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Department of Computer Science
Department of Statistics
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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

National Institute of Health Postdoctoral Fellow Sep 2014 – Present

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

Post-doctoral Research Associate Jan 2013 – Sep 2014

Dept. of Computer Science at Virginia Tech, Sponsor: 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

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

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

Total award: \$165,354

JOURNAL PUBLICATIONS

Ritz A, Poirel CL, Tegge AN, Sharp N, Powell A, Simmons K, Kale S, Murali TM. “Pathways on Demand: Automated Reconstruction of Human Signaling Networks.” *To appear in npj: Systems Biology and Applications*.

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.

PROCEEDINGS

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.

SUBMITTED PAPERS

Ritz A, Poirel CL, **Tegge AN**, Murali TM. “Automated prioritization of receptors and transcription factors in human signaling pathways.” *In revision*.

MANUSCRIPTS IN PREPARATION

Tegge AN, Rodrigues RR, Larkin AL, Murali TM, Rajagopalan P. “Transcriptomic analysis of hepatic cells in multicellular organotypic liver models.” *In preparation*.

Baptista PM, Vyas D, Talhaden T, Moran E, Wathier E, Walker S, **Tegge AN**, Murali TM, Furth M, Reid L, Soker S. “Self-assembled liver organoids recapitulate hepato-biliary organogenesis *in vitro*.” *In preparation*.

PRESENTATIONS

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.

SERVICE

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

REFEREEING

International Conference on Research in Computational Molecular Biology 2014
International Conference on Intelligent Systems for Molecular Biology 2014 – 2015
ACM Conference on Bioinformatics, Computational Biology, and Health Informatics 2015
Scientific Reports 2015

TEACHING

STAT 5674: Methods in Biostatistics Fall 2015
Virginia Tec

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 – present
Research Project: The Annotation and Documentation of Pathway Crosstalk

Sarah Sam *Undergraduate Student* September 2014 – present
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

SKILLS AND TOPICS OF INTEREST

Graphical Models, Data Mining, Support Vector Machines, Neural Networks, Hidden Markov Models, Classification, Statistical Computation, Protein-Protein Interaction Networks, Computational Systems Biology, Gene Expression Analysis, Cellular Signaling and Regulation.