

Ryan Suderman

Curriculum Vitae

Education

2010–2016 **Ph.D. in Computational Biology**, *University of Kansas*, GPA – 3.72 / 4.00.

2005–2009 **B.A. in Mathematics**, *Goshen College*, GPA – 3.54 / 4.00.
Concentration in Biology

Ph.D. Thesis

Title *Heterogeneity and Decision-Making in Cellular Signaling Networks*
Supervisor Professor Eric J. Deeds
Description This thesis examined how different forms of heterogeneity in intracellular signaling networks impact the ability of cells to respond to environmental stimuli.

Experience

Research

- 2016–Present **Postdoctoral Research Associate**, *Los Alamos Nat'l Lab*, Los Alamos, NM.
Funded jointly by the Center for Nonlinear Studies at Los Alamos National Lab and the Spatiotemporal Modeling Center at the University of New Mexico (an NIH National Center for Systems Biology)
- Worked with cell biologists to develop a model of cytokine-induced endosome maturation
 - Drove a collaboration with experimentalists to characterize receptor aggregation in mast cells
 - Developed a set of dynamical models to understand the role of Syk in immune response regulation
- 2011–2016 **Graduate Research Assistant**, *University of Kansas*, Lawrence, KS.
- Constructed and analyzed rule-based models of biochemical interaction networks
 - Applied information theoretic techniques to determine statistical dependencies in biological data
 - Performed statistical analyses of protein interaction data using hierarchical clustering algorithms

Programming

- 2016–Present **Postdoctoral Research Associate**, *Los Alamos Nat'l Lab*, Los Alamos, NM.
- Contributed to software for fitting rule-based models to experimental data (BioNetFit)
 - Adapted a web-based visualization client for use as a standalone application (RuleBuilder)
 - Developed a Python library to facilitate analysis of simulation data from rule-based models
 - Built an application for translating between two rule-based modeling languages (TRuML)

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- Summer 2015 **Software Engineer Intern**, *Orion Health*, Scottsdale, AZ.
- Implemented parallelized calculations with Apache Spark for analyzing healthcare data
 - Contributed to an existing code base for patient stratification using Elasticsearch
 - Participated in an Agile software development environment
- 2011–2016 **Graduate Research Assistant**, *University of Kansas*, Lawrence, KS.
- Developed a tool to estimate unbiased information theoretic quantities (ryants.github.io/EstCC)
 - Implemented custom Monte Carlo algorithms for sampling chemical kinetics
 - Managed cluster-based jobs via the TORQUE queueing system
- Independent.**
- Contributed to open-source projects designed to facilitate systems biology modeling (PySB.org)

Technical Skills

- Languages Proficient: SCALA, PYTHON | Intermediate: JAVA, C++, R
- Frameworks Rule-based modeling: BioNetGen, Kappa, ML-Rules | Other: Apache Spark, octave, L^AT_EX
- Utilities git, bash, sbt, Apache Maven, Unix core utilities
- OS OS X, Linux

Teaching

- 2016–Present **Mentor**, Los Alamos, NM.
- Guided summer students visiting Los Alamos National Lab in various modeling projects
- 2016 **Guest Lecturer**, *q-bio Summer School*, Albuquerque, NM.
- Lectured on global parameter fitting algorithms for kinetic Monte Carlo simulations
 - Lead a tutorial on developing models using the ML-Rules multi-level rule-based modeling framework
- 2011–2012 **Teaching Assistant**, *University of Kansas*, Lawrence, KS.
- Taught two semesters of an introductory biology laboratory (3 sections per semester)
 - Lectured on the theory behind methods in molecular biology
 - Guided students through basic experimental techniques

Conferences

Talks

- 2015 *q-bio*: Information flow in single cells and cellular populations

Posters

- 2017 *q-bio*, *Biophysical Society Meeting*: A theoretical analysis of the potential influence of ITAM pairs on Syk recruitment dynamics
- 2016 *Systems Approaches in Immunology and Infectious Diseases*: Dynamical effects of multimeric ring formation in multivalent antigen-antibody interactions
- 2016 *q-bio*: Intrinsic limits of information transmission in biochemical signaling networks
- 2014–2015 *Biophysical Society Meeting*, *MPI*, *q-bio*: Rules for scaffold assembly in signaling networks

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2012 *MPI, q-bio*: Ensemble signaling in MAPK cascades

Outreach

2015 **Judge**, *KU Undergraduate Research Symposium*, Lawrence, KS.

- Judged undergraduate research projects in the biological sciences

2015 **Volunteer**, *Kansas DNA Day*, Kansas City area schools, Kansas City, KS.

- Discussed recent scientific advances with high school students and organized appropriate classroom activities

2014 **Judge**, *Douglas Co. Science Fair*, Lawrence, KS.

- Judged science, math, and engineering projects for elementary, middle, and high school students

Awards

2015 University of Kansas Graduate Fellowship

2012 Finalist in KU Graduate Research Competition

Publications

Ryan Suderman, G Matthew Fricke, and William S Hlavacek. *RuleBuilder: a tool for drawing BioNetGen graphs*. *Methods in Molecular Biology*. 2018, accepted.

Ryan Suderman and Eric J Deeds. *When to use Rule-based models*. *Methods in Molecular Biology*. 2018, accepted.

Raquel Dias, Ryan Suderman, Brandon Thomas, Abolfazi Razi, Andrew H A Clayton, William S Hlavacek, and Richard G Posner. *Using BioNetFit to estimate parameters of rule-based models*. *Methods in Molecular Biology*. 2018, accepted.

Tess Schideler*, Ryan Suderman*, Charuta Palsuledesai, Cedric Cleyrat, William S Hlavacek, and Angela Wandinger-Ness. Epidermal growth factor receptor signaling exerts control over endosomal transport through activation of rab5 and rab7. *manuscript in submission*, 2017.

Ryan Suderman and William S Hlavacek. TRuML: A translator for rule-based modeling languages. *manuscript in submission*, 2017.

Ryan Suderman, Addison Schauer, and Eric J Deeds. Dynamical properties of distinct scaffold assembly paradigms. *manuscript in submission*, 2017.

Ryan Suderman, John Bachman, Adam Smith, Peter Sorger, and Eric J Deeds. Fundamental trade-offs between information flow in single cells and cellular populations. *Proc Natl Acad Sci, USA*, 2017.

Ryan Suderman and Eric J Deeds. Machines vs. Ensembles: Effective MAPK signaling through heterogeneous sets of protein complexes. *PLoS Computational Biology*, 9(10):e1003278, October 2013.

Ryan Suderman and Eric J Deeds. Intrinsic limits of information flow in biochemical networks. *manuscript in preparation*.

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Raquel Dias*, Ryan Suderman*, Brandon Thomas, Abolfazi Razi, Marisa L Martin-Fernandez, Andrew H A Clayton, William S Hlavacek, and Richard G Posner. Bionetfit2: Global fitting of multiple models using metaheuristic optimization. *manuscript in preparation*.

Ryan Suderman, Samantha L Schwartz, Diane S Lidke, and William S Hlavacek. The role of paired ITAMs in Syk recruitment. *manuscript in preparation*.