

RACHEL SHERMAN

Baltimore, MD 21211

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EDUCATION

Ph.D. Candidate, Computer Science

Johns Hopkins University, Baltimore, MD
August 2015 – December 2020 (expected)
M.S.E. awarded August 2017
Advised by Steven Salzberg

B.S., Mathematical and Computational Biology

Harvey Mudd College, Claremont, CA
September 2011 – May 2015
Graduated with Honors in Computer Science

RESEARCH PROJECTS

Structural variation analysis using long reads

2017 – Present

Johns Hopkins University, Schatz Lab

My work focuses on analyzing novel variants undiscoverable in short read data. Using long read data, we catalog variants of interest and can analyze their frequency in public short-read data sets to determine their disease relevance. I have a particular focus on variant discovery in breast cancer patient data, as well as examining several unsolved Mendelian disease cases.

Insertion discovery in African ancestry populations

2016 – Present

Johns Hopkins University, Salzberg Lab

By combining assembly and alignment techniques we discovered nearly 300 Mb of novel sequence in large insertions in a short read data set of 910 individuals of African descent. We are performing additional work to determine the potential functionality of these sequences, and hope our findings will ultimately help provide a better reference genome for African descended populations.

Valley Oak genome assembly

2015

Johns Hopkins University, Salzberg Lab

Estimated genome size of the Valley Oak using a variety of methods and assembled the Valley Oak chloroplast.

Protein prediction from amino acid-ribonucleobase interactions

2014 – 2015

Collaboration with Carleton College and University of Cambridge undergraduates

Yielded predictions of protein sequence from RNA solely from interaction data and examined the potential of such interactions for ribosome-free encoding.

Simulation of artificial RNA molecules with long folding pathways

2014 – 2015

Harvey Mudd College and University of British Columbia, Condon Lab

As project manager of a team of four, I aided in simulation based testing of a theoretically designed RNA molecule.

NSF REU in Computational Biology and Bioinformatics

Summer 2014

Cold Spring Harbor Laboratory, Schatz Lab

Extended an algorithm for detecting structural variations between genomes, and streamlined the process pipeline.

TEACHING EXPERIENCE

Adjunct Faculty, Mount St Mary's University, Introduction to Computer Science

Fall 2019

Designed materials for and taught 3-credit CMSCI120: Intro to Computer Science. The course was taught in Python and covered topics including problem-solving methods, development of basic algorithms, and modular program design, in addition to programming basics.

Instructor, Johns Hopkins, What's in a Mutt: An intro to dog DNA analyses

January 2019

Designed and taught a three week intersession course on determining a mutt's breed by analyzing its DNA sequence as the sole instructor. The 16 hours of class time was split between lectures and a hands-on data analysis project.

Research Mentor, Johns Hopkins, BDP Summer Research Program

Summer 2019

Acted as the primary mentor for a summer undergraduate researcher. I designed a summer-long project analyzing

RNA-seq data to determine if any novel human sequences from my recent Nature Genetics paper appeared to be transcribed, and worked with my student to help him develop an understanding of the biological motivations of the project, in addition to advising him on technical aspects of the project.

Research Mentor, Johns Hopkins, Computer Science Summer Research Expeditions **Summer 2017**
Acted as the primary mentor for a summer undergraduate researcher. Guided her in analyzing alignments of novel sequence insertion data to multiple human and primate genome assemblies, which resulted in her being second author on a *Nature Genetics* paper.

Teaching Assistant, Johns Hopkins, Introduction to Genomic Research **Spring 2017**
As a TA for the debut of this course, I helped design the four project assignments which made up the student's work for the semester. I also held office hours, answered questions via Piazza, and graded. Course taught by Steven Salzberg.

Grader/Tutor, Harvey Mudd College, Computer Science **2013 – 2015**
Held office hours and graded for four classes; Intro to Computer Science, Data Structures, Software Development, and Computational Biology.

INDUSTRY EXPERIENCE

Software Engineering Intern, Adobe Systems **Summer 2013**
Worked to optimize iOS-Creative Cloud's synchronization back end. Collected and analyzed data, and implemented optimizations in Objective-C.

CERTIFICATES AND AWARDS

Teaching Academy Certificate of Completion **2018 – 2020**
Attended short workshops and a 3-day intensive Teaching Institute through the Johns Hopkins Center for Educational Resources Teaching Academy to learn best pedagogical practices and gain hands-on teaching experience.

CRA-W Grad Cohort **2016**
Sponsored attendance to a workshop for career development of female-identifying graduate students in their first through third years of a computing-related graduate program.

Harriet H. Cohen Fellowship **2015 – 2016**
Received a departmental fellowship granted to one first year PhD student.

SERVICE

Reviewer, *Molecular Biology and Evolution*, *Nature Communications Biology*, *Trends in Genetics*
Faculty Liaison, *Computer Science Graduate Student Council* 2016 – Present
PhD Visit Day Coordinator, *Computer Science Graduate Student Council* 2016 – Present
Council Head, *Computer Science Graduate Student Council* 2017 – 2019
President, *Jewish Graduate Student Association* 2017 – 2018

PUBLICATIONS AND PRESENTED WORK

PEER-REVIEWED PUBLICATIONS

Aganezov, S., Goodwin, S., **Sherman, R. M.**, Sedlazeck, F. J., Arun, G., Bhatia, S., ... & Schatz, M. C. (2020). Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. *Genome Research*.

Shumate, A. *, Zimin, A. V. *, **Sherman, R. M.**, Puiu, D., Wagner, J. M., Olson, N. D., ..., & Salzberg, S. L. (2020). Assembly and Annotation of an Ashkenazi Human Reference Genome. *Genome Biology*, 21, 129.

Sherman, R. M. & Salzberg, S. L. (2020). Pan-genomics in the human genome era. *Nature Reviews Genetics*, 21, 243-254.

Chen, S. *, Krusche, P. *, Dolzhenko, E., **Sherman, R. M.**, Petrovski, R., Schlesinger, F., ... & Eberle, M. A. (2019). Paragraph: A graph-based structural variant genotyper for short-read sequence data. *Genome Biology*, 20, 291.

- Sherman, R. M.**, Forman, J., Antonescu, V., Puiu, D., Daya, M., Rafaels, N., ... & Salzberg, S. L. (2019). Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *Nature Genetics*, 51(1), 30.
- Sork, V. L., Fitz-Gibbon, S. T., Puiu, D., Crepeau, M., Gugger, P. F., **Sherman, R.**, ... & Salzberg, S. L. (2016). First Draft Assembly and Annotation of the Genome of a California Endemic Oak *Quercus lobata* Née (Fagaceae). *G3: Genes/ Genomes/ Genetics*, g3-116.
- Cannon, J.G.D., **Sherman, R.M.**, Wang, V.M.Y., & Newman, G.A. (2015). Cross-species conservation of complementary amino acid-ribonucleobase interactions and their potential for ribosome-free encoding. *Scientific Reports*.

CONFERENCE TALKS

- Discovering non-reference sequences to assemble a pan-genome of 910 African-ancestry individuals. *Personal Genomics and International Cooperation Conference*. Shanghai, China. October 2019.
- Assembly of a pan-genome from deep sequencing of 910 humans of African descent. *RECOMB*. Washington D.C., May 2019.
- Analyzing structural variation in breast cancer with long read sequencing of patient-derived organoids. *Biological Data Science*. Cold Spring Harbor, NY. November 2018.

PRESENTED POSTERS

- Sherman, R.M.**, Salzberg, S.L.. Evidence of transcription in novel human genomic sequences. *RECOMB*. Washington, DC. May 2019.
- Sherman, R.M.**, Antonescu, V., Rasika M.A., Taub, M.A., Beaty, T.H., Ruczinski, I., Barnes, K.C., & Salzberg, S.L.. Discovery of long novel insertions in African descent populations. *The Biology of Genomes*. Cold Spring Harbor, NY. May 2018.
- Agwamba, K.* , Heinen, S.* , Ramsden, C.* , **Sherman, R.*** , Sweedyk, E., & Condon, A.. Designing and analyzing RNA molecules with long and diverse folding pathways. *21st International Conference on DNA Computing and Molecular Programming*. Boston, MA. August 2015.

MISCELLANEOUS

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| Invited Lecture, Diversifying genomics, <i>Baltimore Underground Science Space</i> | March 2019 |
| Interview, African pan-genome work, <i>FutureProof on Ireland's NewsTalk Radio</i> (24:00) | February 2019 |
| Interview, Dog DNA intersession course, <i>Johns Hopkins Hub</i> | January 2019 |
| Interview, African pan-genome work, <i>The Atlantic</i> | November 2018 |