Ryan Suderman

Curriculum Vitae

Education

2010–2016	**Ph.D. in Computational Biology**, *University of Kansas*.
2005–2009	**B.A. in Mathematics**, *Goshen College*.
	Concentration in Biology

Ph.D. Thesis

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

Experience

Industry

2018–present **Mathematical Modeler**, *Immunetrics, Inc.*, Pittsburgh, PA.

Modeling
- Develop, troubleshoot, and analyze systems pharmacology models
- Work directly with clients to provide model-based predictions of potential clinical trials
- Present Immunetrics' work to potential clients and other interested parties

Project Management
- Define and develop scope for new projects
- Estimate and track effort to completion for new and ongoing projects
- Oversee projects with less-experienced modelers

Miscellaneous
- Recruit and train new modelers
- Test and document scientific software for quantitative systems pharmacology modeling

Academic Research

2016–2018 **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 to characterize receptor aggregation in mast cells
- Developed 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 find statistical dependencies in biological data
- Performed exploratory data analysis on protein interaction data

Programming

2016–Present **Postdoctoral Research Associate**, *Los Alamos Nat'l Lab*, Los Alamos, NM.
- Contributed to software for fitting experimental data with metaheuristic algorithms (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 rule-based modeling languages (TRuML)

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 analytical tools to estimate information theoretic quantities (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, BioNetGen)

Teaching

2016–2018 **Mentor**, Los Alamos, NM.
- Guided summer students visiting Los Alamos National Lab in various modeling and software development 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

2017 *ACM-BCB* – TRuML: A translator for rule-based modeling languages

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

Publications

Eshan D. Mitra, **Suderman, Ryan**, Joshua Colvin, Alexander Ionkov, Andrew Hu, Herbert M. Sauro, Richard G. Posner, and William S. Hlavacek. PyBioNetFit and the biological property specification language. *IScience*, 19:1012–1036, 2019.

Suderman, Ryan, Eshan D. Mitra, Yen Ting Lin, Keesha E. Erickson, Song Feng, and William S. Hlavacek. Generalizing Gillespie's direct method to enable network-free simulations. *Bulletin of Mathematical Biology*, 81:2822–2848, 2018.

Keesha E. Erickson, Oleksii S. Rukhlenko, Md Shahinuzzaman, Kalina P. Slavkova, Yen Ting Lin, **Suderman, Ryan**, Edward C. Stites, Marian Anghel, Richard G. Posner, Dipak Barua, Boris N. Kholodenko, and William S. Hlavacek. Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. *Plos Comp Biol*, 15:e1006706, 2019.

William S. Hlavacek, Jennifer Longo, Lewis R. Baker, María del Carmen Ramos Álamo, Alexander Ionkov, Eshan D. Mitra, **Suderman, Ryan**, Keesha E. Erickson, Raquel Dias, Joshua Colvin, Brandon R. Thomas, and Richard G. Posner. *A step-by-step guide to using BioNetFit*, pages 391–419. Methods in Molecular Biology. Humana Press, New York, NY, 2019.

Suderman, Ryan, G Matthew Fricke, and William S Hlavacek. *Using RuleBuilder to graphically define and visualize BioNetGen-language patterns and reaction rules*, pages 33–42. Methods in Molecular Biology. Humana Press, New York, NY.

Suderman, Ryan and Eric J Deeds. Intrinsic limits of information transmission in biochemical signalling motifs. *J R Soc Interface Focus*, 8:20180039, 2018.

Srgjan Civciristov, Andrew M. Ellisdon, **Suderman, Ryan**, Cindy K. Pon, Bronwyn A. Evans, Oded Kleifeld, Steven J. Charlton, William S. Hlavacek, Meritxell Canals, and Michelle L. Halls. Preassembled GPCR signaling complexes mediate unique cellular responses to ultra-low ligand concentrations. *Science Signaling*, 11, 2018.

Suderman, Ryan and William S. Hlavacek. TRuML: A Translator for Rule-Based Modeling Languages. In *Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology,and Health Informatics*, ACM-BCB '17, pages 372–377, New York, NY, USA, 2017. ACM.

Suderman, Ryan, 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*, 114(22):5755–5760, 2017a.

Suderman, Ryan, Addison Schauer, and Eric J Deeds. Understanding the dynamics of scaffold-mediated signaling. *bioRxiv*, 2017b.

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