Tyler **Bradshaw, PhD**

Molecular, Cellular, and Computational Biologist

Durham NC, USA

(+1) 952-212-4563 | twesleyb10@gmail.com | twesleyb | twbradshaw

Summary

I am a diligent and driven computational and molecular biologist. In my PhD work, I combined cutting-edge spatial and proximity proteomics tools to solve problems in molecular neuroscience. I am a self-taught programmer and data scientist, and have pioneered novel computational pipelines and molecular techniques in numerous projects aimed at understanding the organization of the neuronal proteome and its dysregulation in disease. I am interested in a career where I can continue to draw together ideas and approaches spread across the fields of cell biology and computer science.

Work Experience

Graduate Research Assistant

Fall 2016 - May 2021

Soderling Laboratory, Duke University — *Department of Neurobiology*

- Developed a novel spatial proteomics analysis pipeline for clustering and statistical inference in spatial proteomics, published in *eLife*.
- Applied and developed CRISPR-based methods for genetic depletion and tagging of endogenous proteins–work which lead to founding of CasTag BioSciences.
- Performed synaptosome subcellular fractionation to assess synaptic protein changes in multiple mouse models of human brain disorders.
- Designed peptide libraries for multiple-reaction monitoring targeted proteomics.
- Experience working with numerous model organisms including immortalized cell lines, bacteria, yeast, and mice.
- Applied and analyzed BioID-based proximity proteomics for identification of subcellular specific compartments.
- Normalization and analysis of RNA transcriptomics and protein proteomics datasets.
- Awarded the Ruth L. Kirschstein National Research Service Award Fellowship to study a protein of unknown function and the mechanisms by which its loss causes a rare epilepsy disorder.

Research Technician

May 2014 - May 2016

Soderling Laboratory, Duke University — *Department of Cell Biology*

- Performed protein co-immunoprecipitation and proximity proteomics for identification of protein-protein interactions and revealing protein interactomes *in vivo*–my work was a part of the first application of BioID *in vivo*, published in the journal *Science*.
- Performed immunoblotting, immunostaining, and cell and tissue culture for assessing protein expression and localization *in vitro* and *in vivo*.
- Molecular cloning and generation of adeno-associated virus for transgene expression *in vivo*.
- Maintained mouse colony with >30 strains of mice; performed mouse surgery, husbandry, genotyping, and analysis of mouse behavior.

Skills

Computational Biology

- Linear models and linear mixed-models in R
- Clustering and visualization of protein networks in R and Python
- Analysis of biological network organization and function
- DevOps toolchain: Windows, Linux, Tmux, Vim, LaTeX, R, Python, Julia, Cytoscape, Adobe Illustrator, PowerPoint

Molecular Biology

- Molecular cloning and plasmid design
- Molecular biology using immortalized human cell lines, E. coli, and yeast
- Protein purification, co-immunoprecipitation and immunoblotting
- Production of adeno associated virus and stereotaxic injection into mouse brain tissue
- Subcellular fractionation and tandem mass tag multiplex proteomics
- Adherent cell culture and transfection

Education

Duke University, Department of Neurobiology

Durham, NC

Doctor of Philosophy - Neurobiology — *Fall 2016 - May 2021*

- Dissertation: *Statistical Inference and Community Detection in Proximity and Spatial Proteomics*; my thesis work establishes a framework for the analysis of proximity and spatial proteomics, extending protein-level inference in spatial proteomics to the level of protein-groups or modules and generates hypotheses that identify foci of biological function and dysfunction which may underlie the neuropathology of disease.

University of Washington

Seattle, Washington

Bachelor of Science - Molecular, Cellular and Developmental Biology — *Fall 2010 - Spring 2014*

- My undergraduate research focused on the pathobiological mechanisms of type I and type II diabetes. In the the Surgical Outcomes Research Center, I worked with Ossabaw pigs to study mechanisms of weight-loss following bariatric surgery. In the Bornfeldt lab, I performed some of my first molecular biology experiments aimed at studying mechanisms of type I diabetes accelerated atherosclerosis.