MoTrPAC Animal data: analysis of the phenotypic data

```
# Set the working directory to the folder with the data
setwd("/Users/David/Desktop/MoTrPAC/march_2019/pheno_data/PASS1A.6M-RLS 0,01/3-Data Sets/")
all_csvs = list.files(".") # get all files in dir
# read all files
csv_data = list()
for(fname in all_csvs){
   csv_data[[fname]] = read.csv(fname,stringsAsFactors = F)
}# sapply(csv_data,dim) # check the dimensions of the different datasets
```

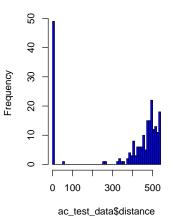
Acute tests

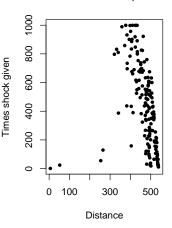
[1] "Treadmill stopped 28:49 (mm:ss) into the acute bout due to problems with the other rat on the s Nest, we analyze the distances. We hypothesized that these are a function of the shocks given or "errors" in the process.

```
# convert the shock lengths to numbers (seconds)
parse_shocktime<-function(x){</pre>
  arr = strsplit(x,split=":")[[1]]
  if(length(arr)<2){return(NA)}</pre>
  return(as.numeric(arr[1])*60+as.numeric(arr[2]))
}
tmp_x = ac_test_data$howlongshock
tmp_x = sapply(tmp_x, parse_shocktime)
ac_test_data$howlongshock = tmp_x
rm(tmp_x)
par(mfrow=c(1,2))
# histogram of distances
hist(ac_test_data$distance,col="blue",breaks=50,main = "Histogram of distances")
# Correlation between distance and number of shocks
# Get the indices of the samples with shock information -
# these the animals that did the acute test
```

Histogram of distances

Dist vs times shocked, rho=-0.67



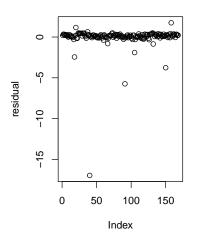


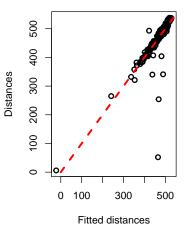
```
##
## Call:
## lm(formula = distance ~ timesshock + howlongshock + weight +
##
       days_start, data = trained_animals_data)
##
## Residuals:
##
      Min
                1Q
                   Median
                                3Q
                                       Max
## -412.69
            -1.46
                      6.48
                             11.87
                                     70.92
##
## Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
                            14.11730 38.851 < 2e-16 ***
              548.46424
## (Intercept)
## timesshock
                  0.02645
                             0.01301
                                       2.033
                                               0.0437 *
## howlongshock -0.29488
                             0.01983 -14.871
                                             < 2e-16 ***
## weight
                 -0.20455
                             0.04091
                                     -5.000 1.47e-06 ***
                                               0.1832
## days_start
                  0.21137
                             0.15813
                                       1.337
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 41.24 on 163 degrees of freedom
## Multiple R-squared: 0.6793, Adjusted R-squared: 0.6714
## F-statistic: 86.32 on 4 and 163 DF, p-value: < 2.2e-16
```

```
# We have some clear outliers:
library(MASS)
par(mfrow=c(1,2))
plot(studres(dist_lm), main="studentized residuals (lm)", ylab="residual")
# Select the top outliers and look at their comments
outliers = abs(studres(dist_lm)) > 2
# how many outliers have we selected?
sum(outliers)
## [1] 4
# their comments:
trained_animals_data[outliers,"comments"]
## [1] ""
## [2] "Halfway through the acute test, the shocker grid malfunctioned and would not shut off even when
## [3] "The shocker grid started to malfunction at time point 18:25 of the run. The distance ran, time
## [4] "Shocker grid malfunctioned. Distance ran, time spent on shocker grid, and number of times rat w
# Plot the fitted values of the linear regression vs.
# the true distances
plot(dist_lm$fitted.values,trained_animals_data$distance,lwd=2,
     main="Fitted vs real values",ylab="Distances",xlab="Fitted distances")
abline(0,1,col="red",lty=2,lwd=3)
```

studentized residuals (Im)

Fitted vs real values

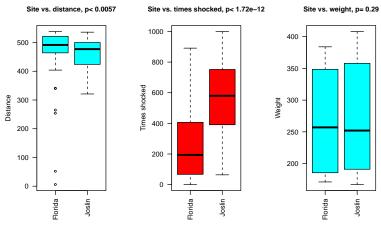


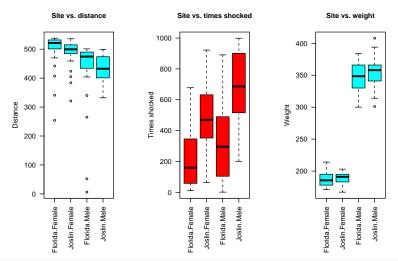


Site comparison

```
# Load additional information about the animals
registr_data = csv_data[[which(grepl("Regist",names(csv_data)))]]
rownames(registr_data) = as.character(registr_data$participantGUID)
# make the rownames in the test data comparable
rownames(trained_animals_data) = trained_animals_data$participantGUID
# add sex to the trained animal data data frame
sex_key = c("Female","Male")
trained_animals_data$sex = sex_key[registr_data[rownames(trained_animals_data),"sex"]]
# Map site Ids to their names
site_names = c("910"="Joslin","930"="Florida")
trained_animals_data$site = site_names[as.character(trained_animals_data$siteID)]
```

```
# Sanity check: the numbers should be the same for both sites
table(ac_test_data$siteID)
##
## 910 930
## 108 108
table(trained_animals_data$site,trained_animals_data$sex)
##
##
             Female Male
##
     Florida
                 42
##
     Joslin
                 42
                      42
run_wilcox<-function(x1,x2){</pre>
  return(wilcox.test(x1[x2==x2[1]],x1[x2!=x2[1]])$p.value)
}
# Compare the distances, shocks, and weight
par(mfrow=c(1,3), mar=c(10,4,4,4))
# Site only
p_dist = run_wilcox(trained_animals_data$distance,trained_animals_data$site)
boxplot(distance~site,data=trained_animals_data,col="cyan",ylab="Distance",
        main=paste("Site vs. distance, p<",format(p dist,digits = 2)),</pre>
        cex.main=1,las=2)
p_timesshock = run_wilcox(trained_animals_data$timesshock,trained_animals_data$site)
boxplot(timesshock~site,data=trained_animals_data,col="red",ylab="Times shocked",
        main=paste("Site vs. times shocked, p<",format(p_timesshock,digits = 3)),</pre>
        cex.main=1,las=2)
p_w = run_wilcox(trained_animals_data$weight,trained_animals_data$site)
boxplot(weight~site,data=trained_animals_data,col="cyan",ylab="Weight",
        main=paste("Site vs. weight, p=",format(p_w,digits = 2)),
        cex.main=1,las=2)
```





Regress time shocked and distance vs. site and sex
summary(lm(timesshock~site+sex,data=trained_animals_data))

```
##
## Call:
## lm(formula = timesshock ~ site + sex, data = trained_animals_data)
##
## Residuals:
##
                1Q Median
                                ЗQ
                                       Max
##
  -453.06 -167.17 -11.96 151.83 543.99
##
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                             31.02
                                     6.380 1.72e-09 ***
                 197.92
## siteJoslin
                 307.05
                             35.82
                                     8.572 7.02e-15 ***
## sexMale
                 149.10
                             35.82
                                     4.162 5.06e-05 ***
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 232.1 on 165 degrees of freedom
## Multiple R-squared: 0.355, Adjusted R-squared: 0.3471
## F-statistic: 45.4 on 2 and 165 DF, p-value: < 2.2e-16
summary(lm(distance~site+sex,data=trained animals data))
##
## Call:
## lm(formula = distance ~ site + sex, data = trained_animals_data)
## Residuals:
      Min
                10 Median
                                3Q
                                       Max
## -435.20 -10.88
                     15.44
                             33.70
                                     67.24
##
## Coefficients:
##
               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 501.780
                            8.745 57.381 < 2e-16 ***
## siteJoslin
                -9.440
                            10.097 -0.935
                                              0.351
## sexMale
                -60.583
                            10.097 -6.000 1.21e-08 ***
```

```
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 65.44 on 165 degrees of freedom
## Multiple R-squared: 0.1827, Adjusted R-squared: 0.1727
## F-statistic: 18.44 on 2 and 165 DF, p-value: 5.937e-08
```