```r
## Input files from a directory
NeuN   <- "raw/NeuN-Overlap"
Nuclei <- "raw/NucleiOverlap"
UpperQ <- "raw/UpperQ"
GFP    <- "raw/GFPonly"

## Output directory
output_dir <- "analysis/NeuN/"

## List files using full file name
files_neun   <- list.files(NeuN, full.names = T)
files_nuclei <- list.files(Nuclei, full.names = T)
files_upperq <- list.files(UpperQ, full.names = T)
files_gfp    <- list.files(GFP, full.names = T)

## Plate analysis will use only NeuN-Overlap data
stat.ntxt <- vector()
stat.txt  <- vector()

## Beginning of script
for (i in seq_along(files_neun)){
  file <- read.csv(files_neun[i])
  colnames(file)[2] <- "Well.R"
  txt1  <- subset(file, Well.R == "2")[,3]
  txt2  <- subset(file, Well.R == "23")[,3]
  ntxt1 <- subset(file, Well.R == "1")[,3]
  ntxt2 <- subset(file, Well.R == "24")[,3]
  nam   <- paste("Plate", i, "_NeuN", sep="")
  data  <- list(ntxt1, ntxt2, txt1, txt2)

  for (j in 1:4){
    treatment <- c("ntxt1","ntxt2", "txt1", "txt2")
    output1   <- mean(data[[j]], na.rm = T)
    output2   <- sd(data[[j]], na.rm = T)

    plate     <- paste(nam, "well-comparison", treatment[j], sep="_")
    analysis  <- data.frame(Mean = output1, Std = output2)
    write.table(analysis, file = paste(output_dir, plate, ".csv", sep = ""), sep = ",", append = F,
row.names = F, col.names = T)
  }

  ## Statistical analysis
  stat.ntxt <- c(stat.ntxt, t.test(ntxt1,ntxt2)$p.value)
  stat.txt  <- c(stat.txt, t.test(txt1,txt2)$p.value)
}

pvalues <- data.frame(Vehicle = stat.ntxt, Topotecan = stat.txt)
write.table(pvalues, file = paste(output_dir, "pvalues_well-comparison_NeuN_analysis.csv", sep = ""), sep
= ",", append = F, row.names = F, col.names = T)
```