

Jisoo Park

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EDUCATION **Tufts University**, Massachusetts, USA 2017
Ph.D. in Computer Science, Advisor: Donna K. Slonim
Dissertation: Discovering molecular mechanisms of human disease through gene sets and networks

Washington University in St. Louis, Missouri, USA 2007
M.S. in Computer Science

Ewha Womans University, Seoul, South Korea 2005
B.S. in Computer Science

PUBLICATIONS Jisoo Park, Benjamin J. Hescott and Donna K. Slonim. Pathway centrality in protein interaction networks identifies functional mediators of pulmonary disease. Submitted manuscript, 2017. (bioRxiv 171942; doi: <https://doi.org/10.1101/171942>)

Jisoo Park, Benjamin J. Hescott and Donna K. Slonim. Towards a more molecular taxonomy of disease. (extended journal version) *Journal of Biomedical Semantics*. Jul 27;8(1):25, 2017.

Jisoo Park. Discovering molecular mechanisms of human disease through gene sets and networks. *Doctoral dissertation, Tufts University*, 2017.

Jisoo Park, Benjamin J. Hescott, and Donna K. Slonim. Towards a More Molecular Taxonomy of Disease. (workshop version) Bio-ontologies SIG at ISMB 2016, Orlando, FL.

Jisoo Park, Heather C. Wick, Daniel E. Kee, Keith Noto, Jill L. Maron and Donna K. Slonim. Finding Novel Molecular Connections between Developmental Processes and Disease. *PLoS Computational Biology*, May 29;10(5):e1003578, 2014.

Mengfei Cao, Christopher M. Pietras, Xian Feng, Kathryn J. Doroschak, Thomas Schaffner, Jisoo Park, Hao Zhang, Lenore J. Cown and Benjamin J. Hescott. New Directions for Diffusion-Based Network Prediction of Protein Function: Incorporating Pathways with Confidence, *Bioinformatics*, 30(12):i219-i227, 2014.

Mengfei Cao, Hao Zhang, Jisoo Park, Noah M. Daniels, Mark E. Crovella, Lenore J. Cowen and Benjamin J. Hescott. Going the Distance for Protein Function Prediction: A New Distance Metric for Protein Interaction Networks, *PLoS ONE*, 8(10):e76339, 2013.

POSTERS Jisoo Park, Benjamin J. Hescott, and Donna K. Slonim. Building a More Molecular Taxonomy of Disease, *ACM-BCB 2017*, Boston, MA.

Jisoo Park, Benjamin J. Hescott, and Donna K. Slonim. Towards a More Molecular Taxonomy of Disease, *Computational Aspects of Biological Information (CABI) 2016* at Microsoft Research in Cambridge, MA.

Jisoo Park, Benjamin J. Hescott, and Donna K. Slonim. Towards a More Molecular Taxonomy of Disease, *Bio-ontologies SIG at ISMB 2016*, Orlando, FL.

Jisoo Park, Keith Noto, Daniel Kee, Heather Wick and Donna Slonim. An Abstract View of Associations Between Diseases and Developmental Gene Sets, *VisWeek 2012*, Seattle, WA.

ONGOING PROJECTS

Investigation of functional overlap between genes responsible for prematurity complications
We hypothesize that immune and developmental functions are connected to multiple prematurity complications. Developed methods to evaluate statistical significance of overlapping functions between the prematurity disease gene sets.

Gene set Disease Association (GDA) analysis using inferred disease ontologies
Integrate results of two prior projects to learn more about how to infer disease ontologies with molecular content.

AWARDS

F1000 best paper/presentation award, Bio-ontologies SIG at ISMB 2016.

GIFT Fellowship, Tufts University, 2014.

Tufts Research Visualization Award (non-interactive media), Tufts University, 2012

Scholarship, Ewha Womans University, 2004.

TEACHING EXPERIENCE

Guest Lecturer in Tufts Courses

The Engineering Method of Technical Writing (COMP 150TW), Spring 2017.

Current Challenges in Computational Biology (COMP 150-05), Fall 2016.

Computational Biology (COMP 167), Spring 2015.

Bioinformatics (COMP 7 / BIO 40), Fall 2014.

Teacher Training

Graduate Institute for Teaching (GIFT) fellow: participated in a selective teacher-training program for graduate students, Tufts University, Summer - Fall 2014.

Teaching Assistant

Computational Biology, Lenore Cowen, Fall 2011.

Introduction to Machine Learning, Carla Brodley, Fall 2011.

Behavioral Based Robotics, Matthias Scheutz, Fall 2010.

Mentoring

Undergraduate summer students at Bioinformatics/Computational Biology (BCB) research group at Tufts University, 2017.

Graduate student, Hao Zhang, on a project developing diffusion based gene prioritization methods.

PROFESSIONAL
ACTIVITIES

Student activity organizer, *Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, Boston, 2017.

Reviewer, *Bioinformatics*, 2016.

Sub-reviewer, *RECOMB*, 2014.

Student volunteer, *Intelligent Systems for Molecular Biology (ISMB) conference*, Boston, 2014.

Student volunteer, *VisWeek*, Seattle, 2012.

Member, *International Society for Computational Biology (ISCB)*, since 2014.

Member, *ACM SIG on Bioinformatics, Computational Biology, and Biomedical Informatics*, since 2017.

APPLICATIONS &
SOFTWARE

Gene set Disease Association (GDA) analysis tool
Web-based application running GDA analysis and visualizing the experimental results. Available at <http://gda.cs.tufts.edu/>

SmurfPreparse module for left-handed alpha helix detection
Annotates indices of residues on left-handed alpha helices from multiple sequence alignments. SmurfPreparse is a part of the Smurf package (Menke et al., 2010).

Automated domain translator for First Order Decision Diagrams (FODD) planner
Transforms sensor data from robots into input for the FODD planner. Written in Prolog. FODD planner (Joshi et al., 2009) is detailed in “Generalized First Order Decision Diagrams for First Order Markov Decision”, *International Joint Conference on Artificial Intelligence (IJCAI)*, pp. 1916-1921, 2009.

INDUSTRY
EXPERIENCE

AstraZeneca, Intern at Research and Development Information (RDI) *Summer 2013*
Analyzed common variants in cancer NGS data and identified regions with significant variants in genome using simulated exome sequence data. Worked with GATK variant calling tools and GenePattern.

XIOS, C#.NET developer *Februaury 2010–August 2010*
Developed inventory management and Point of Service (PoS) system

PROGRAMMING
LANGUAGES

Python, R(with Bioconductor package), Java, C#.NET, Matlab, C/C++, Prolog