

**BIOGRAPHICAL SKETCH**

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NAME: Daniel Beck

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

POSITION TITLE: Postdoc Research Associate

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
University of Alaska, Fairbanks	BS	05/2006	Biology
University of Idaho	PhD	05/2014	Bioinformatics

**A.****Personal Statement**

I am interested in complex systems with many interacting components. My previous research has used machine-learning techniques to identify links between microbial communities and disease. I am currently focused on epigenetics, studying how environmental influences change methylation patterns and other epigenetic markers. I have experience analyzing large next-generation sequencing datasets. This includes developing pipelines that clean and process raw sequencing reads, perform statistical tests, and summarize the analysis results. I have also developed software tools for visualizing complex datasets.

**B.****Positions and Honors**

2009-2014 Research Assistant in Dr. James Foster's lab at University of Idaho

2015-present Post doc in Dr. Mike Skinner's lab at Washington State University

**C.****Contributions to Science****Complete list of published work in MyBibliography:**

<https://www.ncbi.nlm.nih.gov/sites/myncbi/16yPpwezeRVQkl/bibliography/56498193/public/?sort=date&direction=ascending>

**Major Contributions:****(1) Epigenetics**

Ben Maamar M, Sadler-Riggelman I, Beck D, Skinner MK (2018) Epigenetic Transgenerational Inheritance of Altered Sperm Histone Retention Sites. *Scientific Reports* 28;8(1):5308. PMID: 29593303

McBirney M, King SE, Pappalardo M, Houser E, Unkefer M, Nilsson E, Sadler-Riggelman I, Beck D, Winchester P, Skinner MK. (2017) Atrazine induced epigenetic transgenerational inheritance of disease, lean phenotype and sperm epimutation pathology biomarkers. *PLoS One*. 12(9):e0184306. PMID: 28931070

Shnorhavorian M, Schwartz S, Sadler-Riggelman I, Beck D, Skinner MK (2017) DNA Methylation Regions in Adult Human Sperm Following Adolescent Chemotherapy: Potential Epigenetic Inheritance from Chemotherapy. *Plos One* 12(2): e0170085. PMID: 28146567

McNew SM, Beck D, Sadler-Riggelman I, Knutie SA, Koop JAH, Clayton DH, Skinner MK. (2017) Epigenetic variation between urban and rural populations of Darwin's finches. *BMC Evol Biol.* 17(1):183. PMID: 28835203

**(2) Bioinformatics tool development for MeDIP-Seq analysis.**

Beck D, Sadler-Riggelman I, Skinner MK (2017) Generational Comparisons (F1 versus F3) of Vinclozolin Induced Epigenetic Transgenerational Inheritance of Sperm Differential DNA Methylation Regions (Epimutations) Using MeDIP-Seq *Environmental Epigenetics* 3(3): dvx016. PMID: 29147574

Ben Maamar M, Sadler-Riggelman I, Beck D, McBirney M, Nilsson E, Klukovich R, Xie Y, Tang C, Yan W, Skinner MK (2018) Alterations in sperm DNA Methylation, Non-Coding RNA expression, and histone retention mediate Vinclozolin induced epigenetic transgenerational inheritance of disease. *Environmental Epigenetics* 4(2):1-19, dvy101. PMID: 29732173

**(3) Microbial ecology.**

Beck D and Foster JA (2015) Machine learning classifiers provide insight into the relationship between microbial communities and bacteria vaginosis. *BioData Mining* 8:23. PMID: 26294933

Beck D and Foster JA (2014) Machine learning techniques accurately classify microbial communities by bacterial vaginosis characteristics. *PLoS ONE* 9(2):e87830. PMID: 24498380

Hunt KM, Foster JA, Forney LJ, Schütte UME, Beck D, Abdo Z, Fox LK, Williams JE, McGuire MK, McGuire MA (2011) Characterization of the diversity and temporal stability of bacterial communities in human milk. *PLoS ONE* 6(6):e21313. PMID: 21695057

**(4) Bioinformatic tool development for microbial community analysis.**

Beck D, Dennis C, and Foster JA (2014) SEED: a user-friendly tool for exploring and visualizing microbial community data. *Bioinformatics* 31(4):602-3. PMID: 25332377

Beck D, Settles M, Foster JA (2011) OTUbase: an R infrastructure package for operational taxonomic unit data. *Bioinformatics* 27(12): 1700-1. PMID: 21498398

Copeland WK, Krishnan V, Beck D, Settles M, Foster JA, Cho KC, Day M, Hickey R, Schütte UME, Zhou X, Williams CJ, Forney LJ, and Abdo Z (2012) mcaGUI: Microbial community analysis R-GUI. *Bioinformatics* 28(16) :2198-9. PMID: 22692220

**D.**  
**Research Support**  
No independent funding