# Curriculum Vitae

# James D. Beck

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| **Current Position:** | Computational Biology Researcher | **Address:** | |
| **Institution:** | Boise State University | 3758 S. Caddis Place | |
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| **Homepage:** | https://jdbeck66.github.io/jimbeck/ | | |

## EDUCATION

2018-2022    **PhD Candidate** – Computational Math, Science, and Engineering
Boise State University, Boise, ID USA

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

**MBA**

Marquette University, Milwaukee, WI USA

**BS Healthcare Administration**

University of Wisconsin, Eau Claire, WI USA

## WORK EXPERIENCE

8/2019 – Current
**Computational Biology Researcher - Hayden Lab at Boise State University, ID, USA.**

Research in Molecular Biology:

- Accurately **predicted the impact of sequence mutations on the functional activity** of CPEB3 ribozyme variants using custom machine learning pipelines. Developed pipelines incorporated Autoencoders, LSTM, and Random Forest models from PyTorch and Scikit-Learn.
- Developed high-throughput, **custom deep mutational scanning libraries measuring relative and epistatic measurement of activity** for multiple ribozyme variants.
- **Built software that increased the read depth** four-fold for self-cleaving ribozyme variants in paired-end Illumina sequencing runs.
- Developed **customized structural visualizations of mutational variation** for CPEB3, HDV, Twister, Hammerhead, and Hairpin self-cleaving ribozyme variants.
- Implemented custom process for **catalytically important parameter selections by fitting exponential decay functions** to functional activity observations.
- Applied **dimensionality reduction techniques using singular value decomposition** on regulatory distal elements of Aquaporin genes within Artemisia tridentata.
- Implemented **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 for undergraduate biology students on the use **of high-performance computing resources, supercomputer clusters, Julia, Python, R and Bash scripting**.

1/2015 – 12/2015
**Owner of Yellow Dog Consulting, ID, USA.** Developed a physician performance software platform. Developed a franchised, neurosciences product and Interim CEO of Neurosurgical Operating Unit.

8/2013 – 12/2014
**Principal at Clifton Larson Allen LLP, MN USA.** Integrated Beck Advisory Group operations post acquisition and led physician practice services for the organization.

7/2006 – 7/2013
**Owner of Beck Advisory Group Boise, ID USA.** A professional consultancy offering strategic, transactional 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.* (bioRxiv: **doi:** https://doi.org/10.1101/2022.05.31.494017

Hudon, S. F., Palencia Hurtado, E., **Beck, J. D.**, Burden, S. J., Bendixsen, D. P., Callery, K. R., ... & Hayden, E. J. (2021). Primers to 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

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| Tools & Pipelines | 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

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| 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

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| Operating Systems | Linux/Unix, MacOS, Windows |
| Code Languages | Broad experience writing code/scripts in Bash/Shell, C, C++, Julia, MATLAB, Python, R, Rust |
| Visualization Tools | ParaView, D3.js, Matplotlib, HTML/CSS/JavaScript, LaTex |
| Databases | JSON, NoSQL, SQL |
| Reproducibility | Docker, Singularity, Jupyter-Notebooks/Lab |
| High Performance Computing | CUDA, Globus, Slurm |