

Curriculum Vitae

James D. Beck

Current Position: Computational Biology Researcher

Institution: Boise State University

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EDUCATION

2022 Ph.D. Computational Math, Science, and Engineering

Boise State University, Boise, ID

Training: Numerical Methods in Linear Algebra and Differential Equations, Network and Graph Analysis, Parallel Computing, Scientific Visualization, Cell Biology, Bioinformatics, Molecular Genetics

Dissertation: *Improved Computational Prediction of Ribozyme Function and Structure with Enhanced Parameter Selection and Library Design*

M.B.A., Marquette University, Milwaukee, WI

B.S. Healthcare Administration, University of Wisconsin, Eau Claire, WI

WORK EXPERIENCE

8/2019 – Current

Computational Biology Researcher - Hayden Lab at Boise State University, ID, USA.

Research in Molecular Biology:

- **Predicted the impact of mutations on the functional activity** of RNA variants using custom machine learning pipelines implementing Autoencoders, LSTM, SVR, and Random Forest models from PyTorch and Scikit-Learn.
- Developed custom Julia code for the **high-throughput processing of deep mutational scanning libraries to characterize relative and epistatic measurements of activity** of multiple RNA molecules and their variants.
- Created software for the **high-speed calling of molecular variants**, increasing the read depth four-fold in FASTQ file reads.
- Developed a **high-volume visualization processing of mutational variation** related to structural significance for self-cleaving ribozymes and their variants.
- Designed custom processing tools to **select catalytically important parameters by fitting exponential decay functions** to functional activity observations.
- Applied **dimensionality reduction techniques** on regulatory distal elements of Aquaporin genes within *Artemisia tridentata*.
- Implemented a **differential gene expression pipeline for Apolipoprotein E4 fragments** to identify up and down regulated genes involved in Alzheimer's disease.
- **Calculated stability values for reference gene primers** used for qPCR amplification of telomeres in vertebrates.

- Developed training materials and programs on the use of **dimensionality reduction and high-performance computing resources, supercomputer clusters, Julia, Python, R and Bash scripting.**

1/2015 – 12/2015

Senior Consultant

Yellow Dog Consulting, ID, USA.

A software development practice creating data driven physician performance software, including specialized development analysis for neurosurgical service expansion.

8/2013 – 12/2014

Senior Consultant

Clifton Larson Allen LLP, MN USA. A consultancy providing operational and physician integration services to physician groups, hospitals, and integrated health systems.

7/2006 – 7/2013

Senior Consultant

Beck Advisory Group Boise, ID USA. A professional consultancy providing operational and physician integration services to physician groups, hospitals, and integrated health systems.

PUBLICATIONS

IN REVIEW

Roberts J. M., **Beck, J. D.**, Pollack, T.B., Bendixsen, D. P. & Hayden, E. J. (2022). RNA sequence to structure analysis from comprehensive pairwise mutagenesis of multiple self-cleaving ribozymes. *eLife*. doi: <https://doi.org/10.3389/fmolb.2022.893864>

PUBLISHED

Beck, J. D., Roberts J. M., Kitzhaber J., Trapp A., Serra, E., Spezzano, F. & Hayden, E. J. (2022). Predicting higher-order mutational effects in an RNA enzyme by machine learning of high-throughput experimental data. *Frontiers in Molecular Biosciences*. doi: <https://doi.org/10.3389/fmolb.2022.893864>

Hudon, S. F., Palencia Hurtado, E., **Beck, J. D.**, Burden, S. J., Bendixsen, D. P., Callery, K. R., ... & Hayden, E. J. (2021). Primers for highly conserved elements optimized for qPCR-based telomere length measurement in vertebrates. *Molecular Ecology Resources*, 21(1), 59-67.

Rohn, T. T., **Beck, J. D.**, Galla, S. J., Isho, N. F., Pollock, T. B., Suresh, T., ... & Hayden, E. J. (2021). Fragmentation of Apolipoprotein E4 is Required for Differential Expression of Inflammation and Activation Related Genes in Microglia Cells. *International journal of neurodegenerative disorders*, 4(1).

Melton, A. E., **Beck, J.**, Galla, S. J., Jenkins, J., Handley, L., Kim, M., ... & Buerki, S. (2021). A draft genome provides hypotheses on drought tolerance in a keystone plant species in Western North America threatened by climate change. *Ecology and evolution*, 11(21), 15417-15429.

ACHIEVEMENTS

GUTT NSF Grant Fellowship, Award #1826801

Awarded GUTT (Genomes Underlying Toxin Tolerance) Fellowship to provide computational support to the investigation of molecular innovations that predict toxin tolerance in wild vertebrate herbivores.

NVIDIA Academic Hardware Grant

Awarded GPU hardware to develop training protocols for the high-throughput processing of sequence data and the implementation of machine learning prediction pipelines of functional activity.

SKILLS

BIOINFORMATICS

Tools & Pipelines	AlphaFold, BLAST, BWA, Bowtie2, DADA2, DESeq2, ENA, FastQC, GenBank, GROMACS, HUMAnN2/ MetaPhlan2, Infernal, K-Seq, PDB, RFam, SAMtools
Statistics	Clustering, Correlation Analysis, Dimensionality Reduction, K-Fold Cross Validation, Regression Analysis

MACHINE LEARNING

PyTorch	Designed successful predictive models using custom built Dataset and Dataloader tools implementing a variety of methods including Autoencoders, LSTM, and Linear Neural Networks.
Scikit-Learn	Designed successful functional and structural predictive models using Random Forest and Support Vector Regression algorithms.

SOFTWARE ENGINEERING

Operating Systems	Linux/Unix, Windows
Code Languages	Proficient: Bash/Shell, C/C++, Julia, Python, R, Familiar: Lua, MATLAB, Rust
Visualization Tools	D3.js, HTML/CSS/JS, LaTeX, Matplotlib, Paraview
Databases	JSON, NoSQL, SQL
Reproducibility	Docker, Jupyter Lab, Singularity
High Performance Computing	CUDA, Globus, Slurm