

Bernie Joseph Daigle, Jr.

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EDUCATION	Ph.D., Genetics <i>Stanford University, Stanford, CA</i> GPA: 4.086 Advisor: Russ B. Altman Thesis: "Using Heterogeneous Sources of Biological Knowledge to Improve the Identification of Differentially Expressed Genes."	January 2010
	B.S., Biology, <i>summa cum laude</i> <i>Cornell University, Ithaca, NY</i> GPA: 4.033 Advisor: Bik Tye Thesis: "Production and Purification of Mcm5p and Investigation of Its Potential Role in Transcriptional Regulation."	May 2002
PROFESSIONAL EXPERIENCE	The University of Memphis, Memphis, TN <i>Associate Professor</i> Departments of Biological Sciences and Computer Science <i>Assistant Professor</i> Departments of Biological Sciences and Computer Science	2021-present 2015-2021
	University of California, Santa Barbara, Santa Barbara, CA <i>Assistant Researcher (Professional Research Series)</i> Institute for Collaborative Biotechnologies <i>Postdoctoral Researcher, Petzold Research Group</i> Department of Computer Science	2011-2015 2009-2011
	Stanford University, Stanford, CA <i>Graduate Student, Altman Research Group</i> Department of Bioengineering <i>Rotation Student, Kay Research Group</i> Department of Genetics	2003-2009 Winter 2003
	Cornell University, Ithaca, NY <i>Undergraduate Student, Tye Research Group</i> Department of Molecular Biology and Genetics	2000-2002
	Allegheny-Singer Research Institute, Pittsburgh, PA <i>Undergraduate Intern, Center for Genomic Sciences</i>	Summers 1999,2000,2002
GRANTS AND FELLOWSHIPS	<ul style="list-style-type: none"><i>U.S. Department of Defense (subcontract through NYU)</i> "Advancing Precision Psychiatry for Military Service-Related PTSD by Enhancing Knowledge of Clinical Subtypes and their Endophenotypes" (\$640,999; Role: PI)<i>UofM FedEx Institute of Technology</i>	2022-2026 2022

- “Accelerated reconstruction of regulatory networks underlying human disease”
(\$2,750; Role: PI)
- *U.S. Army Research Office* Summer 2020
“Identification of Prognostic and Diagnostic Biomarkers for PTSD”
(\$7,500; Role: PI)
 - *UofM FedEx Institute of Technology* 2020
“Optimizing biological network inference using deep learning”
(\$1,750; Role: PI)
 - *UofM College of Arts & Sciences* 2019-2020
“High-Speed Regulatory Network Inference Using Deep Neural Networks”
(\$10,000; Role: PI)
 - *U.S. Army Research Office* Summer 2019
“Identification of Robust Biomarkers for Posttraumatic Stress Disorder Using Longitudinal Analysis”
(\$6,458; Role: PI)
 - *UofM FedEx Institute of Technology* 2019
“Preliminary Study of a Novel Unbiased Machine Learning Approach, Hybrid Clustering with Multi-Dimensional Vectors”
(\$13,018; Role: co-I)
 - *UofM Division of Research and Innovation* 2019
“Community of Research Scholars: Synthesis of Research and Teaching Practices with the UofM High Performance Computer”
(\$2,500; Role: co-I)
 - *U.S. Army Research Office* Summer 2018
“Identifying Prognostic Biomarkers for Posttraumatic Stress Disorder”
(\$6,561; Role: PI)
 - *U.S. Army Research Laboratory* 2017-2023
“Knowledge-Driven Multi-omic Biomarker Identification for Posttraumatic Stress Disorder”
(\$485,239; Role: PI)
 - *Leidos Biomedical Research, Inc.* Winter 2017
“Gene Expression and DNA Methylation Biomarker Identification for Posttraumatic Stress Disorder”
(\$12,013; Role: PI)
 - *Leidos Biomedical Research, Inc.* Summer 2016
“Multi-omic Biomarker Identification for Posttraumatic Stress Disorder”
(\$29,766; Role: PI)
 - *Army Research Office* 2014-2015
“A Systems Approach to Understanding Post-Traumatic Stress Disorder”
(\$1,500,000; Role: co-PI)
 - *National Library of Medicine* 2008-2009
Biomedical Informatics Research Training Fellowship
 - *Howard Hughes Medical Institute* 2003-2008
Predoctoral Research Fellowship
 - *Stanford University* 2002-2005
Geraldine Jackson Fuhrman Predoctoral Fellowship
 - *Cornell University* Summer 2001
Hughes Scholars Program Research Fellowship

HONORS AND AWARDS	• CAS Travel Enrichment Award, The University of Memphis	2023
	• NSF MODULUS Conference Travel Award, George Mason University	2022
	• CAS Early Career Research Award, The University of Memphis	2018
	• Child Care Grant, SIAM Conference on the Life Sciences	2018
	• CAS Travel Enrichment Award, The University of Memphis	2018
	• Steve Hsia Biomedical Paper Award, WCICA Conference	2012
	• NSF Travel Award, MCQMC Conference	2012
	• SAMSI Travel Award, Uncertainty Quantification Workshop	2011
	• MSRI Travel Award, BIRS Biochemical Stochasticity Workshop	2011
	• Los Alamos National Laboratory Scholarship, q-bio Summer School	2009
	• AAAS/Science Award, Program for Excellence in Science	2009
	• DOE Travel Award, Pacific Symposium on Biocomputing Conference	2005

PEER-REVIEWED JOURNAL ARTICLES **Total Citations: 1250** **h-index: 15** **i10-index: 19**

1. Kathryn M. Parsley, Bernie J Daigle Jr, and Jaime L. Sabel. Initial Development and Validation of the Plant Awareness Disparity Index. *CBE—Life Sciences Education*, 21(4):ar64, December 2022. Publisher: American Society for Cell Biology (lse).
2. Sohini Banerjee, Mazen Istanbouli, and Bernie J Daigle Jr. Post-Traumatic Stress Disorder (PTSD) biomarker identification using a deep learning model. *Journal of Emerging Investigators*, 5:1–8, September 2022.
3. Gwyneth W. Y Wu, Owen M. Wolkowitz, Victor I. Reus, Jee In Kang, Mathea El-nar, Reuben Sarwal, Janine D. Flory, Duna Abu-Amara, Rasha Hammamieh, Aarti Gautam, Francis J. Doyle, Rachel Yehuda, Charles R. Marmar, Marti Jett, Synthia H. Mellon, Kerry J. Ressler*, Ruoting Yang*, Seid Muhie*, Bernie J Daigle Jr*, Linda M. Bierer*, Leroy Hood*, Kai Wang*, Inyoul Lee*, Kelsey R. Dean*, and Pramod R. Somvanshi*. Serum brain-derived neurotrophic factor remains elevated after long term follow-up of combat veterans with chronic post-traumatic stress disorder. *Psychoneuroendocrinology*, page 105360, Jul 2021. *As member of SBPBC.
4. Carole E. Siegel, Eugene M. Laska, Ziqiang Lin, Mu Xu, Duna Abu-Amara, Michelle K. Jeffers, Meng Qian, Nicholas Milton, Janine D. Flory, Rasha Hammamieh, Bernie J Daigle Jr, Aarti Gautam, Kelsey R. Dean, Victor I. Reus, Owen M. Wolkowitz, Synthia H. Mellon, Kerry J. Ressler, Rachel Yehuda, Kai Wang, Leroy Hood, Francis J. Doyle, Marti Jett, and Charles R. Marmar. Utilization of machine learning for identifying symptom severity military-related PTSD subtypes and their biological correlates. *Translational Psychiatry*, 11(1):1–12, Apr 2021.
5. Liangqun Lu, Kevin A. Townsend, and Bernie J Daigle Jr. GEOLimma: differential expression analysis and feature selection using pre-existing microarray data. *BMC Bioinformatics*, 22(1):44, Feb 2021.
6. Ruoting Yang, Aarti Gautam, Derese Getnet, Bernie J Daigle Jr, Stacy Miller, Burook Misganaw, Kelsey R. Dean, Raina Kumar, Seid Muhie, Kai Wang, Inyoul Lee, Duna Abu-Amara, Janine D. Flory, Leroy Hood, Owen M. Wolkowitz, Synthia H. Mellon, Francis J. Doyle, Rachel Yehuda, Charles R. Marmar, Kerry J. Ressler, Rasha Hammamieh, and Marti Jett. Epigenetic biotypes of post-traumatic stress disorder in war-zone exposed veteran and active duty males. *Molecular Psychiatry*, 26:4300–4314, Dec 2020.

7. Jee In Kang, Susanne G. Mueller, Gwyneth W. Y. Wu, Jue Lin, Peter Ng, Rachel Yehuda, Janine D. Flory, Duna Abu-Amara, Victor I. Reus, Aarti Gautam, Leroy Hood*, Kerry J. Ressler*, Daniel Lindqvist*, Ji Hoon Cho*, Michelle Coy*, Frank Desarnaud*, Saverio Bersani*, Silvia Fossati*, Allison Hoke*, Raina Kumar*, Meng Li*, Iouri Makotkine*, Stacy-Ann Miller*, Linda Petzold*, Laura Price*, Meng Qian*, Kelsey Scherler*, Seshamalini Srinivasan*, Anna Suessbrick*, Li Tang*, Xiaogang Wu*, David Baxter*, Esther Blessing*, Kelsey R. Dean*, Bernie J Daigle Jr*, Guia Guffanti*, Kai Wang*, Lynn M. Almli*, F. Nabarun Chakraborty*, Duncan Donohue*, Kimberly Kerley*, Taek-Kyun Kim*, Eugene Laska*, Inyoul Lee*, Min Young Lee*, Adriana Lori*, Liangqun Lu*, Burook Misganaw*, Seid Muhie*, Jennifer Newman*, Nathan Price*, Shizhen Qin*, Carole Siegel*, Pramod R. Somvanshi*, Gunjan S. Thakur*, Young Zhou*, Ruoting Yang*, Rasha Hammamieh, Francis J. Doyle, Marti Jett, Charles R. Marmar, Synthia H. Mellon, and Owen M. Wolkowitz. Effect of combat exposure and posttraumatic stress disorder on telomere length and amygdala volume. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, 5(7):678–687, Jul 2020. *As member of PTSD Systems Biology Consortium.
8. Liangqun Lu and Bernie J Daigle Jr. Prognostic analysis of histopathological images using pre-trained convolutional neural networks: Application to hepatocellular carcinoma. *PeerJ*, 8:e8668, March 2020.
9. Vinhthuy Phan, Diem-Trang Pham, Caroline Melton, Adam J. Ramsey, Bernie J Daigle Jr, and Jennifer R. Mandel. icHET: Interactive visualization of cytoplasmic heteroplasmy. *Bioinformatics*, 35(21):4411–4412, November 2019.
10. Kelsey R. Dean, Rasha Hammamieh, Synthia H. Mellon, Duna Abu-Amara, Janine D. Flory, Guia Guffanti, Kai Wang, Bernie J Daigle Jr, Aarti Gautam, Inyoul Lee, Ruoting Yang, Lynn M. Almli, F. Saverio Bersani, Nabarun Chakraborty, Duncan Donohue, Kimberly Kerley, Taek-Kyun Kim, Eugene Laska, Min Young Lee, Daniel Lindqvist, Adriana Lori, Liangqun Lu, Burook Misganaw, Seid Muhie, Jennifer Newman, Nathan D. Price, Shizhen Qin, Victor I. Reus, Carole Siegel, Pramod R. Somvanshi, Gunjan S. Thakur, Yong Zhou, Leroy Hood, Kerry J. Ressler, Owen M. Wolkowitz, Rachel Yehuda, Marti Jett, Francis J. Doyle, and Charles Marmar. Multi-omic biomarker identification and validation for diagnosing warzone-related post-traumatic stress disorder. *Molecular Psychiatry*, pages 1–13, September 2019.
11. Pramod R. Somvanshi, Synthia H. Mellon, Janine D. Flory, Duna Abu-amara, Rasha Hammamieh*, Aarti Gautam*, Kai Wang*, Inyoul Lee*, Bernie J Daigle Jr*, Ruoting Yang*, Owen M. Wolkowitz, Rachel Yehuda, Marti Jett, Leroy Hood, Charles Marmar, and Francis J. Doyle. Mechanistic inferences on metabolic dysfunction in PTSD from an integrated model and multi-omic analysis: Role of glucocorticoid receptor sensitivity. *American Journal of Physiology-Endocrinology and Metabolism*, July 2019. *As member of PTSD Systems Biology Consortium.
12. Burook Misganaw, Guia Guffanti, Adriana Lori, Duna Abu-Amara, Janine D. Flory, Rasha Hammamieh*, Aarti Gautam*, Ruoting Yang*, Bernie J Daigle Jr*, Leroy Hood*, Kai Wang*, Inyoul Lee*, Synthia H. Mellon*, Owen M. Wolkowitz*, Susanne Mueller, Rachel Yehuda, Marti Jett, Charles R. Marmar, Kerry J. Ressler, and Francis J. Doyle. Polygenic risk associated with post-traumatic stress disorder onset and severity. *Translational Psychiatry*, 9(1):1–8, June 2019. *As member of SBPBC.
13. Rasha Hammamieh, Nabarun Chakraborty, Aarti Gautam, Seid Muhie, Ruoting Yang, Duncan Donohue, Raina Kumar, Bernie J Daigle Jr, Yuanyang Zhang, Duna Abu-Amara, Stacy-Ann Miller, Seshmalini Srinivasan, Janine Flory, Rachel Yehuda, Linda Petzold, Owen M. Wolkowitz, Synthia H. Mellon, Leroy Hood, Francis J.

- Doyle III, Charles Marmar, and Marti Jett. Whole-genome DNA methylation status associated with clinical PTSD measures of OIF/OEF veterans. *Translational Psychiatry*, 7(7):e1169, July 2017.
14. Brian Drawert, Andreas Hellander, Ben Bales, Debjani Banerjee, Giovanni Bellesia, Bernie J Daigle Jr, Geoffrey Douglas, Mengyuan Gu, Anand Gupta, Stefan Hellander, Chris Horuk, Dibyendu Nath, Aviral Takkar, Sheng Wu, Per Lötstedt, Chandra Krintz, and Linda R. Petzold. Stochastic Simulation Service: Bridging the Gap between the Computational Expert and the Biologist. *PLOS Computational Biology*, 12(12):e1005220, December 2016.
 15. Min K. Roh and Bernie J Daigle Jr. SParse++: Improved event-based stochastic parameter search. *BMC Systems Biology*, 10:109, November 2016.
 16. Gunjan S Thakur, Bernie J Daigle Jr, Meng Qian, Kelsey R Dean, Yuanyang Zhang, Ruoting Yang, Taek-Kyun Kim, Xiaogang Wu, Meng Li, Inyoul Lee, Linda R Petzold, and Francis J Doyle III. A Multi-Metric Evaluation of Stratified Random Sampling for Classification: A Case Study. *IEEE Life Sciences Letters*, PP(99):1–1, October 2016.
 17. Yuanyang Zhang, Tie Bo Wu, Bernie J Daigle Jr, Mitchell Cohen, and Linda Petzold. Identification of disease states associated with coagulopathy in trauma. *BMC Medical Informatics and Decision Making*, 16:124, September 2016.
 18. Bernie J Daigle Jr, Mohammad Soltani, Linda R Petzold, and Abhyudai Singh. Inferring single-cell gene expression mechanisms using stochastic simulation. *Bioinformatics*, 31(9):1428–35, May 2015.
 19. Gunjan S Thakur, Bernie J Daigle Jr, Kelsey R Dean, Yuanyang Zhang, Maria Rodriguez-Fernandez, Rasha Hammamieh, Ruoting Yang, Marti Jett, Joseph Palma, Linda R Petzold, and Francis J Doyle Iii. Systems biology approach to understanding post-traumatic stress disorder. *Mol Biosyst*, 11(4):980–93, Mar 2015. **Cover Article.**
 20. Ruoting Yang*, Bernie J Daigle Jr*, Seid Y Muhie, Rasha Hammamieh, Marti Jett, Linda R Petzold, and Francis J Doyle III. Core modular blood and brain biomarkers in social defeat mouse model for post traumatic stress disorder. *BMC Syst Biol*, 7:80, Aug 2013. *Contributed equally.
 21. Robin E White, Curtis J Palm, Lijun Xu, Evelyn B Ling, Mitchell Ginsburg, Bernie J Daigle Jr, Ruquan Han, Andrew J Patterson, Russ B Altman, and Rona G Giffard. Mice lacking the 2 adrenergic receptor have a unique genetic profile before and after focal brain ischemia. *ASN Neuro*, Aug 2012.
 22. Bernie J Daigle Jr, Min K Roh, Linda R Petzold, and Jarad Niemi. Accelerated maximum likelihood parameter estimation for stochastic biochemical systems. *BMC Bioinformatics*, 13(1):68, May 2012.
 23. Ruoting Yang*, Bernie J Daigle Jr*, Linda R Petzold, and Francis J Doyle III. Core module biomarker identification with network exploration for breast cancer metastasis. *BMC Bioinformatics*, 13:12, Jan 2012. *Contributed equally. **Highly accessed article on BioMed Central.**
 24. Min K Roh*, Bernie J Daigle Jr*, Dan T Gillespie, and Linda R Petzold. State-dependent doubly weighted stochastic simulation algorithm for automatic characterization of stochastic biochemical rare events. *J Chem Phys*, 135(23):234108, Dec 2011. *Contributed equally. **Featured as a Research Highlight by J Chem Phys.**
 25. Bernie J Daigle Jr*, Min K Roh*, Dan T Gillespie, and Linda R Petzold. Automated estimation of rare event probabilities in biochemical systems. *J Chem Phys*,

134(4):044110, Jan 2011. *Contributed equally. **Featured in *Virtual Journal of Biological Physics Research*.**

26. Jesse M Engreitz, Bernie J Daigle Jr, Jonathan J Marshall, and Russ B Altman. Independent component analysis: Mining microarray data for fundamental human gene expression modules. *J Biomed Inform*, 43(6):932–44, Dec 2010.
27. Bernie J Daigle Jr, Alicia Deng, Tracey McLaughlin, Samuel W Cushman, Margaret C Cam, Gerald Reaven, Philip S Tsao, and Russ B Altman. Using pre-existing microarray datasets to increase experimental power: application to insulin resistance. *PLoS Comput Biol*, 6(3):e1000718, Mar 2010. **Faculty of 1000 Recommended article.**
28. Bernie J Daigle Jr and Russ B Altman. M-bison: microarray-based integration of data sources using networks. *BMC Bioinformatics*, 9:214, 2008. **Highly accessed article on BioMed Central.**
29. Garth D Ehrlich, Richard Veeh, Xue Wang, J William Costerton, Jay D Hayes, Fen Ze Hu, Bernie J Daigle Jr, Miles D Ehrlich, and J Christopher Post. Mucosal biofilm formation on middle-ear mucosa in the chinchilla model of otitis media. *JAMA*, 287(13):1710–1715, Apr 2002.

PEER-REVIEWED
CONFERENCE
PROCEEDINGS

1. Yuanyang Zhang, Bernie J Daigle Jr, Mitchell Cohen, and Linda R. Petzold. A Cure Time Model for Joint Prediction of Outcome and Time-to-Outcome. In *2015 IEEE International Conference on Data Mining (ICDM)*, pages 1117–1122, November 2015.
2. Gunjan S Thakur, Bernie J Daigle Jr, Kelsey Dean, Linda R Petzold, and Francis J Doyle III. Metric focused feature selection for customized biomarker identification. In *The Fifth International Conference on Foundations of Systems Biology in Engineering (FOSBE 2015)*, Aug 2015.
3. Yuanyang Zhang, Bernie J Daigle Jr, Lisa Ferrigno, Mitchell Cohen, and Linda Petzold. Data-driven mortality prediction for trauma patients. Selected for presentation at the *Machine Learning in Computational Biology workshop (MLCB 2014) in the Twenty-eighth Annual Conference on Neural Information Processing Systems (NIPS 2014)*, Dec 2014.
4. Gunjan S Thakur, Bernie J Daigle Jr, Linda R Petzold, and Francis J Doyle III. A multivariate ensemble approach for identification of biomarkers: application to breast cancer. In *The 19th World Congress of the International Federation of Automatic Control (IFAC)*, pages 809–814, Aug 2014.
5. Ruoting Yang, Bernie J Daigle Jr, Linda R Petzold, and Francis J Doyle III. Core module network construction for breast cancer metastasis. In *10th World Congress on Intelligent Control and Automation (WCICA)*, pages 5083–5089, Jul 2012. **Received Steve Hsia Biomedical Paper Award.**

ABSTRACTS

- Liangqun Lu and Bernie J Daigle Jr. Multi-Omic PTSD Subgroup Identification and Clinical Characterization. *Biological Psychiatry*, 87(9):S9, May 2020.
- Ruoting Yang, Aarti Gautam, Derese Getnet, Bernie J Daigle Jr, Stacy Ann Miller, Kelsey Dean, Seid Muhie, Kai Wang, Inyoul Lee, Duna Abu Amara, Janine D. Flory, Leroy Hood, Owen Wolkowitz, Synthia Mellon, Francis J. Doyle, Rachel Yehuda, Charles Marmar, Kerry Ressler, Rasha Hammamieh, and Marti Jett. Epigenetic Biotypes of PTSD in War-Zone Exposed Veteran and Active Duty Males. *Biological Psychiatry*, 87(9):S8–S9, May 2020.

- Rasha Hammamieh, Aarti Gautam, Nabarun Chakraborty, Seid Muhie, Ruoting Yang, Duncan Donohue, Bernie J Daigle Jr, Yuanyang Zhang, Duna Abu Amara, Janine Flory, Rachel Yehuda, Linda Petzhold, Frank Doyle, Charles Marmar, and Marti Jett. 229. A Cohort Study of OIF/OEF Veterans: A Blood Epigenomic Assessment. *Biological Psychiatry*, 85(10):S95, May 2019.
- Eric C. Rouchka, Julia H. Chariker, David A. Tieri, Juw Won Park, Shreedharkumar Rajurkar, Vikas Singh, Nishchal K. Verma, Yan Cui, Mark Farman, Bradford Condon, Neil Moore, Jerzy Jaromczyk, Jolanta Jaromczyk, Daniel Harris, Patrick Calie, Eun Kyong Shin, Robert L. Davis, Arash Shaban-Nejad, Joshua M. Mitchell, Robert M. Flight, Qing Jun Wang, Richard M. Higashi, Teresa W-M Fan, Andrew N. Lane, Hunter N. B. Moseley, Liangqun Lu, Bernie J Daigle Jr, et al. Proceedings of the 16th Annual UT-KBRIN Bioinformatics Summit 2016: Bioinformatics. *BMC Bioinformatics*, 18(9):377, October 2017.
- Eric C. Rouchka, Julia H. Chariker, Benjamin J. Harrison, Juw Won Park, Xueyuan Cao, Stanley Pounds, Susana Raimondi, James Downing, Raul Ribeiro, Jeffery Rubnitz, Jatinder Lamba, Bernie J Daigle Jr, et al. Proceedings of the 15th Annual UT-KBRIN Bioinformatics Summit 2016. *BMC Bioinformatics*, 17(10):297, August 2016.
- Nabarun Chakraborty, Seid Muhie, Ruoting Yang, Aarti Gautam, Duncan Donohue, Bernie J Daigle Jr, Yuanyang Zhang, Duna Abu Amara, Jannie Flory, Rachel Yehuda, Frank Doyle, Rasha Hammamieh, Charles Marmar, and Marti Jett. Characterization of the Epigenomic Status of the US OEF/OIF War Veterans: A Pilot Clinical Study. *The FASEB Journal*, 30(1 Supplement):831.3–831.3, January 2016.
- Linda Petzold, Yuanyang Zhang, Bernie J Daigle Jr, Lisa Ferrigno, and Mitch Cohen. Toward a data-driven model of trauma dynamics. *Journal of Critical Care*, 28(6):e37, Dec 2013.
- Stephen R Yant, Xiaolin Wu, Yong Huang, Bernie J Daigle Jr, Brian A Garrison, Shawn M Burgess, and Mark A Kay. Nonrandom insertion site preferences for the sb transposon in vitro and in vivo. *Molecular Therapy*, 9:S309–S310, Jan 2004.
- Stephen R Yant, Brian Garrison, Bernie J Daigle Jr, and Mark A Kay. Analysis of target site selection for the sleeping beauty transposon in mouse liver. *Molecular Therapy*, 7(5):S63–S63, Jan 2003.

BOOK CHAPTERS

- Bernie J Daigle Jr. Bayesian Parameter Estimation and Markov Chain Monte Carlo. In *Quantitative Biology: Theory, Computational Methods, and Models*, pages 339–355. MIT Press, 2018.
- Bernie J Daigle Jr*, Balaji S Srinivasan*, Jason A Flannick, Antal F Novak, and Serafim Batzoglou. *Systems Biology for Signaling Networks*, volume 1 of *Systems biology*, chapter in Current Progress in Static and Dynamic Modeling of Biological Networks, pages 13–74. Springer, New York, 1st edition, 2010. *Contributed equally.

TUTORIALS AND LECTURES

- “Stochastic Simulation of Biochemical Systems.” *Invited lecture*, MATH 3410/1: Honors Seminar in Math, The University of Memphis, Memphis, TN, Sep 24, 2021.
- “Systems Biology Approaches to Disease Biomarker Discovery.” PUBH 7/8153: Biostatistics in Bioinformatics, The University of Memphis, Memphis, TN, April 6, 2021.
- “Increasing Experimental Power with Knowledge-Guided Integration of Biological Datasets.” PUBH 7/8153: Biostatistics in Bioinformatics, The University of Memphis, Memphis, TN, April 7, 2020.

- “Inferring Gene Expression Mechanisms from Single-Cell RNA-Seq Data.” BINF 7980: Research Seminar in Bioinformatics, The University of Memphis, Memphis, TN, Oct 19, 2018.
- “Increasing Experimental Power with Knowledge-Guided Integration of Biological Datasets.” PUBH 7/8153: Biostatistics in Bioinformatics, The University of Memphis, Memphis, TN, Mar 27, 2018.
- “Characterizing Biochemical Rare Events Using Stochastic Simulation.” BINF 7980: Research Seminar in Bioinformatics, The University of Memphis, Memphis, TN, Nov 17, 2017.
- “Meet the Scientist.” *Invited lecture*, Graduate Women in Science, The University of Memphis, Memphis, TN, Apr 7, 2017.
- “Stochastic Simulation of Biochemical Systems.” *Invited lecture*, MATH 3410/1: Honors Seminar in Math, The University of Memphis, Memphis, TN, Nov 16, 2016.
- “Computational Inference of Single-Cell Biological Mechanisms.” BINF 7980: Research Seminar in Bioinformatics, The University of Memphis, Memphis, TN, Oct 28, 2016.
- “Efficient Characterization of Rare Events in Biochemical Systems.” *Invited lecture*, Machine Learning Journal Club, The University of Memphis, Memphis, TN, Mar 18, 2016.
- “Efficient Characterization of Biological Rare Events.” *Invited lecture*, Bio 291C: Exploring BioMath, St. Olaf College, Northfield, MN, May 8, 2014.
- “A Tutorial for Using R/Bioconductor to Perform DNA Microarray Analysis.” UCSB NSF-IGERT systems biology seminar series, Santa Barbara, CA, Jan 31, 2011.
- “Microarray data preprocessing and differential expression analysis.” *Invited lecture*, ARL/ICB Crash Course in Systems Biology, Lawrence Berkeley National Laboratory, Berkeley, CA, Aug 10, 2010.

INVITED TALKS

- “Multi-omics Approaches to PTSD Biomarker Discovery.” Department of Genetics, Genomics, and Informatics, The University of Tennessee Health Science Center, Memphis, TN, May 20, 2022.
- “Systems Biology Approaches to Disease Biomarker Discovery.” Department of Biological Sciences, The University of Memphis, Memphis, TN, September 3, 2020.
- “Integration of microRNA-mRNA Interaction Networks with Transcriptomics Data to Increase Experimental Power.” Data Management Symposium, The University of Tennessee Health Science Center, Memphis, TN, April 15, 2019.
- “Inferring Gene Expression Mechanisms from Single-Cell RNA-Seq Data.” Department of Biomedical Engineering, The University of Memphis, Memphis, TN, April 12, 2019.
- “Maximum Likelihood Parameter Estimation and Model Identification from Single-Cell Distribution Data.” Division of Biostatistics, Department of Preventive Medicine, The University of Tennessee Health Science Center, Memphis, TN, April 8, 2019.
- “Bayesian Network-Based Integration of High-Dimensional Biological Data to Increase Experimental Power.” International Conference on Mathematics and Statistics (ICOMAS 2018), The University of Memphis, Memphis, TN, May 9, 2018.
- “MLE to ABC: Parameter Estimation for Stochastic Biochemical Systems.” Seminar Program in Scientific Computing, Department of Information Technology, Uppsala University, Uppsala, Sweden, September 13, 2017.

- “Computational Inference of Single-Cell Gene Expression Mechanisms.” Memphis Mathematical Biology Seminar, St. Jude Children’s Research Hospital, Memphis, TN, May 11, 2017.
- “Inferring Single-Cell Biochemical Mechanisms Using Stochastic Simulation.” Department of Microbiology, Immunology, and Biochemistry, The University of Tennessee Health Science Center, Memphis, TN, May 8, 2017.
- “Knowledge-Guided Integration of Biological Datasets to Increase Experimental Power.” Department of Microbiology and Immunology, Drexel University College of Medicine, Philadelphia, PA, October 12, 2016.
- “Increasing Experimental Power by Integrating Heterogeneous Biological Datasets.” Computer Science Colloquium, The University of Memphis, Memphis, TN, February 5, 2016.
- “Integrating Heterogeneous Microarray Datasets to Increase Experimental Power.” Department of Biological Sciences, The University of Memphis, Memphis, TN, February 9, 2015.
- “Inferring Single-Cell Biological Mechanisms Using Stochastic Simulation.” Sanford-Burnham Medical Research Institute, La Jolla, CA, May 14, 2014.
- “Stochastic Simulation-Based Methods for Inferring Biological Mechanisms.” Department of Mathematics, Statistics, and Computer Science, St. Olaf College, Northfield, MN, May 9, 2014.
- “Inferring Single-Cell Biological Mechanisms Using Stochastic Simulation.” Computer Science and Engineering Department, University of Connecticut, Storrs, CT, April 25, 2014.
- “Inferring Single-Cell Biological Mechanisms Using Stochastic Simulation.” Department of Systems & Computational Biology, Albert Einstein College of Medicine, Bronx, NY, April 2, 2014.

SELECTED ORAL
PRESENTATIONS

- “Multi-omic PTSD Subgroup Identification and Clinical Characterization.” *Selected for Presentation* at the Society of Biological Psychiatry (SOBP) Virtual Symposium, May 26, 2020.
- “Efficient Maximum Likelihood Model Identification and Parameter Inference from Single-Cell Distribution Data.” *Selected for Presentation* at the Society for Industrial and Applied Mathematics (SIAM) Conference on the Life Sciences, Minneapolis, MN, Aug 7, 2018.
- “Integration of microRNA-mRNA Interaction Networks with Microarray Data to Increase Experimental Power.” *Selected for Presentation* at the 13th Annual Mid-South Computational Biology and Bioinformatics Society (MCBIOS) Conference, Memphis, TN, Mar 3, 2016.
- “Increasing Experimental Power by Integrating microRNA-mRNA Interaction Networks with Microarray Data.” *Selected for Presentation* at The Fourth Annual Winter q-bio Meeting, Honolulu, HI, Feb 16, 2016.
- “Efficient Estimation of Rare Event Probabilities in Biochemical Systems.” *Selected for Presentation* at the Tenth International Conference on Monte Carlo and Quasi-Monte Carlo Methods in Scientific Computing (MCQMC 2012), Sydney, Australia, Feb 13, 2012.
- “Efficient Biochemical Parameter Estimation Using Rare Event Simulation Techniques.” The Third International Workshop on Stochasticity in Biochemical Reaction Networks, Banff, Canada, Sep 16, 2011.

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- “Accelerated Maximum Likelihood Estimation for Stochastic Biochemical Systems.” *Selected for Presentation* at The Fifth Annual q-bio Conference on Cellular Information Processing, Santa Fe, NM, Aug 13, 2011.
 - “An information-theoretic approach to improve the estimation of rare event probabilities in biochemical systems.” *Selected for Presentation* at the 11th International Conference on Systems Biology (ICSB 2010), Edinburgh, UK, Oct 11, 2010.
- SELECTED
POSTER
PRESENTATIONS
- Sohini Banerjee, Mazen Istambouli, Bernie J Daigle Jr. Post-Traumatic Stress Disorder (PTSD) Biomarker Identification using Integrative Network Fusion and Deep Learning with Bayesian Hyperparameter Optimization. *Poster session at the 18th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference*, virtual, Apr 2022.
 - Mazen Istambouli, Kristoffer S. Berlin, Bernie J Daigle Jr. Structural Equation Modeling of Neuroendocrine and Clinical PTSD Measures. *Poster session at the 17th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference*, virtual, Apr 2021. **Winner, 2nd prize in undergraduate/graduate student category.**
 - Ted Ling Hu, Bernie J Daigle Jr. Singular Value Decomposition: Data-Driven Feature Selection for Transcriptomics Data Sets. *Poster session at the Memphis DATA Conference*, Memphis, TN, Mar 2019.
 - Mazen Istambouli, Bernie J Daigle Jr. Multi-Omics Biomarker Discovery for PTSD. *Poster session at the 16th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference*, Birmingham, AL, Mar 2019.
 - Liangqun Lu, Bernie J Daigle Jr. Clinical Subgroup-Specific PTSD Classification and Biomarker Discovery. *Poster session at the Big Data in Precision Health Conference*, Stanford, CA, May 2018.
 - Pulin Agrawal, Bernie J Daigle Jr. Characterization and Classification of Gene Expression Data with Sparse Autoencoders. *Poster session at the 15th Annual Mid-South Computational Biology and Bioinformatics Society (MCBIOS) Conference*, Starkville, MS, Mar 2018.
 - Liangqun Lu, Bernie J Daigle Jr. Large-scale Microarray Data Based Feature Selection for Improved Molecular Classification. *Poster session at the UT-KBRIN Bioinformatics Summit*, Burns, TN, Apr 2017.
 - Caroline E. Melton, Jennifer R. Mandel, Bernie J Daigle Jr. Identifying Heteroplasmy in *D. carota* Using Whole Genome Shotgun Sequencing Without Known Variants. *Poster session at the 14th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference*, Little Rock, AR, Mar 2017.
 - Bernie J Daigle Jr. Integration of microRNA-mRNA Interaction Networks with Gene Expression Data to Increase Experimental Power. *Poster session at the UT-KBRIN Bioinformatics Summit*, Cadiz, KY, Apr 2016.
 - Kevin A Townsend, Bernie J Daigle Jr. Large-scale Microarray Data Integration for Improved Differential Expression Analysis. *Poster session at the 13th Annual Mid-South Computational Biology and Bioinformatics Society (MCBIOS) Conference*, Memphis, TN, Mar 2016.
 - Bernie J Daigle Jr., Mohammed Soltani, Linda R Petzold, Abhyudai Singh. Inferring Single-Cell Gene Expression Mechanisms using Stochastic Simulation. *Poster Session at the 3rd Stochastic Physics in Biology Gordon Research Conference*, Ventura, CA, Jan 2015.

- Bernie J Daigle Jr. PTSD: Trauma and Anxiety—Understanding the Molecular Pathways of Trauma. *UCSB Engineering Medicine Biology Discovery Innovation (EMBoDI) Open House*, Santa Barbara, CA, Apr 2013.
- Bernie J Daigle Jr, Min K Roh, Linda R Petzold, Jarad Niemi. MCEM²: Monte Carlo Expectation-Maximization with Modified Cross-Entropy Method. *Poster session at the 2nd Annual Southern California Systems Biology Conference (SoCal SysBio)*, Irvine, CA, Jan 2012.
- Bernie J Daigle Jr, Philip S Tsao, Russ B Altman. Using pre-existing microarray datasets to increase experimental power: Application to insulin resistance. *Poster session at The Third q-bio Conference on Cellular Information Processing*, Santa Fe, NM, Aug 2009.
- Bernie J Daigle Jr, Caroline F Thorn, Russ B Altman. Use of prior biological knowledge to strengthen inferences drawn from a drug response microarray experiment. *Poster session at the Pacific Symposium on Biocomputing (PSB) 2005*, Kona, HI.

SOFTWARE
RELEASED

icHET: Interactive Visualization of Cytoplasmic Heteroplasmy

icHET 0.5 is a high-performance computing-based workflow that produces an interactive visualization to facilitate the exploration, analysis and discovery of heteroplasmy across multiple genomic samples.

Availability: <https://github.com/vtphan/HeteroplasmyWorkflow>

StochSS: Stochastic Simulation Service

StochSS 1.5.1 provides an integrated development environment and cloud computing framework for modeling and simulation of stochastic biochemical systems. *Availability:* <http://www.stochss.org>

SAGAT: SVD-Augmented Gene expression Analysis Tool

The `sagat.1.0-1` R package provides a computationally efficient statistical method for integrating pre-existing gene expression data with a microarray dataset. *Availability:* <https://simtk.org/home/sagat>

M-BISON: Microarray-Based Integration of data SOURces using Networks

The `mBison.1.0-1` R package is a fully documented implementation of a robust graphical model for integrating heterogeneous biological knowledge with microarray data. *Availability:* <https://simtk.org/home/m-bison>

STUDENT
MENTORING

The University of Memphis, Memphis, TN

- Kevin Townsend 2015-2016
B.S., Computer Science
- Pulin Agrawal 2016-2019
Ph.D., Computer Science
- Caroline Melton 2016-2019
Ph.D., Biological Sciences
- Liangqun Lu 2016-2020
Ph.D., Biological Sciences
- Ted Ling Hu 2017-2019
M.S., Bioinformatics
- Mazen Istanbouli 2017-present
M.S., Bioinformatics
Ph.D., Biological Sciences

- Vibha Tripathi 2018-2020
M.S., Bioinformatics
- James Courtney 2018
B.S., Biomedical Engineering
- Hunter Franks 2019
B.S., Psychology
- Daniel O'Malley 2020
B.S., Chemistry
- Sohini Banerjee 2020-2022
Thomas Jefferson High School for Science and Technology
- Shreya Shivpuje 2021
M.Tech., Indian Institute of Technology, Madras
- Adil Abdurahaman 2022-present
M.D., The University of Tennessee Health Science Center
- Jalyssa Smith 2022-present
B.S., Biomedical Engineering
- Christine Odero 2023-present
M.S., Data Science
- Serena Zhao 2023-present
A.B., Harvard College

TEACHING
EXPERIENCE

The University of Memphis, Memphis, TN

- *BIOL 7060/8060* Spring 2023
Biological Data Analysis
- *BIOL 7708/8708* Fall 2016, Spring 2019, Spring 2021
Data Science for Biologists
- *BIOL 4092/6092* Spring 2017, Fall 2017
Survey of Genomics and Bioinformatics
- *BIOL 4490/6490* Fall 2018, Fall 2019, Fall 2020, Fall 2021, Fall 2022
Introduction to Genomics and Bioinformatics
- *BINF 7970* Spring 2019, Spring 2020
Current Literature in Bioinformatics
- *BIOL 1110* Spring 2021, Fall 2021, Spring 2022
General Biology I

SERVICE

Local Arrangements Co-chair, Mid-South DATA Conference 2023.

University Council for Graduate Studies Natural Sciences representative, The University of Memphis, 2022-present.

Young Scientist Award Chair, 18th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference, 2022.

Founding member, The University of Memphis Center for Data Science, 2022.

Local Arrangements Chair, Memphis DATA Conference 2022.

Ad Hoc Proposal Reviewer, Congressionally Directed Medical Research Programs (CDMRP),

2021.

Tenure and Promotion Committee member, Department of Biological Sciences, The University of Memphis, 2021-present.

Co-chair, Strategic Planning Committee, Department of Biological Sciences, The University of Memphis, 2021-present.

Board of Directors member, MidSouth Computational Biology and Bioinformatics Society (MCBIOS), 2021-present.

Speaker's Chair, Memphis DATA Conference 2021.

Faculty Research Grant Review Committee member, The University of Memphis CAS Research Grants programs, 2020.

Founding Advisory Board member, The University of Memphis Center for Biodiversity Research, 2019.

Speaker's Chair, Memphis DATA Conference 2019.

Data Science Master's Degree Program Planning Committee member, The University of Memphis, 2018-present.

High Performance Computing Steering Committee member, The University of Memphis, 2018-present.

High Performance Computing RFP Evaluation Committee member, The University of Memphis, 2018.

Faculty Search Committee member, Department of Biological Sciences, The University of Memphis, 2017-2018.

Program Committee member, 2017 International Workshop on Translational Bioinformatics in Precision Medicine, IEEE International Conference on Bioinformatics and Biomedicine (BIBM).

Strategic Planning Committee member, Department of Biological Sciences, The University of Memphis, 2016-present.

Faculty Search Committee member, Department of Biological Sciences, The University of Memphis, 2016-2017.

Professional Researcher Merit Review Committee member, UCSB Institute for Collaborative Biotechnologies, Feb 2015.

Professional Researcher Merit Review Committee member, UCSB Institute for Collaborative Biotechnologies, Feb 2013.

Strategic Planning Group member, Army Research Office Mathematical Sciences Division Strategy Planning Workshop, May 2011.

Journals refereed: Bioinformatics, BMC Bioinformatics, Genomics, IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), PLoS Computational

Biology, Journal of Chemical Physics, Journal of Biomedical Informatics, Computational and Mathematical Methods in Medicine, Computational Statistics & Data Analysis (CSDA), BMC Cancer, Frontiers in Psychiatry, BMC Veterinary Research, npj Precision Oncology, International Journal for Computer Assisted Radiology and Surgery, Frontiers in Artificial Intelligence, Frontiers in Big Data, PLoS One.

Conferences refereed: The 12th European Control Conference (ECC13), the 14th European Control Conference (ECC15), the 14th Annual MidSouth Computational Biology and Bioinformatics Society (MCBIOS) Conference, the 2017 International Workshop on Translational Bioinformatics in Precision Medicine (IEEE BIBM 2017), the 15th Annual MCBIOS Conference, the 16th Annual MCBIOS Conference, the 17th Annual MCBIOS Conference.