

# SEAN HACKETT

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## Summary of Qualifications:

- Investigates questions in systems biology and biochemistry from an experimentally-driven, computational perspective
- Analyzes genomic datasets using statistically rigorous methods and integrates resulting data in principled ways
- Has a deep understanding of biology and biochemistry
- Excels at communicating with diverse audiences both in writing and orally

**Skills:** *Research:* statistics, machine learning, systems biology, metabolomics, proteomics, genetics

*Computational:* R (dplyr, purrr, ggplot2, devtools, shiny), Python (Pandas, Jupyter, RDKit), Git, UNIX, L<sup>A</sup>T<sub>E</sub>X, SQL

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EDUCATION	Princeton University <b>Ph.D., Quantitative and Computational Biology</b> <ul style="list-style-type: none"><li>• Thesis: <i>Quantitative Analysis of Metabolism and Protein Abundance Using Integrative 'Omics</i></li><li>• DOE Office of Science Graduate Fellowship (SCGF): 2012 - 2015</li></ul> Cornell University <b>B.S., Biological Sciences</b> <ul style="list-style-type: none"><li>• Thesis: <i>Candidate gene analysis of German shepherd dogs to identify genes contributing to arrhythmogenesis</i></li><li>• Concentration in Genetics and Development</li><li>• <i>Magna Cum Laude</i> with Distinction in Research</li></ul>	Princeton, New Jersey November 2015  Ithaca, New York June 2006
RESEARCH MANAGER	Calico Labs <ul style="list-style-type: none"><li>• Managed five data scientists and one project manager where I helped to reorganize the Computing group to improve impact and collaboration.</li></ul>	S. San Francisco, CA Feb 2018 - Present
DATA SCIENTIST	<ul style="list-style-type: none"><li>• Developed an automated metabolomics pipeline which streamlined data normalization and compound identification.</li><li>• Improved approaches for finding causal regulatory connections from a massive transcriptional perturbation experiment.</li></ul>	Jan 2017 - Present
POSTDOCTORAL ASSOCIATE	Princeton University, Lewis-Sigler Institute <ul style="list-style-type: none"><li>• Supervisor: John Storey, Director of the Center for Statistics and ML</li><li>• Applied methods from topic modeling to identify latent variables affecting high-dimensional sport data.</li><li>• Mapped QTLs of yeast competitive growth phenotypes.</li></ul>	Princeton, NJ Dec 2015 - Jan 2017
GRADUATE FELLOW	Princeton University, Quantitative and Computational Biology <ul style="list-style-type: none"><li>• Adviser: Josh Rabinowitz, Professor of Chemistry and Genomics</li><li>• Supervized two graduate students performing systems biology research.</li><li>• Developed a scalable algorithm for combining metabolomics, proteomics and fluxes to provide novel insight into how metabolism is controlled. This allowed me to identify 3 novel instances of metabolic regulation and to dissect how metabolite and enzyme concentrations jointly drive metabolic flux. (DOE grant DE-SC0012461 was awarded to continue this research.)</li><li>• Identified a pattern of metabolite changes in primary human pancreatic tumors, which led to the discovery that intact extracellular proteins are a major source of nutrients in cancer.</li></ul>	Princeton, NJ Sep 2010 - Dec 2015
RESEARCH SPECIALIST	Cornell University, Molecular Biology and Genetics <ul style="list-style-type: none"><li>• Supervisor: Andy Clark, Professor of Population Genetics</li><li>• Mentored five undergraduates working on <i>Drosophila</i> genetics.</li></ul>	Ithaca, NY June 2006 - Sep 2010

## SELECTED PUBLICATIONS

- [Sean R. Hackett](#), Edward A. Baltz, Marc Coram, Bernd J. Wranik, Griffin Kim, Adam Baker, Minjie Fan, David G. Hendrickson, Marc Brendl, R. Scott McIsaac. *Learning causal networks using inducible transcription factors and transcriptome-wide time serie*. *Molecular Systems Biology*, 16 (3), 2020.
- Sam S. Schoenholz, [Sean Hackett](#), Laura Deming, Eugene Melamud, Navdeep Jaitly, Fiona McAllister, Jonathon O'Brien, George Dahl, Bryson Bennett, Andrew Dai, Daphne Kohler. *Peptide-spectrum matching from weak supervision*. ArXiv.
- [Sean R. Hackett](#) and John D. Storey. *Mixed Membership Martial Arts: Data-Driven Analysis of Winning Martial Arts Styles*. MIT Sloane Sports Conference, 2017.
- [Sean R. Hackett](#), Vito R.T. Zanolli, Wenxin Xu, Jonathan Goya, Junyoung O. Park, David H. Perlman, Patrick A. Gibney, David Botstein, John D. Storey, and Joshua D. Rabinowitz. *Systems-level analysis of mechanisms regulating yeast metabolic flux*. *Science*, 345, 2016.
- JK Grenier, JR Arguello, M Cardoso Moreira, S Gottipati, J Mohammed, [SR Hackett](#), R Boughton, AJ Greenberg & AG Clark. *Global Diversity Lines - A five-continent reference panel of sequenced Drosophila melanogaster strains*. *G3*, 5(4), 2015.
- J Kamphorst, M Nofal, C Commisso, [SR Hackett](#), W Lu, E Grabocka, G Miller, JA Drebin, MG Vander Heiden, D Bar-Sagi, CB Thompson, JD Rabinowitz. *Human pancreatic cancer tumors are nutrient poor and the tumor cells actively scavenge extracellular protein*. *Cancer Research*, 75, 2015.
- Robin Mathew, Sinan Khor, [Sean R. Hackett](#), Joshua D. Rabinowitz, David H. Perlman & Eileen White. *Functional role of autophagy-mediated proteome remodeling in cell survival signaling and innate immunity*. *Molecular Cell*, 55(6), 2014.
- Jeffrey S. Bruenig, [Sean R. Hackett](#), Joshua D. Rabinowitz & Leonid Kruglyak. *Genetic basis of metabolome variation in yeast*. *PLoS Genetics*, 2013.
- C Commisso., SM Davidson, RG Soydaner-Azeloglu, SJ Parker, JJ Kamphorst, [SR Hackett](#), E Grabocka, M Nofal, JA Drebin, CB Thompson, JD Rabinowitz, CM Metallo, MG Vander Heiden & D Bar-Sagi. *Macropinocytosis of protein is an amino acid supply route in Ras-transformed cells*. *Nature*, 497, 2013.
- AJ Greenberg, [SR Hackett](#), LG Harshman & AG Clark. *Environmental and genetic perturbations reveal different networks of metabolic regulation*. *Molecular Systems Biology*, 7:563, 2011.
- AJ Greenberg, [SR Hackett](#), LG Harshman & AG Clark. *A hierarchical bayesian model for a novel sparse partial diallel crossing design*. *Genetics*, 185(1):361-373, June 2010.

## TALKS

- 2019 Cold Spring Harbor Cellular Dynamics and Models.  
*Expansive perturbation profiling reveals a causal transcriptional network*
- 2017 MIT Sloane Sports Analytics Conference. Research Paper Competition finalist.  
*Mixed Membership Martial Arts: Data-Driven Analysis of Winning Martial Arts Styles*
- 2016 Genomic Sciences Program Annual PI Meeting.  
*Systems-Level Analysis of Mechanisms Controlling Yeast Metabolic Flux*
- 2014 Agilent Emerging Omics Research Tour: 'Omics and Integrated Biology.  
*Exploring Metabolic Regulation Via Integrative 'Omics*.
- 2014 Yeast Genetics Meeting. Plenary Talk: Environmental Sensing Networks.  
*An Integrated 'Omics Approach to Large-Scale Quantitative Analysis of Cellular Metabolic Regulation*
- 2013 International Conference on Systems Biology. Parallel Session: Complex Genetic Traits  
*Genetic Basis of Metabolome Variation in Yeast*

## TEACHING EXPERIENCE

INSTRUCTOR	Introductory Data Analysis with R Course (3 sessions at Calico)	Fall 2017
TEACHING ASSISTANT	RStudio Master R Developer Workshop (advanced R workshop taught by Hadley Wickham)	September 2016
INSTRUCTOR	Statistical Programming with R workshop (Princeton)	March 2015
	Statistical Programming with R workshop (Princeton)	October 2014
TEACHING ASSISTANT	An integrated, mathematically and computationally sophisticated introduction to biochemistry, molecular biology, genetics, genomics and evolution (undergraduate course taught by David Botstein, Eric Weichaus & Peter Andolfatto)	Fall 2012
	Advanced Statistics for Biology (graduate course taught by John Storey)	Spring 2012