

Ruth Johnson

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Education

- **University of California, Los Angeles** **Los Angeles, CA**
PhD Computer Science *Sept 2017-present*
- **University of California, Los Angeles** **Los Angeles, CA**
B.S. Mathematics, Minor in Bioinformatics *Sept 2013-June 2017*

Academic Honors.....

- RECOMB Travel Fellowship (2020)
- NRT-Modeling and Understanding Human Behavior Fellowship (2018)
- Ford Fellowship Predoctoral Competition - Honorable Mention (2018)
- NSF Graduate Research Fellowships Program - Honorable Mention (2017)
- Eugene V. Cota-Robles Fellowship, UCLA (2017)

Research Experiences

- **Machine Learning in Biomedical Lab at UCLA** **Los Angeles, CA**
Graduate Student Researcher *July 2017 – current*
 - Leveraging electronic health records to predict common variable immune deficiency and other rare disorders through phenotype risk scores
 - Developed Bayesian statistical framework to model genetic architecture of complex traits
 - Emphasis on probabilistic modeling, Markov Chain Monte Carlo, variational inference, graphical models
 - Under supervision of Prof. Sriram Sankararaman and Prof. Bogdan Pasaniuc
- **Illumina** **Foster City, CA**
Deep Learning Engineering Intern *June 2018-Sept 2018*
 - Developed end-to-end parallelizable training data generation pipeline for deep learning base calling models
 - Utilized Keras, convolutional neural networks, Python
 - Under supervision of Amirali Kia
- **Bioinformatics Lab at UCLA** **Los Angeles, CA**
Undergraduate Student Researcher *March 2016 – June 2017*
 - Constructed software pipeline for fine-mapping analyses with the integration of functional annotation data
 - Created Python based data visualization tool that produces publication-ready figures of integrated fine-mapping experiments
 - Under supervision of Prof. Bogdan Pasaniuc
- **Sandia National Laboratory** **Albuquerque, NM**
R&D Engineering Intern *June 2016 – August 2016*
 - Researched satellite anomaly detection methods through supervised classification algorithms such as DBSCAN
 - Designed components of an object-oriented, dynamic web UI for satellite control systems using ReactJS and ExtJS

Journal Publications

* - denotes joint authors

1. **Localizing components of shared transethnic genetic architecture of complex traits from GWAS summary data.**
Huwenbo Shi*, Kathryn S Burch*, [Ruth Johnson](#), Malika K Freund, Gleb Kichaev, Nicholas Mancuso, Astrid M Manuel, Natalie Dong, Bogdan Pasaniuc; *American Journal of Human Genetics* 2020.
2. **An automated machine learning-based model predicts postoperative mortality using readily-extractable preoperative electronic health record data**
Brian Hill, Robert Brown, Eilon Gabel, Christine Lee, Maxime Cannesson, Loes Olde Loohuis, [Ruth Johnson](#), Brandon Jew, Uri Maoz, Aman Mahajan, Sriram Sankararaman, Ira Hofer, Eran Halperin; *British Journal of Anaesthesia* 2019.
3. **Probabilistic fine-mapping of transcriptome-wide association studies**
Nicholas Mancuso, Malika K. Freund, [Ruth Johnson](#), Huwenbo Shi, Gleb Kichaev, Alexander Gusev, and Bogdan Pasaniuc; *Nature Genetics* 2019.
4. **A unifying framework for joint trait analysis under a non-infinitesimal model**
[Ruth Johnson](#), Huwenbo Shi, Bogdan Pasaniuc*, Sriram Sankararaman*; *Bioinformatics* 2019.
5. **Improved methods for multi-trait fine mapping of pleiotropic risk loci**
Gleb Kichaev*, Megan Roytman*, [Ruth Johnson](#), Eleazar Eskin, Sara Lindström, Peter Kraft, Bogdan Pasaniuc; *Bioinformatics* 2017.

Conference Publications

1. **A scalable method for estimating the regional polygenicity of complex traits**
[Ruth Johnson](#), Kathryn S. Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc, Sriram Sankararaman; *RECOMB 2020*.
2. **A unifying framework for joint trait analysis under a non-infinitesimal model**
[Ruth Johnson](#), Huwenbo Shi, Bogdan Pasaniuc*, Sriram Sankararaman*; *ISMB 2018*.

Preprints

1. **Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits**
[Ruth Johnson](#), Kathryn S. Burch, Kangcheng Hou, Mario Paciuc, Bogdan Pasaniuc, Sriram Sankararaman; under review at *American Journal of Human Genetics*.
2. **Prior diagnoses and medications as risk factors for COVID-19 in a Los Angeles Health System**
Timothy S Chang, Yi Ding, Malika K Freund, [Ruth Johnson](#), Tommer Schwarz, Julie M Yabu, Chad Hazlett, Jeffrey N Chiang, Ami Wulf, Daniel H Geschwind, Manish J Butte, Bogdan Pasaniuc; *medRxiv* 2020.

Oral Presentations

1. **A scalable method for estimating the regional polygenicity of complex traits**
RECOMB, July 2020. Virtual meeting.
2. **Leveraging electronic health record signatures identify undiagnosed patients with Common Variable Immunodeficiency Disease**
Undiagnosed Diseases Network - Steering Committee Meeting, March 2020. Los Angeles, CA, USA. (cancelled due to COVID-19)

3. **Leveraging electronic health record signatures identify undiagnosed patients with Common Variable Immunodeficiency Disease**
Institute for Quantitative and Computational Biosciences - Research Seminar, February 2020. Los Angeles, CA, USA.
4. **Electronic health record signatures identify undiagnosed patients with of CVID**
Medical and Population Genetics seminar - Computational Genomics and Health, November 2019. Los Angeles, CA, USA.
5. **Dissecting the genetic architecture of complex traits through local polygenicity using summary statistics from genome-wide association studies**
Biology of Genomes 2019, May 2019. Long Island, NY, USA.
6. **Dissecting the genetic architecture of complex traits through local polygenicity using summary statistics from genome-wide association studies**
Medical and Population Genetics, May 2019. Los Angeles, CA, USA.
7. **A scalable Bayesian model for estimating the genetic architecture of complex traits using summary statistics from GWAS**
Probabilistic Modeling in Genomics Meeting 2018, November 2018. Long Island, NY, USA.
8. **A unifying framework for joint trait analysis under a non-infinitesimal model**
ISMB 2018, July 2018. Chicago, IL, USA.
9. **Combining genetic correlation and colocalization into a unifying model**
Medical and Population Genetics, May 2019. Los Angeles, CA, USA.
10. **CANVIS: Correlation Annotation VISualization**
RECOMB Genetics Satellite Meeting, July 2017. Los Angeles, CA, USA.

Poster Presentations

1. **Fine-scale estimates of regional polygenicity provide insights into the genetic architecture of complex traits**
Ruth Johnson, Kathryn S. Burch, Kangcheng Hou, Bogdan Pasaniuc, Sriram Sankararaman; Annual meeting of the American Society of Human Genetics, Oct 2019. Houston, TX, USA.
2. **An analysis of the genetic overlap of 20 complex traits under a non-infinitesimal model**
Ruth Johnson, Huwenbo Shi, Kathryn Burch, Bogdan Pasaniuc, Sriram Sankararaman; Annual meeting of the American Society of Human Genetics, Oct 2018. San Diego, CA, USA.
3. **Integrative fine-mapping of 34 complex phenotypes**
Ruth Johnson, Gleb Kichaev, Kathryn Burch, Bogdan Pasaniuc; Annual meeting of the American Society of Human Genetics, Oct 2017. Orlando, FL, USA.
4. **Leveraging functional annotations in fine-mapping of causal variants for complex traits**
Ruth Johnson, Gleb Kichaev, Kathryn Burch, Bogdan Pasaniuc; UCLA Undergraduate Research Poster Day, May 2017. Los Angeles, CA, USA.
**Dean's Prize Science Award Honoring Outstanding Undergraduate Researcher*
5. **Visualizing correlated causal variants**
Ruth Johnson, Gleb Kichaev, Bogdan Pasaniuc; Annual meeting of the American Society of Human Genetics, October 2016. Vancouver, CN.

Mentoring Experience

- Jessie Chen. Undergraduate student, Bruins in Genomics Summer Program.
Project title: "ATLAS-hub: an R Shiny App for PheWAS results on the ATLAS BioBank"
 - Research Excellence award and Top Presentation award
- Mario Paciuc. Undergraduate student, Rice University.
Project title: "Genetic correlation of complex traits under a non-infinitesimal model"
 - co-author on Johnson et al. RECOMB 2020
 - award for Distinction in Research and Creative Works from the Department of Statistics
- Gary Hu. Undergraduate student, Bruins in Genomics Summer Program.
Project title: "Trans-ethnic genetic overlap in complex traits."
- Hugo Mainguy. Undergraduate student, Bruins in Genomics Summer Program.
Project title: "Assessing the overlap of complex traits through the shared proportion of causal SNPs and genetic correlation"
- Engineering Undergraduate Research Program - Graduate Student Mentor.
 - Taught weekly workshops about scientific presentations and guided 10-15 students through creating abstracts, posters, and presentations about their research projects.

Software

- **BEAVR** *Estimating regional polygenicity*
Software that estimates the proportion of causal variants (*i.e.* polygenicity) within a given region from GWAS summary statistics and in-sample LD.
<https://github.com/bogdanlab/BEAVR>
- **UNITY** *Quantifying genetic overlap of complex traits*
Software that uses a fully Bayesian framework to calculate the proportion of shared causal variants between two complex traits through GWAS summary statistics. The method also explicitly models the genetic correlation present between both traits.
<https://github.com/bogdanlab/UNITY>
- **CANVIS** *Fine-mapping visualization*
A fine-mapping tool that visually summarizes an integrative fine-mapping experiment. The tool provides visual representation of the local correlation structure (LD), the functional annotations used, as well as association statistics and posterior probabilities for each SNP.
<https://github.com/bogdanlab/PAINTOR/tree/master/CANVIS>