# Tyler Wied

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#### DATA SCIENCE SKILLS

- Languages: Python, SQL, R, Bash
- Machine Learning & Statistics: supervised and unsupervised learning, dimensionality reduction, natural language processing, network analysis, feature engineering, modeling and simulations, time series, Monte Carlo methods, bootstrap, ANOVA,  $\chi^2$  test, A/B testing
- Tools: NumPy, pandas, Git, scikit-learn, gensim, NLTK, Dash, Jupyter, Matplotlib
- Computing: High-performance and parallel computing, Unix, SSH

#### EXPERIENCE

# • Insight Data Science

Seattle, WA

Data Science Fellow

Jan 2019 - Present

- Consulted for a cryptocurrency hedge fund to identify trends across five key 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 (principal component analysis).
- Wrote **custom Python scripts** to validate simulation results with comparisons to real-world observations ( $\chi^2$  test), with a **6-fold improvement** over previous predictions.
- Built pipeline to simultaneously run hundreds of simulations on cluster compute nodes.
- Collaborated cross-functionally to identify the most promising targets in a toxin study by combining features from diverse datasets, **reducing search space more than 90%**.
- Leadership and communication: trained and led a team of undergraduate and graduate students. Served as tutor to 15+ students in two graduate-level biophysics courses.

# • University of Wisconsin-Madison

Madison, WI

2009 - 2012

Research Assistant

 Developed first genetic mouse model for mania. Conducted behavioral experiments for hyperactivity and identified 15+ statistically significant indicators of mania (one-way ANOVA). This mouse line was subsequently used to identify key genetic similarities to humans with bipolar disorder.

• Isolated individual contributions of key features affecting DNA stability across 50+ experimental conditions in MATLAB, enabling prediction with those single 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