# 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)
```

Take all fcs and load them as a dataframe of exprs, store in a list

```r
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

```r
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)) +
  scale_y_log10(limits=c(1e5,1e7)) +
  xlim(c(0,750000)) + ylim(c(0,3e6)) +
  geom_abline(intercept=0,slope=15)
```

Now that we know how to gate those suckas, we loop through and build a pretty dataframe ammenable to ggplot

```r
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 * 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)

```r
names(sdatz) <- c("blank","653","fy4","blank","mix1","mix2")
```

So now you can explore your results

```r
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

```r
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

```r
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," densities of GFP signal per cell")))
```

How many GFP "pos" cells are detected as such?

```r
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)
```