library(GenomicRanges)

# Specify the directory path of my narrowPeak files

directory <- "/Users/yulongqiu/Desktop/Biostats/Master\_Thesis/Peaks\_bysample/By\_sample\_Narrowpeaks"

# Gets the file names of all narrowPeak files in the directory

files <- list.files(path = directory, pattern = "\*.narrowPeak", full.names = TRUE)

# Create an empty list to store the GRanges objects generated by each file

granges\_list <- list()

# Use a loop to iterate through each file and convert it to a GRanges object

for (file in files) {

df <- read.table(file = file,

col.names = c("chr", "start", "end", "name", "score", "strand",

"fold\_change", "neg\_log10pvalue\_summit",

"neg\_log10qvalue\_summit", "relative\_summit\_position"))

# Convert each file to Grange object

peaks <- makeGRangesFromDataFrame(df = df, keep.extra.columns = TRUE)

granges\_list[[basename(file)]] <- peaks

#print Granges\_list

print(granges\_list)

combined.granges <- unlist(GRangesList(granges\_list))

# Use reduce to combine

combined.peaks <- reduce(x = combined.granges)

print(combined.peaks)

###Save rds and rdata

save(combined.peaks, file = "/Users/yulongqiu/Desktop/Biostats/Master\_Thesis/combined\_peaks.RData")

saveRDS(combined.peaks, file = "/Users/yulongqiu/Desktop/Biostats/Master\_Thesis/combined\_peaks.rds")