

# Tyler Wied

Seattle, WA  
(920) 634-9618

tjwied@gmail.com  
LinkedIn: tylerwied  
GitHub: tjwied

## DATA SCIENCE SKILLS

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- **Machine Learning:** Supervised (logistic & linear regression, random forests, 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

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- **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 ( $\chi^2$  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

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- **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