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| **Current Position:** | Computational Biology Researcher | **Address:**  3758 S. Caddis Place  Boise, ID 83716 |
| **Institution:** | Boise State University |
| **Email:** | jimbeck@u.boisestate.edu |
| **Homepage:** | https://jdbeck66.github.io/jimbeck/ |

Education

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| **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:

* P**redicted 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

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| 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

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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, 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 |