Calcium Flux Trace Plotting

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## Load R functions

source("ChiuPeakProcessingAlgorithm.R")

## Warning: package 'stringr' was built under R version 3.4.3

source("ChiuPeakProcessingUtilities.R")  
source("tcpl\_fit\_functions.R")

## Load and process multiple plates

### Read files

seq1.file.list<- get.seq1.file.list(".")  
n.files<-length(seq1.file.list)  
dat.list<-list()  
for (n in 1:n.files) {  
 fname<-seq1.file.list[n]  
 dat.list[[n]]<-get.seq1.dat(fname)  
}

### Produce Trace plots

## While file?  
  
filenum<-1  
  
## "dat" is a data frame with Well (e.g., E3) in the first column, and the data in the other columns  
  
dat<-dat.list[[filenum]]  
  
t<-as.numeric(sub("X","",colnames(dat)[-1]))  
  
##Set up loop to export each trace as a .png into new directory folder  
  
##change working directory to new folder where you want the traces  
  
setwd("C:\\Users\\ablanchette\\Documents\\CM Peak Processing\\Cardiotox\_Repeat Experiment\\1083\\1083\_Traces")  
  
for (i in 1:length(dat$Well)) {  
  
 plotname<-paste("1083\_Trace\_", dat$Well[i], ".png", sep="")   
   
 rownum<-i  
  
 y<-dat[rownum,-1]  
  
 well<-dat[rownum,1]  
  
 png(plotname)  
   
 plot(t,y,cex=0.5,type="l");  
  
 mtext(paste(seq1.file.list[filenum]," Row ",rownum," (Well ",well,")",sep=""),side=3,cex=0.75)  
   
 dev.off()  
}