi, S., Emrich, S. and M.A. McDowell. *Phlebotomus papatasi* sand fly predicted salivary protein diversity and immune response potential based on *in silico* prediction in Egypt and Jordan populations. *PLOS Neglected Tropical Diseases*, 14(7): e0007489.

2020 Wright, G., Rodriguez, A., Li, J., Clark, P.L., Milenkovic, T. and S.J. Emrich. Analysis of computational codon usage models and their association with translationally slow codons, *PLOS One*, 15 (4), e0232003.

- 2020 Waterhouse, R.M., Aganezov, S., Anselmetti, Y., Lee, J., Ruzzante, L., Reijnders, M.J., Feron, R., B  rard, S., George, P. Hahn, M.W., Howell, P.I., Kamali, M., Koren, S., Lawson, D., Maslen, G., Peery, A., Phillippy, A.M., Sharakhova, M.V., Tannier E., Unger, M.F., Zhang, S.V., Alekseyev, M.A., Besansky, N.J., Chauve, C., **Emrich, S.J.**, and I.V. Sharakhov. Evolutionary superscaffolding and chromosome anchoring to improve *Anopheles* genome assemblies, *BMC Biology*, 18(1), 1.
- 2020 Molik, D.C., Pfrender, M. and **S.J. Emrich**. Uncovering effects from the structure of metabarcoding sequences for metagenetic and microbiome analysis, *Methods and Protocols*, 3(1)22.
- 2019 Li, X., Kumar, S., McDew-White, M. Haile M., Cheeseman, I.H., **Emrich, S.J.**, Button-Simons, K., Nosten, F., Kappe, S.H., Ferdig, M.F., Anderson, T.J.C., and A. M Vaughan. Genetic mapping of fitness determinants across the malaria parasite *Plasmodium falciparum* life cycle, *PLoS Genetics*, 10.
- 2019 S. Zhu, **S. J. Emrich** and D. Chen. Predicting Local Inversions Using Rectangle Clustering and Representative Rectangle Prediction, *IEEE Transactions on Nanobioscience*, 18(3):316–323.
- 2019 RJ Nowling and **S.J. Emrich**. Adjusted Likelihood-Ratio Test for variants with unknown genotypes, *J. Bioinformatics and Computational Biology*, 16(5):1840020.
- 2019 S. Zhu, **S. J. Emrich** and D. Chen. Inversion detection using PacBio long reads. *Int. J. Data Mining and Bioinformatics*, 20(3):230–246.
- 2019 Rund, S S., C. Braak, K., Cator, L., Copas, K., **Emrich, S.J.**, Giraldo-Calderon, G.I., Johansson, M. A., Heydari, N., Hobern, D., Kelly, S.A., Lawson, D., Lord, C., MacCallum, R.M., Roche, D.G., Ryan, S.J., Schigel, D., Vandegrift, K., Watts, M., Zaspel, J. M. and Pawar, S. MIREAD, a minimum information standard for reporting arthropod abundance data, *Scientific Data*, 6(1):40.
- 2018 Wiltshire, R.M., Bergey, C.M., Kayondo, J.R., Birungi, J., Mukwaya, L.G., **Emrich, S.J.**, Besansky, N.J. and F. H Collins. Reduced-representation sequencing identifies small effective population sizes of *Anopheles gambiae* in the north-western Lake Victoria basin, Uganda, *Malaria journal*, 17(1):285.
- 2018 Choudhury, O., Chakrabarty, A., and **S.J. Emrich**. HECIL: a hybrid error correction algorithm for long reads with iterative learning, *Scientific Reports*, 8(1):9936 (Google: 3 citations).
- 2018 Ryan, S.F., Deines, J.M., Scriber, J.M., Pfrender, M.E., Jones, S.E., **Emrich, S.J.** and J.J. Hellmann. Climate-mediated hybrid zone movement revealed with genomics, museum collection, and simulation modeling. *Proceedings of National Academy of Sciences (USA)*, 201714950 (cover article; Google: 12 citations).
- 2018 Li, L., Cheng, Y., **Emrich, S.** and J. Schorey. Activation of endothelial cells by extracellular vesicles derived from *Mycobacterium tuberculosis* infected macrophages or mice, *PLoS one*, 13(5):e0198337. (Google: 1 citation).
- 2018 Choudhury, O., Chakrabarty, A., and **S.J. Emrich**. Highly accurate and efficient data-driven methods for genotype imputation, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8(1): 9936.
- 2018 Rodriguez, A., Wright, G., **Emrich, S.J.**, and P.L. Clark. % MinMax: A versatile tool for calculating and comparing synonymous codon usage and its impact on protein folding. *Protein Science*, 27(1):356–362 (Google: 9 citations).

- 2017 [Zhu, S.](#), [Chen, D.Z.](#), and **[S.J. Emrich](#)**. Single molecule sequencing-guided scaffolding and correction of draft assemblies, *BMC Genomics*, 18(10):879 (Google: 1 citation).
- 2017 [Hazekamp, N.](#), [Kremer-Herman, N.](#), [Tovar, B.](#), [Meng, H.](#), [Choudhury, O.](#), **[Emrich, S.J.](#)** and [D. Thain](#). Combining static and dynamic storage management for data intensive scientific workflows, *IEEE Transactions on Parallel and Distributed Systems* (Google: 3 citations).
- 2017 [Faisal, F.E.](#), [Newaz, K.](#), [Chaney, J.L.](#), [Li, J.](#), **[Emrich, S.J.](#)**, [Clark, P.L.](#), and [T. Milenkovic](#). GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison, *Scientific Reports*, 7: 14890 (Google: 6 citations).
- 2017 [Horsman, M.E.](#), [Marous, D.R.](#), [Li, R.](#), [Oliver, R.A.](#), [Byun, B.](#), **[Emrich, S.J.](#)**, [Bogges, W.](#), [Townsend, C.A.](#) and [S. Mobashery](#). Whole-genome shotgun sequencing of two beta-Proteobacterial species in search of the bulgecin biosynthetic cluster, *ACS Chemical Biology*, 12 (10), 2552–2557 (Google: 3 citations).
- 2017 [Konar, A.](#), [Choudhury, O.](#), [Bullis, R.](#), [Fiedler, L.](#), [Kruser, J.M.](#), [Stephens, M.T.](#), [Gailing, O.](#), [Schlarbaum, S.](#), [Coggeshall, M.V.](#), [Staton, M.E.](#), [Carlson, J.E.](#), **[Emrich, S.](#)** and [J. Romero-Severson](#). High-quality genetic mapping with ddRADseq in the non-model tree *Quercus rubra*, *BMC genomics* 18 (1), 417 (Google: 5 citations).
- 2017 [Chaney, J.L.*](#), [Steele, A.*](#), [Carmichael, R.](#), [Rodriguez, A.](#), [Specht, A.T.](#), [Ngo, K.](#), [Li, J.](#), **[Emrich, S.*](#)** and [P.L. Clark*](#). Widespread position-specific conservation of synonymous rare codons within coding sequences. *PLoS Computational Biology*, 13(5), e1005531 (Google: 30 citations).
- 2017 [Adema, C.](#), [Hillier, L.](#), [Jones, C.](#), [Loker, E.S.](#), [Knight, M.](#), [Minx, P.](#), [Oliveira, G.](#), [Raghavan, N.](#), [Shedlock, A.](#), [Amaral, L.](#) et al. Whole genome analysis of a schistosomiasis-transmitting freshwater snail. *Nature Communications*, 8, 15451 (Google: 55 citations).
- 2016 [Siwo, G.](#), [Rider, A.](#), [Tan, A.](#), [Pinapati, R.](#), **[Emrich, S.](#)**, [Chawla, N.](#) and [M. Ferdig](#). Prediction of fine-tuned promoter activity from DNA sequence. *F1000Res*, 5: 158. (Google: 2 citations)
- 2016 [Love, R.R.](#), [Steele, A.](#), [Mamadou B.](#), [Coulibaly, M.B.](#), [Traore, S.](#), **[Emrich, S.J.](#)**, [Fontaine, M.C.](#) and [N. J. Besansky](#). Chromosomal inversions and ecotypic differentiation in *Anopheles gambiae*: the perspective from whole-genome sequencing. *Molecular Ecology*, 25(23), 5889–5906 (Google: 12 citations).
- 2016 [Behura, S.K.](#), [Sarro, J.](#), [Li, P.](#), [Mysore, K.](#), [Severson, D.W.](#), **[Emrich, S.J.*](#)** and [M. Duman-Scheel*](#). High-throughput cis-regulatory element discovery in the vector mosquito *Aedes aegypti*. *BMC Genomics*, 17 (1), 341 (Google: 9 citations).
- 2016 [Hall, A.B.*](#), [Papathanos, P.-A.*](#), [Sharma, A.*](#), [Cheng, C.*](#), [Akbari, O.S.](#), [Assour, L.](#), [Bergman, N.H.](#), [Cagnetti, A.](#), [Crisanti, A.](#), [Dottorini, T.](#), [Fiorentini, E.](#), [Galizi, R.](#), [Hnath, J.](#), [Jiang, X.](#), [Koren, S.](#), [Nolan, T.](#), [Radune, D.](#), [Sharakhova, M.V.](#), [Steele, A.](#), [Timoshchevskiy, V.](#), [Windbichler, N.](#), [Zhang, S.](#), [Hahn, M.W.](#), [Phillippy, A.M.](#), **[Emrich, S.J.](#)**, [Sharakhov, I.V.](#), [Tu, Z.J.](#), and [N.J. Besansky](#). Radical remodeling of the Y chromosome in a recent radiation of malaria mosquitoes. *Proceedings of the National Academy of Sciences*, 113(15):E2114-E2123 (Google: 44 citations).
- 2015 [Mesquita, R.D. et al.](#) (120 authors total). The genome of *Rhodnius prolixus*, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite transmission. *Proceedings of the National Academy of Science*, 112 (48), 14936-14941 (Google: 140 citations).

- 2015 Choudhury, O., Hazekamp, N., Thain, D. and **S. Emrich**. Accelerating comparative genomics workflows in a distributed environment with optimized data partitioning and workflow fusion. *Scalable Computing: Practice and Experience*, 16 (1), 53-70 (Google: 7 citations).
- 2015 Ramalho-Ortigao, M., Coutinho-Abreu, I.V., Balbino, V.Q., Figueiredo, C.A.S., Mukbel, R., Dayem, H., Hanafi, H.A., El-Hossary, S.S., Fawaz, E., Abo-Shehada, M., Hoel, D.F., Stayback, G., Wadsworth, M., Shoue, D.A., Abrudan, J., Lobo, N.F., Mahon, A.R., **Emrich, S. J.**, Kamhawi, S., Collins, F.H. and M. A. McDowell. *Phlebotomus papatasi* SP15: mRNA expression variability and amino acid sequence polymorphisms of field populations. *Parasites and Vectors*, 8(1):298 (Google: 5 citations).
- 2015 Egan, S.P.*, *Ragland, G.**, Assour, L., Powell, T.H.Q., Hood, G.R., **Emrich, S.**, Nosil, P. and J. L. Feder. Experimental evidence of genome-wide impact of ecological selection during early stages of speciation-with-gene-flow. *Ecology Letters*, 18(8):817–825 (Google: 70 citations).
- 2015 Mbengue, A.*, Bhattacharjee*, S., Pandharkar, T. , Haining, L., Estiu, G., Stahelin, R.V., Rizk, S., Njimoh, D.L., Ryan, Y., Chotivanich, K., Nguon, C., Ghorbal, M., Lopez-Rubio, J.J., Pfrender, M., **Emrich, S.**, Mohandas, N., Dondorp, A.M., Wiest, O. and K. Haldar. A molecular mechanism of artemisinin resistance in *Plasmodium falciparum* malaria. *Nature*, 520(7549):683–687 (Google: 315 citations).
- 2015 Warren, A.S., Aurrecochea, C., Brunk, B. Desai, P., **Emrich, S.**, *Giraldo-Calderon, G.*, Harb, O., Hix, D., Lawson, D., Machi, D., Mao, C., McClelland, M., Nordbergm E., Shukla, M., Wattam, A.R., Will, R., Yo, H.S. and B. Sobral. RNA-Rocket: An RNaseq analysis tool for infectious disease research. *Bioinformatics*, btv002 (Google: 10 citations).
- 2015 *Fontaine, M.C.**, Pease, J.B.* , *Steele, A.*, Waterhouse, R.M., Neafsey, D.E., Sharakhovm I.V., Jiang, X., Hall, A.B., Catteruccia, F., Kakani, E., Mitchell, S.N., Wu, Y.-C., Smith, H.A., Love, R.R., Lawniczak, M.K., Slotman, M.A., **Emrich, S.J.**, Hahn, M.W. and N.J. Besansky. Extensive introgression in a malaria vector species complex revealed by phylogenomics. *Science*, 347(6217):1258524 (Google: 271 citations).
- 2015 The Anopheles Genomes Cluster Consortium. Highly evolvable malaria vectors: the genomes of 16 Anopheles mosquitoes. *Science*, 347(6217):1258522 (Google: 289 citations).
- 2014 *Giraldo-Calderon, G.**, **Emrich, S.***, MacCallum, B., Maslen, G., Gesing, S., Dialynas, E., Topalis, P., Ho, N., Madey, G., Colins, F., Lawson, D. and the VectorBase Consortium. VectorBase: an updated bioinformatics resource for invertebrate vectors of human pathogens *Nucleic Acids Research*, gku1117 (Google: 201 citations).
- 2014 Tomchaney, M., Mysore, K., Sun, L., Li, P., **Emrich, S.J.**, Severson, D.W. and M. Duman-Scheel. Examination of the genetic basis for sexual dimorphism in the *Aedes aegypti* (dengue vector mosquito) pupal brain. *Biology of Sex Differences*, 5:10 (Google: 9 citations).
- 2014 Rider, A.K., Milenkovic, T., Siwo, G.H., Pinpati, R.S., **Emrich, S.J.**, Ferdig, M.T. and *N.V. Chawla*. Networks' characteristics are important for systems biology. *Network Science*, 2(2):139–161 (Google: 4 citations).
- 2014 Jiang, X., Peery, A., Hall, A.B., Sharma, A., Chen, X.-G. Waterhouse, R.M., Komissarov, A., Riehle, M.M. Shouche, Y., Sharakhova, M.V. *et al.*. Genome analysis of a major urban malaria vector mosquito, *Anopheles stephensi*. *Genome Biology*, 15(9):459 (Google: 75 citations).

- 2014 Dugan, V.G., **Emrich, S.J.**, *Giraldo-Calderon, G.I.*, Harb, O.S., Newman, R.M., Pickett, B.E., Schriml, L.M., Stockwell, T.B., Stoeckert, C.J. Sullivan, D.E., *et al.*, Standardized metadata for human pathogen/vector genomic sequences. *PLoS One*, 9(6):e99979 (Google: 24 citations).
- 2014 O’Neil, S.T., Dzurisin, J.D.K., Williams, C.M. , Lobo, N.F., Higgins, J.K., Deines, J.M., Carmichael, R.D., *Zeng, E.*, Tan, J.C., Wu, G.C. **Emrich, S.J.** and J.J. Hellmann. Gene expression in closely related species mirrors local adaptation: consequences for responses to a warming world. *Molecular Ecology*, 23(11):2686–2698 (Google : 16 citations).
- 2014 Thrasher, A., Musgrave, Z., Kachmark, B., Thain, D. and **S. J. Emrich**. Shifting the bioinformatics computing paradigm: A case study in parallelizing genome annotation using MAKER and Work Queue. *Int. J. Bioinformatics Research and Applications*, 10(4)447–460 (Google: 6 citations).
- 2014 Geng, P., Li, W., Lin, L., de Miranda, J.R., **Emrich, S.**, An, L. and O. Terenius. Genetic characterization of a novel Iflavirus associated with vomiting disease in the Chinese oak silkworm *Antheraea pernyi*. *PLoS One*, 9(3):e92107 (Google : 13 citations).
- 2014 *Zhang, W.*, *Zeng, E.*, *Livermore, J.*, Liu, D., Jones, S. and **S. Emrich**. Mapping genomic features to functional traits through microbial whole genome sequences. *Int. J. Bioinformatics Research and Applications*, 10(4):461–478 (Google: 5 citations).
- 2013 Meyer, P., Siwo, G., Zeevi, D., Sharon, E., Norel, R., Segal, E., Stolovitzky, G., *et al.* Inferring gene expression from ribosomal promoter sequences, a crowdsourcing approach. *Genome Research*, 23(11), 1928–1937 (Google: 10 citations).
- 2013 Evans, J.D., Brown, S.J., Hackett, K.J., Robinson, G., Richards, S., Lawson, D., Elsik, C., Coddington, J., Edwards, O., **Emrich, S.**, Gabaldon, T., Goldsmith, M., Hanes, G., Misof, B., Munoz-Torres, M., Niehuis, O., Papanicolaou, A., Pfrender, M., Poelchau, M., Purcell-Miramontes, M., Robertson, H.M., Ryder, O., Tagu, D., Torres, T., Zdobnov, E., Zhang, G. and X. Zhou. The i5K Initiative: Advancing Arthropod Genomics for Knowledge, Human Health, Agriculture, and the Environment. *Journal of Heredity*, 5: 595–600 (Google: 172 citations).
- 2013 O’Neil, S.T. and **S. J. Emrich**. Assessing *de novo* transcriptome assembly metrics for consistency and utility. *BMC Genomics*, 14(1):465 (Google: 97 citations).
- 2013 Neafsey, D.E., Christophides, G.K., Collins, F.H., **Emrich, S.J.**, *Fontaine, M.C.*, Gelbart, W., Hahn, M.W., Howell, P.I., Kafatos, F.C., Lawson, D., Muskavitch, M.A.T, Waterhouse, R.M., Williams, L.J. and N. J. Besansky. The evolution of the *Anopheles* 16 genomes project. *G3*, 3:(7), 1191–1194 (Google: 56 citations).
- 2013 *Livermore, J.A.*, **Emrich, S.J.**, Tan, J. and S. E. Jones. Freshwater bacterial lifestyles inferred from comparative genomics. *Environmental Microbiology*, 16(3):746–758 (Google: 27 citations).
- 2013 Abrudan, J., Ramalho-Ortigao, M., O’Neil, S., Stayback, G., Wadsworth, M., Bernard, M., Shoue,D., **Emrich, S.**, Lawyer, P., Kamhawi, S., Rowton, E.D., Lehane, M.J., Bates, P.A., Valenzeula, J.G., Tomlinson, C., Appelbaum, E., Moeller, D., Thiesing, B., Dillon, R., Clifton, S., Lobo, N.F., Wilson, R.K., Collins, F.H. and M.A. McDowell. The characterization of the *Phlebotomus papatasi* transcriptome. *Insect Molecular Biology*,22(2):211–232 (Google: 11 citations).
- 2013 Bradnam, K.R., Fass, J.N., Alexandrov, A., *Baranay, P.*, Bechner, M., Birol, I., Boisvert, J., Chapman, J.A., Chapuis, G., Chikhi, R. *et al.* Assemblathon 2: evaluating *de novo* methods of genome assembly in three vertebrate species, *GigaScience*, 2(1):1–31 (Google: 490 citations).

- 2012 Moretti, C., Thrasher, A., Yu, L., Olson, M., **Emrich, S.** and D. Thain. A framework for scalable genome assembly on clusters, clouds and grids. *IEEE Transactions on Parallel and Distributed Systems*, 23(12):2189–2197 (Google: 23 citations).
- 2012 O’Neil, S. T. and **S. J. Emrich**. Haplotype and minimum-chimerism consensus determination using short sequence data. *BMC Genomics* 13(Suppl 2), S4 (Google: 18 citations).
- 2012 Megy, K.*, **Emrich, S. J.***, Lawson, D., Campbell, D., Dialynas, E., Hughes, D.S., Koscielny, G., Louis, C., MacCallum, R.M., Redmond, S.N., Sheehan, A., Topalis, P., Wilson, D. and the VectorBase Consortium. VectorBase: improvements to a bioinformatics resource for invertebrate vector genomics. *Nucleic Acids Research*, 40:D729-734 (Google: 172 citations).
- 2012 Lanc, I., Bui, P., Thain, D. and **S.J. Emrich**. Adapting bioinformatics applications for heterogeneous systems: a case study. *Concurrency and Computation: Practice and Experience* (Google: 13 citations).
- 2011 Rider, A.K., Siwo, G., Chawla, N.V., Ferdig, M.T. and **S. J. Emrich**. A supervised learning approach to the ensemble clustering of genes. *International Journal of Data Mining and Bioinformatics*, 12:116 (Google: 7 citations).
- 2011 Carmichael, R., Braga-Henebry, P. Thain, D. and **S. J. Emrich**: Biocompute 2.0: an improved collaborative workspace for data intensive bio-science. *Concurrency and Computation: Practice and Experience*, 23(17): 2305-2314 (Google: 12 citations).
- 2011 Samarakoon, U., Regier, A., Tan, A., Desany, B.A., Collins, B., Tan, J.C., **Emrich, S.J.** and M. T. Ferdig. High-throughput 454 sequencing for allele discovery and recombination mapping in *Plasmodium falciparum*. *BMC Genomics*, 12:116 (Google: 30 citations).
- 2010 Lawniczak, M.K.*, **Emrich, S.J.***, Holloway, A.K., Regier, A.P., Olson, M., White, B., Redmond, S., Fulton, L., Appelbaum, E., Godfrey, J., Farmer, C., Chinwalla, A., Yang, S.P., Minx ,P., Nelson, J., Kyung, K., Walenz, B.P., Garcia-Hernandez, E., Aguiar, M., Viswanathan, L.D., Rogers, Y.H., Strausberg, R.L., Sasaki, C.A., Lawson, D., Collins, F.H., Kafatos, F.C., Christophides, G.K., Clifton, S.W., Kirkness, E.F. and N. J. Besansky. Widespread divergence between incipient *Anopheles gambiae* species revealed by whole genome sequences. *Science*, 330(6003): 512–514 (Google: 243 citations).
- 2010 Rider, A.K., Siwo, G., Chawla, N.V., Ferdig, M. and **S. J. Emrich**, A statistical approach to finding overlooked genetic associations. *BMC Bioinformatics*, 11:526 (Google: 4 citations).
- 2010 Lobo, N.F., Sangare, D.M., Regier, A.A., Reidenbach, K.R., Bretz, D.A., Sharakhova, M.V., **Emrich, S.J.**, Traore, S.F., Costantini, C., Besansky, N.J. and F. C. Collins, Breakpoint structure of the *Anopheles gambiae* 2Rb chromosomal inversion. *Malaria Journal*, 9:293 (Google: 21 citations).
- 2010 Yu, L., Moretti, C., Thrasher, A. **Emrich, S.**, Judd, K. and D. Thain, Harnessing parallelism in multicore clusters with the All-Pairs, Wavefront, and Makeflow abstractions. *Cluster Computing*, 13:243–246 (Google: 57 citations).
- 2010 O’Neil, S.T., Dzurisin, J.D., Carmichael, R.D., Lobo, N.F., **Emrich, S.J.** and J.J. Hellmann, Population-level transcriptome sequencing of nonmodel organisms *Erynnis propertius* and *Papilio zelicaon*. *BMC Genomics*, 11:310 (Google: 133 citations).
- 2009 Liu, S., Chen, H.D., Makarevitch, I., Shirmer, R., **Emrich, S.J.**, Dietrich, C.R., Barbazuk, W.B., Springer, N.M., and P.S. Schnable. High-throughput genetic mapping of mutants via Quantitative SNP-typing. *Genetics*, 184(1):19–26 (Google: 73 citations).

- 2009 Schnable, P.S., Ware, D., Fulton, R.S., Stein, J.C., Wei, F., Pasternak, S., Liang, C., Zhang, J., Fulton, L., Graves, T.A., et al. The B73 maize genome: complexity, diversity, and dynamics. *Science*, 326:1112-1115 (cover of Nov 20th, 2009 issue; Google: 2956 citations).
- 2007 Ohtsu, K., Smith, M., **Emrich, S.J.**, Borsuk, L.A., Zhou, R., Chen, T., Zhang, X., Timmermans, M., Beck, J., Buckner, B., Janick-Buckner, D., Nettleton, D., Scanlon, M.J., and P.S. Schnable. Global gene expression analysis of the shoot apical meristem of maize (*Zea mays* L.). *Plant Journal*, **52**:391–404 (Google: 147 citations).
- 2007 Barbazuk, W.B.* , **Emrich, S.J.*** , Chen, H.D., Li, L., and P.S. Schnable. SNP discovery in maize via 454 transcriptome sequencing. *Plant Journal*, **51**:910–918 (Google: 449 citations).
- 2007 Kalyanaraman, A.* , **Emrich, S.J.*** , Schnable, P.S., and S. Aluru. Assembling genomes on large-scale parallel computers. *Journal of Parallel and Distributed Computing*, **67**:1240–1255 (Google: 41 citations).
- 2007 **Emrich, S.J.***, Barbazuk, W.B*., Li, L. and P.S. Schnable. Gene discovery and annotation using LCM-454 transcriptome sequencing. *Genome Research*, **17**:69–73 (Google: 347 citations).
- 2007 **Emrich, S.J.***, Li, L.* , Wen, T.-J., Yandea-Nelson, M.D., Fu, Y., Guo, L., Chou, H.-H., Aluru, S., Ashlock, D.A., and P.S. Schnable. Nearly identical paralogs (NIPs): implications for maize (*Zea mays* L.) genome evolution. *Genetics*, **175**:429–439 (Google: 46 citations; featured in *Science*, Vol. 315, No. 5810, pp. 302 in Editor’s Choice: Highlights of recent literature). (Google: 70 citations)
- 2005 Fu, Y.* , **Emrich, S.J.*** , Guo, L., Wen, T.-J., Aluru, S., Ashlock, D.A., and P.S. Schnable. Quality assessment of Maize Assembled Genomic Islands (MAGIs) and experimental validation of predicted novel genes, *Proceedings of the National Academy of Science, USA*, **102**:12282–12287 (Google: 81 citations).
- 2005 Yao, H., Guo, L., Fu, Y., Borsuk, L.A., Wen, T.-J., Skibbe, D.S., Cui, X., Scheffler, B.E., Cao, J., **Emrich, S.J.**, Ashlock, D.A., and P.S. Schnable. Evaluation of seven *ab initio* gene prediction programs for the discovery of maize genes, *Plant Molecular Biology*, **3**:445–460 (Google: 52 citations).
- 2004 **Emrich, S.J.**, Aluru, S., Fu, Y., Wen, T., Narayanan, M., Guo, L., Ashlock, D.A., and P.S. Schnable. A strategy for assembling the maize (*Zea mays* L.) genome, *Bioinformatics*, **20**:140–147. (Google: 67 citations)
- 2003 **Emrich, S.J.**, Lowe, M., and A.L. Delcher. PROBEmer: A web-based software tool for selecting optimal DNA oligos. *Nucleic Acids Res.*, **31**:3746–3750. (Google: 73 citations)
- 2002 Lowe, M., Madsen, E. L., Schindler, K., Smith, C., **Emrich, S.**, Robb, F., and R. U. Halden. Geochemistry and microbial diversity of a Trichloroethene-contaminated superfund site undergoing intrinsic in situ reductive dechlorination. *FEMS Microbiol. Ecol.*, **40**:123–134. (Google: 64 citations)

* denotes equal contribution

Peer-reviewed Conference

- 2020 Lu, Z., Gilchrist, M. and **S.J. Emrich**. Mutational bias in shaping codon usage bias and its association with gene expression across species, *Proceedings of the 12th International conference on Bioinformatics and Computational Biology*.

- 2019 Wright, G., Rodriguez, A., Clark, P. and S.J. Emrich. A new look at codon usage and protein expression, *Proceedings of 11th International Conference on Bioinformatics and Computational Biology.*
- 2018 Zhu, S., Emrich, S.J. and D.Z. Chen. Predicting local inversions using rectangle clustering and representative rectangle prediction, In *Proceedings of IEEE International Conference on Bioinformatics and Biomedicine (BIBM).*
- 2018 Molik, D.C., Pfrender, M.E. and S.J. Emrich. Effects from structure of metabarcoding sequences on lossy analysis of microbiome data. In *Proceedings of 2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM).*
- 2018 Newaz, K., Faisal, F.E., Chaney, J.L, Li, J., Emrich, S.J., Clark, P.L. and T. Milenkovic. GRAFENE: Graphlet-based alignment-free network approach integrates 3D structural and sequence (residue order) data to improve protein structural comparison, BIODDD.
- 2018 Nowling, R.J. and S.J. Emrich. Adjusted likelihood-ratio test for variants with unknown genotypes, in *Proceedings of the 10th International Conference on Bioinformatics and Computational Biology (BiCOB)*
- 2018 Nowling, R.J. and S.J. Emrich. Detecting chromosomal inversions from dense SNPs by combining PCA and association tests, *ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB)*, Washington DC.
- 2018 Newaz, K., Faisal, F.E., Chaney, J.L, Li, J., Emrich, S.J., Clark, P.L. and T. Milenkovic. Network approach integrates 3D structural and sequence data to improve protein structural comparison, *Proceedings of the 26th Conference on Intelligent Systems for Molecular Biology (ISMB)*, Chicago.
- 2018 Nowling, R.J. and S.J. Emrich. Adjusted Likelihood-Ratio test for variants with unknown genotypes. *Proceedings of the 7th International Conference on Bioinformatics and Computational Biology (BICoB)* (Google: 2 citations).
- 2017 Nowling, R.J. and S.J. Emrich. Stable feature ranking with logistic regression ensembles. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*
- 2017 Zhu, S., Emrich, S.J. and D. Chen. Inversion detection using PacBio long reads. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)* (Google: 1 citation).
- 2016 Zhu, S., Chen, D. and S.J. Emrich. Single molecule sequencing-guided scaffolding and correction of draft assemblies. *6th IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Atlanta.
- 2016 Choudhury, O.C., Chakrabarty, A. and S.J. Emrich. HAPI-Gen: Highly accurate phasing and imputation of genotype data. *ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB)*, 78–87 (Google: 2 citations).
- 2015 Zeng, E., Zhang, W., Emrich, S., Liu, D., Livermore, J. and S. Jones. A computational framework for integrative analysis of large microbial genomics data. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM).*
- 2015 Hazekamp, N., Sarro, J., Choudhury, O., Gesing, S., Emrich, S., and D. Thain. Scaling up bioinformatics workflows with dynamic job expansion: a case study using Galaxy and Makeflow. *IEEE 11th International Conference on e-Science (e-Science)* (Google: 5 citations).
- 2015 Assour, L.A. and S.J. Emrich. Global Maximum-parsimony based ancestral reconstruction with non-universal genes. *5th IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Miami.

- 2015 Choudhury, O., Rajan, D., Hazekamp, N., Gesing, S., Thain, D. and **S. Emrich**. Balancing thread-level and task-level parallelism for data-intensive workloads on clusters and clouds. *Proceedings of IEEE Cluster*, 2015 (Google: 3 citation).
- 2015 Assour, L. and **S.J. Emrich**. Multi-genome synteny for assembly improvement. *Proceedings of the 7th International Conference on Bioinformatics and Computational Biology (BICoB)* (Google: 4 citations).
- 2015 Steele, A. and **S.J. Emrich**. pbSandwich: Scaffolding draft genomes with long reads. *Proceedings of the 7th International Conference on Bioinformatics and Computational Biology (BICoB)*.
- 2014 Choudhury, O., Hazekamp, N.L., Thain, D. and **S.J. Emrich**. Accelerating comparative genomics workflows in a distributed environment with optimized data partitioning. *Proceedings of C4Bio (part of 14th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGrid))* (Google: 7 citations)
- 2014 Hazekamp, N.L., Choudhury, O., Gesing, S., **Emrich, S.** and D. Thain. Expansion of logical workflows into series of independent encapsulated workflows. *Proceedings of the 14th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGrid)*.
- 2013 Lanc, I. and **S.J. Emrich**. An unsupervised learning approach to assembly validation. *3rd IEEE International Conference on Computational Advances in Bio and medical Sciences*, New Orleans (Google: 3 citations).
- 2013 Lumibao, C.Y., McLachlan, J., Kuch, M., **Emrich, S.J.**, Jackson, S.T. and H. Poinar. Unlocking the Past: Genetic Clues of Historical Shifts in Forest Community Composition from Ancient DNA in Lake Sediments. *Proceedings of the 98th Annual Meeting of the Ecological Society of America (ESA)*, Minneapolis, MN.
- 2013 Zhang, W., Zeng, E., Livermore, J., Liu, D., Jones, S. and **S. Emrich**. Predicting bacterial functional traits from whole genome sequences Using random forests. *3rd IEEE International Conference on Computational Advances in Bio and medical Sciences*, New Orleans (Google: 1 citation)
- 2013 Rajan, D., Thrasher, A., Abdul-Wahid. B., Izaguirre, J.A., **Emrich, S.** and D. Thain. Case studies in designing elastic applications. *13th IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGrid)* (Google: 2 citations)
- 2012 Thrasher, A., Musgrave, Z., Thain, D. and **S. J. Emrich**. Shifting the bioinformatics computing paradigm: A case study in parallelizing genome annotation using MAKER and Work Queue. *2nd IEEE International Conference on Computational Advances in Bio and medical Sciences*, Las Vegas. (Google: 6 citations)
- 2012 Zhang, W., Zeng, E., Liu, D., Jones, S. and **S. J. Emrich**. A machine learning framework for trait based genomics. *2nd IEEE International Conference on Computational Advances in Bio and medical Sciences*, Las Vegas (Google: 5 citations).
- 2011 Theresa, C.B., A.N. Colaco, **S.J. Emrich**, S.T. O'Neil, and J.S. McLachlan. New genetic tools for estimating long-term changes in forest composition, 96th Annual ESA Conference.
- 2011 Lanc, I., Bui, P, Thain, D. and **S. J. Emrich**. Adapting bioinformatics applications for heterogeneous systems: a case study. *Proceedings of the Second International Workshop on Emerging Computational Methods for the Life Sciences*. (Google: 6 citations)

- 2011 O’Neil, S.T. and **S. J. Emrich**. Robust haplotype reconstruction of eukaryotic sequence data with Hapler. *1st IEEE International Conference on Computational Advances in Bio and Medical Sciences*, Orlando. (Google: 7 citations)
- 2010 Rider, A., Siwo, G., Emrich, S.J., Ferdig, M. and N. V. Chawla. A supervised learning approach to the unsupervised clustering of genes. *IEEE International Conference on Bioinformatics and Biomedicine*, Hong Kong. (Google: 2 citations)
- 2010 Zhang, W., Zeng, E., and S.J. Emrich. A two-stage machine learning approach for pathway analysis. *IEEE International Conference on Bioinformatics and Biomedicine*, Hong Kong. (Google: 6 citations)
- 2010 Thrasher, A., Carmichael, R., Bui, P., Thain, D., and S.J. Emrich. Taming complex bioinformatics workflows with Weaver, Makeflow, and Starch. *Workflows in Support of Large-Scale Science* held in conjunction with *Supercomputing 10*. (Google: 20 citations)
- 2010 Carmichael, R., Braga-Henebry, P., Thain, D. and S.J. Emrich. Biocompute: Towards a collaborative workspace for data intensive bio-science. *Emerging Computational Methods for the Life Sciences Workshop* held in conjunction with *19th International Symposium on High Performance Distributed Computing (HPDC)*. (Google: 9 citations)
- 2009 Yu, L., Moretti, C., Emrich, S., Judd, K. and D. Thain. Harnessing parallelism in multicore clusters with the All-Pairs and Wavefront abstractions. *18th International Symposium on High Performance Distributed Computing (HPDC)*. (Google: 57 citations)
- 2009 Regier, A., Olson, M. and S.J. Emrich. Alignment and analysis of closely related genomes, *International Conference on Bioinformatics and Computational Biology (BiCoB)* (Google: 1 citation)
- 2006 Kalyanaraman, A.*, Emrich, S.J.*, Schnable, P.S., and S. Aluru. Assembling genomes on large-scale parallel computers. *IEEE International Parallel and Distributed Processing Symposium (IPDPS’06 ; Acceptance Ratio: 23%; best paper award)*. (Google: 33 citations).
- 2004 Ashlock, D.A., Emrich, S.J., Bryden, K.M., Corns, S.A., T.-J. Wen, and P.S. Schnable. A comparison of evolved finite state classifiers and Interpolated Markov Models for improving PCR primer design, *IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology*, 190–197 (Google: 8 citations).

Invited papers

- 2012 **S.J. Emrich**. Opportunities and challenges of non-model ecoinformatics. *2nd IEEE International Conference on Computational Advances in Bio and medical Sciences*, Las Vegas
- 2009 Moretti, C., Olson, M., Emrich, S., and D. Thain. Highly scalable genome assembly on campus grids. 2nd Workshop on Many-Task Computing on Grids and Supercomputers, Portland, OR. (Google: 19 citations)

BOOK CHAPTERS

- 2013 Rider, A.K, Chawla, N.V. and S.J. Emrich. A survey of current integrative network algorithms for systems biology. Ales Prokop and Bela Csukas (Eds.) Springer, *Systems Biology*, 479–495. (Google: 3 citations)

- 2012 Thain, D., Albrecht, M., Bui, H., Bui, P., Carmichael, R., **Emrich, S.** and P. Flynn. Data intensive computing with clustered chirp servers. *Data Intensive Distributed Computing: Challenges and Solutions for Large-scale Information Management*, IGI Global, Chapter 7. (Google: 3 citations)
- 2007 Barbazuk, W.B., **Emrich, S.J.** and P.S. Schnable. SNP mining from maize 454 EST sequences. *Cold Spring Harbor Protocols* (Google: 15 citations)
- 2005 **Emrich, S.J.**, Kalyanaraman, A and S. Aluru. Algorithms for large-scale sequence clustering and assembly of biological sequence data. *Handbook of Computational Molecular Biology*, CRC Press, Chapter 13 (Google: 8 citations).

INVITED PRESENTATIONS OVER THE LAST SIX YEARS

- 9/27/18 Data-driven approaches for uncovering genotype/phenotype relationships
Invited seminar, Tennessee Plant Research Center
- 7/9/18 Problem-driven bioinformatics
Invited seminar, Oak Ridge National Laboratory
- 1/28/18 Speciation and informatics
Invited seminar, Ecology and Evolutionary Biology, University of Tennessee
- 9/29/16 Single molecule sequencing to improve genomes
Invited talk, International Congress of Entomology (ICE)
- 4/5/16 VectorBase, your improved arthropod bioinformatics resource
Invited talk, Entomological Society of America (ESA) Pacific branch, Honolulu, HI
- 2/20/16 Genome assembly improvement as applied to mosquitoes
Invited seminar, Virginia Tech (Entomology)
- 6/17/15 Assembly assessment and improvement in the Anophelines
Invited talk, 9th Annual Arthropod Genomics Symposium, Manhattan, KS.
- 4/28/15 Non-model genome assembly improvement
Invited seminar, University of Georgia (Institute for Bioinformatics)

EXTERNAL SUPPORT

Current

M. Blum (PI) (w/ Emrich, McLachlan, Megonigal, Mozdzer, and Weston as co-PIs) Developing genomic resources for *Schoenoplectus americanus*, a foundational plant governing ecosystem processes at the coastal terrestrial-aquatic interface. US Department of Energy/Joint Genome Institute, Community Science Program (CSP).

K. Gwinn (PI) (w/ Emrich, Staton, others as co-PIs) BiGG FACTS in One Health: Training Next Generation of Women Bioinformatics, Genetics, and Genome Scientists. US Dept. of Agriculture NIFA, \$475,895, 6/1/19–5/31/24.

S. Emrich (PI w/ Milenkovic, Clark and Li). Integrative Computational Framework for Pattern Mining in Big -omics Data: Linking Synonymous Codon Usage to Biogenesis. National Institutes of Health, \$1,094,400, 6/1/16–5/31/20.

Remaining at Notre Dame

M. Ferdig (PI) (w/ Anderson, Kappe as project PIs, Cheeseman, Emrich, and Vaughan as core PIs). Harnessing the power of experimental genetic crosses and systems genetics to probe drug resistance in malaria, NIH, \$12,300,983, 7/1/17–6/30/22.

Completed

S. Emrich and F. Collins (PIs): VectorBase: A Bioinformatics Resource Center for invertebrate vectors of human pathogens. National Institutes of Health, \$14,714,077 with all options, 9/15/14–09/14/19.

S. Emrich (PI). Improving the *Culex quinquefasciatus* genome for improved population-level analysis. National Institutes of Health, \$391,312, 3/1/16–2/28/19

N. Besansky (PI) and S. Emrich. Anchoring and uniting the *An. funestus* assembly for improved vector analysis. National Institutes of Health, \$427,052, 07/01/14–06/30/17.

F. Collins (PI): VectorBase: An NIAID Bioinformatics Resource Center for Invertebrate Vectors of Human Pathogens. National Institutes of Health. \$14,671,665 (5 years; Emrich scientific manager and co-PI, 50% effort)

P. Clark and S. Emrich (PIs): Influence of Translation on Protein Folding. National Institutes of Health collaborative supplement to 5R01GM074807-07: \$290,704 (2 years)

RECENT INTERNAL COMPETITIVE FUNDING (1/2014 – PRESENT)

S. Emrich (PI) and M. Pfrender, J. Nabrzyski (co-PIs): Replacement of the Notre Dame Bioinformatics data analysis rig, \$98,000 (inc. cost share from the Eck Institute for Global Health and ND Environmental Change Initiative)

N. Besansky and S. Emrich (PIs): Building multi-disciplinary teams for Global Health research and training: “Decoding the Y chromosome of a killer: the African malaria mosquito,” \$24,12, Eck Institute for Global Health.

J. McLachlan and S. Emrich (PIs): “Using ancient DNA to resolve longstanding questions in global change ecology,” \$63,025, ND Environmental Change Initiative

COURSE EXPERIENCE AT U. OF TENN

COSC302/307 Advanced Data Structures and Algorithms, Spring 2019,2020
– Second part of a traditional CS data structures course. Over 80 students.

COSC494/594 Special topic: Bioinformatics Computing, Spring and Fall 2018
– A more graduate student focused of CSE40532 from ND

PRIOR COURSE EXPERIENCE (NOTRE DAME)

CSE40532/60532 Bioinformatics Computing, Fall 2008, 2010, 2012–2013, 2015, 2017
– Developed from scratch. One of the most multidisciplinary classes in CSE with 1/3 Biology, 1/3 CSE grad and 1/3 CSE undergrad.

CSE20312 Data Structures, Spring 2017
– C++ Object-oriented programming look at data structures with a capstone team project

CSE20212 Fundamentals of Computing, 2008–2016
– C++ Object-oriented programming with a capstone team project

- CSE66560 Advanced Bioinformatics Computing, Spring 2012
 – Active learning for bioinformatics algorithms and implementations at a graduate-only level. Developed from scratch.
- BIOS/CSE60132 Basic Computing for Bioinformatics, 2011–2016
 – Introduction to bioinformatics tailored for non-Computer Science majors built based on my and my students’ collaborations by Shawn O’Neil (now at Oregon State doing similar training). Was the highest rated fall CSE class, now taught by BIOS (Stuart Jones)
- CSE40833/60833 Introduction to Parallel Algorithms and Programming, Fall 2007 + 2009
 – Text based on comprehensive lecture notes by Prof. Aluru at ISU, otherwise redeveloped
-

CURRENT GRADUATE STUDENTS

- Ashley Babjac PhD student, joined 2020, EECS@UT
- Katrina Schlum PhD candidate, Genome Science and Technology@UT, joined 2018
- Zhixiu Lu PhD student, joined 2018, EECS@UT
- Rachel Offut MS student, joined 2018, EECS@UT
- Cai John PhD student, joined 2019, Bredescen Center @UT/ORNL
- Gabriel Wright PhD; joined in 2016 (co-advised by Tijana Milenkovic @ND)
- David Molik PhD candidate in IBMS; joined in 2017 (primarily advised by Michael Pfrender @ND)
-

THESES SUPERVISED

- 2019 Shenglong Zhu
 “Algorithms for Assembly Consolidation and Prediction of Large-Scale Genome Structure”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2017 Olivia Choudhury
 “Expediting analysis and improving fidelity of ‘Big Data’ genomics”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2016 RJ Nowling
 “Replacing domain-specific methods in bioinformatics with machine learning techniques”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2015 Lauren Assour
 “Species divergence: Computational methods to explore and resolve biological questions related to the evolution of species”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2014 Irena Lanc
 “Novel methods for assembly validation and improvement”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2013 Andrew Thrasher
 ”Leveraging large-scale distributed systems for massive biological datasets”
 Doctoral Thesis, Computer Science and Engineering, University of Notre Dame

- 2013 Wei Zhang
"Data mining for biological data learning: Algorithms and application"
Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2013 Andrew Rider (co-advised with Nitesh Chawla)
"Data and network science for noisy heterogeneous systems"
Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2013 Rory Carmichael
"Scaling collaborative bioinformatics"
Masters Thesis, Computer Science and Engineering, University of Notre Dame
- 2012 Shawn O'Neil
"Non-model transcriptomics: Applications, assessments, and algorithms"
Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2011 Allison A.P. Regier
"A flexible comparative genomics framework for integrating heterogeneous sequence data"
Doctoral Thesis, Computer Science and Engineering, University of Notre Dame
- 2010 Benjamin Drda
"Hive: an alignment tool for distributed systems"
Honors Thesis. Undergraduate Engineering Honors, University of Notre Dame
- 2009 Michael R. Olson
"New methods for assembly and validation of large genomes"
Master's Thesis, Computer Science and Engineering, University of Notre Dame
- 2008 Allison A.P. Regier
"Challenges in working with draft genomes"
Master's Thesis, Computer Science and Engineering, University of Notre Dame

ALUMNI (GRADUATE AND POSTDOCTORAL*)

- Shenglong Zhu 2016–2019 (now at Amazon in Seattle)
- RJ Nowling 2015– 2017 (now Assistant Professor, Milwaukee School of Engineering)
- Olivia Choudhury 2012 – 2017 (**Eck Global Health fellow**), postdoctoral fellow at IBM
- Lauren Assour 2010 – 2015 (**Naughton Fellow**, coadvised by Ken Wolfe at Trinity College Dublin), works in data-driven finance in Chicago
- Erliang Zeng* 2009-2014 – Former managing director of ND Bioinformatics Core, now Associate Professor at University of Iowa
- Irena Lanc 2009–2014 – faculty researcher at WashU (St. Louis)
- Wei Zhang 2010-2013 – Now at Facebook
- Josh Livermore* 2011-2013 - Environmental Change postdoctoral fellow; now at a biotech firm in Iowa
- Andrew Thrasher 2009–2013 – Senior Software Engineer at St. Jude Children's Research Hospital
- Andrew Rider 2008–2013 (**Global Health Fellow**; coadvised with Nitesh Chawla)
- Rory Carmichael 2011–2012 – Now at QuantCast
- Shawn O'Neil 2009–2012 (**Schmidt Fellow, Global Health Fellow**); currently a non-tenure track teaching and research faculty member at Oregon State

Alison Regier 2007–2011 (**Presidential Fellow**); currently a research scientist at WashU (St. Louis)
Michael Olson 2007–2009 ; currently software architect for CenterX

UNDERGRADUATE RESEARCH ALUMNI

Abigail Prorise 2018–2020
Alex Bahna 2018
Kirolis Shahat 2018
Will Markley 2015–2018; job at Amazon Robotics
Mara Staines 2016–2017; job in financial sector as programmer
Connor Howington Summer 2017 REU (now works on VB)
Chris Ray 2014–2016
Xuanyi (Lexi) Li Fall 2013–2016
Brian Bishop Summer 2016 REU (back at U. of New Hampshire)
Kim Ngo 2014–2015
Nick LaRosa Summer 2012–2015 (MS at Notre Dame, job at start up)
Brian Kachmarck Summer 2010–2012; job at Amazon (Seattle)
Paul Baranay Summer 2010–2012; **NSF Graduate fellow**, doing PhD at Yale
Benjamin Drda 2007–2010; software job at Epic (Madison)

UNIVERSITY SERVICE

University-wide

2011–2017 Co-director, ND Genomics and Bioinformatics Core Facility (GBCF)
2008–2011 Director, NDBioinformatics Core Facility (BCF)

Departmental Committees

2007–2010 CSE@ND Graduate Studies Committee
2008–2017 CSE@ND Curriculum Committee (mostly undergrad-focused)
2006 BCB Graduate Curriculum Committee, which redesigned the PhD core curriculum in bioinformatics and computational biology at Iowa State University.

Student Committees

CSE: Scott Christley (2008 PhD), Chris Moretti (2010 PhD), Ryan Kennedy (2010 PhD), Darcy Davis (2011 PhD), Ryan Connaughton (2011 PhD), Peter Bui (2012 PhD), Hoang Bui (2012 PhD), James Gentile (2013 PhD), Li Yu (2014 PhD), Dinesh Rajan (2015 PhD), Patrick Donnelly (2016 PhD), Fattaneh Bayatbabolghani (2017 PhD)
Biology: Upeka Samaroon (2012 PhD), Jenica Abrudan (2013 PhD), Changde Cheng (2014 PhD), Masha Unger (2014 PhD), Candice Lumibao (2014 PhD), Sheri Sanders (2016 PhD), Rachel Love (2017 PhD), Yiyuan Li (2018 PhD)

PROFESSIONAL MEMBERSHIPS

International Society for Computational Biology (ISCB)

Association for Computing Machinery (ACM)

EXTERNAL SERVICE ACTIVITIES

Journal Editorial Boards

2017–present Associate editor, *PeerJ*

2013–present Associate editor, *BMC Genomics*

Grant proposal reviewing

2009, 2011, 2012 ad hoc, NSF BIOS directorate

2015, 2017 Panelist, NSF BIOS directorate

2019 Panelist, NSF CISE directorate

Steering Committee Member

2010–2017 Arthropod Genomics Symposium

Program Chair

2016 Program Co-chair
6th IEEE International Conference on Computational Advances in Bio and Medical Sciences, Atlanta, GA.

2013 Sequence Analysis Co-chair
ACM Conference on Bioinformatics, Computational Biology, and Biomedical Informatics, Washington DC.

2012 Emerging Computational Methods for the Life Sciences Workshop
ACM Symposium on High-Performance Parallel and Distributed Computing (HPDC)

2011 Parallel Bio-Computing Workshop
International Conference on Parallel Processing and Applied Mathematics

Program Committee Member

2011–2018 IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS)

2009–2018 International Conference on Bioinformatics and Computational Biology (BiCoB)

2010–2012 IEEE International Conference on Cloud Computing Technology and Science (CloudCom)

2009–2012 Using Emerging Parallel Architectures for Computation Science Workshop
International Conference on Computational Science

2011, 2013, 2016, 2017 ACM Conference on Bioinformatics, Computational Biology and Biomedicine

2011 ACM Symposium on High-Performance Parallel and Distributed Computing (HPDC)

- 2010 Workshop on Parallel Programming and Applications on Accelerator Clusters, IEEE Cluster
- 2007–2011 Parallel Bio-Computing Workshop
International Conference on Parallel Processing and Applied Mathematics
- 2009, 2011 International Conference on Contemporary Computing, Applications
- 2008-2009 IEEE/ACM Supercomputing (SC), Applications
- 2008, 2013 HICOMB Workshop, IEEE International Parallel and Distributed Processing Symposium (IPDPS)

Tutorials

- 2007 Computational Problems in Maize Genomics
International Conference on Computational Systems Bioinformatics (CSB)
- 2006 Exploring Computational Biology with a Massively Parallel
High Performance Computing Environment
International Conference on Intelligent Systems for Molecular Biology (ISMB)

Recent reviewer for the following journals: (roughly past year)

Nature

IEEE/ACM Transactions on Computational Biology and Bioinformatics

Bioinformatics

PLoS One

Nucleic Acids Research

BMC Bioinformatics