

Tyler Bradshaw, PhD

MOLECULAR, CELLULAR, AND COMPUTATIONAL BIOLOGIST

Durham NC, USA

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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

- Development of novel spatial proteomics analysis pipeline for clustering and statistical inference in multiplex spatial proteomics.
- Application and development of CRISPR-based methods for genetic depletion and tagging of endogenous proteins leading to founding of CasTag BioSciences.
- Performed synaptosome subcellular fractionation to assess synaptic changes in multiple mouse models of human brain disorders.
- Experience working with numerous model organisms including immortalized cell lines, bacteria, yeast, and mice.
- Application and analysis of BioID-based proximity proteomics for identification of subcellular specific compartments.
- Normalization and analysis of RNA transcriptomics and protein proteomics datasets.
- Recipient of a Ruth L. Kirschstein National Research Service Award Fellowship (NRSA F31) 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

- Protein co-immunoprecipitation and proximity proteomics for identification of protein-protein interactions and revealing protein interactomes *in vivo*-first application of BioID *in vivo* and proteome of inhibitory post-synapse published in *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
- Analysis of biological network organization and function
- DevOps toolchain: Windows, Linux, Tmux, Vim, LaTex, R, Python, Julia, Cytoscape, Adobe Illustrator
- 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 TMT multiplex proteomics
- Primary neuronal culture

Molecular Biology

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

University of Washington

Seattle, Washington

BACHELOR OF SCIENCE - MOLECULAR, CELLULAR AND DEVELOPMENTAL BIOLOGY

Fall 2010 - Spring 2014

- My undergraduate research focused on type II and type I diabetes in the Surgical Outcomes Research Center and Bornfeldt Laboratory, respectively.