

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 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. My previous research has used machine-learning techniques to identify links between microbial communities and disease. 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**

<http://www.ncbi.nlm.nih.gov/sites/myncbi/1PiX8IHGveyAh/bibliography/41624451/public/?sort=date&direction=ascending>.

Major Contributions:

(1) Application epigenetic bioinformatics tools.

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

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

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.

(2) Developed epigenetic bioinformatics tools for MeDIP-Seq analysis.

Shnorhavorian M, Schwartz S, Sadler-Riggleman 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

(3) Developed bioinformatics tools for microbial community analysis.

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, 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

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) Application bioinformatics tools for microbial communities.

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

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

Day MD, Beck D, Foster JA (2011) Microbial communities as experimental units. *Bioscience* 61(5):398-406. PMID: 21731083

D.

Research Support

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