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Education

2018   Ph.D., Zoology
University of Wisconsin-Madison (Madison, WI, USA)

2013   B.S., Biopsychology (*cum laude*)
Tufts University (Medford, MA, USA)

Employment

Senior Scientist Bioinformatics, Biomarkers & Genomic Medicine   Jan. 2022—Present
Parexel International (Remote from Dallas, TX, USA)

- Perform ETL for large bioinformatics files at scale
- Develop data ingestion pipelines for genomic sequencing datasets (GWAS & xQTL)
  Examples of tools created for a major pharmaceutical client:
  - Lift over genomic regions from datasets on human genome build 37 to build 38
  - Update genomic coordinates for rsIDs from older builds of dbSNP
  - Generate custom entity flat files for xQTL studies
- Define and implement quality control of raw data and metadata

Postdoctoral Researcher, Department of Neuroscience   Jun. 2018—Jan. 2022
University of Texas Southwestern Medical Center (Dallas, TX, USA)

- Implemented single-cell transcriptomics (10X Genomics Chromium) in songbirds, from molecular to computational components
- Published co-first-author paper in *Science*, second-author paper in *Nature Communications*, and received an NIH Postdoctoral Fellowship (NRSA F32)
  - Colquitt, B. M.*, **Merullo, D. P.***, et al. (2021). Cellular transcriptomics reveals evolutionary identities of songbird vocal circuits. *Science*, 371(6530), eabd9704. *co-first author
  - Xiao, L., **Merullo, D. P.**, et al. (2021). Expression of FoxP2 in the basal ganglia regulates vocal motor sequences in the adult songbird. *Nature Communications*, 12(1), 2617.

Technical Skills

Languages:	R, Python, Julia, Bash, SQL, Git, Markdown, LaTeX
HPC/Cloud Environments:	Linux, GCP, HDFS
Bioinformatics:	GWAS, xQTL, single-cell RNA sequencing, spatial transcriptomics, clustering (UMAP/tSNE), differential expression tests, linear regression