This script wants fcs files as exported by the C6 Accuri Magic Flow Cytometer.

Get into the directory with the fcs files.

```r
require(ggplot2)
require(flowViz)
#this loads library(flowCore)

#Take all fcs and load them as a dataframe of exprs, store in a list
datz <- list()
for (fz in dir()[grep("fcs",dir())]) {
  datz[[fz]] <- data.frame(exprs(read.FCS(fz,transformation=F))
}

#Exploratory plot to figure out gating
ggplot(data.frame(datz[[1]][1:1e4,]),aes(x=FL1.A,y=FSC.A))+
  theme_bw()+geom_point(cex=0.01)+
  scale_x_log10(limits=c(1e1,1e7))+ #If you want log10
  scale_y_log10(limits=c(1e5,1e7))+ #If you just want limits
  xlim(c(0,750000))+ylim(c(0,3e6))+
  geom_abline(intercept=0,slope=15) #An exploratory gating line for
  # GFP pos/neg, can also use
  # something complex like
  # stat_function, or simple
  # like geom_vline

#Now that we know how to gate those suckas, we loop through and build
# a pretty dataframe ammenable to ggplot
#Change stuff to change your gates, what channels you're gating on etc
sdatz <- list()
for (fz in names(datz)) {
  sdatz[[fz]] <- cbind(datz[[fz]][,c("FSC.A","FL1.A")],
    datz[[fz]]$FSC.A > 1e5 & datz[[fz]]$FL1.A > 1e5 & datz[[fz]]$FSC.A < 1e7,
    datz[[fz]]$FL1.A * 15 > datz[[fz]]$FSC.A)
  names(sdatz[[fz]]) <- c("FSC","FL1","cell","gfp")
}

#And easier names than the names of the files from names(datz)
names(sdatz) <- c("blank","653","fy4","blank","mix1","mix2")

#So now you can explore your results
print(ggplot(sdatz[[fz]]$cell,.)
  aes(x=FL1,y=FSC,col=gfp)) +
  theme_bw()+geom_point(cex=0.01,alpha=0.1)+
  scale_x_log10(limits=c(1e1,1e6)) +
  scale_y_log10(limits=c(1e5,5e6))+
  ggtitle(paste0(fz," scatterplot")))

#Once you’re happy, adjust this look to output a bunch of pngs
for (fz in names(sdatz)) {
  png(paste0(fz,"scatter",".png"))
  print(ggplot(sdatz[[fz]]$cell,.)
    aes(x=FL1,y=FSC,col=gfp)) +
    theme_bw()+geom_point(cex=0.01,alpha=0.1)+
    scale_x_log10(limits=c(1e1,1e6)) +
    scale_y_log10(limits=c(1e5,5e6))+
    ggtitle(paste0(fz," scatterplot")))
  dev.off()
  #This is a density plot, if you like that kind of thing
  #print(ggplot(sdatz[[fz]]$cell,.)
  #  aes(x=FL1,col=gfp))+
  #  theme_bw()+geom_density(adjust=0.1)+
  #  scale_x_log10(limits=c(1e1,1e6)) +
  #  xlab("FL1-A signal") +
  #  ggtitle(paste0(fz," distributions of GFP signal per cell")))
  #dev.off()
}

#How many GFP "pos" cells are detected as such?
frac653 <- sum(sdatz$`653`$gfp & sdatz$`653`$cell)/sum(sdatz$`653`$cell)
frac1 <- sum(sdatz$fy4$gfp & sdatz$fy4$cell)/sum(sdatz$fy4$cell)
fracmix1 <- sum(sdatz$mix1$gfp & sdatz$mix1$cell)/sum(sdatz$mix1$cell)
fracmix2 <- sum(sdatz$mix2$gfp & sdatz$mix2$cell)/sum(sdatz$mix2$cell)
fracmix3 <- sum(sdatz$mix3$gfp & sdatz$mix3$cell)/sum(sdatz$mix3$cell)
```
And so forth