

Matt Niederhuber, PhD

I am a molecular biologist and bioinformatician with experience generating and analyzing a range of genomics datatypes. I care about reproducible code, engaging data visualization, and writing about amazing new science.

Education

PhD - Genetics & Molecular Biology

University of North Carolina

2016 - 2023

Chapel Hill, NC

– NSF Graduate Research Fellow

– Thesis: “Fine-tuning Enhancer Activity in Development”

Certificate - Premedical Sciences

Columbia University

2011 - 2013

New York, NY

BA - English Literature

Kenyon College

2006 - 2010

Gambier, OH

Experience

Postdoctoral Fellow

Bioinformatics and Analytics Research Collaborative

November 2023 - Current

UNC - Chapel Hill, NC

– Led analysis of multiple client RNA-seq and CUT&RUN projects

– Produced high-quality reports, figures, and communicated results to clients

– Refactored and containerized codebase for multi-institute COPD RNA-seq study

– Developed LLM-based Python package to automate annotation of SRA metadata

– Customized Nextflow nf-core pipelines and taught Nextflow basics

– Wrote and led workshops on R/RStudio, Nextflow, Containerization, and ATAC-seq

– Mentored two entry-level bioinformatics

Graduate Research Student

PI: Dr. Daniel J. McKay

August 2016 - October 2023

UNC - Chapel Hill, NC

– Led two projects developmental gene regulation and enhancer biology

– Wrote custom analysis of CUT&RUN and FAIRE-seq data in R

– Designed a novel fluorescent reporter system to capture dynamic enhancer activity *in vivo*

– Automated quantification of RNAi-screen confocal imaging with Python

Research Assistant II

PI: Dr. Pamela A. Silver

June 2014 - July 2016

Harvard Medical School - Boston, MA

– Led a project studying the cyanobacterial carboxysome using super-resolution microscopy

– Helped characterize a novel bacterial memory device for inflammation detection

– Mentored the 2015 Harvard undergraduate IGEM team

Research Assistant

PI: Dr. Jerard Hurwitz

June 2013 - June 2014

Memorial Sloan Kettering Cancer Center - New York, NY

– Hands-on experience with cell culture and standard protein biochemistry methodologies

Skills

Programming: R, Python, Bash/Unix command line, HTML

Computational and Software: Nextflow/nf-core, Snakemake, Git, Docker, Singularity/Apptainer, NGS data processing and QC, High-Performance Computing, image analysis, SQL, ImageJ, Napari, Adobe Creative Suite

Wet lab: molecular cloning, protein biochemistry, cell culture, fluorescent microscopy, FAIRE-seq, CUT&RUN, NGS library preparation and QC, Drosophila genetics

Teaching

How to Learn to Code - Python (Taught 6 classes)	June 2024
Intro to R/RStudio (1 day workshop)	August 2024
UNC BARC Internal Workshops (ATAC-seq, Nextflow, Containerization)	Feb., April, June 2024

Publications

Academic:

Niederhuber MJ, Leatham-Jensen M, McKay DJ. 2024. [The SWI-SNF nucleosome remodeler constrains enhancer activity during *Drosophila* wing development](#). Genetics.

Niederhuber MJ, McKay DJ. 2021. [Mechanisms underlying the control of dynamic regulatory element activity and chromatin accessibility during metamorphosis](#). COIS.

Nystrom SL*, **Niederhuber MJ***, McKay DJ. 2020. [Expression of E93 provides an instructive cue to control dynamic enhancer activity and chromatin accessibility during development](#). Development. *equal contributors

Naydich AD, Nangle SN, Bues JJ, Trivedi D, Nissar N, Inniss MC, **Niederhuber MJ**, Way JC, Silver PA, Riglar DT. 2019. [Synthetic gene circuits enable systems-level biosensor discovery at the host-microbe interface](#). mSystems.

Niederhuber MJ, Lambert TJ, Yapp C, Silver PA, Polka JK. 2017. [Superresolution microscopy of the \$\beta\$ -carboxysome reveals a homogeneous matrix](#). MBoC.

Uyehara CM, Nystrom SL, **Niederhuber MJ**, Leatham-Jensen M, Ma Y, Buttitta LA, McKay DJ. 2017. [Hormone-dependent control of developmental timing through regulation of chromatin accessibility](#). *Genes and Development*. Genes and Development.

Riglar DT, Giessen TW, Baym M, Kerns JS, **Niederhuber MJ**, Bronson RT, Kotula JW, Gerber GK, Way JC, Silver PA. 2017. [Engineered bacteria can function in the mammalian gut long-term as live diagnostics of inflammation](#). Nature Biotechnology.

Selected Popular (see mattniederhuber.com for full list):

[AlphaFold Unlocks Protein Structure Prediction with Artificial Intelligence](#).
UNC: The Pipettepen, 2021.

[UNC Scientists Partner with Citizen Scientists to Map Earth's River Obstructions](#).
UNC Institute for the Environment, 2019.

[CUT&RUN: An Improved Method for Studying Protein-DNA Interactions](#).
Addgene Blog, 2018.

[Making Time Matter: How Hormone Pulses Direct Chromatin Accessibility During Development](#).
Development: The Node, 2017.

Yes, This Exists: A Biohacker Hotline.
Popular Science, 2013. (out of print)