

## SHARON GREENBLUM, PhD

240-506-0587 • 951 Marina Way S Unit I, Richmond CA 94804 • greensi@lbl.gov

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### Professional Summary

- *Computational biologist with breadth and depth*: drove analysis on projects spanning genomic, transcriptomic and metabolomic profiling of plants, population genetics of rapid adaptation in fruitflies, systems biology applied to the human gut microbiome, and pathway analysis of drug response in cancer patients
- *Trained communicator*: sought out enrichment from a number of selective and interactive communication training programs; coordinated SF's annual *taste of science* festival
- *Engaged advocate*: mentored high school, undergraduate, and graduate-level students; served as a community tutor and STEM education facilitator, co-chaired Stanford's Postdoctoral Association

### Professional Experience

**Joint Genome Institute, Genome Technologies Group, Berkeley, CA** **May 2019-present**

- Computational Biology Research Scientist supporting user projects and new technologies
- Developing robust analytic methods for single-cell transcriptomic profiling of various plant species
- Creating frameworks for integrating transcriptome and metabolome data to understand systems-level processes associated with biofuel production

**Stanford University, Department of Biology, Stanford, CA** **Nov 2015-April 2019**

- Postdoctoral Research Fellow in the laboratory of Dr. Dmitri Petrov
- Led computational analysis on a series of large-scale projects investigating the genomic basis of rapid seasonal adaptation in *Drosophila melanogaster*
- Engaged in long-term collaboration with Dr. Paul Schmidt's lab at the University of Pennsylvania

### Education

**University of Washington, Department of Genome Sciences, Seattle, WA** **Sept 2009-Dec 2014**

- PhD, Genome Sciences; Certificate in Computational Molecular Biology
- Thesis: *Metagenomic Systems Biology of the Human Gut Microbiome* (Adviser: Dr. Elhanan Borenstein)
- Applied network-based analyses to shotgun metagenomic data and uncovered systems-level properties associated with obesity and digestive disorders
- Designed an *in silico* pipeline to perform the first large-scale analysis of intra-species copy number variation among dominant human gut species directly from shotgun data

**Northwestern University, McCormick School of Engineering, Evanston, IL** **Sept 2003-June 2007**

- BS, Biomedical Engineering
- Specialization: Bioinformatics + Biomechanics

### Additional Research Experience

**Santa Fe Institute, Summer School in Complex Systems, Santa Fe, NM** **June-July 2015**

- Selected for intensive program on complex systems approaches to social and physical sciences
- Collaboratively designed an agent-based model of informal economies

**Stanford University, Hopkins Microbiology Course, Pacific Grove, CA** **June-July 2012**

- Selected for residential training course in microbiology, combining field work, theory, and informatics to isolate and identify bacterial populations in local ecosystems

**National Institutes of Health, National Cancer Institute, Rockville, MD** **Aug 2007-Sept 2009**

- Designed an informatics tool to score gene expression within the context of molecular pathways and identify pathways implicated in disease

- DePaul University, REU program in Medical Informatics, Chicago, IL** **June-Sept 2006**
- Developed a novel algorithm to automatically analyze DNA microarray images for DNA fingerprinting
- Denmark's International School/Roskilde University, Copenhagen, Denmark** **Jan 2006-May 2006**
- Completed an immersive study abroad program with coursework concentration in bioinformatics
- National Institutes of Health, Diagnostic Radiology Department, Bethesda, MD** **June-Sept 2005**
- Adapted wavelet analysis for colon polyp detection in virtual colonoscopy

## Communication Training

- HRP271: Scientific Communication & Media, Stanford University, Stanford, CA** **July-August 2018**
- Participated in career development course combining lecture, case study, and practical final project to develop critical skills for communicating science in academic and general media
- Improv for Communication Short Course, Stanford University, Stanford, CA** **May-June 2016**
- Participated in improvisational exercises to communicate scientific ideas
- Science Communication Fellowship, Pacific Science Center, Seattle, WA** **Sept 2014-Feb 2015**
- Selected for funded workshop series and mentoring on communication of science to general audiences
  - Developed and presented solo interactive exhibit at a nationally-renowned science museum
- UW Engage Communication Training Program, University of Washington, Seattle, WA** **Jan-May 2014**
- Selected for competitive program focused on oral and written science communication
  - Delivered research talk for a public audience at Town Hall Seattle *Science Now! Speaker Series*

## Leadership

- Founder + Coordinator, JGI Single Cell Journal Club** **2019-present**
- Lead a weekly discussion group of recent literature focused on new single cell 'omics technologies and analysis techniques
- Co-Chair, Stanford University Postdoctoral Association** **2016-2017**
- Led >2,200 Stanford postdocs in advocacy and community-building initiatives
  - Helped achieve 13% minimum salary increase for all Stanford postdocs
  - Elected Communications Officer (2017-present) and council member (2015-2019)
- Vice President, Stanford's Interdisciplinary Microbiome Perspectives group** **2016-2017**
- Secured funding, established a list-serve, and moderated meetings, for discussion group evaluating recent microbiome literature

## Teaching/Mentorship Experience

- Summer Research Mentor, Joint Genome Institute** **July-August 2020; 2021**
- Co-mentored a UC Merced undergraduate student in a project to automate single cell data visualization
  - Co-mentored a UC Merced graduate student in a project to develop an interactive app for exploring large-scale mutation data; mentee's project was selected for a talk at the annual JGI User Meeting
- Guest Lecturer, UC Berkeley** **February 2020, February 2022**
- Delivered lectures and created interactive coding activities on topics related to genomic resequencing and transcriptome data analysis in graduate level *Genomics and Computational Biology* course
- Tutor, Richmond Literacy For All Program (LEAP)** **August 2019-present**
- Work with Richmond community members 1-3 hours per week to help them prepare to take the GED
- Guest Lecturer, Stanford University** **May 2017; June 2018**

- Delivered lectures on *Current Topics in Population Biology* to first-year graduate students

**Summer Research Mentor, Stanford University**

**June-Sept 2016; 2017**

- Mentored/co-mentored three female high school students in computational biology, evolutionary genetics, and machine learning
- Guided co-mentee to achieve national semifinalist designation in the Siemens Competition

**Teaching Assistant, University of Washington, Seattle, WA**

**Sept - Dec 2011; Jan-March 2013**

- Led discussion sections, developed instructional content, provided individual support, assisted with exam design and grading, and delivered guest lectures for Intro to Genetics (senior-level undergraduate course) and Intro to Computational Molecular Biology (graduate level programming course)

**Tutor, Broadview Women's and Children's Shelter, Seattle, WA**

**June 2010-Feb 2015**

- Provided weekly individual assistance to K-12 students and single mothers enrolled in educational and career-development courses
- Received 2014 Volunteer of the Year Award for 100+ hours of service

## Awards

- NIH F32/NRSA Fellowship; 3 years of full funding (2017-2019)
- Stanford's CEHG (Center for Evolutionary and Human Genetics) Fellowship; 1 year of full funding (2016)
- EMBO Next Gen Immunology Conference travel scholarship (2015)
- Department nomination, UW Distinguished Thesis Award (2015)

## Academic Service

- Poster competition organizer: JGI User Meeting (2021)
- Steering committee member: 2021 LBNL Biosciences Annual Meeting (2021)
- NIH Library of Medicine Literature Selection Technical Review Committee (2020-present)
- Junior session chair and poster judge: 'Population Genetics and Evolution' at the *Drosophila Research Conference* (2018)
- Session co-organizer: 'Probing Microbiome Dynamics' at *SMBE 2017* (2017)
- Co-organizer: *Bay Area Postdoc Symposium* (2016)
- Session chair and poster judge: 'Evolution and Quantitative Biology' at the *GSA Allied Genome Conference* (2016)
- Reviewer for *NSF, Bioinformatics, Cell, Genome Biology, Nature Communications, PLoS Computational Biology, PLoS ONE, RECOMB Conference on Research in Computational Molecular Biology, Cell Metabolism*
- Associate Faculty Member: *Faculty of 1000* online reviewer database (2013-2015)

## Outreach

- Committee lead: Lawrence Berkeley Lab's Early Career resource group, Outreach committee (2022)
- Committee lead: Sustainable JGI, Remote/hybrid employee committee (2021-2022)
- Facilitator: Lawrence Berkeley Lab's 'Live Science' virtual demo on coding + hip-hop beats (2021)
- Facilitator + lecturer: Berkeley Lab Director's Apprenticeship program (2020-2022)
- Panelist: Science Accelerating Girls' Engagement in STEM (SAGE) virtual summer camp (2021)
- Team lead: National *taste of science* Festival, San Francisco chapter (2017-2018)
- Judge: Santa Clara's 'Synopsys Science + Tech Championship' (2016)
- Activity lead: Pacific Science Center's 'Science on Wheels' outreach program (2014)
- Mentor: NWABR Student Bio Expo program (Nov-Dec 2012)
- Exhibitor: Yakima Science Festival (2012) and Pacific Life Sciences Expo Day (June 2010-12)

## Publications

### Journal Articles

- Rudman S\*, Greenblum S\*, Rajpurohit S\*, Betancourt N, Hanna J, Tilk S, Yokoyama T, Petrov D, Schmidt P. (2022) Direct observation of adaptive tracking on ecological timescales in *Drosophila*. *Science*, in press. (prep-

rint at doi.org/10.1101/2021.04.27.441526). \*co-first authors

- Rudman S, **Greenblum S**, Hughes R, Rajpurohit S, Kiratli O, Lowder D, Lemmon S, Petrov D, Chaston J, Schmidt P (2019). Microbiome composition shapes rapid genomic adaptation of *Drosophila melanogaster*. *Proceedings of the National Academy of Sciences*, 116(40):20025-20032. (featured in *Science Daily*)
- Tilk S, Bergland A, Goodman A, Schmidt P, Petrov D, **Greenblum S** (2019). Accurate Allele Frequencies from Ultra-low Coverage Pool-Seq Samples in Evolve-and-Resequencing Experiments. *G3: GENES, GENOMES, GENETICS*, 9(12):4159-4168.
- **Greenblum S**, Carr R, Borenstein E (2015). Extensive strain-level copy number variation across human gut microbiome species. *Cell* 160:583-594. (featured on *Cell* cover, *Genomeweb*, *UW NewsBeat*, and *Science Daily*)
- **Greenblum S**, Chiu H, Levy R, Carr R, Borenstein E (2013). Towards a predictive systems-level model of the human microbiome: Progress, challenges, and opportunities. *Current Opinion in Biotechnology*, 24:810-820.
- Efroni S, Meerzaman D, Schaefer CF, **Greenblum S**, Soo-Lyu M, Hu Y, Cultraro C, Meshorer E, Buetow KH (2013). Systems analysis utilising pathway interactions identifies sonic hedgehog pathway as a primary biomarker and oncogenic target in hepatocellular carcinoma. *IET Systems Biology*, 7(6):243-51.
- **Greenblum S**, Turnbaugh PJ, Borenstein E (2011). Metagenomic systems biology of the human gut microbiome reveals topological shifts associated with obesity and inflammatory bowel disease. *Proceedings of the National Academy of Sciences*, 109(2):594-599. (featured in *This Week in PNAS*, *UW Today*, and *Science Daily*)
- **Greenblum S**, Efroni S, Schaefer C, Buetow K (2011). The Pathologist: An automated tool for pathway-centric analysis. *BMC Bioinformatics*, 12:133.
- Efroni S, Ben-Hamo R, Edmonson M, **Greenblum S**, Schaefer CF, Buetow KH (2011). Detecting Cancer Gene Networks Characterized by Recurrent Genomic Alterations in a Population. *PLoS ONE*, 6(1):e14437.
- Clifford R, Zhang J, Meerzaman D, Lyu M, Hu Y, Cultraro C, Finney R, Kelley J, Efroni S, **Greenblum S**, Nguyen C, Row W, Sharm S, Wu G, Yan C, Zhang H, Chung Y, Kim J, Park N, Song H, Buetow K (2010). Genetic variations at loci involved in the immune response are risk factors for hepatocellular carcinoma. *Hepatology* 52(6):2034-43.

#### Patents

- Summers R, Li J, Greenblum S (2008). Virtual Colonoscopy Via Wavelets. Patent No. 20080194946.

#### Presentations

##### Selected Talks

- “Parallelism of genomic response during rapid seasonal adaptation in *Drosophila melanogaster*”, *Society of Molecular Biology and Evolution (SMBE)*. Yokohama, Japan (July 2018).
- “Tracking parallel seasonal adaptation in *Drosophila melanogaster* populations”, *Bay Area Population Genetics Symposium*. UC Santa Cruz; Santa Cruz, CA (April 2018).
- “Tracking adaptation in *Drosophila melanogaster* populations”, *Stanford Postdoctoral Research Symposium*. Stanford University; Stanford, CA (Oct 2017).
- “Viewing Human Gut Strain Variation through a Functional Lens”, *Stanford Microbiome Bioinformatics Symposium*. Stanford University; Stanford, CA (May 2016).
- “Microbiome functional landscapes through a systems-level lens”, *EMBO Next Gen Immunology conference: From Host Genome to the Microbiome*. Weizmann Institute of Science; Tel Aviv, Israel (Feb 2016).
- “Metagenomic Systems Biology”, *UW Genome Sciences 10-year Anniversary Symposium*. University of Washington; Seattle, WA (Sept 2011).
- “Automated image analysis of noisy microarrays.” *Undergraduate Research Symposium*. Argonne National Laboratories; Chicago IL (Sept 2006).

##### Poster Presentations

- Greenblum S, Bergland A, Berner M, Rajpurohit S, Tilk S, Schmidt P, Petrov D. Genomics of rapid adaptation on seasonal timescales in *D. melanogaster*. *European Society of Evolutionary Biology*, Groningen, Netherlands (August 2017).
- Greenblum S, Bergland A, Berner M, Rajpurohit S, Tilk S, Schmidt P, Petrov D. Ultra low coverage evolve-and-resequence studies reveal the genomics of rapid adaptation on seasonal timescales in *D. melanogaster*.

*Drosophila Research Conference*, San Diego CA (April 2017).

- Greenblum S, Tilk S, Bergland A, Petrov D. Leveraging haplotype-aware inference for evolve-and- resequence studies. *GSA: The Allied Genome Conference*, Orlando, Florida (July 2016).
- Greenblum S, Carr R, Borenstein E. Bacteria Get Personal. *Keystone Conference on Chemical Transformations in the Human Microbiome*, Big Sky, Montana (March 2014).
- Greenblum S, Turnbaugh P, Borenstein E. Metagenomic Systems Biology: A New Framework for Studying the Human Gut Microbiome. *Institute for Systems Biology International Symposium: Systems Biology and the Microbiome*, Seattle (April 2012).
- Greenblum S, Turnbaugh P, Borenstein E. Metagenomic Systems Biology of the Human Gut Microbiome. *International Human Microbiome Congress*, Vancouver (March 2011).
- Greenblum S, Turnbaugh P, Borenstein E. Systems biology of the human microbiome: Linking microbiome-level network topology to host phenotype. *RECOMB Satellite on Systems Biology*, New York (November 2010).
- Greenblum S, Efroni S, Schaefer C, Buetow K. The PathOlogist: An Automated Tool for Pathway-Centric Analysis. *ISMB 2008*, Toronto, Ontario (July 2008).
- Greenblum S, Krucoff M, Furst J, Raicu D. Automated image analysis of noisy microarrays. *VISAPP:International Conference on Computer Vision Theory and Applications*, 371-3757, Barcelona, Spain (March 2007).
- Greenblum S, Li J, Huang A, Summers RM. Wavelet Analysis in Virtual Colonoscopy. *SPIE Medical Imaging 2006*, (6143) 992-999, Orlando, FL (April 2006).