Matthew DeJongh

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Education

M.A. in Theological Studies, Winebrenner Theological Seminary, 1998.
Ph.D. in Computer Science (Artificial Intelligence), The Ohio State University, 1991.
M.S. in Computer Science, The Ohio State University, 1986.
B.S. in Computer Science and Mathematics, The Ohio State University, 1985.

Employment

Professor of Computer Science, Hope College, Holland, Michigan, (2014 - present)
Associate Professor of Computer Science, Hope College, Holland, Michigan, (2008 – 2014)
Assistant Professor of Computer Science, Hope College, Holland, Michigan, (2002 – 2008)
Senior Software Engineer, NetGenics, Inc./LION bioscience Inc. (1998 – 2002)
Campus Minister, Great Commission Ministries (1991 – 1998)
Graduate Research Assistant, The Ohio State University (1987 – 1991)
Graduate Teaching Assistant, The Ohio State University (1986 – 1987)

Publications

(* designates Student co-author)

SMD Seaver, F Liu, Q Zhang, J Jeffryes, JP Faria, JN Edirisinghe, M Mundy, N Chia, E Noor, ME Beber, AA Best, M DeJongh, JA Kimbrel, P D'haeseleer, SR McCorkle, JR Bolton, E Pearson, S Canon, EM Wood-Charlson, RW Cottingham, AP Arkin, CS Henry, The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes, *Nucleic Acids Research*, Vol. 49, Issue D1, January 2021.

Li K, Chen R, Lindsey W, Best AA, DeJongh M, Henry C, Tintle N, "Implementing and evaluating a Gaussian mixture framework for identifying gene function from TnSeq data," *Pacific Symposium on Biocomputing 2019*, World Scientific Press, November, 2018.

Arkin A, Cottingham R, Henry C, *et al.*, "KBase: The United States Department of Energy Systems Biology Knowledgebase," *Nature Biotechnology*, Vol. 36, July, 2018.

*Bowerman N, Tintle N, DeJongh M, Best AA, "Identification and Analysis of Bacterial Genomic Metabolic Signatures," *Pacific Symposium on Biocomputing*, Vol. 22, January, 2017.

Faria J, Davis J, Edirisinghe J, Taylor R, Weisenhorn P, Olson R, Stevens R, Rocha M, Rocha I, Best AA, DeJongh M, Tintle N, Parrelo B, Overbeek R, Henry C, "Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation," *Frontiers in Microbiology: Systems Microbiology*, Vol. 7, November, 2016.

Disselkoen C, *Greco B, *Cook K, *Koch K, *Lerebours R, *Viss C, *Cape J, *Held E, *Ashenafi Y, *Fischer K, *Acosta A, *Cunningham M, Best AA, DeJongh M, Tintle N, "A Bayesian Framework for the Classification of Microbial Gene Activity States," *Frontiers in Microbiology: Systems Microbiology*, Vol. 7, August, 2016.

Faria J, Khazaei T, Edirisinghe J, Weisenhorn P, Seaver S, Conrad N, Harris N, DeJongh M, Henry C, "Constructing and Analyzing Metabolic Flux Models of Microbial Communities", Book Chapter in *Springer Protocol Handbooks*, Humana Press, June, 2016.

*Powers S, DeJongh M, Best AA, and Tintle N, "Cautions about the reliability of pairwise gene correlations based on expression data" *Frontiers in Microbiology: Systems Microbiology*, Vol. 6, No. 650, June, 2015.

Devoid, S, Overbeek, R, DeJongh, M, Vonstein, V, Best, A, Henry, C, "Automated Genome Annotation and Metabolic Model Reconstruction in the SEED and Model SEED", Book Chapter in *Systems Metabolic Engineering*, Series: Methods in Molecular Biology, ed. Hal Alper, Humana Press, February, 2013.

Tintle, N, *Sitarik, A, *Boerema, B, *Young, K, Best, A, DeJongh, M, "Evaluating the consistency of gene sets used in the analysis of bacterial gene expression data" *BMC Bioinformatics*, Vol. 13, No. 193, August, 2012.

DeJongh, M, *Bockstege, B, *Frybarger, P, *Hazekamp, N, *Kammeraad, J, *McGeehan, T, "CytoSEED: a Cytoscape Plugin for Viewing, Manipulating and Analyzing Metabolic Models Created by the Model SEED" *Bioinformatics*, Vol. 28, Issue 6, Advance Access, December 2011.

Henry, C, Overbeek, R, Xia, F, Best, A, Glass, E, Gilbert, J, Larsen, P, Edwards, R, Disz, T, Meyer, F, Vonstein, V, DeJongh, M, Bartels, D, Desai, N, D'Souza, M, Devoid, S, Keegan, K, Olson, R, Wilke, A, Wilkening, J, Stevens, R, "Connecting genotype to phenotype in the era of high-throughput sequencing," *Biochimica et Biophysica Acta (BBA) - General Subjects*, Vol. 1810, No. 10, October, 2011.

Ravcheev, D, Best, A, Tintle, N, DeJongh, M, Osterman, A, Novichkov, P, Rodionov, D, "Inference of the Transcriptional Regulatory Network in Staphylococcus aureus by Integration of Experimental and Genomics-Based Evidence," *Journal of Bacteriology*, Vol. 193, No. 13, July, 2011.

McFall, R, DeJongh, M, "Increasing Engagement and Enrollment in Breadth-First Introductory Courses Using Authentic Computing Tasks," *Proceedings of the 2011*

SIGCSE Technical Symposium on Computer Science Education, 2011.

Henry, C, DeJongh, M, Best, A, *Frybarger, P, Linsay, B, Stevens, R, “High-throughput generation, optimization and analysis of genome-scale metabolic models,” *Nature Biotechnology*, Vol. 28, No. 9, published online 29 August 2010.

Tintle, N, Best, A, DeJongh, M, *VanBruggen, D, Heffron, F, Porwollik, S, Taylor, R, “Gene set analyses for interpreting microarray experiments on prokaryotic organisms,” *BMC Bioinformatics*, Vol. 9, No. 469, November, 2008.

Aziz, R, Bartels, D, Best, A, DeJongh, M, Disz, T, Edwards, R, *Formsma, K, Gerdes, S, Glass, E, Kubal, M, Meyer, F, Olsen, G, Olson, R, Osterman, A, Overbeek, R, McNeil, L, Paarmann, D, Paczian, T, Parrello, B, Pusch, G, Reich, C, Stevens, R, Vassieva, O, Vonstein, V, Wilke, A, Zagnitko, O, “The RAST Server: Rapid Annotations using Subsystems Technology ,” *BMC Genomics*, Vol. 9, No. 75, February, 2008.

Best, A, DeJongh, M, Barton, A, Brown, J, Barney, C, “Models of Interdisciplinary Research and Service Learning at Hope College,” *Council on Undergraduate Research Quarterly*, December, 2007.

DeJongh, M, *Formsma, K, *Boillot, P, *Gould, J, *Rycenga, M, Best, A, “Toward the automated generation of genome-scale metabolic networks in the SEED,” *BMC Bioinformatics*, Vol. 8, No. 139, April, 2007.

DeJongh, M, *Van Dort, P, *Ramsay, B, “Linking Molecular Function and Biological Process Terms in the Gene Ontology for Gene Expression Data Analysis,” *Conference Proceedings of the IEEE Engineering in Medicine and Biology Society*, Vol. 4, pp. 2984-6, September, 2004.

DeJongh, M, Burnatowska-Hledin, M, “Development and Implementation of an Introductory Bioinformatics Course at Hope College,” Special Issue on Bioinformatics of *Transformations: Liberal Arts in the Digital Age*, Vol. 2, No. 1, April, 2004.

McEntire, R, Karp, P, Abernethy, N, Olken, F, Kent, R, DeJongh, M, Tarczy-Hornoch, P, Benton, D, Pathak, D, Helt, G, Lewis, S, Kosky, A, Neumann, E, Hodnett, D, Tolda, L, and Topaloglou, T, “An Evaluation of Ontology Exchange Languages for Bioinformatics,” in *Proceedings of the Eighth International Conference on Intelligent Systems for Molecular Biology,* pp. 239-250, AAAI Press, Menlo Park, CA, 2000.

Johnson, T, Smith, J, Johnson, K, Amra, N, and DeJongh, M. “Diagrammatic Reasoning of Tabular Data,” in Narayanan, N. H, (ed.), *Reasoning with Diagrammatic Representations: Papers from the 1992 AAAI Spring Symposium*, pp. 161-164, AAAI Press, Menlo Park, CA, 1992.

Johnson, K, Johnson, T, Smith, J, DeJongh, M, Fischer, O, Amra, N, and Bayazitoglu, A, “RedSoar-A System for Red Blood Cell Antibody Identification,” in *Proceedings of the Fifteenth Annual Symposium on Computer Applications in Medical Care*, pp. 664-668, McGraw Hill, Washington, D.C, 1991.

DeJongh, M and Smith, J, “Integrating Models of a Domain for Problem Solving,” in *Proceedings of the Eleventh International Conference on Expert Systems and Their Applications*, pp. 125-135, Avignon, France, 1991.

Presentations

(* designates Student co-author)

DeJongh M, "How to Play a Piano Concerto without an Orchestra," Westmont Impact Conference, Westmont College, Santa Barbara, California, July 25, 2025.

DeJongh M, "How to Play a Piano Concerto without an Orchestra," Hope Academy of Senior Professionals, Hope College, Holland, Michigan, April 8, 2025.

DeJongh M, "How to Play a Piano Concerto without an Orchestra," Osher Lifelong Learning Institute, Aquinas College, Grand Rapids, Michigan, November 14, 2024.

DeJongh M, "How to Play a Piano Concerto without an Orchestra," Music Department Seminar, Westmont College, Santa Barbara, California, October 8, 2024.

DeJongh M, "Reverse Karaoke for Piano Concertos," Economics Department Seminar, Meiji Gakuin University, Tokyo, Japan, December 1, 2023.

DeJongh M, "Reverse Karaoke for Piano Concertos," Computer Science Department Seminar, Hope College, Holland, MI, September 5, 2023.

DeJongh M, "Reverse Karaoke for Piano Concertos," Research Presentation, Liverpool Hope University, Liverpool, UK, June 13, 2023.

DeJongh M, “Building the Killer App for Modeling Microbial Metabolism: from ModelSEED to KBase,” Invited Keynote Address, Network and Pathways Session, Metabolomics 2016, Dublin, Ireland, June 28, 2016.

DeJongh M, “Building the Killer App for Modeling Microbial Metabolism: from ModelSEED to KBase,” Luxembourg Centre for Systems Biomedicine, September 25, 2015.

DeJongh M, Henry C, Arkin A, *et al*, “Metabolic Modeling in the DOE Systems Biology Knowledgebase,” *COBRA 2014 - 3rd Conference on Constraint-Based Reconstruction and Analysis*, Charlottesville, VA, May, 2014.

*Hazekamp N, *Kammeraad J, *Bockstege B, DeJongh M, “Comparative Analysis of M. pneumoniae models using the CytoSEED plugin for metabolic model visualization,” Invited presentation at *ASBMB 2012*, San Diego, CA, April, 2012.

DeJongh, M, *Poel, N, Best, A, Henry, C, “Genome-scale Metabolic Models for Mollicutes reveal novel route through the Pentose Phosphate Pathway,” Invited presentation at

ASBMB 2010, Anaheim, CA, April, 2010.

Henry, C, DeJongh, M, Best, A, *Frybarger, P, Stevens, R, "High-throughput construction and optimization of 140 new genome-scale metabolic models," Poster presentation at *JOBIM 2009*, Nantes, France, June, 2009.

Best, A, DeJongh, M, *Boillot, P, *Bowerman, N, *Formsma, K, *Frybarger, P, *Wilkening, J, "Toward the Automated Generation of Genome-scale Metabolic Networks in the SEED," Poster presentation at the *American Society for Microbiology 107th General Meeting*, Toronto, Ontario, May, 2007.

Best, A, DeJongh, M, Tintle, N. "Interdisciplinary Research across Biology, Mathematics and Computer Science: Genome-scale Metabolic Reconstruction and Modeling of Microbial Life," Invited Presentation at *Midstates Consortium for Mathematics and Science: Interdisciplinary Science Education*, St. Olaf College, Northfield, Minnesota, February 23-24, 2007.

DeJongh, M, Best, A, "Toward the Automatic Generation of Genome-Scale Metabolic Models in the SEED," Poster Presentation at *Department of Energy Genomics:GTL Awardee Workshop V*, Bethesda, Maryland, February 11-14, 2007.

DeJongh, M, Burnatowska-Hledin, M, "Two Complementary Approaches to Teaching Bioinformatics at Hope College," Invited Presentation at *NITLE Bioinformatics Practicum*, Bates College, Lewiston, Maine, June 19-21, 2006.

Best, A and DeJongh, M. "A Research-based Approach to Teaching Bioinformatics: Microbial Genome Annotation and Metabolic Modeling using the SEED," *13th American Society for Microbiology Conference for Undergraduate Educators*, University of Central Florida, Orlando, Florida, May 19-21, 2006.

DeJongh, M and Best, A. "Bioinformatics at Hope College," Invited Presentation at *Albion College Math and Biology Colloquium Series*, Albion, Michigan, March 31, 2005.

DeJongh, M, "Beginning Programming in Perl for Bioinformatics," Invited Presentation at the Education Workshop of the *American Society for Cell Biology 44th Annual Meeting*, Washington, D.C, December 4-8, 2004.

DeJongh, M and Burnatowska-Hledin, M, "Report On the MITC Hands-on Teaching of Bioinformatics Workshop," Invited Presentation at *Voyage to Ithaka: Technology, Collaboration, and the Future of Liberal Arts Colleges*, National Institute for Technology and Liberal Education, Chicago, Illinois, November 7-9, 2004.

DeJongh, M, "Beginning Programming in Perl for Bioinformatics," at the *Midwest Instructional Technology Center's Hands-on Teaching of Bioinformatics Workshop*, Hope College, Holland, Michigan, May 13-15, 2004.

DeJongh, M, Burnatowska-Hledin, M, "An Introductory Course in Bioinformatics," at the *Midwest Instructional Technology Center's Hands-on Teaching of Bioinformatics*

Workshop, Hope College, Holland, Michigan, May 13-15, 2004.

DeJongh, M, Burhans, D, Doom, T, LeBlanc, M, “Bioinformatics in the Undergraduate Curriculum: Opportunities for Computer Science Educators,” at *SIGCSE 2004*, Norfolk, Virginia, March 3-7, 2004.

DeJongh, M, LeBlanc, M, “SIGCSE Special Projects Showcase: Bioinformatics in the Computer Science Curriculum,” at *SIGCSE 2004*, Norfolk, Virginia, March 3-7, 2004.

DeJongh, M, *Van Dort, P, *Ramsay, B, “Linking Molecular Function and Biological Process Terms in the Gene Ontology for Gene Expression Data Analysis,” Poster Presentation at *Pacific Symposium in Biocomputing 2004*, Kona, Hawaii, January 6-10, 2004.

DeJongh, M, “Introducing Bioinformatics into the Undergraduate Curriculum,” at *Bio2010: Computational Solutions to Biological Problems*, Washington University School of Medicine, June 24-26, 2003.

DeJongh, M and Burnatowska-Hledin, M, “Introducing Bioinformatics into the Undergraduate Curriculum,” at *Innovative Science Teaching: Enhancing Learning with Technology*, DePauw University, May 31-June 1, 2003.

DeJongh, M and Burnatowska-Hledin, M, “Introductory Bioinformatics Exercises using Internet Resources,” at *Bioinformatics in the Undergraduate Curriculum*, Dickinson College, March 21-22, 2003.

DeJongh, M and Smith, J, “The Use of Functional and Causal Knowledge in RED,” presented at the Eighth SOAR Workshop, University of Southern California, October, 1990.

DeJongh, M and Smith, J, “Integrating Multiple Models of Expertise,” presented at the AAAI Spring Symposium on Artificial Intelligence in Medicine, Stanford University, March, 1990.

DeJongh, M and Smith, J, “Bridging the Knowledge and Symbol Levels: Towards An Integrated Knowledge Engineering Environment,” presented at the AAAI Spring Symposium on Knowledge System Development Tools and Languages, Stanford University, March, 1989.

Student Research Presentations

Grimes M, Satkiewicz L, "Characterizing Metabolic Diversity in the Bacterial World," at *COBRA 2018*, Seattle, WA, October 14, 2018.

Kondo S, “Modeling Bacterial Metabolism and Genetic Regulation,” at the *Celebration of Undergraduate Research and Creative Performance*, Hope College, Holland, Michigan, April 15, 2015.

Deeg C, Kondo S, “Proposing Genes for Gap Reactions in Metabolic Pathways,” at the *Celebration of Undergraduate Research and Creative Performance*, Hope College, Holland, Michigan, April 11, 2014.

Kammeraad, J, Houg, A, Kondo, S, DeJongh, M, “Comparative Analysis of M. pneumoniae models using the CytoSEED plugin for metabolic model visualization,” at the *Pew Midstates Science and Mathematics Consortium's Undergraduate Research Symposium*, St. Louis, Missouri, November, 2012.

Hazekamp N, Kammeraad J, Bockstege B, DeJongh M, “Comparative Analysis of M. pneumoniae models using the CytoSEED plugin for metabolic model visualization,” Poster presentation and winner of Honorable Mention at *ASBMB 2012*, San Diego, CA, April, 2012.

Frybarger, P, DeJongh, M, “Generation and Refinement of Metabolic Reaction Networks in the SEED ,” at *ISMB 2008*, Toronto, Ontario, July 19-23, 2008.

Frybarger, P, “Expanding the Scope of Genome-Scale Metabolic Models,” at the *Seventh Annual Celebration of Undergraduate Research and Creative Performance*, Hope College, Holland, Michigan, March 28, 2008.

Formsma, K, Boillot, P, “Comparative Metabolic Modeling of Prokaryotic Genomes,” at the *Council for Undergraduate Research 2007 Posters on the Hill*, Washington, DC, April 25, 2007.

Formsma, K, “Automatic Generation of Genome-Scale Metabolic Models,” at the *SIGCSE 2007 Student Research Competition*, Covington, Kentucky, March 7-10, 2007.

Boillot, P, Formsma, K, “Automatic Generation of Genome-Scale Metabolic Models,” at the *Sixth Annual Celebration of Undergraduate Research and Creative Performance*, Hope College, Holland, Michigan, January 29, 2007.

Ambrose, J, Formsma, K, Gould, J, “Integration of KEGG pathways into the SEED,” at the *Argonne National Laboratory Symposium for Undergraduates in Science, Engineering and Mathematics*, Argonne National Laboratory, Argonne, Illinois, November 4-5, 2005.

Blumenberg, K, Wilkening, M, “Mining Implicit Links in the Gene Ontology,” at the *Eleventh Annual Consortium for Computing Sciences in Colleges: Midwest Conference*, Kalamazoo College, Kalamzoo, Michigan, October 1-2, 2004.

Sumner, N, Evans, T, DeJongh, M, “Simulating the Effects of Speciation and Extinction Rates on Branch Lengths in Phylogenetic Trees,” at the *International Conference for Mathematics in Biology and Medicine*, University of Michigan, Ann Arbor, Michigan, July 25-28, 2004.

Ramsay, B, Van Dort, P, “Functional Modeling of Genes and Cellular Processes for Gene Expression Analysis,” at the *SIGCSE 2004 Student Research Competition*, Norfolk, Virginia, March 3-7, 2004.

Ramsay, B, Van Dort, P, "Functional Modeling of Genes and Cellular Processes," at the *Pew Midstates Science and Mathematics Consortium's Undergraduate Research Symposium*, St. Louis, Missouri, November 14-16, 2003.

Grants, Awards, Visiting Professorships

Visiting Professor, Meiji Gakuin University, Tokyo, Japan, September - December 2023.

Visiting Professor, Liverpool Hope University, Liverpool, UK, September 2022 - June 2023.

National Science Foundation, *Collaborative Research: RUI: Modeling Transcriptome Inferred Gene Activity States for the Investigation of Metabolic and Regulatory Diversity of Sequenced Microbes*, Award Number MCB-1775211, August 2017 - August 2022.

National Science Foundation, *RUI: Dynamics of genomic mosaicism in non-host associated Escherichia populations*, Award Number MCB-1616737, August 2016 through July 2019.

Fulbright Research Scholar at the Luxembourg Centre for Systems Biomedicine, University of Luxembourg, February to June 2016.

National Science Foundation, *Collaborative Research: RUI: Developing Integrated Metabolic Regulatory Models (iMRMs) for the Investigation of Metabolic and Regulatory Diversity of Sequenced Microbes*, Award Number MCB-1330734, October 2013 through September 2016.

Department of Energy, *KBase: An Integrated Knowledgebase for Predictive Biology and Environmental Research*, Subcontract to Argonne National Laboratory, September 2011 through August 2016.

National Science Foundation, *Extending the RAST server to support reconstruction and modeling of cellular networks*, Award Number DBI-0850546, September 2009 through August 2013.

Fulbright Research Scholar at the Laboratoire Bordelais de Recherche en Informatique, Bordeaux, France, *Fulbright-Aquitaine Regional Council Award*, January to June 2009.

National Science Foundation, *RUI: Automated Metabolic Reconstruction for All Sequenced Microbial Genomes* with Dr. Aaron Best (Biology), Award Number MCB-0745100, August 2008 through July 2012.

Argonne National Laboratory, *Guest Faculty Program*, 2006 to 2020.

Hope College, *Howard Hughes Medical Institute Faculty Development Grant for Interdisciplinary Research* with Dr. Aaron Best (Biology) and Dr. Nathan Tintle (Mathematics), Summer, 2006.

Hope College, *Howard Hughes Medical Institute Faculty Development Grant for Interdisciplinary Research* with Dr. Aaron Best (Biology), Summer, 2005.

Hope College, *Towsley Research Scholar Award*, January, 2005.

National Computational Science Institute, *Development of Virtual Applets to Increase the Understanding of Concepts in the Undergraduate Biology Curriculum at Hope College*, with Debbie Swarthout, September, 2004.

Hope College Faculty Development Fund, *Functional Modeling of Genes and Cellular Processes for Gene Expression Data Analysis*, June, 2004.

Midwest Instructional Technology Center, *Hands-on Teaching of Bioinformatics Workshop*, with Maria Burnatowska-Hledin, May, 2004.

The Association for Computing Machinery, Special Interest Group in Computer Science Education: *Bioinformatics in the Computer Science Curriculum*, with Maria Burnatowska-Hledin at Hope College, and Mark LeBlanc and Betsey Dyer at Wheaton College, MA, July 2003.

Recent Service to Hope College

Presidential Advisory Committee, 2023-2025

Computer Science Department Chair, 2018-2022, Spring 2024

Senior Seminar Director, 2018-2022

Presidential Search Committee, 2018

Faculty Moderator, 2016-18

Provost Transition Committee, 2017

Campus Master Planning Committee, 2016-17

Strategic Plan - Academic Distinctiveness Study Group, 2015 (Chair)

Professional Interests Committee, 2010, 2011-13 (Chair), 2016-18

Administrative Affairs Board, 2014-15 (Secretary)

Critical Issues Symposium Planning Committee, 2013-14

Computer Science Department Chair, 2013