Miranda Galey

Seattle, WA 98103 | (214) 809-7642 | galey004@umn.edu
linkedin.com/in/miranda-galey-6055a7126

Early career molecular biologist with 3+ years of experience with high throughput data set analysis and long read sequencing. Has strong organizational ability and experience in the administrative, bioinformatic, and molecular lab bench spheres.

SKILLS AND ACCOMPLISHMENTS

- Molecular Lab Bench: HMW DNA/RNA Extraction | Mammalian Cell Culture | Long Read Sequencing | Oxford Nanopore | PCR | Genomic Sequencing Assays
- Programming and Bioinformatics: R | Python | Rust | Unix bash shell| Mothur | HTML5 | LaTeX | HPC Scripting | minimap2 | flye | clair3 | EPI2ME | snakemake | git
- Analysis Skills: Long Read Sequencing WGS Alignment and Variant Detection | Metagenomic Dataset Analysis | Machine Learning | spatial analysis with ArcGIS | Workflow Management

- Authored and implemented ELNs, LIMs, and ONT analysis pipeline for a genomic sequencing lab
- Set up and trained staff to run a new oxford nanopore sequencing cost center resulting in quality datasets for 115 projects and more than 1000 genomes.
- Presented a new differential methylation detection software developed in Rust and R as an invited speaker at Oxford Nanopore's London Calling event.
- Acting consultant for troubleshooting ONT library preps and data analysis for genomic sequencing cxore

WORK EXPERIENCE

Research Scientist III | University of Washington, Seattle WA
(06/2021) – Present

- Consult with research collaborators to design studies and implement analysis of Long Read Sequencing datasets and short read sequencing datasets using a variety of command line tools
- Developed a clinical tool in R and Rust to graphically display SNP phasing, coverage, annotated genes, and statistically significant differences in methylation for loci associated with imprinting disorders.
- Supervised and managed the day to day activities of a small genomics lab, including training all staff, acting as safety officer, prioritizing projects, maintaining equipment and reagent levels, vetting new protocols, and leading projects.

- Managed a long read cost center by working with both academic and corporate collaborators from project design, DNA/RNA quality control consulting, custom library preparation, PromethION, flongle, gridION, and minION operation, genome alignment, and data analysis.
- Optimized mammalian cell culture, DNA isolation and library preparation protocols to increase average read lengths to more than 50kb and shared new protocols with many collaborative labs.

Bioinformatics Researcher | Natural Resources Research Institute, Duluth MN (01/2020) – (06/2021)

- Analysed MiSeq High Throughput Datasets from alignment, through taxonomic identification and pathogen detection to correlation with other environmental variables and datasets
- Developed custom pipelines in the bash shell, with mothur, other command line programs, and python for analysis of fungal ITS MiSeq datasets.
- Trained other staff and graduate students in the use of R, compositional data analysis, multivariate compositional analysis, source sink flow, and other statistical analyses on datasets including wastewater effluent 16S, fungal COI from rhizospheres, and wild rice composite datasets.

Graduate Research Assistant | University of Minnesota, Duluth, MN (08/2016) – (08/2019)

- Designed and implemented a study of mitochondrial and DNA markers present in bat feces using DNA extraction kits, PCR, and Illumina sequencing
- Developed a generalized hidden Markov model of mRNA transcript polyadenylation/uridylation in *Trypanosoma brucei* using RNAseq data, RT-PCR data, and Python
- Led radiotelemetry crews and mist netting crews to capture and track insectivorous bats throughout public lands in Minnesota.

EDUCATION

M.S. Integrated Biosciences | University of Minnesota, Duluth, MN (2020)
B.A. Human Ecology | College of the Atlantic, Bar Harbor, ME (2016)

RECENT PUBLICATIONS

For a more complete list, look at my orcid entry: https://orcid.org/0000-0002-4721-7499

Li, H., Berent, E., Hadjipanteli, S., **Galey, M.**, Muhammad-Lahbabi, N., Miller, D. E., & Crown, K. N. (2023). Heterozygous inversion breakpoints suppress meiotic crossovers by altering recombination repair outcomes. *PLoS Genetics*, *19*(4), e1010702.

Galey, M., Reed, P., Wenger, T., Beckman, E., Chang, I. J., Paschal, C. R., ... & Miller, D. E. (2022). 3-hour genome sequencing and targeted analysis to rapidly assess genetic risk. *medRxiv*, 2022-09.

Miller, D. E., Lee, L., **Galey, M.,** Kandhaya-Pillai, R., Tischkowitz, M., Amalnath, D., ... & Oshima, J. (2022). Targeted long-read sequencing identifies missing pathogenic variants in unsolved Werner syndrome cases. *Journal of Medical Genetics*, *59*(11), 1087-1094.

Miller, D. E., Hanna, P., **Galey, M.,** Reyes, M., Linglart, A., Eichler, E. E., & Jüppner, H. (2022). Targeted Long-Read Sequencing Identifies a Retrotransposon Insertion as a Cause of Altered GNAS Exon A/B Methylation in a Family With Autosomal Dominant Pseudohypoparathyroidism Type 1b (PHP1B). *Journal of Bone and Mineral Research*, *37*(9), 1711-1719.