

Samantha J. Riesenfeld

CONTACT INFORMATION	Broad Institute of MIT and Harvard 415 Main St, Rm 6035 Cambridge, MA 02142	riesen@broadinstitute.org http://www.broadinstitute.org/~riesen/
RESEARCH INTERESTS	<ul style="list-style-type: none">• Data science, including statistical modeling and algorithms, in molecular biology• Immunology, with emphasis on the interaction of the immune and nervous systems and the role of innate lymphoid cells in inflammatory responses• Intra- and intercellular circuits regulating gene expression, function, and development• Comparative genomics, evolution, and metagenomics	
EDUCATION	<p>University of California, Berkeley, CA Ph.D., Computer Science, December 2007 Advisor: Richard M. Karp Dissertation: <i>Optimization and Reconstruction over Graphs</i></p> <p>Harvard University, Cambridge, MA B.A., Mathematics and Computer Science, June 2000</p>	
TRAINING AND WORK EXPERIENCE	<p>Postdoctoral Fellow / Associate, June 2013–Present Broad Institute of MIT and Harvard, Cambridge, MA Advisor: Aviv Regev</p> <p>Postdoctoral Research Fellow / Sponsored Staff (joint appointment), January 2014–Present Brigham and Women’s Hospital, Harvard Medical School, Boston, MA Advisor: Vijay K. Kuchroo</p> <ul style="list-style-type: none">• Analyzed single-cell transcriptomic data to characterize subpopulations of innate lymphoid cells (ILCs) resident in lung and skin, in mouse models of allergy and disease.• Collaboratively discovered new ILC response pathways, including a neuronal-ILC interaction in the lung and a trajectory through mixed immunity types in skin ILCs.• Adapted statistical machine learning techniques, such as latent Dirichlet allocation and zero-inflated negative binomial regression, to novel biological contexts.• Collaboratively developed a diffusion-based computational approach to reconstruct the transcriptional trajectories of 25 cell types during zebrafish embryogenesis. <p>Postdoctoral Fellow, November 2008–May 2013 Gladstone Institutes, University of California, San Francisco, CA Advisor: Katherine S. Pollard</p> <ul style="list-style-type: none">• Designed DNA oligomer libraries with provably optimal k-mer coverage using reverse-complementary de-Bruijn-like sequences. Analyzed data from <i>in vivo</i> transgenic zebrafish assays to infer tiny enhancer-like elements (<15 vs. typical 500 base pairs).• Implemented pipeline to simulate gene-family shotgun metagenomic data, and used it to characterize accuracy of phylogenetic methods in novel contexts. <p>Postdoctoral Intern, January–June 2008 University of California, Berkeley, CA Advisor: Dorit S. Hochbaum</p> <ul style="list-style-type: none">• Researched applications of advanced convex optimization techniques.	

Graduate Student Researcher, August 2002–December 2007

University of California, Berkeley, CA

Advisor: Richard M. Karp

- Solved discrete optimization problems in theoretical computer science, such as designing approximation algorithms for minimum-cost bounded-degree spanning trees and establishing the query complexity of sorting partially ordered sets.

Medical Assistant, September 2000–July 2001

Planned Parenthood Santa Fe Medical Office, Santa Fe, NM

Supervisor: Kristen Kikut

- Performed phlebotomies, patient intake, counseling on family planning.

Research Intern, February–August 1998

INRIA, Sophia-Antipolis, France

Advisor: Olivier Faugeras

- Programmed a pilot project in image-based-rendering for computer vision.

HONORS AND
AWARDS

- *BroadIgnite award*, supports highly innovative, high-risk projects at Broad, 2018–19
- *Top Poster award* (\$1000), Brigham Research Institute Lung Research Center Annual Symposium & Poster Session, 2017
- *NIH Ruth L. Kirschstein National Research Service Award for Individual Postdoctoral Fellows* (Parent F32), 2011–14
- *PhRMA Foundation Post Doctoral Fellowship in Informatics*, 2011
- *NSF Graduate Research Fellowship*, 2001–03, 2004–05
- *B.A. awarded cum laude with Honors in Field* for the senior thesis, 2000
- *John Harvard Scholarships (Annual Rank Group I)*, 1997–99
- *Undergraduate Teaching Fellow* (paid, selective position) for three courses, 1997–99
- *NSF Research Experiences for Undergraduates* (summer internship), 1997
- *National Merit Scholar*, 1995

LANGUAGES

Programming: Skilled in R, recent convert to Python; experienced in C, C++, Perl; familiar with Java, Lisp, MATLAB.

Human: Working proficiency in Italian and French.

KEY
PUBLICATIONS

Lun A*, **Riesenfeld SJ***, Andrews T*, Dao P*, Gomes T*, participants in the 1st Human Cell Atlas Jamboree, Marioni JC[†]. **Distinguishing cells from empty droplets in droplet-based single-cell RNA sequencing data.** *Genome Biology*. 20:63 (2019).

Wallrapp A*, Burkett PR*, **Riesenfeld SJ***, Kim S, Christian E, Abdulnour RE, Herbst RH, Khan P, Chiu IM, Levy BD, Regev A, Kuchroo VK[†]. **CGRP negatively regulates alarmin-driven ILC2 responses.** (2019) [In review]

* These authors contributed equally to this work. In theoretical computer science, author order is typically alphabetical.

[†] Corresponding author.

Bielecki, P*, **Riesenfeld SJ***, Kowalczyk MS*, Vesely MCA, Kroehling L, Yaghoubi P, Dionne D, Jarret A, Steach HR, McGee HM, Porter CBM, Licon-Limon P, Bailis W, Jackson R, Gagliani N, Locksley RM, Regev A[†], Flavell RA[†]. **Skin inflammation driven by differentiation of quiescent tissue-resident ILCs into a spectrum of pathogenic effectors.** *bioRxiv* 461228 [Preprint] (2018).

Farrell JA*, Wang Y*, **Riesenfeld SJ**, Shekhar K, Regev A[†], Schier A[†]. **Single-cell reconstruction of developmental trajectories during zebrafish embryogenesis.** *Science*. 360(6392), eaar3131 (2018).

Wallrapp A*, **Riesenfeld SJ***, Burkett PR*, Abdulnour RE, Nyman J, Dionne D, Hofree M, Cuoco MS, Rodman C, Farouq D, Haas BJ, Tickle TL, Trombetta JJ, Baral P, Klose CSN, Mahlaköiv T, Artis D, Rozenblatt-Rosen O, Chiu IM, Levy BD, Kowalczyk MS[†], Regev A[†], Kuchroo VK[†]. **The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation.** *Nature*. 549(7672):351-356 (2017).

Highlighted in: “Neuroimmunology: ILC2s touch a nerve.” *Nature Reviews Immunology*. 17:661 (2017). “Commentary: Neuronal regulation of type 2 innate lymphoid cells via neuromedin U.” *Frontiers in Pharmacology*. 9:230 (2018).

Smith RP*, **Riesenfeld SJ***, Holloway AK, Li Q, Murphy KK, Feliciano NM, Orecchia L, Oksenberg N, Pollard KS[†], Ahituv N[†]. **A Compact, In Vivo Screen of All 6-mers Reveals Drivers of Tissue-Specific Expression and Guides Synthetic Regulatory Element Design.** *Genome Biology*. 14:R72 (2013).

Highlighted in: “What makes for a powerful enhancer sequence?” BioMed Central blog *Biome* (2013). <http://www.biomedcentral.com/biome/what-makes-for-a-powerful-enhancer-sequence/>

Riesenfeld SJ[†], Pollard KS. **Beyond Classification: Gene-Family Phylogenies from Shotgun Metagenomic Reads Enable Accurate Community Analysis.** *BMC Genomics*, 14:419 (2013).

Daskalakis C*, Karp RM*, Mossel E*, **Riesenfeld S***, Verbin E*. **Sorting and Selection in Posets.** *SIAM Journal on Computing*, 40(3), 597–622 (2011).

Chaudhuri K*, Rao S*, **Riesenfeld S***, Talwar K*. **A Push-Relabel Algorithm for Approximating the Minimum-Degree MST Problem and Its Generalization to Matroids.** *Theoretical Computer Science*, 410(44): 4489–4503 (2009). Invited submission.

Chaudhuri K*, Rao S*, **Riesenfeld S***, Talwar K*. **What Would Edmonds Do? Augmenting Paths and Witnesses for Degree-Bounded MSTs.** *Algorithmica*, 55(1):157–189 (2009). Invited submission.

ADDITIONAL PUBLICATIONS

Dani N*, Herbst RH*, Habib N*, Head J, Dionne D, Nguyen L, McCabe C, Cui J, Shipley F, Jang A, Rodman C, **Riesenfeld SJ**, Zhang F, Rozenblatt-Rosen O, Regev A[†], Lehtinen MK[†]. **A cellular and spatial map of the choroid plexus across brain ventricles and ages.** (2019) [Submitted]

Burkett PR, Kim S, **Riesenfeld SJ**, Wallrapp A, Christian E, Abdulnour RE, Regev A, Levy BD, Kuchroo VK[†]. **Alveolar macrophages regulate type 2 immunity via CLEC-2.** (2019) [In review]

Wallrapp A, **Riesenfeld SJ**, Burkett PR, Kuchroo VK[†]. **Type 2 innate lymphoid cells in the induction and resolution of tissue inflammation.** *Immunological Reviews*. 286:53–73 (2018). [Invited review]

Capra JA, Carbone L, **Riesenfeld SJ**, Wall JD[†]. **Genomics Through the Lens of Next-Generation Sequencing.** *Genome Biology*, 11:306 (2010). [Invited review]

Sharpton TJ[†], **Riesenfeld SJ**, Kembel SW, Ladau J, O’Dwyer JP, Green JL, Eisen JA, Pollard KS. **PHYLOTU: A High-Throughput Procedure Quantifies Microbial Community Diversity and Resolves Novel Taxa from Metagenomic Data.** *PLoS Computational Biology*, 7(1): e1001061 (2011).

Daskalakis C*, Karp RM*, Mossel E*, **Riesenfeld S***, Verbin E*. **Sorting and Selection in Posets.** *Proc. 20th Annual ACM-SIAM Symposium on Discrete Algorithms*, 392–401 (2009).[‡]

Highlighted in: Fortnow L, Gasarch W. “Sorting a Partial Order.” *Computational Complexity Weblog* (2009). <http://blog.computationalcomplexity.org/2009/01/sorting-partial-order.html>

Riesenfeld S. Optimization and Reconstruction over Graphs. Ph.D. Thesis, Electrical Engineering and Computer Sciences Department, UC Berkeley, CA. 150 p. *Technical Report*, No. UCB/EECS-2008-6 (2008).

Chaudhuri K*, Rao S*, **Riesenfeld S***, Talwar K*. **A Push-Relabel Algorithm for Approximating Degree Bounded MSTs.** *Proc. 33rd Intl. Colloq. on Automata, Languages, and Programming*, 191–201 (2006).[‡]

Chaudhuri K*, Rao S*, **Riesenfeld S***, Talwar K*. **What Would Edmonds Do? Augmenting Paths and Witnesses for Degree-Bounded MSTs.** *Proc. 8th Intl. Workshop on Approximation Algorithms for Combinatorial Optimization Problems*, 26–39 (2005).[‡]

Bogdanov A*, Maneva E*, **Riesenfeld S***. **Power-Aware Base Station Positioning for Sensor Networks.** *Proc. INFOCOM 23rd Annual Joint Conf. of IEEE Computer and Communications Societies*, 1:575–585 (2004).[‡]

SELECTED
PRESENTATIONS

“Quiescent tissue resident ILCs give rise to a continuous spectrum of ILC2 and ILC3 populations in response to the IL-23 stimulation.” (talk) *ILC2018*, University of Tokyo, Tokyo, Japan (2018).

“Using topic models to analyze the spectrum of ILC states in homeostatic and psoriatic skin.” (talk) *Single-Cell Genomics 2018*, Broad Institute, Cambridge, MA (2018).

“Topic modeling the transcriptional spectrum of innate lymphoid cells.” (talk) Models, Inference & Algorithms seminar, Broad Institute, Cambridge, MA (2018).

“Neuropeptide receptors and regulation of ILC2 function.” (talk) *Food Allergy Science Initiative Scientific Advisory Board Meeting*, Broad Institute, Cambridge, MA (2018).

“Using single-cell RNA-seq to identify novel neuro-immune pathways in allergy.” (talk) *Broad Institute’s Thirteenth Annual Retreat*, Hynes Convention Center, Boston, MA (2017).

[‡] In computer science, full papers are typically submitted first to conferences for peer review, and may be later published in journals.

- “Using single-cell RNA-seq to identify novel neuro-immune pathways in allergic inflammation.” (talk) *Physical Concepts and Computational Models in Immunology Symposium*, MIT, Cambridge, MA (2017).
- “Neuropeptide amplification of allergic inflammation.” (talk) *Broad Institute Board of Scientific Counselors Meeting*, Broad Institute, Cambridge, MA (2017).
- “Neuromedin U receptor-1 signaling promotes IL-25-driven inflammatory innate lymphoid cells.” (Top Poster, \$1000) *Brigham Research Institute Lung Research Center Annual Symposium & Poster Session*, Brigham and Women’s Hospital, Boston, MA (2017).
- “Identifying T-cell Subpopulations from Single-Cell Proteomic Data Using Locality-Sensitive Hashing and Markov Clustering.” (poster) *Systems Biology: Global Regulation of Gene Expression Meeting*, Cold Spring Harbor, NY (2014).
- “Optimized Oligomer Libraries to Screen Short Synthetic Enhancers *in Vivo*.” (talk) *Statistics and Genomics Seminar*, UC Berkeley, CA (2012).
- “A Novel Algorithm Enables *in Vivo* Characterization of Short Regulatory Sequences.” (talk) *Gladstone Scientific Advisory Board Meeting*, Gladstone Institutes, UCSF, San Francisco, CA (2010).
- “Building Phylogenies with Metagenomic Sequence Reads.” (talk) *Biology of Genomes Meeting*, Cold Spring Harbor, NY (2010).
- “Sorting Algorithms for Partial Orders.” (talk) *Bay Area Theory Symposium (BATS)*, IBM Almaden Research Center, Almaden, CA (2006).
- “A Push-Relabel Algorithm for Approximating Degree Bounded MSTs.” (talk) *33rd International Colloquium on Automata, Languages, and Programming (ICALP 2006)*, Venice, Italy (2006).
- “Inferring Reticulate Evolution Networks from Consensus Gene Trees.” (talk) *Cyberinfrastructure for Phylogenetic Research (CIPRES) Annual All-Hands Meeting*, San Diego, CA (2005).
- “Power-Aware Base Station Positioning for Sensor Networks.” (talk) *INFOCOM 2004, 23rd Annual Joint Conference of the IEEE Computer and Communications Societies*, Hong Kong, China (2004).

TEACHING
EXPERIENCE

Mentor for PhD students and computational scientists

Broad Institute, Cambridge, MA

- Caroline B. M. Porter (2017–18): Single-cell RNA-seq analysis of placental NK cells
- Rebecca H. Herbst (2017–18): Single-cell RNA-seq analysis in tumor immunology
- Brian Cleary (2013–14): Locality-sensitive hashing for single-cell proteomic T-cell data

Gladstone Institutes, University of California, San Francisco, CA

- Aram Avila-Herrera (2011): Phylogeny and simulations of DNA sequences
- Genevieve D. Erwin (2009): Programming and algorithms for biology

Graduate Student Instructor, Spring Semester 2004

University of California, Berkeley, CA

- Efficient Algorithms and Intractable Problems

Teaching Fellow, Fall Semesters 1997–99

Harvard University, Cambridge, MA

- Efficient Algorithms (1999, graduate level), Honors Linear Algebra and Real Analysis I (1998), Introduction to Formal Systems and Computation (1997)

SERVICE

Steering Committee member, Models, Inference & Algorithms Broad Initiative (<https://www.broadinstitute.org/scientific-community/science/mia/models-inference-algorithms>)

Reviewer for: Bioinformatics, Statistical Applications in Genetics and Molecular Biology, ACM-SIAM Symposium on Discrete Algorithms

SOFTWARE

Software developed for research and made available to the community:

- **CITE-seq Analysis** (https://github.com/sriesenfeld/CITE-seq_Analysis)
Custom alignment script and pipeline framework to quantify digital expression in an antibody-derived tag (ADT) library.
- **CompoHeatMap** (<https://github.com/sriesenfeld/CompoHeatMap>)
R code for very customizable, annotated heatmaps
- **MRCC Libraries** (<https://github.com/sriesenfeld/MRCC-Libraries/>)
Computes minimal reverse-complementary-covering DNA oligomer libraries
- **MetaPASSAGE** (<https://github.com/sriesenfeld/MetaPASSAGE/>)
Automates shotgun metagenomic simulations and streamlines data analysis

GRANTS

BroadIgnite Award, March 2018–February 2019.

“Machine learning approaches to explore connections between the nervous and immune systems”

Role: PI (Postdoctoral Associate)

\$40,000

NIH Ruth L. Kirschstein National Research Service Award for Individual Postdoctoral Fellows (Parent F32), September 2011–December 2014

“A Novel Approach to Decoding Vertebrate Gene Regulation” (# 5F32HD069168)

Role: PI (Postdoctoral Fellow)

Annual award: \$53,042 (2011); \$55,670 (2012); \$57,734 (2013)

PhRMA Foundation Postdoctoral Fellowship in Informatics, March–August 2011

“A Novel Approach to Decoding Vertebrate Gene Regulation”

Role: PI (Postdoctoral Fellow)

\$20,000 (Annual award: \$40,000 for 2011–13; relinquished after six months)

UCSF Program for Breakthrough Biomedical Research Integrative Research Award, 2009–10

“In Vivo Characterization of the Vertebrate Regulatory Code”

Role: Postdoctoral Fellow (Joint PIs: Katherine S. Pollard, Nadav Ahituv)

\$197,387

NSF Graduate Research Fellowship, 2001–05

Field: Computer Science – Theory

Role: PI/Fellow (Graduate Student Researcher)

Annual stipend: \$18,000 (2001); \$20,500 (2002); \$30,000 (2004)