

ALLISON N. TEGGE

Department of Statistics
Virginia Tech, Blacksburg, VA 24061

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RESEARCH INTERESTS

Methods: Graphical Models, Support Vector Machines, Neural Networks, Hidden Markov Models.
Topics: Computational Systems Biology, Gene Expression Analysis, Cellular Signaling and Regulation.

EDUCATION

Ph.D. Informatics 2008 – 2012

University of Missouri–Columbia; Columbia, Missouri

- Thesis: “Using Pathway Correlation Profiles for Understanding Biological Pathway Perturbation”
- Advisor: Dong Xu

M.S. Bioinformatics 2006 – 2008

University of Illinois Urbana–Champaign; Urbana, Illinois

- Thesis: “Prediction of Neuropeptide Cleavage in Four Mammalian Species Using Artificial Neural Networks and Logistic Regression Models”
- Advisor: Sandra Rodriguez-Zas

B.S. Animal Sciences 2003 – 2006

University of Illinois Urbana–Champaign; Urbana, Illinois

PROFESSIONAL EXPERIENCE

Research Assistant Professor Dec 2016 – Present

Dept. of Statistics at Virginia Tech

Assistant Professor Dec 2016 – Present

Basic Science Education at Virginia Tech Carilion School of Medicine

National Institute of Health Postdoctoral Fellow Sep 2014 – Dec 2016

Dept. of Computer Science at Virginia Tech, Advisors: T. M. Murali, Padma Rajagopalan

Post-doctoral Research Associate Jan 2013 – Sep 2014

Dept. of Computer Science at Virginia Tech, Advisor: T. M. Murali

Graduate Research Assistant Aug 2008 – Dec 2012

Informatics Institute at University of Missouri – Columbia

Database Programmer May 2008 – Aug 2008

Dept. of Animal Sciences at University of Illinois Urbana – Champaign

Graduate Research Assistant Aug 2006 – Aug 2008

Dept. of Animal Sciences at University of Illinois Urbana – Champaign

Undergraduate Research Assistant Aug 2005 – Aug 2006

Dept. of Animal Sciences at University of Illinois Urbana – Champaign

HONORS AND AWARDS

National Institute of Health F32 Fellowship Sep 2014 – Aug 2017

Best Bioinformatics Poster Award at Missouri Informatics Symposium Oct 2012

National Library of Medicine Biomedical Informatics Training Fellowship 2008 – 2012

Outstanding Graduate Student in MU Informatics Institute, University of Missouri 2010

Jonathan Baldwin Turner Scholarship, University of Illinois Urbana – Champaign 2003 – 2006

James Scholar, University of Illinois Urbana – Champaign 2003 – 2005

FUNDING

National Institute of Environmental Health Sciences F32 Postdoctoral Fellowship Sep 2014 – Aug 2017

Title: “Computing hepatic intercellular communications in response to toxicant exposures.”

Total award: \$165,354

- Stein JS, **Tegge AN**, Turner JK, Bickel WK (2017). Episodic future thinking reduces delay discounting and cigarette demand: an investigation of the good-subject effect. *Journal of behavioral medicine*.
- Moody LN, **Tegge AN**, Poe LM, Koffarnus MN, Bickel WK (2017). “To drink or to drink less? Distinguishing between effects of implementation intentions on decisions to drink and how much to drink in treatment-seeking individuals with alcohol use disorder.” *Addictive behaviors*.
- Bharadwaj A, Singh DP, Ritz A, **Tegge AN**, Poirel CL, Kraikivski P, ..., Murali TM (2017). “GraphSpace: stimulating interdisciplinary collaborations in network biology.” *Bioinformatics*, 33(19), 3134-3136.
- Moody LN, **Tegge AN**, Bickel WK (2017). “Cross-Commodity Delay Discounting of Alcohol and Money in Alcohol Users.” *Psychological Record*, 67(2), 285-292.
- Sam SA*, Teel J*, **Tegge AN***, Bharadwaj A, Murali TM (2017). “XTalkDB: a database of signaling pathway crosstalk.” *Nucleic Acids Research (Database Issue)*, to appear. * co-first authors.
- Ritz A, Poirel CL, **Tegge AN**, Sharp N, Powell A, Simmons K, Kale S, Murali TM (2016). “Pathways on Demand: Automated Reconstruction of Human Signaling Networks.” *npj: Systems Biology and Applications*, a Nature Partner Journal, 2, Article number 16002.
- Tegge AN**, Sharp N, Murali TM (2016). “XTalk: a path-based approach to identifying crosstalk between signaling pathways.” *Bioinformatics*, 32(2), 242–251.
- Santos MCT*, **Tegge AN***, Correa BRS, Mahesula S, Kohnke LQ, Qiao M, Ferreira MAR, Kokovay E, Penalva LOF (2016). “miR-124, -128 and -137 orchestrate neural differentiation by acting on overlapping gene sets containing a highly connected transcription factor network.” *Stem Cells*, 34, 220–232. * co-first authors.
- Cui S, Guha S, Ferreira MAR, **Tegge AN** (2015). “hmmSeq: A Hidden Markov Model for Detecting Differentially Expressed Genes from RNA-Seq Data.” *Annals of Applied Statistics*, 9, 901–925.
- Ritz A*, **Tegge AN***, Kim H, Poirel CL, Murali TM (2014). “Signaling Hypergraphs.” *Trends in Biotechnology*, 32(7), 356–362. * co-first authors.
- Tegge AN**, Caldwell CW, Xu D (2012). “Pathway Correlation Profile of Gene-Gene Co-expression for Identifying Pathway Perturbation.” *PLoS One*, 7(12), e52127.
- Cheng J, Wang Z, **Tegge AN**, Eickholt J (2009). “Prediction of Global and Local Quality of CASP8 Models by MULTICOM series.” *Proteins*, 77, 181–184.
- Tegge AN**, Wang Z, Eickholt J, Cheng J (2009). “NNcon: Improved Protein Contact Map Prediction Using 2D-Recursive Neural Networks.” *Nucleic Acids Research*, 37, w515–w518.
- Wang Z, **Tegge AN**, Cheng J (2009). “Evaluating the Absolute Quality of a Single Protein Model Using Support Vector Machines and Structural Features.” *Proteins*, 75(3), 638–647.
- Cheng J, **Tegge AN**, Baldi P (2008). “Machine Learning Methods for Protein Structure Prediction.” *IEEE Reviews in Biomedical Engineering*, 1, 41–49.
- Tegge AN**, Southey BR, Sweedler JV, Rodriguez-Zas SL (2008). “Comparative Analysis of Neuropeptide Cleavage Sites in Human, Mouse, Rat, and Cattle.” *Mammalian Genome*, 19(2), 106–120.

CONFERENCE PUBLICATIONS

- Tegge AN**, Rodriguez-Zas SL, Sweedler JV, Southey BR (2007). “Comparative Analysis of Binary Logistic Regression to Artificial Neural Networks in Predicting Precursor Sequence Cleavage.” *Bioinformatics and Biomedicine Workshops*, 101–108.
- Tegge AN**, Rodriguez-Zas SL, Southey BR (2007). “Binary Logistic Regression Modeling of Precursor Sequence Cleavage.” *Proceedings of the American Statistical Association*, Biometrics Section [CDROM], Alexandria, VA. American Statistical Association, 389–393.

BOOK CHAPTERS

- Tegge AN**, Wang Z, Cheng J (2010). “Integrative Protein Fold Recognition by Alignments and Machine Learning.” *Protein Structure Prediction: Method and Algorithms*, vol. 12, Wiley.
- Tegge AN**, Rodriguez-Zas SL, Sweedler JV, Southey BR (2007). “Enhanced Prediction of Cleavage in Bovine Precursor Sequences.” *Bioinformatics Research and Applications*. Springer Berlin Heidelberg, 350–360.

Tegge AN, Rodrigues RR, Larkin AL, Murali TM, Rajagopalan P. “Transcriptomic analysis of hepatic cells in multicellular organotypic liver models.” *Revisions submitted to Scientific Reports*.

PRESENTATIONS

Bayesian Analysis for Multi-Subject Time Course RNA-Seq Experiments . *2017 Joint Statistical Meeting*, Baltimore, Maryland, USA. Aug 2017.

A computational approach to the identification of pathway crosstalk. *The Virginia Tech Carilion School of Medicine and Research Institute*, Roanoke, Virginia, USA. Oct 2016. (Invited)

Bayesian analysis for multi-subject time course RNA-seq experiments. *2016 International Conference on Statistical Distributions and Applications*, Niagara Falls, Ontario, Canada. Oct 2016. (Invited)

XTalk: a path-based approach to identifying pathway crosstalk. *2016 Joint Statistical Meeting*, Chicago, Illinois, USA. July 2016.

Bayesian analysis for multi-subject time course RNA-seq experiments. *60th ISI World Statistics Congress*, Rio de Janeiro, Brazil. July 2015.

Using *in vitro* liver models to study hepatic intercellular signaling. *Second Annual Regenerative Medicine IGEP Retreat*, Regenerative Medicine IGEP, Virginia Tech. May 2015.

XTalk: a path-based approach to identifying pathway crosstalk. *Department Seminar*, Department of Statistics, Virginia Tech. March 2014.

Pathway Analysis of ToxCast Data. *Workshop on Computational Toxicology*, Institute for Critical Technology and Applied Science, Virginia Tech. September 2013.

Pathway Correlation Profile of Gene-Gene Co-Expression for Identifying Pathway Perturbation. *National Library of Medicine Informatics Training Conference*, Madison, Wisconsin. June 2012.

A Pathway Based Correlation Method for Identifying Perturbation in Follicular Lymphoma from Microarray Gene Expression Data. *National Library of Medicine Informatics Training Conference*, Denver, Colorado. June 2010.

Integrative Protein Fold Recognition by Alignment and Machine Learning. *National Library of Medicine Informatics Training Conference*, Portland, Oregon. June 2009.

Comparative Analysis of Binary Logistic Regression to Artificial Neural Networks in Predicting Precursor Sequence Cleavage. *Bioinformatics and Biomedicine Workshops*, San Jose, California. November 2007.

Enhanced Prediction of Cleavage in Bovine Precursor Sequences. *Third International Symposium on Bioinformatics Research and Applications*, Atlanta, Georgia. May 2007.

POSTERS

Rodrigues RR, Larkin AL, Vu LT, **Tegge AN**, Murali TM, Rajagopalan P. “Transcriptome Analysis of Multi-cellular Signaling in an Organotypic 3D Liver Model.” Annual Meeting of the Biomedical Engineering Society, Seattle, Washington. September 2013.

Cui S, Guha S, Ferreira MAR, **Tegge AN**. “A hidden Markov model for detecting differentially expressed genes from RNA-Seq data.” *Frontiers in Methodological and Applied Statistics: A Celebration of 50 Years of MU’s Department of Statistics*, Columbia, Missouri. September 2013.

Tegge AN, Caldwell CW, Xu D. “Pathway Correlation Profiles for the Identification of Pathway Perturbation.” *International Conference on Intelligent Systems for Molecular Biology*, Long Beach, California. July 2012.

Tegge AN, Xu D, Caldwell CW. “Interpreting Discordant Results Between Two Diagnosis-Relapse Datasets.” *National Library of Medicine Informatics Training Conference*, Bethesda, Maryland. June 2011.

Tegge AN, Arthur G, Bennett L, Caldwell CW, Xu D, Cheng J. “A Pathway Based Correlation Method for Identifying Perturbation in Follicular Lymphoma from Microarray Gene Expression Data.” *International Conference on Intelligent Systems for Molecular Biology*, Boston, Massachusetts. July 2010.

Tegge AN, Wang Z, Deng X, Compani B, Su T, Chang I, Shapiro B, Vaughn MW, Cheng J, Mjolsness E. “Sigmoid: A Visualization, Simulation and Retrieval Tool for Biological Networks and Systems Biology.” *Pacific Symposium on Biocomputing*, Big Island, Hawaii. January 2009.

Tegge AN, Rodriguez-Zas SL, Southey BR. “Binary logistic regression modeling of precursor sequence cleavage.” *Institute for Genomic Biology Symposium*, Urbana, IL. October 2008.

Tegge AN, Rodriguez-Zas SL, Southey BR. “Binary logistic regression modeling of precursor sequence cleavage.” *Joint Statistical Meeting of the American Statistical Association*, Salt Lake City, Utah. July 2007.

Tegge AN, Southey BR, Andinet A, Sweedler JV, Rodriguez-Zas SL. “Bioinformatics analysis of bovine neuropeptides.” *American Dairy Science Association/American Society of Animal Science Joint Annual Meeting*, Minneapolis, Minnesota. July 2006.

TEACHING

STAT 2984: SS – Statistical Programming I *Spring 2018*
Virginia Tech

Biostatistics *Fall 2017*
Virginia Tech School of Medicine

STAT 5674: Methods in Biostatistics *Fall 2015, 2016*
Virginia Tech

Howard Hughes Medical Institute Summer Biomedical Informatics Institute *May 2011, 2012*
University of Missouri Columbia

Guest lecture on epigenetics biological and computational methodologies.

INFOINST 7005: Introduction to Bioinformatics *Spring 2010, 2011, 2012*
University of Missouri Columbia

Guest lecture on microarray analysis.

ANSC 542: Applied Bioinformatics *Spring 2009*
University of Illinois Urbana-Champaign

Guest lectures on biology related databases, graded homework, and answered student’s questions.

MENTORING

Joelle Teel Undergraduate Student *May 2015 – May 2016*

Research Project: The Annotation and Documentation of Pathway Crosstalk

Sarah Sam Undergraduate Student *September 2014 – August 2016*

Research Project: The Annotation and Documentation of Pathway Crosstalk

Peter Burnham Undergraduate Student *April 2013 – June 2015*

Research Project: Finding High Impact Drug Targets through Viral Dependency Factors

Richard Rodrigues Graduate Student *April 2013 – February 2014*

Research Project: Elucidating the Multi-cellular Signaling in an Organotypic 3D Liver Model

INSTITUTIONAL SERVICE

Member of Policy and Procedures Committee *Aug 2016 – present*
Department of Statistics, Virginia Tech

President, MU Informatics Institute Graduate Student Association *Aug 2009 – May 2012*
University of Missouri – Columbia

Student Member of Curriculum Committee *Aug 2010-Dec 2012*
MU Informatics Institute, University of Missouri – Columbia

Student Coordinator *May 2011*
Howard Hughes Medical Institute Summer Biomedical Informatics Institute, Columbia, Missouri

PROFESSIONAL SERVICE

Reviewer, International Conference on Research in Computational Molecular Biology *2014*

Reviewer, International Conference on Intelligent Systems for Molecular Biology *2014 – 2015*

Reviewer, ACM Conference on Bioinformatics, Computational Biology, and Health Informatics *2015*

Reviewer, Scientific Reports *2015*

Reviewer, IEEE Transactions on Computational Biology and Bioinformatics *2016 – 2017*

Reviewer, BMC Bioinformatics *2016*