RYAN SUDERMAN

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http://ryants.github.io

RESEARCH EXPERIENCE

Los Alamos National Laboratory ⠀⠀⠀⠀⠀⠀April 2016 - present
Postdoctoral Research Associate ⠀⠀⠀⠀⠀⠀*Los Alamos, NM*

· Worked with cell biologists to develop a model of 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
· Co-appointment with the Spatiotemporal Modeling Center at the University of New Mexico, a National Center for Systems Biology as designated by the NIH

University of Kansas ⠀⠀⠀⠀⠀⠀February 2011 - March 2016
Graduate Research Assistant ⠀⠀⠀⠀⠀⠀*Lawrence, KS*

· Constructed and analyzed rule-based models of biochemical interaction networks
· Applied information theoretic techniques to determine statistical dependencies in biological data sets
· Performed statistical analyses of protein interaction data using hierarchical clustering algorithms

Goshen College ⠀⠀⠀⠀⠀⠀January 2009 - August 2009
Independent Study ⠀⠀⠀⠀⠀⠀*Goshen, IN*

· Implemented a model of cancer resource consumption using cellular automata with Maple modeling software

EDUCATION

University of Kansas ⠀⠀⠀⠀⠀⠀*March 2016*
Ph.D. in Computational Biology ⠀⠀⠀⠀⠀⠀3.72 / 4.00

Goshen College ⠀⠀⠀⠀⠀⠀*August 2009*
B.A. in Mathematics ⠀⠀⠀⠀⠀⠀3.54 / 4.00
Concentration in Biology

COURSE HIGHLIGHTS

Graduate

· Dynamical Systems Biology, Formal Languages and Automata, Phys. Chemistry, Structural Biophysics

Undergraduate

· Differential Equations, Linear Algebra, Discrete Mathematics, Programming Techniques

Independent

· Functional Programming Techniques

TEACHING EXPERIENCE

q-bio Summer School ⠀⠀⠀⠀⠀⠀July 2016
Guest Lecturer ⠀⠀⠀⠀⠀⠀*Albuquerque, NM*

- Lectured on various global parameter fitting algorithms for kinetic Monte Carlo simulations
- Discussed the implementation of computational tools used for fitting experimental data in systems biology
- Lead a tutorial on developing models using the ML-Rules multi-level rule-based modeling framework

Independent   June 2012-May 2015
Tutor   *Lawrence, KS*

- Tutored in mathematics and biology (middle school though college-level material)

University of Kansas   September 2011 - May 2012
Graduate Teaching Assistant   *Lawrence, KS*

- Taught two semesters of an introductory biology laboratory (3 sections per semester)
- Lectured on the theory behind the methods used in the lab
- Guided students through basic experimental methods in molecular biology

PROGRAMMING EXPERIENCE

Los Alamos National Laboratory   April 2016-present
Postdoctoral Research Associate   *Los Alamos, NM*

- Tested and debugged software for fitting rule-based models to experimental data
- Adapted a web-based visualization client for use as a standalone Java application
- 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)

Orion Health   June 2015 - August 2015
Software Engineer Intern   *Scottsdale, AZ*

- Implemented parallelized calculations with Apache Spark for analyzing healthcare data
- Contributed to an existing code base for stratification of patient populations using Elasticsearch
- Participated in an Agile software development environment

University of Kansas   February 2011 - March 2016
Graduate Research Assistant   *Lawrence, KS*

- Developed an tool to estimate unbiased information theoretic quantities (ryants.github.io/EstCC)
- Implemented algorithms to sample continuous-time Markov chains using Monte Carlo methods
- Submitted and managed cluster-based jobs via the PBS queuing system

Independent

- Contributed to open-source projects designed to facilitate systems biology modeling in Python (PySB.org)

TECHNICAL SKILLS

Programming Languages	Scala, Python Java, C++, Perl, R
Domain Specific Languages	Kappa, BioNetGen, ML-Rules (rule-based modeling) Maple, octave, LaTeX
Tools & Utilities	git, bash, sbt/maven, IntelliJ IDEA, eclipse, xmgrace
Operating Systems	Mac OS X, Linux
Productivity Suites	Microsoft Office, Omnigraffle

OUTREACH

Undergraduate Research Symposium
Judge

April 25, 2015
University of Kansas, Lawrence, KS

· Judged undergraduate research projects in the biological sciences

Kansas DNA Day
Ambassador

April 22, 2015
Olathe Northwest High School, Olathe, KS

· Discussed recent scientific advances with high school students and organized relevant classroom activities

Douglas Co. Science Fair
Judge

February 6, 2014
West Middle School, Lawrence, KS

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

AWARDS

· University Graduate Fellowship for 2015-16

· Finalist in 2012 KU Graduate Research Competition (advanced graduate studies category)

SOCIETY MEMBERSHIPS

National Postdoctoral Association	April 2016-present
Biophysical Society	December 2014-present
Sigma Chi Research Organization	May 2012-May 2013
AAAS	April 2012-March 2016

CONFERENCES

Date	Conference	Contributed Talk
August 2015	q-bio	*Information flow in single cells and cellular populations*

Date	Conference	Contributed Poster
February 2017	Biophysical Society	*A theoretical analysis of the potential influence of ITAM pairs on Syk recruitment dynamics*
September 2016	Systems Approaches in Immunology and Infectious Diseases	*Dynamical effects of multimeric ring ring formation in multivalent antigen-antibody interactions*
August 2016	q-bio	*Intrinsic limits of information transmission in biochemical signaling networks*
February 2015	Biophysical Society	
October 2014	MPI	*Rules for scaffold assembly in signaling networks*
August 2014	q-bio	
November 2012	MPI	*Machines vs. Ensembles*
August 2012	q-bio	*Ensemble signaling in MAPK cascades*

PUBLICATIONS

1. Dias*, R., Suderman*, R., Thomas, B., Razi, A., Martin-Fernandez, M. L., Clayton, A. H. A., Hlavacek, W. S. & Posner, R. G. BioNetFit2: Global fitting of multiple models using metaheuristic optimization. *manuscript in preparation* (2017).

2. Dias, R., Suderman, R., Thomas, B., Razi, A., Clayton, A. H. A., Hlavacek, W. S. & Posner, R. G. in *Modeling Biomolecular Site Dynamics* (ed Hlavacek, W. S.) (2017, accepted).

3. Schideler*, T., Suderman*, R., Palsuledesai, C., Cleyrat, C., Hlavacek, W. S. & Wandinger-Ness, A. Epidermal growth factor receptor signaling exerts control over endosomal transport through activation of Rab5 and Rab7. *manuscript in preparation* (2017).

4. Suderman, R. & Deeds, E. J. Intrinsic Limits of Information Flow in Biochemical Networks. *manuscript in preparation* (2017).

5. Suderman, R. & Deeds, E. J. in *Modeling Biomolecular Site Dynamics* (ed Hlavacek, W. S.) (2017, accepted).

6. Suderman, R. & Hlavacek, W. S. TRuML: A Translator for Rule-Based Modeling Languages. *manuscript in submission* (2017).

7. Suderman, R., Schauer, A. & Deeds, E. J. Dynamical Properties of Distinct Scaffold Assembly Paradigms. *manuscript in submission* (2017).

8. Suderman, R., Bachman, J., Smith, A., Sorger, P. & Deeds, E. J. Fundamental trade-offs between information flow in single cells and cellular populations. *PNAS, manuscript in press.* doi:`10.1073/pnas.1615660114` (2017).

9. Suderman, R., Fricke, G. M. & Hlavacek, W. S. in *Modeling Biomolecular Site Dynamics* (ed Hlavacek, W. S.) (2017, accepted).

10. Suderman, R., Schwartz, S. L., Lidke, D. S. & Hlavacek, W. S. The Role of Paired ITAMs in Syk recruitment. *manuscript in preparation* (2017).

11. Suderman, R. & Deeds, E. J. Machines vs. Ensembles: Effective MAPK Signaling through Heterogeneous Sets of Protein Complexes. *PLoS Computational Biology* **9,** e1003278 (Oct. 2013).