

**David L Gibbs**  
Institute for Systems Biology  
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## **Education**

*PhD*, Bioinformatics, Oregon Health and Science University, 2012  
Dissertation Title: Integrated Signatures of Disease Using Network Methods  
Advisor: Shannon K McWeeney

*Postbac*, Computer Science, Portland State University, 2005 - 2008

*B.A.*, Chemistry, Reed College, 1999

## **Experience**

*Postdoctoral Fellow*: The Institute for Systems Biology, 2015-present  
Employed with Shmulevich Lab at ISB working on a large multi-site collaboration with Inova and a project with the Cancer Genome Atlas group.

*Postdoctoral Fellow*: OHSU & The Institute for Systems Biology, 2012-2015  
External collaborator with the Shmulevich Lab at ISB working on a large multi-site collaboration researching the genetic regulatory basis underlying preterm birth.

*Graduate Research Assistant*: OHSU, OCTRI 2011-2012  
Bioinformatics programming and analysis on large multi-center proteomics collaboration.

*Research Assistant*: OHSU, OCTRI 2009  
Performed copy number variant analysis of SNP array data in a Leukemia study for Beth Wilmot.

*Teaching Assistant*: OHSU, DMICE 2009  
Met with students and graded homework in Introduction to Java for Michelle Hribar.

*Research Assistant*: OHSU, Center for Hematologic Malignancies, Summer 2009  
Provided computational support in cancer research collaboration.

*Grader*: Portland State University, Computer Science Dept. 2005-2006  
Graded Introduction to Computer Science I & II, and Data Structures for Karla Fant.

## **Publications**

Varsha, D.\*, Gibbs D. L.\*, Knijnenburg T., Kramer R., Vockley J., Niederhuber J., Shmulevich I., Bernard B. (2016) Using incomplete trios to boost confidence in family based association studies, *Front. Genet.* 7:34. doi: 10.3389/fgene.2016.00034

Gibbs, D. L., Gralinski L. E., Baric, R. S. & McWeeney, S. K. (2014). Multi-omic network signatures of disease. *Front. Genet.* 4:309. doi: 10.3389/fgene.2013.00309

Gibbs, D. L., Baratt, A., Baric, R., Kawaoka, Y., Orwoll, E., Smith, R. D., Katze, M., McWeeney, S. K. (2013). Protein co-expression network analysis (ProCoNA). *J Clin Bioinforma*, 3(1). doi: 10.1186/2043-9113-3-11.

Siegel, D. H., Shieh J., Kwon, E. K., Basalga, E., Blei, F., Bruer, H., Cordisco, M., Dobyns, W., Duffy, K., Galliner, Garzon, M., Gibbs, D. L., Hayflick, S., Haggstrom, A., Knopper, A., Krol, A., Kwok, P., Lorier, R., Mancini, A., McWheeney, S. K., Metry, D., Morel, K., Newell, B., Pope, E., Santoro, J., Wagner, A., Wargon, O., Wilmot, B., Wilson-Bracket, Worthey, E., Frieden, I., Drolet, B., Broeckel, U. (2012) Copy number variation analysis in 94 individuals with PHACE syndrome. *J Invest Dermatol*, 133, 677–684. doi:10.1038/jid.2012.367

## **Manuscripts in preparation:**

“Combining Dependent P-values with an Empirical Adaption of Brown’s Method” – utilized the author’s code to produce an R package, submitted to bioconductor. Accepted for oral presentation to ECCB2016.

“Inova preterm birth study” – Multi-omic characterization of preterm birth using a diverse cohort of mothers and trios. Planning for late-June submission.

“Influence analysis on biological pathways using ant colony optimization” – Exploration of how time series data can be used to characterize dynamics on networks, and the relation to biological function. Draft to be submitted to BioRxiv soon.

## **Journal Reviews**

Bioinformatics

Computers in Biology and Medicine

## **Podium Presentations**

Gibbs, D. L., Shmulevich, I. (2016). Solving the maximum influence problem on biological networks. ISMB, Late Breaking Research, Orlando.

Gibbs, D. L., Shmulevich, I. (2014). Using information flow models and ant optimization to solve the influence maximization problem on biological networks as line digraphs. OHSU Research Week.

Gibbs, D. L., McWeeney, S. (2013). Mind the gap: strategies for integrating proteomic data. ISMB Berlin, Mass Spec Special Interest Group.

Gibbs, D. L., McWeeney, S. (2013). Multi-omic network signatures of disease. NLM Informatics Training Conference, Bethesda MD, Plenary session.

Gibbs, D. L., McWeeney, S. (2013). Multi-omic network signatures of disease. OHSU Research Week.

Gibbs, D. L., McWeeney, S., (2012). Peptides, Proteins and Networks: Removing obstacles and getting on the road to systems integration. OHSU Research Week.

Gibbs, D. L., Bankhead III, A. (2011). Reducing Variability in Co-Expression Network Construction. NLM Informatics Training Conference, Bethesda MD.

## **Poster Presentations**

Gibbs, D. L., Shmulevich I. (2014) Solving the Influence Maximization Problem with network flows, ant optimization, and regulatory line graphs. ISB Retreat.

Lee, C. G., Baraff, A., Smith, R., Baker, E., Petyuk, V., Cawthon, P. M., Bauer, D. C., Gibbs, D. L., Baratt, A., McWeeney, S. K., Lapidus, J., Orwoll, E. S. (2013). Novel Markers of Obesity: a Population-Based Proteomic Approach. ENDO

Gibbs, D. L., McWeeney, S., (2012). Peptides, Proteins and Networks: Removing obstacles and getting on the road to systems integration. ISMB, Boston.

Vingara, L. K., Gibbs, D. L., Bankhead III, A., Boudreau, E. (2012). Robust Information Recovery for Statistical Spectroscopy. Experimental NMR Conference.

Baratt, A., Baraff, A., Petyuk, V., Gibbs, D. L., Woffedin, C., Sarver, S., Sandoval, J., Anderson, F., Smith, R., Lapidus, J., McWeeney, S. K., Orwoll, E. S. (2011). Statistical and Bioinformatics Considerations for Population Level Proteomic Biomarker Studies. RECOMB Satellite Conference on Computational Proteomics.

Gibbs, D. L., Bankhead III, A. (2011). Managing Variability in Co-Expression Network Construction. AMIA Summit on Translational Bioinformatics, San Francisco.

Siegel, D., Gibbs, D. L., Frieden, I., Drolet, B., Broeckel, U. (2011). Copy number variation analysis in PHACE syndrome. Society for Investigative Dermatology Annual Meeting, Pheonix AZ.

Wilmot, B., Gibbs, D. L., Hsieh, P. H., McWeeney, S. K. (2009). Considerations for Algorithm Selection and Experimental Design in Detection of Copy Number Variation in Cancer” ISMB.

### **Awards**

NLM Postdoctoral Fellowship, 2012

ISCB Travel Fellowship, Long Beach Meeting 2012

NLM Predoctoral Fellowship (ARRA Grant) 2009-2011

### **Teaching**

Bio-Algorithms, OHSU BMI 550, Mentored and gave two lectures.

Bioinformatics seminar, OHSU BMI 553, class co-lead, focus on Bayesian networks.

### **Professional Activities**

ISB Postdoc Board Member 2015-current

Member of the International Society for Computational Biology (ISCB) 2010-current

Member of student counsel ISCB 2013-2014