

# Deborah Chasman

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## Recent Experience

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- 2018–Present **Postdoctoral research associate** (Laboratory of Professor Irene Ong)  
*Department of Obstetrics and Gynecology, University of Wisconsin–Madison*
- Developing computational methods to study how prenatal and early life environmental exposures influence immune system development
- 2014–2018 **Postdoctoral research associate** (Laboratory of Professor Sushmita Roy)  
*Wisconsin Institute for Discovery, University of Wisconsin–Madison*
- Developing computational methods for inferring cell type-specific gene regulatory networks by integrating multiple data types
  - Developing and assessing methods to prioritize experimental targets
- 2008–2014 **Graduate research assistant** (Laboratory of Professor Mark Craven)  
*UW–Madison, Depts. of Computer Sciences and Biostatistics and Medical Informatics*
- Developing integer linear programming-based methods for inferring interpretable and accurate biological subnetworks

## Education

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- 2014 **PhD**, Computer Sciences. *University of Wisconsin–Madison, Madison, WI*  
Advisor: Professor Mark Craven  
*Thesis: Improving the interpretability of integer linear programming methods for biological subnetwork inference*  
Thesis committee: Mark Craven, Paul Ahlquist, Michael Ferris, Audrey Gasch, David Page, Xiaojin Xu  
Research focus in machine learning and biomedical informatics  
Graduate minor in biology and biostatistics
- 2009 **MS**, Computer Sciences. *University of Wisconsin–Madison, Madison, WI*
- 2007 **BA magna cum laude**, Computer Science. *Carleton College, Northfield, MN*

## Honors

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- 2018–Present Postdoctoral Fellow, Computation and Informatics in Biology and Medicine Training Program (Environmental Exposures Informatics)
- 2016–2017 Postdoctoral Fellow, Computation and Informatics in Biology and Medicine Training Program
- 2008–2011 Predoctoral Fellow, Computation and Informatics in Biology and Medicine Training Program
- June 2007 Awarded Distinction in undergraduate major and senior integrative exercises

## Publications

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Chasman D, Walters KB, Lopes TJS, Eisfeld AJ, Kawaoka Y, Roy S (2016) Integrating Transcriptomic and Proteomic Data Using Predictive Regulatory Network Models of Host Response to Pathogens. *PLOS Computational Biology* 12(7): e1005013. doi:10.1371/journal.pcbi.1005013 **Top 10 recommended papers by RECOMB/ISCB Regulatory and Systems Genomics, 2015-2016.**

Chasman D, Ho YH, Berry DB, Nemecek CM, MacGilvray ME, Hose J, Merrill AE, Lee MV, Will JL, Coon JJ, Ansari AZ, Craven M, Gasch AP (2014) Pathway connectivity and signaling coordination in the yeast stress-activated signaling network. *Mol Syst Biol* 10(11):759. doi: 10.15252/msb.20145120

Chasman D, Gancarz B, Hao L, Ferris M, Ahlquist P, Craven M (2014) Inferring host gene subnetworks involved in viral replication. *PLoS Comput Biol* 10(5): e1003626. doi:10.1371/journal.pcbi.1003626

MacGilvray ME, Shishkova E, Chasman D, Place M, Gitter A, Coon JJ, Gasch AP (2018) Network inference reveals novel connections in pathways regulating growth and defense in the yeast salt response. *PLoS Comput Biol* 13(5): e1006088. doi:10.1371/journal.pcbi.1006088

Garcia K, Chasman D, Roy S, Ané J (2017) Physiological responses and gene co-expression network of mycorrhizal roots under K<sup>+</sup> deprivation. *Plant Physiol.* pp.01959.2016. doi:10.1104/pp.16.01959

Niu Z, Chasman D, Eisfeld AJ, Kawaoka Y Roy S. (2016) Multi-task Consensus Clustering of Genome-wide Transcriptomes from Related Biological Conditions. *Bioinformatics.* doi:10.1093/bioinformatics/btw007

Roy S, Fotuhi Siahpirani A, Chasman D, Knaack S, Ay F, Stewart R, Wilson M, Sridharan S. (2015) A predictive modeling approach for cell line-specific long-range regulatory interactions. *Nucleic Acids Research.* 43(18): 8694-8712. doi:10.1093/nar/gkv865

Zhang Y, Majunath M, Zhang S, Chasman D, Roy S, Song JS. (2018) Integrative genomic analysis predicts causative cis-regulatory mechanisms of the breast cancer-associated genetic variant rs4415084. *Cancer Reseach. Early Epub.* doi:10.1158/0008-5472.CAN-17-3486

Larrainzar E, Riely BK, Kim SC, Carrasquilla-Garcia N, Yu HJ, Hwang HJ, Oh M, Kim GB, Surendrarao AK, Chasman D, Fotuhi Siahpirani A, Penmetsa RV, Lee GS, Kim N, Roy S, Mun JH, Cook DR (2015) Deep Sequencing of the Medicago truncatula Root Transcriptome Reveals a Massive and Early Interaction between Nodulation Factor and Ethylene Signals. *Plant Physiol.* 2015 Sep;169(1):233-65. doi:10.1104/pp.15.00350.

Azencott, CA, Aittokallio T, Roy S, DREAM Idea Challenge Consortium, Norman T, Friend S, Stolovitsky G, Goldenberg A (2017) The inconvenience of data of convenience: computational research beyond post-mortem analyses. *Nature Methods* 14:937-938. Member of consortium as a participant in one of the two winning submissions.

Chasman D, Gancarz B, Ahlquist P, Craven M (2009) Explaining effects of host gene knockouts on Brome Mosaic Virus replication. *IJCAI'09 Workshop on Abductive and Inductive Knowledge Development.*

## Theses

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Chasman D (2014) Improving the interpretability of integer linear programming methods for biological sub-network inference.

## Review Articles

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Chasman D, Roy S (2017) Inference of cell type specific regulatory networks on mammalian lineages. *Current Opinion in Systems Biology* 2:129–138. doi:10.1016/j.coisb.2017.04.001

Chasman D, Fotuhi Siahpirani A, Roy S (2016) Network-based approaches for analysis of complex biological systems. *Current Opinion in Biotechnology* 39:157–166. doi:10.1016/j.copbio.2016.04.007

## Presentations

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| Conference talk | <ul style="list-style-type: none"><li>• Dynamic Regulatory Module Networks for integrative inference of cell type-specific regulatory programs. Abstract presentation. <i>Intelligent Systems in Molecular Biology (ISMB) 2018.</i></li><li>• Integrative reconstruction of the regulatory network controlling host response to influenza infections. Presentation, <i>Great Lakes Bioinformatics Conference (GLBIO) 2015. <b>Best Short Talk.</b></i></li><li>• Integrating transcriptomic and proteomic data with predictive regulatory network models of host response to pathogens. Presentation, <i>RECOMB Conference on Regulatory and Systems Genomics 2015.</i></li><li>• An abductive approach to explaining genome-wide experimental observations. Plenary session at <i>National Library of Medicine Informatics Training Conference 2010, Denver, CO.</i></li><li>• Explaining effects of host gene knockouts on Brome Mosaic Virus replication. Presentation at <i>Abductive &amp; Inductive Knowledge Development Workshop. IJCAI 2009, Pasadena, CA.</i></li></ul> |
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- Poster presentations
- Society of Toxicology Annual Meeting 2017.
  - Great Lakes Bioinformatics Conferences (GLBIO) 2017.
  - RECOMB Conference on Regulatory and Systems Genomics 2013.
  - Intelligent Systems in Molecular Biology (ISMB) 2011–2013.

## Other Professional Activities

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- Trainee Ethical Conduct of Research for Data Scientists (Spring 2017)
- Participant NIAID Systems Biology of Infectious Diseases working groups on Computational Modeling and Data Dissemination (Sept 2014–April 2015)
- Mentor
- Undergraduate independent study (Spring 2015)
  - Integrated Biological Sciences Summer Research Program (Summer 2013, Summer 2015)
- Reviewer *PLoS Computational Biology, Bioinformatics, PLoS ONE, Journal of Computational Biology*
- Coordinator UW–Madison Artificial Intelligence reading group (2013–2014)
- Outreach instructor Introduction to Systems Biology for Experimental Biologists (2015), Wisconsin Science Festival, Expand Your Horizons

## Skills and Qualifications

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- Programming languages and systems: Java, Python, optimization modeling with GAMS and ILOG CPLEX, Matlab, C/C++, bash, Linux/Unix, L<sup>A</sup>T<sub>E</sub>X, Condor High-Throughput Computing
- Extensive collaboration with biological researchers
- Selected graduate coursework: machine learning, artificial intelligence, bioinformatics, databases, algorithms, biochemistry, genetics, biostatistics