Ruth Johnson

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Education

- **University of California, Los Angeles** **Los Angeles, CA**
  PhD Computer Science *Sept 2017-present*
  GPA: 3.95/4.0
- **University of California, Los Angeles** **Los Angeles, CA**
  B.S. Mathematics, Minor in Bioinformatics *Sept 2013-June 2017*

Academic Honors

- 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 ($40,000) (2017)

Research Experiences

- **Mahine Learning in Genomics Lab at UCLA** **Los Angeles, CA**
  Graduate Student Researcher *July 2017 – current*
  - Developed Bayesian statistical framework to model genetic architecture of complex traits
  - Emphasis on probabilistic modeling, Markov Chain Monte Carlo, variational inference, graphical models
  - Prior experience with machine learning programming languages: TensorFlow, Stan, Edward
  - Under supervision of Prof. Sriram Sankararaman
- **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

Publications

* - denotes joint authors

1. **A unifying framework for joint trait analysis under a non-infinitesimal model**
   Ruth Johnson, Huwenbo Shi, Bogdan Pasaniuc*, Sriram Sankararaman*; *ISMB Proceedings 2018 [simultaneously published in Bioinformatics].*
2. **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.*

Preprints

1. **Preoperative predictions of in-hospital mortality using electronic medical record data**
   Brian Hill, Robert P Brown, Eilon Gabel, Christine Lee, Maxime Cannesson, Loes Olde Loohuis, Ruth Johnson, Brandon Jew, Uri Maoz, Aman Mahajan, Sriram Sankararaman, Ira Hofer, Eran Halperin; *bioRxiv*. (submitted to *PLOS Medicine*)

Oral Presentations

1. **A unifying framework for joint trait analysis under a non-infinitesimal model**
   ISMB 2018, July 2018. Chicago, IL, USA.
2. **CANVIS: Correlation Annotation VISualization**
   RECOMB Genetics Satellite Meeting, July 2017. Los Angeles, CA, USA.

Poster Presentations

1. **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.
2. **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*
3. **Visualizing correlated causal variants**
   Ruth Johnson, Gleb Kichaev, Bogdan Pasaniuc; Annual meeting of the American Society of Human Genetics, October 2016. Vancouver, CN.

Software

- **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`