

BIOGRAPHICAL SKETCH

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NAME: Dreyfuss, Jonathan Michael

eRA COMMONS USER NAME (credential, e.g., agency login): DREYFUSSJ

POSITION TITLE: Director, Bioinformatics & Biostatistics Core

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

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
McGill University, Canada	B.A.	06/2004	Economics
University of North Carolina - Chapel Hill, USA	M.S.	05/2006	Statistics and Operations Research
Boston University, USA	Ph.D.	12/2013	Bioinformatics

A. Personal Statement

After my BA, I received an MS from the Department of Statistics and Operations Research at UNC Chapel Hill. I joined the Harvard Partners Center for Genetics and Genomics as a Bioinformatics Analyst in 2006, and then completed my PhD in the Graduate Program in Bioinformatics at Boston University, where I was advised by James Galagan. My thesis focused on new methods for the reconstruction and analysis of metabolic networks, with an application to the filamentous fungus *Neurospora crassa*.

Overall, I have been applying and developing biostatistics and bioinformatics methods for clinical data, physiological outcomes, genomics, metagenomics, epigenomics, transcriptomics, proteomics, metabolomics, metabolic networks, and data integration. Thus, I have the expertise and experience to carry on the biostatistics and bioinformatics analysis for this proposal.

B. Positions and Honors**Professional Positions**

07/2006–07/2009 Bioinformatics Analyst, Harvard Medical School – Partners HealthCare Center for Genetics and Genomics, Boston, MA
 11/2013–06/2017 Research Scientist, Department of Biomedical Engineering, Boston University, Boston, MA
 11/2013–06/2017 Bioinformatics/Systems Biology Core Coordinator, Joslin Diabetes Center, Boston, MA
 07/2017–10/2019 Associate Director, Bioinformatics & Biostatistics Core, Joslin Diabetes Center, Boston, MA
 11/2019–04/20 Co-Director, Bioinformatics & Biostatistics Core, Joslin Diabetes Center, Boston, MA
 05/20– Director, Bioinformatics & Biostatistics Core, Joslin Diabetes Center, Boston, MA

Awards and Professional Recognition

2009–2011 NSF Integrative Graduate Education and Research Traineeship (IGERT) program fellowship
 2013–2015 Program Committee, ISMB 2014 and ISMB/ECCB 2015 (Disease Models & Epidemiology)
 2018 Mary K. Iacocca Senior Visiting Research Fellow
 2019 Developmental Core Committee, Harvard Center for AIDS Research

C. Contributions to Science

1. The majority of my publications document my contribution by supporting studies involving multiple types of high-throughput data, such as metabolomics, transcriptomics, and genomics, by applying state-of-the-art statistics/bioinformatics methods.
 - a. Xue R, Lynes MD, Dreyfuss JM, Shamsi F, Schulz TJ, Zhang H, Huang TL, Townsend KL, Li Y, Takahashi H, Weiner LS, White AP, Lynes MS, Rubin LL, Goodyear LJ, Cypess AM, Tseng YH. Clonal analyses and gene profiling identify genetic biomarkers of the thermogenic potential of human brown and white preadipocytes. *Nat Med.* 2015 Jul;21(7):760-8. PubMed PMID: 26076036; PubMed Central PMCID: PMC4496292
 - b. Thomou T, Mori MA, Dreyfuss JM, Konishi M, Sakaguchi M, Wolfrum C, Rao TN, Winnay JN, Garcia-Martin R, Grinspoon SK, Gorden P, Kahn CR. Adipose Tissue is a Major Source of Circulating microRNAs That Can Regulate Gene Expression in Other Tissues. *Nature.* 2017 Feb 23;542(7642):450-455. PubMed PMID: 28199304; PubMed Central PMCID: PMC5330251.
 - c. Galagan, Minch, Peterson, Lyubetskya, Azzizi, Sweet, Gomez, Rustad, Dolganov, Glotova, Abeel, Mahwinney, Kennedy, Allard, Brabant, Krueger, Jaini, Honda, Yu, Hickey, Zucker, Garay, Weiner, Sisk, Stolte, Camacho, Dreyfuss J, Lui, Dorhoi, Mollenkopf, Drogaris, Lamontagne, Zhou, Piquenet, Park, Raman, Kaufmann, Mohny, Chelsky, Moody, Sherman, Schoolnik. The Mycobacterium tuberculosis regulatory network and hypoxia. *Nature.* 2013 Jul 11;499(7457):178-83. PubMed PMID: 23823726; PubMed Central PMCID: PMC4087036.
 - d. Dreyfuss JM, Johnson MD, Park PJ. Meta-analysis of glioblastoma multiforme versus anaplastic astrocytoma identifies robust gene markers. *Mol Cancer.* 2009 Sep 4;8:71. PubMed PMID: 19732454; PubMed Central PMCID: PMC2743637.
2. I have a number of publications where I've applied machine learning methods to gene expression, clinical, and genome-wide association data, and I have derived fundamental limits on the accuracy that can be achieved predicting a trait with genetics based on the prevalence and heritability of the trait.
 - a. McGeachie M, Ramoni RL, Mychaleckyj JC, Furie KL, Dreyfuss JM, Liu Y, Herrington D, Guo X, Lima JA, Post W, Rotter JI, Rich S, Sale M, Ramoni MF. Integrative predictive model of coronary artery calcification in atherosclerosis. *Circulation.* 2009 Dec 15;120(24):2448-54. PubMed PMID: 19948975; PubMed Central PMCID: PMC2810344.
 - b. Chang HH, Dreyfuss JM, Ramoni MF. A transcriptional network signature characterizes lung cancer subtypes. *Cancer.* 2011 Jan 15;117(2):353-60. PubMed PMID: 20839314; PubMed Central PMCID: PMC3017227.
 - c. Ward MM, Pajevic S, Dreyfuss J, Malley JD. Short-term prediction of mortality in patients with systemic lupus erythematosus: classification of outcomes using random forests. *Arthritis Rheum.* 2006 Feb 15;55(1):74-80. PubMed PMID: 16463416.
 - d. Dreyfuss JM*, Levner D*, Galagan JE, Church GM, Ramoni MF. How accurate can genetic predictions be? *BMC Genomics.* 2012 Jul 24;13(1):340. [*=Equal contribution]. PubMed PMID: 22827772; PubMed Central PMCID: PMC3534619.
3. I have developed new methods for analysis of metabolomics data, and for reconstruction and analysis of metabolic networks during my PhD at Boston University, and I have continued studying metabolic networks in adipose and in the context of diabetes.
 - a. Dreyfuss JM*, Jacobs C*, Gindin Y*, Benson G, Staples GO, Zaia J. Targeted analysis of glycomics liquid chromatography/mass spectrometry data. *Anal Bioanal Chem.* 2011 Jan;399(2):727-35. [*=Equal contribution]. PubMed PMID: 20953780; PubMed Central PMCID: PMC3254673.
 - b. Dreyfuss JM*, Zucker JD*, Hood HM, Ocasio LR, Sachs MS, Galagan JE. Reconstruction and validation of a genome-scale metabolic model for the filamentous fungus *Neurospora crassa* using FARM. *PLoS Comput. Biol.* 9(7): e1003126. [*=Equal contribution]. PubMed PMID: 23935467; PubMed Central PMCID: PMC3730674.
 - c. Nogiec C, Burkart A, Dreyfuss JM, Lerin C, Kasif S, Patti ME. Metabolic modeling of muscle metabolism identifies key reactions linked to insulin resistance phenotypes. *Mol Metab.* 2015 Jan 2;4(3):151-63. PubMed PMID: 25737951; PubMed Central PMCID: PMC4338313.

- d. Ramirez AK, Lynes MD, Shamsi F, Xue R, Tseng YH, Kahn CR, Kasif S, Dreyfuss JM. Integrating Extracellular Flux Measurements and Genome-Scale Modeling Reveals Differences between Brown and White Adipocytes. Cell Rep. 2017 Dec 12;21(11):3040-3048. PubMed PMID: 29241534.

Complete List of Published Work in MyBibliography:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/1ZawtCqNHYIAL/bibliography/46780426/public/>

D. Additional Information: Research Support and/or Scholastic Performance

5 P30 DK036836-27

King (PI)

02/15/97-06/30/17

Diabetes Research Center

The DRC at the Joslin Diabetes Center consists of six core laboratories, pilot and feasibility studies, and an enrichment program. The DRC is intended to stabilize, promote, integrate, and coordinate interdisciplinary programs already in existence.

Role: Bioinformatics/Systems Biology Core Coordinator