# Sunnie Grace McCalla

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## Professional Summary

Bioinformatics scientist with extensive expertise in single-cell RNA sequencing, gene regulatory network inference, and multi-omics integration to uncover mechanisms of disease and guide therapeutic discovery. Proven success in developing reproducible computational workflows and delivering biological insights that support actionable findings for therapeutic discovery and translational research. Adept collaborator across computational and wetlab teams and bridging algorithmic development with experimental validation.

## Technical Skills

- **Programming & Data Analysis:** Python, R (tidyverse, Seurat, Shiny), MATLAB, Docker, Git, Linux, HTCondor
- **Bioinformatics Tools:** GSVA, SCENIC, PAGA, xCell, CIBERSORT, DESeq2, edgeR, MERLIN
- **High-Throughput Sequencing:** Bowtie2, FastQC, Trimmomatic, BLAST, QIIME2, CellRanger
- **Workflow & Visualization:** Snakemake, Nextflow, ggplot2, Seaborn, Cytoscape
- **Molecular Techniques:** qPCR/dPCR, RNA/DNA extraction, Illumina NextSeq 500 operation, eDNA sampling
- **Laboratory Techniques:** RNA/DNA isolation and analysis, qPCR, dPCR, siRNA screening, Illumina NextSeq 500 operation, environmental DNA (eDNA) sample processing.

## Professional Experience

### University of Wisconsin–Madison | Graduate Research Assistant, Roy Lab | 2018–Present

- Developed graph-based methods to infer cell-cell interaction networks from single-cell RNA-seq data, improving subtype identification and network resolution.
- Integrated multi-omic datasets to construct regulatory networks driving maize autophagy.
- Modeled CRISPR off-target effects in human retinal organoids using network perturbation approaches.
- Authored 6+ peer-reviewed papers and collaborated with interdisciplinary teams on experimental validation.

### EMD Serono Research & Development Institute | Bioinformatics Co-op Intern | 2024

- Conducted pathway and cellular deconvolution analyses to assess drug efficacy using bulk and single-cell RNA-seq datasets.
- Automated reprocessing and QC of 15+ GEO/SRA datasets; standardized reproducible analysis pipelines.
- Applied GSVA to identify pharmacodynamic gene signatures and developed an RNA-seq exploration tool for internal teams.
- Built frameworks for indication prioritization analyses supporting fusion molecule development programs.

### U.S. Geological Survey | Geneticist | 2012–2017

- Designed and implemented environmental (eDNA) metabarcoding pipelines for invasive species detection and conservation genetics.
- Sequenced mitochondrial genomes and validated species-specific assays for endangered taxa.
- Led multi-agency collaborations and secured >$230 K in research funding through competitive grants.

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## Education

Ph.D. Candidate, Genetics — University of Wisconsin–Madison (Expected 2026)
M.S., Biology (Ecology) — Purdue University
B.S., Biology (Ecology), Cum Laude — Minnesota State University Mankato

## Grants & Awards

- NIH Predoctoral Program in Genetics Training Grant (2017–2020)
- USGS Community for Data Integration Grant "High-Throughput Computing for Big Data and Next-Gen Sequencing" ($43,904)
- USFWS Science Support Partnership Grant — eDNA Detection for Endangered Species ($194,922)

## Selected Publications

Alireza Fotuhi Siahpirani (co–first), **Sunnie Grace McCalla (co–first)**, Saptarshi Pyne, Caleb M. Dillingham, Rupa Sridharan, and Sushmita Roy. 2025. "Uncovering Functional Gene Regulatory Networks in Bulk and Single-Cell Data through Robust Transcription Factor Activity Estimation and Model-Guided Experimental Validation." *bioRxiv*. doi: 10.1101/2025.06.09.658650.

Shilu Zhang, Saptarshi Pyne, Stefan Pietrzak, Spencer Halberg, **Sunnie Grace McCalla**, Alireza Fotuhi Siahpirani, Rupa Sridharan, and Sushmita Roy. 2023. "Inference of cell type-specific gene regulatory networks on cell lineages from single cell omic datasets." *Nature Communications*. doi: 10.1038/s41467-023-38637-9.

**Sunnie Grace McCalla**, Alireza Fotuhi Siahpirani, Jiaxin Li, Saptarshi Pyne, Matthew Stone, Viswesh Periyasamy, Junha Shin, and Sushmita Roy. 2023. "Identifying strengths and weaknesses of methods for computational network inference from single-cell RNA-seq data." *G3: Genes, Genomes, Genetics*. doi: 10.1093/g3journal/jkad004.

Nisha R. Iyer, Junha Shin, Stephanie Cuskey, Yucheng Tian, Noah R. Nicol, Tessa E. Doersch, Frank Seipel, **Sunnie Grace McCalla**, Sushmita Roy, and Randolph S. Ashton. 2022. "Modular derivation of diverse, regionally discrete human posterior CNS neurons enables discovery of transcriptomic patterns." *Science Advances*. doi: 10.1126/sciadv.abn7430.

Full publication list available upon request or via Google Scholar.

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