

# 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