BIOGRAPHICAL SKETCH

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NAME James Lyons-Weiler	POSITION TITLE CEO/President/Director Institute for Pure and Applied Knowledge
eRA COMMONS USER NAME (credential, e.g., agency login) jameslyonsweiler	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	MM/YY	FIELD OF STUDY
State University of New York, Oswego, NY	B.A.	8, 1991	Biology
Ohio State University	M. Sc.	6, 1993	Zoology
The University of Nevada, Reno	Ph.D.	6, 1998	Ecology, Evol & Conservation Biology
Pennsylvania State University	Postdoctoral	2000	Computational Molecular Biology

A. Personal Statement

My research program is focused on improving healthcare via the development of treatment efficacy and risk biomarkers, optimizing clinical interventions after adverse events, and understanding the neurological and immunological basis of vaccine injuries. I have been performing collaborative research with DNA sequence data since 1996, microarray gene expression data since 1998, proteomic data since 2003, and next generation sequencing since 2009. I have participated in program-level consortia including the NCI's Early Detection Research Network, caBIG, and managed a large multi-institutional consortium in Proteomics and Bioinformatics (funded via TATRC). With a deep understanding of the effects of data pre-processing algorithms on the validity of downstream statistical inferences, and fundamental comprehension of principles of ecology and evolutionary theory, I have developed novel paradigms for high-dimensional – omic analyses, including advances in statistical methods for variant calling, transcriptional profiling, machine-learning based prediction modeling, integrative translational research via decision modeling, covariate matching for case/control selection, and for the statistical evaluation of survivorship prediction models. These advances are applied via intelligent methods optimization, in which empirically optimized data analysis protocols are arrived at routinely via systematic comparative evaluative methodological research & development to insure reproducibility. I have directed the successful analysis of at least twenty-five Next Generation Sequence data sets with various applications from whole microbial and mouse genome sequencing to from various platforms for transcriptomics, variant detection, ChipSeq, methylomics, and whole genome/exome sequencing. The algorithms I have developed are current in use by many labs as they provide information measures reflective of both data quality and algorithm performance using objective evaluation measures. I have written books on Ebola, Translational Research and Autism. I founded the Institute for Pure and Applied Knowledge to conduct biomedical and translational research in the public interest.

Positions and Honors

1998-2000   AP Sloan/US Department of Energy Postdoctoral Fellow in Computational Molecular Biology
1998-2001   (Awarded but declined) NIH National Research Service Award in Bioinformatics
2000-2002   Assistant Professor, University of Massachusetts, Lowell, Department of Biological Sciences
2000-2002   Co-Director, Center for Bioinformatics and Computational Biology, University of Massachusetts, Lowell
2002-2007   Assistant Professor, University of Pittsburgh School of Medicine, Department of Biomedical Informatics; Core Faculty Member, Biomedical Informatics Training Program; Department of Pathology; Fully Associated Faculty Member, University of Pittsburgh Cancer Institute
2007-2014   Scientific Director, Bioinformatics Analysis Core Service, University of Pittsburgh; Adjunct Assistant Professor, Department of Biomedical Informatics, University of Pittsburgh
2014-present CEO/Director, Institute for Pure and Applied Knowledge

Other Experience and Professional Membership
2016-present Editorial Board, Cancer Research
2004-present Member, Society for Experimental Biology
2004-2006. Associate Editor, *Applied Bioinformatics.*
2006-2007. Founding Editor-in-Chief, *Cancer Informatics*
2008-2010. Grant Review Committee, New Jersey Commission on Cancer Research
2009. Member, The Society for Clinical and Translational Science

B. Selected Peer-Reviewed Publications (Selected from 42 peer-reviewed publications)
<u>**Most relevant to the current application**</u>
Dobrowolski SF, **Lyons-Weiler J**, Spridik K, Vockley J, Skvorak K, Biery A. 2016. DNA methylation in the pathophysiology of hyperphenylalaninemia in the PAHenu2 mouse model of phenylketonuria.
Mol Genet Metab. pii: S1096-7192(16)30001-4. doi: 10.1016/j.ymgme.2016.01.001. PMID 26822703.
Dobrowolski SF, **Lyons-Weiler J,** Spridik K, Biery A, Breck J, Vockley J, Yatsenko S, Sultana T.
Altered DNA methylation in PAH deficient phenylketonuria. Mol Genet Metab. 115(2-3):72-7. doi: 10.1016/j.ymgme.2015.04.002. PMID: 25990862.
Ozburn AR, Falcon E, Twaddle A, Nugent AL, Gillman AG, Spencer SM, Arey RN, Mukherjee S, **Lyons-Weiler J**, Self DW, McClung CA. 2014 Direct Regulation of Diurnal Drd3 Expression and Cocaine Reward by NPAS2. Biol Psychiatry. 2014 Aug 13. pii: S0006-3223(14)00594-0. doi: 10.1016/j.biopsych.2014.07.030. PMID: 25444159.
Zubenko GS, Hughes HB 3rd, Jordan RM, **Lyons-Weiler J**, Cohen BM. 2014. Differential hippocampal gene expression and pathway analysis in an etiology-based mouse model of major depressive disorder. Am J Med Genet B Neuropsychiatr Genet. 165(6):457-66. doi: 10.1002/ajmg.b.32257. PMID: 25059218.
Dobrowolski, SF, A. Biery, K Sprydik, E. Kranik, K. Skvorak, J. Vockley, **J. Lyons-Weiler**, T. Sultana. 2014. Methylome repatterning in a mouse model of Maternal PKU Syndrome. Molecular Genetics and Metabolism 113(3):194-9. doi: 10.1016/j.ymgme.2014.08.006.
Shin SS, Bales JW, Yan HQ, Kline AE, Wagner AK, **Lyons-Weiler J**, Dixon CE. 2013. The effect of environmental enrichment on substantia nigra gene expression after traumatic brain injury in rats. *J Neurotrauma*. 30:259-70. PMID 23094804
Tanaka Y, Shigemura N, Kawamura T, Noda K, Isse K, Stolz DB, Billiar TR, Toyoda Y, Bermudez CA, **Lyons-Weiler J**, Nakao A. 2012. Profiling molecular changes induced by hydrogen treatment of lung allografts prior to procurement. *Biochem Biophys Res Commun*. 425:873-9. PMID 22902635
Hsu E, Shi H, Jordan RM, **Lyons-Weiler J**, Pilewski JM, Feghali-Bostwick CA. 2011. Lung tissues in patients with systemic sclerosis have gene expression patterns unique to pulmonary fibrosis and pulmonary hypertension. *Arthritis Rheum*. 63:783-94. PMID 21360508
Founds SA, Shi H, Conley YP, Jeyabalan A, Roberts JM, **Lyons-Weiler J**. 2012. Variations in discovery-based preeclampsia candidate genes. Clin Transl Sci. 5:333-9. PMID 22883611
Montecalvo A, Larregina AT, Shufesky WJ, Stolz DB, Sullivan ML, Karlsson JM, Baty CJ, Gibson GA, Erdos G, Wang Z, Milosevic J, Tkacheva OA, Divito SJ, Jordan R, **Lyons-Weiler J**, Watkins SC, Morelli AE. 2012. Mechanism of transfer of functional microRNAs between mouse dendritic cells via exosomes. *Blood.* 119:756-66. PMID 22031862.
Hsu E, Shi H, Jordan RM, **Lyons-Weiler J**, Pilewski JM, Feghali-Bostwick CA. 2011. Lung tissues in patients with systemic sclerosis have gene expression patterns unique to pulmonary fibrosis and pulmonary hypertension. *Arthritis Rheum.* 63:783-94. PMID 21360508
Sultana, T., R. Jordan & **J. Lyons-Weiler**. 2009. Optimization of the use of consensus methods for the detection and putative identification of peptides via mass-spectrometry using protein standard mixtures. *J. of Proteomics & Bioinformatics* 2:262-273. PMID 19779596
http://www.omicsonline.com/ArchiveJPB/2009/June/02/JPB2.262.html
Davies, M.L., S. Xu, **J. Lyons-Weiler**, A. Rosendorff, L.R. Wasil; S.A. Webber, D. Metes, D.T. Rowe. 2011. Cellular factors associated with latency and spontaneous Epstein-Barr virus reactivation in B-lymphoblastoid cell lines. *Virology* 400:53-67. PMID 20153012

Additional recent publications of importance to the field (in chronological order)

Dagda RK, Sultana T, **Lyons-Weiler J**. 2010. Evaluation of the consensus of four peptide identification algorithms for tandem mass spectrometry based proteomics. *J Proteomics & Bioinformatics* 3:39-47. PMID 20589240.

Founds SA, Conley YP, Lyons-Weiler JF, Jeyabalan A, Allen Hogge W, Conrad KP. 2009. Altered global gene expression in first trimester placentas of women destined to develop preeclampsia. *Placenta.* 30:15-24. PMID19027158

Ranganathan S, Polshyna A, Lutka F, Nicholl G, **Lyons-Weiler J**, and Bowser R. Assessment of protein stability in cerebrospinal fluid by mass spectrometry based proteomics. *Clinical Proteomics* 2:91-101. *http://www.springerlink.com/content/81778847577u8h73/* PMID 20200596

Lyons-Weiler, J, S Patel and S Bhattacharya. 2003. A classification-based machine learning approach for the analysis of genome-wide expression data. *Genome Research* 13:503-512. PMID 12618382

Bhattacharya, S, D Long, **J Lyons-Weiler.** 2004. Overcoming confounded controls in the analysis of gene expression data from microarray experiments. *Applied Bioinformatics* 2:197-208. PMID 15130791

Patel, S, **J Lyons-Weiler**. 2004. caGEDA: A web application for the integrated analysis of global gene expression patterns in cancer. *Applied Bioinformatics* 3:49-62. PMID 16323966

Lyons-Weiler, J, S Patel, MJ Becich and T Godfrey. 2004. Tests for finding complex patterns of differential expression in cancer: towards individualized medicine. *BMC Bioinformatics,*5:110. PMID 15307894

Lyons-Weiler, J, R Pelikan, HJ Zeh, III, DC Whitcomb, DE Malehorn, WL Bigbee, and M Hauskrecht. 2005. Assessing the statistical significance of the achieved classification error of classifiers constructed using serum peptide profiles, and a prescription for random sampling repeated studies for massive high-throughput genomic and proteomic studies. *Cancer Informatics* 1(1) 53-77. PMID19325865

Shi H, **Lyons-Weiler J**. 2007. Clinical decision modeling system. *BMC Med Inform Decis Mak.* Aug 13;7(1):23. PMID17697328

Jordan R, Patel S, Hu H, and **Lyons-Weiler J.** 2008. Efficiency analysis of competing tests for finding differentially expressed genes in lung adenocarcinoma. *Cancer Informatics,* 6: 389-421. http://www.la-press.com/journal.php?journal_id=10&issue_id=101 PMID 19259419

Berty, H.P., H. Shi & **J. Lyons-Weiler**. 2010. Determining the statistical significance of survivorship prediction models. *J. Clinical Evaluation 16:155-165.*