

Tyler Wied

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DATA SCIENCE SKILLS

- **Machine Learning:** Supervised (logistic & linear regression, random forests, neural networks, boosted trees, support vector machines, k-nearest neighbors, naive bayes), Unsupervised (PCA, k-means clustering, hierarchical clustering), Feature engineering, Natural language processing, Network analysis
- **Statistics:** experimental design, bootstrap, probability, A/B tests, ANOVA, Chi-squared tests, time series, computational simulations, Monte Carlo methods
- **Programming & Tools:** Python (pandas, scikit-learn, NumPy, Jupyter, gensim, Matplotlib, Seaborn, Dash), SQL, NoSQL, R, Unix/Bash, Git, MPI, SSH, Tableau, job scheduling (SLURM, LSF)

EXPERIENCE

- **Insight Data Science** Seattle, WA
Data Science Fellow Jan 2019 - Present
 - Consulted for a hedge fund to identify key trends across five major cryptocurrencies.
 - Developed project road map and architected solution using **machine learning**, **natural language processing** (topic modeling, tf-idf, sentiment analysis), and **network analysis**.
 - Delivered an **interactive dashboard** that displays networks, attitude levels, and the top 20 topics across 200k+ Tweets and 25k+ Twitter users.
- **Johns Hopkins University School of Medicine** Baltimore, MD
Post-Doctoral Research Fellow & PhD Candidate 2012 - 2019
 - Discovered key flexibility in a protein essential for cognitive function from **10+ TB of data** using **simulations**, **numerical analysis**, **unsupervised machine learning**, and **PCA**.
 - Designed an **automated classification algorithm** using geometric metrics to identify protein bottlenecks, enabling straightforward model interpretation.
 - Wrote Python scripts to validate simulation results with statistical tests (Chi-squared test); achieved **6-fold improvement** over previous predictions.
 - **Parallelized** jobs on cluster compute nodes with MPI; **engineered** 10x simulation speed-up.
 - Combined diverse datasets in a cross-functional collaboration for a toxin study: **engineered key features**, performed analysis, and **reduced search space more than 90%**.
 - Directed and trained teams in experiments, experimental design, data analysis and interpretation across four research projects.
- **University of Wisconsin-Madison** Madison, WI
Research Assistant 2009 - 2012
 - Developed first genetic mouse model of mania, now used to understand mania in humans.
 - Used one-way ANOVA to identify **15+ statistically significant** indicators of mania.
 - Enabled prediction of DNA stability by isolating contribution of key features across 50+ experimental conditions.

EDUCATION

- **Johns Hopkins University School of Medicine** Baltimore, MD
PhD, Computational Biophysics (NSF Graduate Research Fellow) 2012 - 2018
- **University of Wisconsin-Madison** Madison, WI
BS, Biochemistry (Honors in Research) 2008 - 2012