#!/bin/bash

#SBATCH --job-name=r\_analysis # Job name

#SBATCH --output=opt\_output.log # Output file

#SBATCH --error=opt\_error.log # Error log

#SBATCH --time=2:00:00 # Adjust the time as needed

#SBATCH --mem-per-cpu=14G # Adjust memory per CPU as needed

#SBATCH --cpus-per-task=8 # Number of CPUs per task

#SBATCH --mail-type=END,FAIL #Email to me when finished

# Initialize Conda for bash shell

source /cluster/home/jfrank/miniconda3/etc/profile.d/conda.sh

# Activate the conda environment

conda activate r\_env

# Navigate to the directory containing the R script

cd "/cluster/scratch/jfrank/Sta426/opt" || { echo "Directory not found"; exit 1; }

# Run the R script using Rscript

echo "Running R script..."

Rscript "opt\_data\_import\_and\_clustering.R" # Replace with your R script name

echo "R script execution finished!"

scp -r C:/Users/julia/Downloads/data [jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426](mailto:jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426)

scp C:/Users/Julia/Studium/Master/STA426/project-snRNAseq-demyelination/Euler/jack\_data\_import\_and\_clustering.R [jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426](mailto:jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426)

scp [jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426](mailto:jfrank@euler.ethz.ch:/cluster/scratch/jfrank/Sta426)/Rplots.pdf C:/Users/julia/Downloads