Todd R. Riley

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EDUCATION

Rutgers University, Piscataway, NJ   August 2008
Ph.D., Computational Biology and Molecular BioPhysics
Dissertation Title: Modeling p53 Transcription Factor Binding Sites
Advisor: Dr. Arnold J. Levine, Co-Advisor: Dr. Eduardo Sontag

University of North Carolina at Chapel Hill, NC   May 2004
Master of Science, Applied Mathematics
Thesis Title: Mathematical Modeling of R1 Plasmid Copy Number Control
Advisor: Dr. Tim Elston

Carnegie Mellon University, Pittsburgh, PA   May 1992
Bachelor of Science, Computer Science/Mathematics

RESEARCH EXPERIENCE

Columbia University, New York, NY   September 2008 – present
Postdoctoral Fellow, Department of Biological Sciences,
Center for Computational Biology and Bioinformatics
Advisor: Dr. Harmen J. Bussemaker

- Co-pioneered a new in vitro high-throughput protocol (called SELEX-seq) to determine the sequence specificity of TF-DNA-cofactor complexes.
- Co-discovered "latent specificity", whereby the binding specificities of proteins of a TF-family change significantly from one another only when bound in complex with a common cofactor.
- Developed novel computational methods to infer accurate, biophysical sequence-to-affinity models from Protein Binding Microarray (PBM) assays.
- Co-discovered that TLS/FUS regulates the gene expression of downstream targets via binding to single-stranded DNA (ssDNA) binding sites.

The Institute for Advanced Study, Princeton, NJ   September 2005 – August 2008
Research Fellow, The Simons Center for Systems Biology
Advisor: Dr. Arnold Levine, Co-Advisor: Dr. Eduardo Sontag

- Developed computational methods to infer the DNA-binding specificities of the p53 protein using a dataset of 160 experimentally validated, functional, human p53 binding elements.

HONORS / AWARDS

"Top Ten Papers of 2011 in Regulatory and Systems Genomics" – RECOMB/ISMB   2012
Associate Faculty Member – Faculty of 1000   November 2012
NCI Integrative Cancer Biology Program Junior Investigator   September 2012
Funded by C2B2/MAGNet Center Grant   September 2010 – present
IAS Graduate Research Fellowship   September 2005 – August 2008
GAANN Fellowship, Rutgers University   September 2004 – August 2005

TEACHING EXPERIENCE

Cold Spring Harbor Laboratory, Cold Spring Harbor, NY   2009 – present
Guest Lecturer – Analyzing protein-DNA binding assays (3 classes)
TA – Integrated Statistical Analysis of Genome Scale Data (4 summer courses)

Columbia University, New York, NY   2009 – present
Guest Lecturer – Computational Biology (4 classes)
Guest Lecturer – R Programming Lab (2 classes)

University of North Carolina at Chapel Hill, NC   2002 – 2004
Instructor – Calculus I (1 semester)
Instructor – Calculus for Business and Social Sciences (2 semesters)
Instructor – Pre-Calculus (1 semester)
Instructor – Math Topics for non-science majors (1 semester)

CONFERENCE/SEMINAR TALKS

RECOMB Conference on Regulatory and Systems Genomics   November 12, 2012
San Francisco, CA
Title: Building accurate sequence-to-affinity models from protein
     binding microarray data using FeatureREDUCE

Department of Biological Sciences Retreat, Tarrytown, NY   September 17, 2011
Columbia University
Title: Dimerization with Extradenticle unlocks latent DNA binding
     specificities that discriminate Hox proteins in Drosophila

Albany 2011: The Seventeenth Conversation, Albany, NY   June 18, 2011
Title: Dimerization with Extradenticle unlocks latent DNA binding
     specificities that discriminate Hox proteins in Drosophila

Systems Biology: Networks, Cold Spring Harbor Lab, NY   March 26, 2011
Title: Dimerization with Extradenticle unlocks latent DNA binding
     specificities that discriminate Hox proteins in Drosophila

Kavli Institute for Theoretical Physics, UC Santa Barbara   January 30, 2007
Title: The Properties of p53 Transcription Factor Binding Sites

INDUSTRY EXPERIENCE

SciQuest Inc., Research Triangle Park, NC   1999 – 2001
- Assisted in designing and implementing the corporate order fulfillment architecture to automate the ordering, invoicing, and tracking processes of purchasing scientific equipment.

Seer Technologies Inc., Cary, NC   1992 – 1999
- Designed and implemented public-key encryption and computer networking software for banking applications. Served as senior systems programmer, systems architect, and development manager.

PUBLICATIONS

Riley, T. R., M. Slattery, R. S. Mann, H. J. Bussemaker. "Building accurate sequence-to-affinity models from high-throughput protein-DNA binding data using FeatureREDUCE." *Manuscript in preparation.*

Gomez-Alcala, P.*, T. R. Riley*, I. Mann, T. R. Hughes, H. J. Bussemaker. "Deciphering the specificity differences within the bHLH transcription factor family." *Manuscript in preparation.*

Riley, T. R., J. Vanicek, G. Atwal, M. Krasnitz, E. Sontag, A. J. Levine. "PURE: a motif finding algorithm that discovers regulatory sequence Patterns Using Relative Entropy." *Manuscript in preparation.*

Lazarovici, A., T. Zhou*, A. Shafer*, A. C. D. Machado*, T. R. Riley, R. Sandstrom, P. J. Sabo, Y. Lu, R. Rohs, J. A. Stamatoyannopoulos, H. J. Bussemaker. "Probing DNA shape and methylation state on a genomic scale with DNase I." **Proc Natl Acad Sci USA** *In Press.*

Weirauch, M., A. Cote1, R. Norel, M. Annala, Y. Zhao, T. R. Riley, J. Saez-Rodriguez, T. Cokelaer, A. Vedenko, S. Talukder, DREAM5 consortium, H. J. Bussemaker, Q. D. Morris, M. L. Bulyk, G. Stolovitzky, T. R. Hughes. "Evaluation of methods for modeling transcription factor sequence specificity." **Nature Biotech**. 31(2): 126-134.

Tan, A. Y., T. R. Riley, T. Coady, H. J. Bussemaker, J. L. Manley. (2012). "TLS/FUS (translocated in liposarcoma/fused in sarcoma) regulates target gene transcription via single-stranded DNA response elements." **Proc Natl Acad Sci USA** 109(16): 6030-6035. PMCID: PMC3341064

Slattery, M.*, T. Riley*, P. Liu*, N. Abe, P. Gomez-Alcala, I. Dror, T. Zhou, R. Rohs, B. Honig, H. J. Bussemaker, R. S. Mann. (2011). "Cofactor binding evokes latent differences in DNA binding specificity between Hox proteins." **Cell** 147(6): 1270-1282. PMCID: PMC3319069

Riley, T., X. Yu, E. Sontag, A. J. Levine. (2009). "The p53HMM algorithm: using profile hidden markov models to detect p53-responsive genes." **BMC Bioinformatics** 10: 111. PMCID: PMC2685388

Yu, X., T. Riley, A. J. Levine. (2009). "The regulation of the endosomal compartment by p53 the tumor suppressor gene." **FEBS J** 276(8): 2201-2212. PMCID: PMC19302216

Riley, T., E. Sontag, P. Chen, A. J. Levine. (2008). "Transcriptional control of human p53-regulated genes." **Nat Rev Mol Cell Biol** 9(5): 402-412. PMCID: PMC18431400

* Equal contribution

UNIVERSITY SERVICE

The BioMaPS Graduate Seminars, Rutgers University 2004 – 2005
- Scheduled speakers, reserved rooms, maintained equipment, and sent announcements for BioMaPS Graduate Seminars. Fostered a friendly, peer-environment for graduate students to present their work.

The Math Learning Center, UNC Mathematics Department 2003 – 2004
- Assisted undergraduate students with mathematics course material, ranging from College Algebra to Calculus III. Managed the Math Learning Center and undergraduate assistants.

PROFESSIONAL AFFILIATIONS

NCI Integrative Cancer Biology Program	2012 – present
International Society for Computational Biology	2012 – present
Society of Industrial and Applied Mathematicians	2003 – present

REFERENCES

Available upon request