Peter E. Larsen

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EDUCATION

M.S., University of Illinois at Chicago	Masters of Science in Bioengineering, 2006 Thesis: "Identifying Gene Interaction Networks from Time Course Microarray Data and Gene Ontology Annotation"
B.S., Purdue University	Bachelor of Science in Ecology and Population Biology, 1993

PROFESSIONAL EMPLOYMENT

Present – January 2009	**Computational Biologist**, *Department of Biosciences, Argonne National Laboratories through Kelly Scientific* Analyze next generation transcriptomic sequencing data, metagenomic data, and metatranscriptomic data. Generate novel analysis methods for structural annotation of gene models, determination of transcriptional profiles, and predict changes in metabolic pathways from NGS data. Developed "GeneShaper" method for structure annotation of gene models using Solexa sequencing reads. Developed "BowStrap" method for assigning confidence intervals to measured gene expression values calculated from deep RNA sequencing data. Developed Function Restricted Value Neighborhood (FRV-N) method for generating putative protein-protein interaction networks from transcriptomic data. Developed Predicted Metabolic Turnover (PRMT) method for generating environmental metabolomic data from metagenomes. Developed Meta Assemblage Prediction (MAP) method for predicting changes in communities in response to changing environmental conditions.
January 2009 – June 2001	**Bioinformatics Specialist,** *Core Genomics Laboratory, University of Illinois at Chicago.* Analyzed high-throughput transcriptomics data in university core laboratory. Developed all lab protocols, documentation, and quality control metrics. Performed all steps of 'Affymetrix' GeneChip and glass slide fabrication, sample labeling, hybridization, data acquisition, and gene sequence annotations. Confirmed microarray results by 386-well RT-PCR. Initiated, developed, and published novel methodologies for data analysis and generation of gene interaction networks from high throughput data including Likelihood of Interaction (LOI) method for prediction of interaction networks from transcriptomic data and text-mining of databases. Maintained collaborative relationships with university researchers, within UIC and at neighboring institutions.

June 2001 – November 1998	**Research and Development,** *Vysis, Inc.* Coordinated between manufacturing team and R&D to generate research use and medical diagnostic FISH probes and DNA genomic microchip arrays in a GMP / ISO 1000 certified laboratory. Generated reliable methods for detection of gene copy number changes with genomic microarrays. Improved production array fabrication protocols to require half previous time and materials while significantly increasing product yield. Served as an Environmental Health and Safety Council Member.
November 1998 – November 1997	**Research Associate,** *ThermoGen, Inc*. Developed methods for directed evolution of thermostable enzymes for increased/altered industrially relevant activities, and screened genomic libraries (plasmid) from thermostable bacteria for enzymes of unique or useful activities. Developed method for identifying regions of protein structure for targeted mutagenesis based on predicted 3D protein structure. Served as Safety Coordinator.
November 1997 – March 1995	**Scientist,** *FermaLogic, Inc.* Researched methods for metabolic engineering of soil microbial species Actinomycetes for the development of new pharmaceutical products and industrial fermentation strain improvement technology. Routine duties included shake flask and stir jar fermentations, bacterial transformations, plasmid construction, chromosomal and plasmid DNA isolations, standard and pulsed field DNA gel electrophoresis, Southern hybridizations, PCR and PCR primer design, and HPLC and HPLC methods development.
February 1995 - January 1996	**Researcher,** *Lakeside Biotechnology, Inc.* Developed proprietary processes for the genetic modification of plants, using model organism *Arabidopsis* and *Agrobacterium tumefaciens*. Maintained laboratory cultures of plants and plant tissue culture micropropagation.

RELEVANT PUBLICATIONS

1. **Peter E. Larsen**, Dawn Field, Yuki Hamada, Jack A. Gilbert. Improving carbon dioxide forecasting through explicit modeling of microbial metabolic dynamics. Submitted to *Nature Climate Change*.

2. Stephen Lumayag, Caroline E Haldin, Colleen Cowan, Beatrix Kovacs, **Peter Larsen**, Dane P. Witmer, David Valle, Shunbin Xu. Inactivation of the miR-183/96/182 Cluster Results in Syndromic Retinal Degeneration. Accepted at *PNAS* 12/21/2012.

3. **Peter E. Larsen**, Jack A. Gilbert. Microbial Bebop: creating music from complex dynamics in microbial ecology. Submitted PLoS ONE.

4. **Peter E Larsen** and Frank R Collart. BowStrap v1.0: Assigning statistical significance to expressed genes using short-read transcriptome data. BMC Research Notes 2012, 5:275. [**HIGHLY ACCESSED**]

5. **Peter E. Larsen**, Sean M. Gibbons and Jack A. Gilbert. Modeling Microbial Community Structure and Functional Diversity Across Time And Space. FEMS Microbiology Letters. Accepted manuscript online: 3 MAY 2012 09:14PM EST | DOI: 10.1111/j.1574-6968.2012.02588.x.

6. **Larsen PE**, Field D, Gilbert JA. Predicting bacterial community assemblages using an artificial neural network approach. Nat Methods. 2012 Apr 15. doi: 10.1038/nmeth.1975. [**Manuscript reviewed in June 2012 Nature Methods, News and Views**]

7. **Larsen P**, Hamada Y, Gilbert J. Modeling microbial communities: Current, developing, and future technologies for predicting microbial community interaction. J Biotechnol. 2012 Mar 23.

8. **Larsen PE**, Collart F, Field D, Meyer F, Keegan KP, Henry CS, McGrath J, Quinn J, Gilbert JA. 2011. Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. Microbial Informatics and Experimentation 2011, 1:4. [**HIGHLY ACCESSED**]

9. **Larsen PE** and Collart FR. Hermaion, ZenoBridge, ZenoArrow and GeneShaper. ANL Invention Report, ANL-SF-09-089

10. Havel VE, Wool NK, Ayad D, Downey KM, Wilson CF, **Larsen P**, Djordjevic JT, Panepinto JC. Ccr4 Promotes Resolution of the ER Stress Response during Host Temperature Adaptation in Cryptococcus neoformans. Eukaryot Cell. 2011 May 20.

11. **Peter E Larsen**, Avinash Sreedasyam, Geetika Trivedi, Gopi K Podila, Leland J Cseke and Frank R Collart. Using Next Generation Transcriptome Sequencing to Predict an Ectomycorrhizal Metabolome. BMC Systems Biology (2011), 5:70. [**HIGHLY ACCESSED**]

12. Adler A, Park YD, **Larsen P**, Nagarajan V, Wollenberg K, Qiu J, Myers TG, Williamson PR. A novel specificity protein 1 (SP1)-like gene, regulating protein kinase C-1 (PKc1)-dependent cell-wall integrity and virulence factors in Cryptococcus neoformans. J Biol Chem. 2011 Apr 12.

13. Henry CS, Overbeek R, Xia F, Best AA, 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 KP, Olson R, Wilke A, Wilkening J, Stevens RL. Connecting genotype to phenotype in the era of high-throughput sequencing. Biochim Biophys Acta. 2011 Mar 21.

14. **Peter Larsen**, Frank Collart and Yang Dai, "Incorporating network topology improves prediction of protein interaction networks from transcriptomic data". International Journal of Knowledge discovery and Bioinformatics, 1(3), pp.1-19. 2010.

15. Park YD, Panepinto J, Shin S, **Larsen P**, Giles S, Williamson PR. Mating pheromone in Cryptococcus neoformans is regulated by a transcriptional/degradative "futile" cycle. J Biol Chem. 2010 Nov 5;285(45):34746-56. Epub 2010 Aug 27.

16. **Peter E Larsen**, Trivedi G, Sreedasyam A, Lu V, Podila GK, Collart FR. Using deep RNA sequencing for the structural annotation of the Laccaria bicolor mycorrhizal transcriptome. PLoS One. 2010 Jul 6;5(7):e9780.

17. **Peter Larsen** and Yang Dai, Using Gene Expression Modeling to Determine Biological Relevance of Putative Regulatory Networks, Proceeding of the 5th International Symposium on Bioinformatics Research and Applications (eds. I. Mandoiu, G. Narasimhan, and Y. Zhang), Lecture Notes in Bioinformatics, Springer Verlag, Vol. 5542 (2009) pp. 40-51, 2009.

18. Kedar Kulkarni, **Peter Larsen** and Andreas A. Linninger, "Assessing chronic liver toxicity based on relative gene expression data", Journal of Theoretical Biology (2008), doi:10.1016/j.jtbi.2008.05.032.

19. **Peter Larsen**, Eyad Almasri, Guanrao Chen and Yang Dai," Incorporating Knowledge of Topology Improves Reconstruction of Interaction Networks from Microarray Data", Lecture Notes in Bioinformatics, Vol. 4983 (eds.by I.I. Mandoiu, Raj Sunderraman, and A. Xelikovsky), Springer Verlag, pp. 434-443, 2008.

20. Eyad Almasri, **Peter Larsen**, Guanrao Chen and Yang Dai, "Incorporating Literature Knowledge in Baysian Network for Inferring Gene Networks with Gene Expression Data", Lecture Notes in

Bioinformatics, Vol. 4983 (eds. by I.I. Mandoiu, Raj Sunderraman, and A. Xelikovsky), Springer Verlag, pp. 184-195, 2008.

21. Guanrao Chen, **Peter Larsen**, Eyad Almasri, Yang Dai, "Rank-based edge reconstruction for scale-free genetic regulatory networks", BMC Bioinformatics (2008), 9:75.

22. **Peter Larsen**, Eyad Almasri, Guanrao Chen, Yang Dai, "A statistical method to incorporate biological knowledge for generating testable novel gene regulatory interactions from microarray experiments", BMC Bioinformatics (2007), 8:317. [**HIGHLY ACCESSED**]

23. **Peter Larsen**, E. Almasri, G. Chen and Y. Dai, "Correlated discretized expression score: a method for identifying gene interaction networks from time course microarray expression data" Proceedings of the 28th International Conference of IEEE Engineering in Medicine and Biology Society (EMBS) (2006). pp. 5842-5845.

24. G. Chen, **P. Larsen**, E. Almasri and Y. Dai, "Sample scale-free gene regulatory network using gene ontology", Proceedings of the 28th International Conference of IEEE Engineering in Medicine and Biology Society (EMBS) (2006). pp.5523-5526.

25. Robert Folberg, Zarema Arbieva, Jonas Moses, Amin Hayee, Tone Sandal, ShriHari Kadkol, Amy Lin, Klara Valyi-Nagy, Suman Setty, Lu Leach, Patricia Chevez-Barrios, **Peter Larsen**, Dibyen Majumdar, Jacob Pe'er, Andrew Maniotis. "The generation of vasculogenic mimicry patterns dampens the invasive melanoma cell genotype and phenotype". Am J Pathol (2006), 166:1187-203.

26. Hessler, PE, **PE Larsen**, AI Constantinou, KH Schram, and JM Weber. "Isolation of isoflavones from soy-based fermentations of the erythromycin-producing bacterium Saccharopolyspora erythraea". Appl. Microbiol. Biotechnol. 1997 47(4) P398-404.

Manuscripts in Preparation

1. **Peter E. Larsen**, Mike Miller, Leland Cseke, Yang Dai, Frank R. Collart. Predicting aspen response to elevated carbon dioxide and ozone using an artificial neural network approach. Targeting PLoS ONE.

2. **Peter E. Larsen**, Avinash Sreedasyam, Geetika Trivedi, Leland J. Cseke, Frank R. Collart. Multi-omics approach to identify sensory mechanisms in mycorrhizal symbiosis. Targeting BMC Bioinformatics.

3. **Peter E. Larsen**, Daniele Armaleo, Frank R. Collart. Using Next Generation Transcriptome Sequencing to Predict a Lichen Metabolome. Targeting BMC Systems Biology.

4. **Peter E. Larsen**, Jack A. Gilbert. Ecosystem scale modeling of microbial CO_2 metabolism in a coastal marine environment. Targeting ISME.

5. Oleg R. Roderick, Ilya Safro, **Peter E. Larsen**, Jack A. Gilbert. Bandura: Modeling 1000 marine microbial OTU's as functions of environmental parameters. Targeting ISME.

Book Chapters

1. Leland J. Cseke, Stan D. Wullschleger, Avinash Shreedasyam, Geetika Trivedi, **Peter Larsen**, Frank Collart. Chapter 12: Carbon Sequestration. *Genomics & Breeding for Climate-Resilient Crops* (ed. Chittaranjan Kole). Springer, New York [In press].

2. Andreas Wilke, **Peter Larsen**, Jack A Gilbert. Chapter 43. *Next Generation Sequencing and the Future of Microbial Metagenomics.* Horizon Scientific Press / Caister Academic Press [In press].

3. **Peter Larsen**, Leland Cseke, Frank R Collart. Using Next Generation Transcriptome Sequencing to Predict an Ectomycorrhizal Metabolome.   *Molecular Microbial Ecology of the Rhizosphere*. (Frans J. de Bruijn ed.), INRA/CNRS Laboratory of Plant-Microbe Interactions. [In press].

4. Yang Dai, Eyad Almasri, **Peter Larsen**, Guanrao Chen, Structure Learning of Genetic Regulatory Networks Based on Knowledge Derived from Literature and Microarray Gene Expression Measurements, *Computational Methodologies in Gene Regulatory Networks*, (S. Das, D. Caragea, W. H. Hsu, S. M. Welch eds.), IGI Global, pp.289-309, 2009.

Relevant Presentations

1. Antarctic MAPs: Predicting the Population Structure of Antarctic Soil Microbial Communities as a Function of Environmental Conditions. Argonne Soils Workshop (ASW) 2011.

2. Biogeography: Everything is Everywhen. International Census of Marine Microorganisms (ICoMM), 2011.

3. Transcriptome profiling identifies the mycorrhizal interaction mechanisms that respond to elevated atmospheric CO_2 and O_3. Argonne Soils Workshop (ASW), 2010

4. Exploring the Aspen-Laccaria Mycorrhizal Interactome using Next Generation Sequencing. Challenges in Environmental Molecular Microbiology (CEMM), 2010.

5. Using Next Generation Sequencing Data for Structural Annotation of L. bicolor Mycorrhizal Transcriptome. Critical Assessment of Massive Data Analysis (CAMDA), 2009.

6. Using Gene Expression Modeling to Determine Biological Relevance of Putative Regulatory Networks. International Symposium on Bioinformatics Research and Applications (ISBRA), 2009.

7. Incorporating Knowledge of Topology Improves Reconstruction of Interaction Networks from Microarray Data. International Symposium on Bioinformatics Research and Applications (ISBRA), 2008.

8. Incorporating Literature Knowledge in Bayesian Network for Inferring Gene Networks with Gene Expression Data. International Symposium on Bioinformatics Research and Applications (ISBRA), 2008.

Patents Issued

J Mark Weber, **Peter E. Larsen**, Mihn B. Luu, and Paul Hessler. 1998. Method and Composition for Enhancing Erythromycin Production. U.S. Serial # 08/852,401.