

Tyler Wied

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DATA SCIENCE SKILLS

- **Programming:** Python, SQL, R, Unix/Bash, MPI, HTML
- **Machine Learning:** supervised (logistic & linear regression, random forests, SVM), unsupervised (PCA, k-means clustering), natural language processing, network analysis, simulations
- **Statistics:** bootstrap, ANOVA, χ^2 tests, A/B tests
- **Tools:** pandas, scikit-learn, NumPy, Jupyter, Matplotlib, Seaborn, Git, gensim, NLTK, Dash

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 roadmap and architected solution using **machine learning** (NLP, topic modeling, sentiment analysis, network analysis).
 - Delivered results in 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 important flexibility in a protein essential for cognitive function from **10+ TB of simulation data**, numerical analysis, and **unsupervised machine learning** (PCA).
 - Developed algorithm to **automatically classify** millions of simulation "snapshots" into a small number of discrete states to create simple, interpretable models.
 - Wrote Python scripts to validate simulation results with respect to real-world observations using statistical tests (χ^2 test), resulting in **6-fold improvement** over previous predictions.
 - Achieved 10x simulation speed-up by **parallelizing** jobs on cluster compute nodes (MPI).
 - Collaborated cross-functionally to identify promising targets in a toxin study by combining diverse datasets and identifying key features, **reducing search space more than 90%**.
 - Trained and led a team of undergraduate and graduate students across four research projects.
- **University of Wisconsin-Madison** Madison, WI
Research Assistant 2009 - 2012
 - Developed first genetic mouse model of mania, which is now used to understand mania in humans.
 - Identified **15+ statistically significant** indicators of mania (one-way ANOVA).
 - Isolated the individual contributions of key features affecting DNA stability across more than 50 experimental conditions in MATLAB, enabling prediction with those features in future studies.

EDUCATION

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