

# John L. Van Hemert, Ph.D.

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## Education

Ph.D. Bioinformatics and Computational Biology (Minor: Statistics),  
Iowa State University, December 2010

*Dissertation:* Methods for Integrated Biochemical Pathway Analysis

*Committee:* Julie Dickerson (Advisor), Basil Nikolau (Co-advisor),  
Roger Wise, Peng Liu, and Gustavo MacIntosh.

B.A. with Honors, Computer Science and Management Information Systems,  
University of Northern Iowa, 2006.

*Specializations:* Software Engineering and International Business.

*Awards:* *Magna Cum Laude*, Provost Scholar, Purple and Old Gold Award, Upsilon Pi Epsilon.

## Experience

### *Iowa State University, Bioinformatics and Computational Biology Program*

Assistant Scientist III, Crop Genome Informatics Laboratory, Iowa State University, 2011-Present  
Research Assistant, Julie Dickerson, 2007-2010.

Journal Referee, Bioinformatics, BMC Bioinformatics

Grape Research Coordination Network Visiting Research Fellow, Mario Pezzotti, Verona, Italy, 2009.

Consultant, Executive Member, Bioinformatics and Computational Biology Laboratory, 2006-2010.

Teaching Assistant, Undergraduate and graduate-level Systems Biology, 2008-2009.

Rotating Research Assistant, Hui-Hsien Chou, Vasant Honavar, and W. Allen Miller, 2006-2007.

## Awards

*ABI Innovation: Model-based Alternative Splicing Analysis Across Expression Platforms, \$424,483*

Co-wrote 2-year NSF ABI program grant proposal with PI Julie A. Dickerson.

*Research Excellence Award*

One doctoral graduate awarded per year per graduate program.

*James Cornette Fellowship, \$5,000*

Awarded based on faculty nomination and publication record in 4/2010.

*Grape Research Coordination Network Travel Fellowship, \$7,000*

Proposal ranked 1/11 in 9/2009.

*Iowa State University Bioinformatics and Computational Biology PhD Program, \$20,000*

Admission in 8/2006 included one fully funded year for laboratory rotations. Partially supported by Graduate Assistance in Areas of National Need program (U.S. Department of Education).

## Research

### Working Manuscripts

**Van Hemert J** and Julie A. Dickerson. Discriminating Omics Response Groups in Biochemical Pathway Networks. *Nucleic Acids Research*. To be submitted.

**Van Hemert J** and Boggess EE. Multivariate analysis of Vitis gene expression during photoperiod-induced bud dormancy. *Plant Physiology*. To be submitted.

### Publications

Schwartz TS, Choi J, Yang Y, Tae H, Mocktalis K, **Van Hemert J**, Proulx S, and Bronikowski AM. A garter snake transcriptome: 454 gs-flx titanium de novo assembly, contig clustering, and sex-specific differences. *BMC Genomics*, 11:694, 2010.

Xia T, **Van Hemert J**, Dickerson JA. CytoModeler: A tool for bridging large-scale network analysis and dynamic quantitative modeling. *Bioinformatics*, In press. 2011.

Xia T, **Van Hemert J**, Dickerson JA. OmicsAnalyzer: a Cytoscape plug-in suite for modeling omics data. *Bioinformatics*, 1;26(23):2995-6. 2010.

**Van Hemert J** and Dickerson JA. Pathwayaccess: Celldesigner plugins for pathway datasources. *Bioinformatics*, 26(18):2345-6, 2010.

**Van Hemert J** and Dickerson JA. Monte carlo randomization tests for large-scale abundance datasets on the gpu. *Computational Methods and Programs in Biomedicine*. 2010.

Grimplett J, Cramer GR, Dickerson JA, Mathiason K, **Van Hemert J**, and Fennell AY. Vitisnet: omics integration through grapevine molecular networks. *PloS One*, 4:e8365, 2009.

Mao L, **Van Hemert J**, Dash S, and Dickerson JA. Arabidopsis gene co-expression network and its functional modules. *BMC Bioinformatics*, 10, 2009.

Sucaet Y, **Van Hemert J**, Tucker B, and Bartholomay L. Iowa-mosquito.net: cyberinfrastructure for monitoring and analyzing mosquito population dynamics. *Journal of Medical Entomology*, 45:775-784, 2008.

### Conferences and Seminars

**Van Hemert J**. JavaCycO: An Object-oriented Redesign of JavaCyc. PathwayTools Workshop. Stanford Research Institute, Menlo Park, California, 2010.

**Van Hemert J**, Alberto Ferrarini, Massimo Delledonne, Mario Pezzotti, Anne Fennell, Julie A. Dickerson. Transcriptomics Platform Integration for Expression and Splice Variant Detection. *International Conference on Intelligent Systems for Molecular Biology*, Boston, Massachusetts and *Grape Research Coordination Network Meeting*, Geneva, New York, 2010.

**Van Hemert J**. Expressional and functional annotation of microarrays for pathway analysis. University of Verona, Italy, 2009. Invited seminar.

**Van Hemert J** and Dickerson JA. Viticyc: a pathway genome database for the grapevine and pathway data integration between metnet and biocyc databases using new celldesigner plugins. In *Plant Sciences Institute Symposium*, Ames, Iowa and *Grape Research Coordination Network Meeting*, Tahoe, California, 2009.

**Van Hemert J**, Sucaet Y, Bartholomay L, Bronikowski A, Warner D, and Janzen F. Eco-informatics: leveraging bioinformatics skills to maximize agility in non-computational environments. In *New Mexico Bioinformatics Symposium*, Santa Fe, New Mexico and *International Conference on Intelligent Systems for Molecular Biology*, Toronto, Ontario, 2008.

**Van Hemert J**. Iowa-mosquito.net: cyberinfrastructure for monitoring and analyzing mosquito population dynamics. Student presentation, Annual Illinois Mosquito and Vector Control Association meeting, 2008. **Best Student Talk**.