

**BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

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**

**Major Contributions:** (1) Developed epigenetic bioinformatics tools for MeDIP-Seq analysis; (2) Developed bioinformatics tools for microbial community analysis.

Shnorhavorian M, Schwartz S, Sadler-Riggelman I, Beck D, Skinner MK (2015) Differential DNA Methylation Regions in Adult Human Sperm Following Adolescent Chemotherapy: Potential Epigenetic Inheritance from Chemotherapy. (Submitted).

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

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

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)

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

Day MD, Beck D, Foster JA (2011) Microbial communities as experimental units. *Bioscience* 61(5)

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)

**D.**

**Research Support**

No independent funding