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EDUCATION

- 2017 PhD, Computational and Systems Biology, Washington University in St. Louis
Advisor: Kristen Naegle
Thesis: Robust algorithms for detecting hidden structure in biological data
- 2009 MS, Biophysics, Ohio State University
Advisor: Michael Paulaitis
Thesis: Mechanical unfolding of solvated α -synuclein studied by Molecular Dynamics simulations
- 2001 BA, Mathematics, Northwestern University

PROFESSIONAL EXPERIENCE

- 2017- Postdoctoral Research Fellow, Lab of Margaret Stratton
Department of Biochemistry and Molecular Biology, University of Massachusetts Amherst
- 2012- Graduate Student, Lab of Kristen Naegle
- 2017 Biomedical Engineering Department, Washington University in St. Louis
- 2009- Graduate Student, Lab of Michael Brent
- 2012 Center for Genome Sciences, Washington University School of Medicine
- 2006- Graduate Student, Lab of Michael Paulaitis
- 2008 Department of Chemical and Biomolecular Engineering, Ohio State University
- 2005- Bioinformatics Intern
- 2006 Comprehensive Cancer Center, Ohio State University
- 2002- Research Assistant
- 2004 Biological Sciences Division, University of Chicago
- 1999- Research Assistant
- 2001 Integrated Genomics, Inc., Chicago, IL

PUBLICATIONS

- 2020 Ozden, C., **Sloutsky, R.**, Santos, N., Agnello, E. Gaubitz, C., Lapinskas, E., Esposito, E., Kelch, B., Garman, S., Hayashi, Y., and Stratton, M.M. (2020), "CaMKII binds both substrates and effectors at the active site", *bioRxiv*, doi.org/10.1101/2020.10.25.354241
- 2020 ***Sloutsky, R.**, *Dziedzic, N., Dunn, M.J., Bates, R.M., Torres-Ocampo, A.P., Boopathy, S. Page, B., Weeks, J.G., Chao, L.H., and Stratton, M.M. (2020), "Heterogeneity in human hippocampal CaMKII transcripts reveals allosteric hub-dependent regulation", *Science Signaling*, vol. 13, no. 641, eaaz0240, doi.org/10.1126/scisignal.aaz0240

- 2020 **Sloutsky, R.** and Stratton, M.M. (2020), “Functional implications of CaMKII alternative splicing”, *European Journal of Neuroscience*, online 28 Apr 2020, (invited review), doi.org/10.1111/ejn.14761
- 2019 **Sloutsky, R.** and Naegle, K.M. (2019), “ASPEN, a methodology for reconstructing protein evolution with improved accuracy using ensemble models”, *Elife*, vol. 8, e47676, doi.org/10.7554/eLife.47676
- 2018 Ronan, T., Anastasio, S., Qi, Z., **Sloutsky, R.**, Naegle, K.M., and Tavares, P.H.S.V. (2018) “Openensembles: a python resource for ensemble clustering”, *The Journal of Machine Learning Research*, vol. 19, no. 1, 956–961
- 2018 **Sloutsky, R.** and Naegle, K.M. (2018), “Proteome-Level analysis indicates global mechanisms for post-translational regulation of RRM domains”, *Journal of Molecular Biology*, vol. 430, no. 1, pp. 41–44, doi.org/10.1016/j.jmb.2017.11.001
- 2016 **Sloutsky, R.** and Naegle, K.M. (2016), “High-resolution identification of specificity determining positions in the LacI protein family using ensembles of sub-sampled alignments”, *PLoS ONE*, vol. 11, no. 9, e0162579, doi.org/10.1371/journal.pone.0162579
- 2013 Cho, Y., **Sloutsky, R.**, Naegle, K.M., and Cavalli V. (2013), “Injury-induced HDAC5 nuclear export is essential for axon regeneration”, *Cell*, vol. 155, no. 4, pp. 894–908, doi.org/10.1016/j.cell.2013.10.004
- 2012 **Sloutsky R.**, Jimenez, N., Swamidass, S.J., and Naegle, K.M. (2013), “Accounting for noise when clustering biological data”, *Briefings in Bioinformatics*, vol. 14, no. 4, pp. 423–36, online 14 Oct 2012, doi.org/10.1093/bib/bbs057
- 2006 Gerdes S.Y., Kurnasov O.V., Shatalin K., Polanuyer B., **Sloutsky R.**, Vonstein V., Overbeek R., and Osterman A.L. (2006), “Comparative genomics of NAD biosynthesis in cyanobacteria”, *Journal of Bacteriology*, vol. 188, no. 8, pp. 3012–23
- 2002 Kurnasov O.V., Polanuyer B., Ananta S., **Sloutsky R.**, Tam A., Gerdes S.Y., Osterman A.L. (2002), “Ribosynicotinamide kinase domain of NadR protein: identification and implications in NAD biosynthesis”, *Journal of Bacteriology*, vol. 184, no. 24, pp. 6906–17

PATENT APPLICATIONS

- 2018 Naegle, K.M. and **Sloutsky, R.** (2018), “Toolkit for the production of post-translationally modified proteins”, United States Patent Application no. 15/710,451; [US20180010102A1](#)

SOFTWARE

- ASPEN** Exhaustive enumeration of phylogenetic topologies under ensemble-derived constraints

AWARDS AND FELLOWSHIPS

- 2018 Protein Science Travel Award, Protein Society Symposium
- 2016 Midwest Quantitative Biology Symposium Travel Award
- 2013 Lockheed Martin Center for Biological Systems Engineering Scholar

PRESENTATIONS

Talks

- 2019 "Conditional Role of Variable Linker in CaMKII Activation"
Joint UMass Amherst / UMass Medical School Chemistry-Biology Interface Retreat
Worcester, MA, USA. June 7
- 2017 "Reconstructing Paralog Divergence Using Ortholog Subsampling"
University of Massachusetts Amherst, Amherst, MA, USA. August 2
- 2017 "Robust Reconstruction of Paralog Divergence Histories"
Center for Biological Systems Engineering seminar series, St. Louis, MO, USA. April 17
- 2016 "Reconstruction of Paralog Divergence Histories by Constrained Topology Enumeration"
Midwest Quantitative Biology Symposium lightning talk, West Lafayette, IN, USA. October 22
- 2015 "Identification of SH2 Domain Recognition Determinants"
Siteman Cancer Center Cell-to-Cell Communications in Cancer seminar series
St. Louis, MO, USA. December 9

Posters

- 2018 "Role of CaMKII Alternative Splicing in Memory Formation"
Protein Society Symposium, July 11
- 2017 "Robust reconstruction of paralog divergence"
Proteins Gordon Research Conference, June 20
- 2016 "Analysis of Complex Specificity Determinant Patterns in Large Protein Families"
Biophysical Society Annual Meeting, March 1

TEACHING EXPERIENCE

- 2019 Biochem 642, Advanced Molecular Biology, Guest Instructor
University of Massachusetts Amherst
- 2009 Bio 5495, Computational Molecular Biology, Teaching Assistant
Washington University in St. Louis
- 2006 Bio 101, An Introduction to Biology, Teaching Assistant and Laboratory Instructor
2007 Ohio State University

OUTREACH

- 2019 Presenter, "Python for scientific applications"
Bioinformatics Users Group instructional seminar series
University of Massachusetts Amherst
- 2014 Software Carpentry workshop facilitator
Washington University School of Medicine