

WORKSHOP: Bulk RNA-seq analysis with R**October 29, 2025****10 am - 4 pm****OGPS Meeting Space - 2955**

Time	Section	Specific topics covered
10:00 – 10:15	General Introduction	
10:15 – 10:30	Introduction to the Great Lakes HPC cluster and Globus	<ul style="list-style-type: none">• Overview of Great Lakes cluster and Turbo and Scratch drives• Globus Connect Personal• Accessing Great Lakes via Globus to retrieve and move data
10:30 – 11:00	Introduction to R and RStudio	<ul style="list-style-type: none">• Overview of FASTQ format• Trimming and cleaning reads• Aligning reads to a reference genome/transcriptome• Performing feature counts
11:00 – 11:30	Initial processing of bulk RNA-seq data	<ul style="list-style-type: none">• Setting up R and RStudio• Setting up a project in RStudio• Using Markdown• Installing and loading packages
11:30 - 12:00	Importing data into RStudio and exploratory analysis	<ul style="list-style-type: none">• Importing counts files into RStudio• Making metadata file• Exploratory analysis• PCA plots• Heatmaps
12:00 - 1:00	Break for lunch	
1:00-2:00	Differential expression analysis with DESeq2	<ul style="list-style-type: none">• Running DESeq2 to identify DE genes• Making volcano plots
2:00-4:00	Making sense of differential expression data	<ul style="list-style-type: none">• Differences between Gene Ontology (GO) and pathway analysis• Overview of various GO and pathway databases• Differences between gene set enrichment analysis (GSEA) and over-representation analysis (ORA)• Performing GSEA with fgsea package in R• Making custom gene sets to run with fgsea• Visualizing GSEA/enrichment output