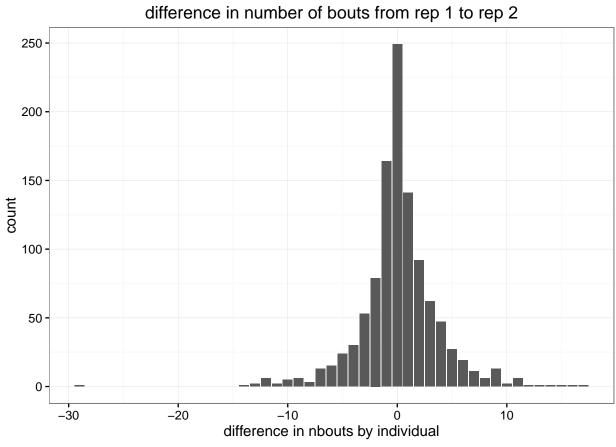
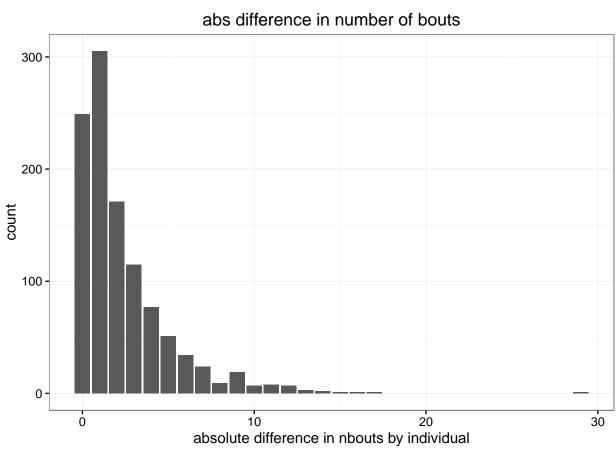
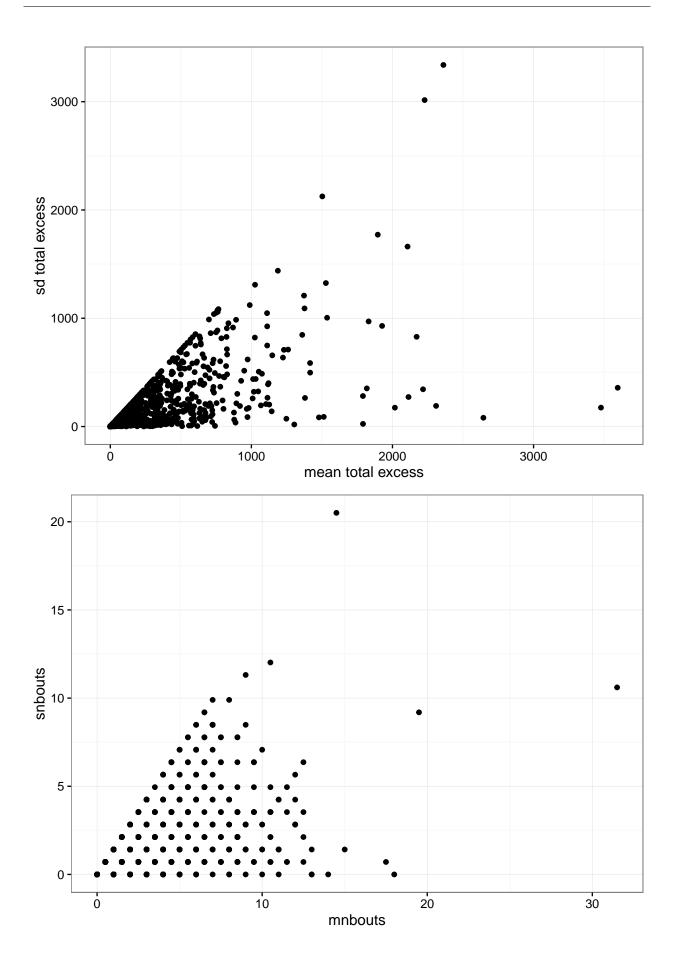
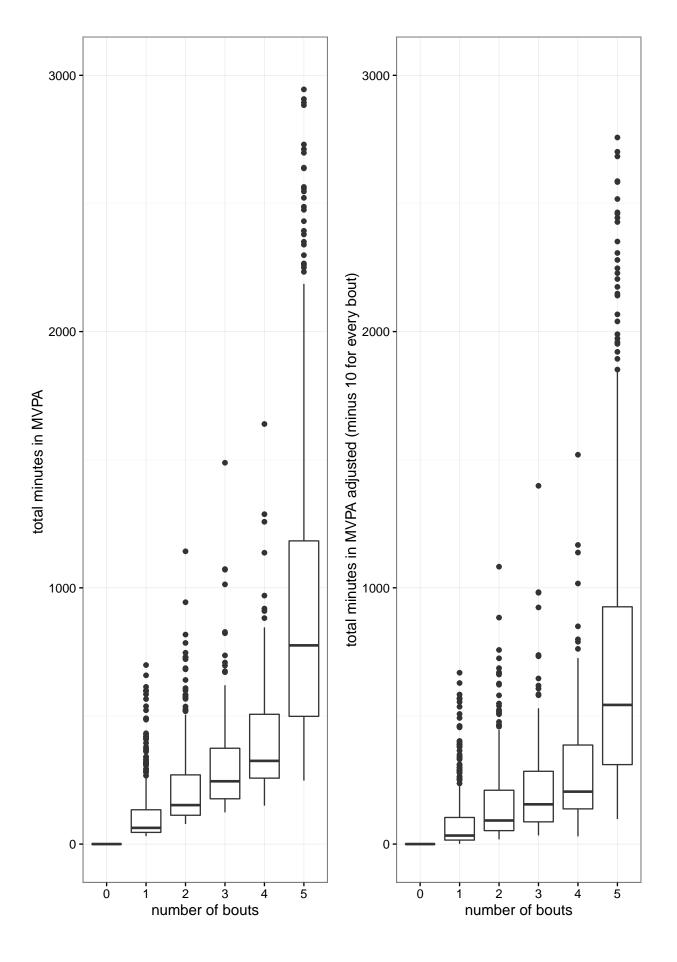
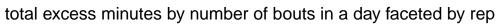
10 -	7	6	6	6	3	4	2	8	4	4	25	
9 -	1	1	1	1	1	1	3	3	4	1	5	count 125
	0	3	4	3	0	2	2	2	2	2	11	
7 -	0	3	8	4	2	3	3	1	2	2	12	
s obs 2	5	3	5	5	5	5	3	6	1	0	7	
number of bouts obs 2	3	3	8	7	7	6	5	9	2	3	6	100 75 50
equnu 4-	12	7	17	15	7	6	4	3	5	0	2	25 0
3 -	21	14	17	19	12	10	7	5	5	3	6	
2 -	23	42	30	15	6	8	11	2	1	4	6	
1 -	65	48	30	21	19	6	2	3	3	1	7	
0 -	126	57	33	16	9	6	6	1	3	3	3	
0 1 2 3 4 5 6 7 8 9 10 number of bouts obs 1												

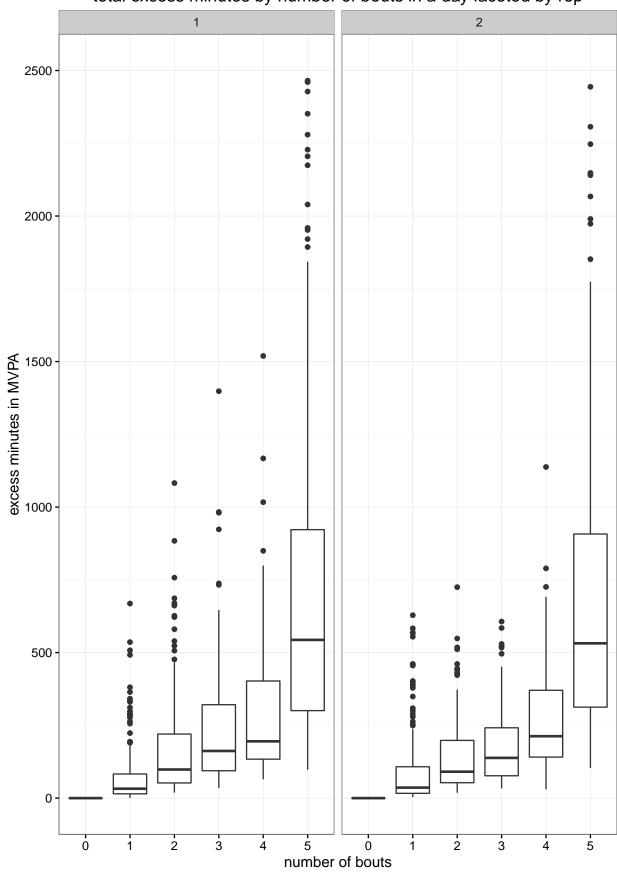


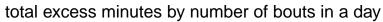


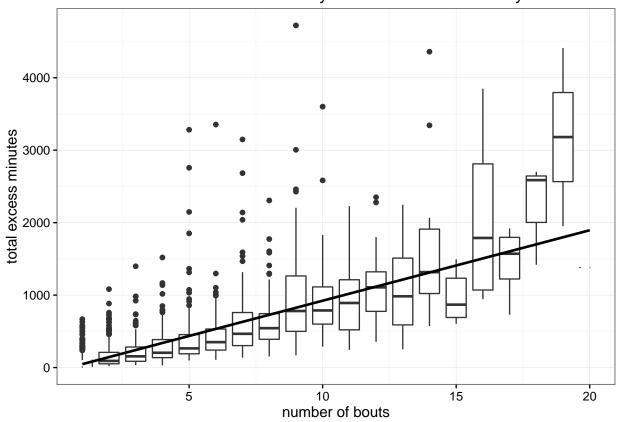




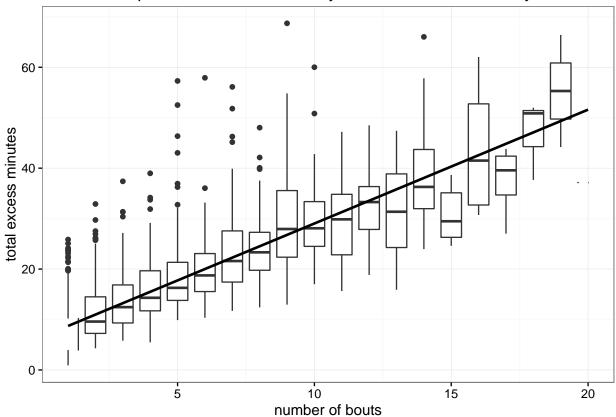


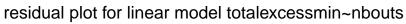


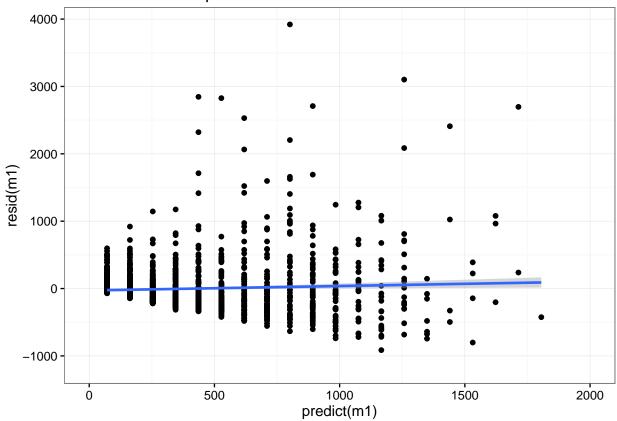




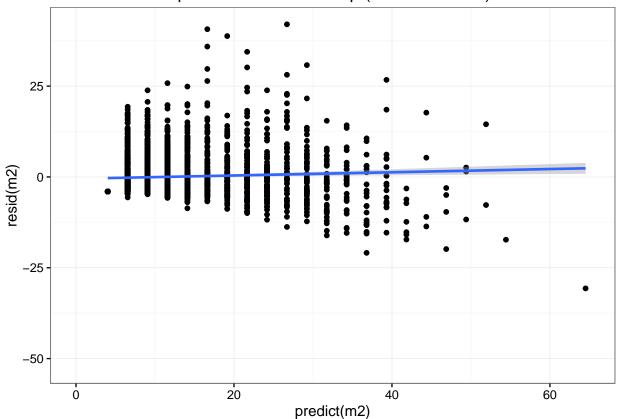
sqrt total excess minutes by number of bouts in a day

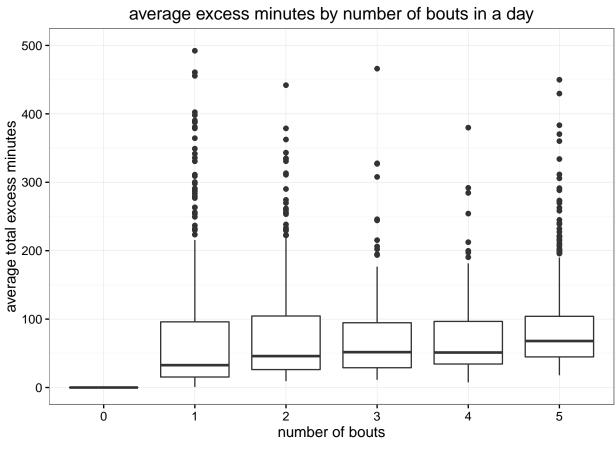


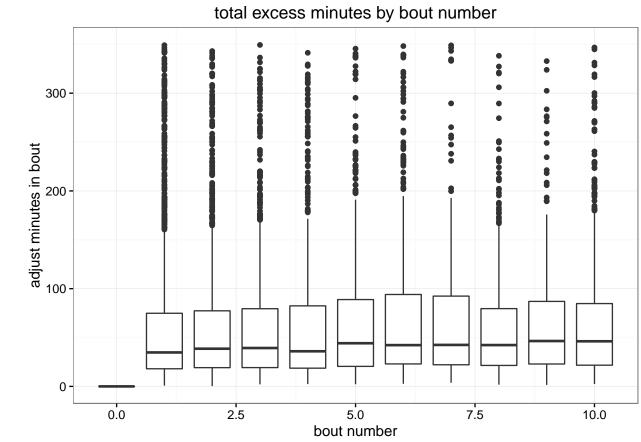


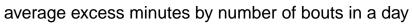


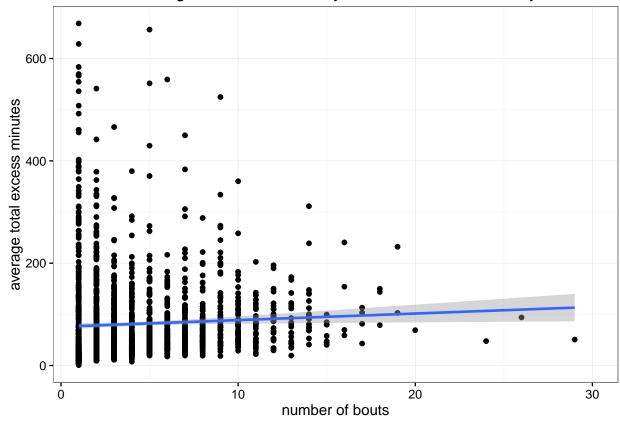
residual plot for linear model sqrt(totalexcessmin)~nbouts



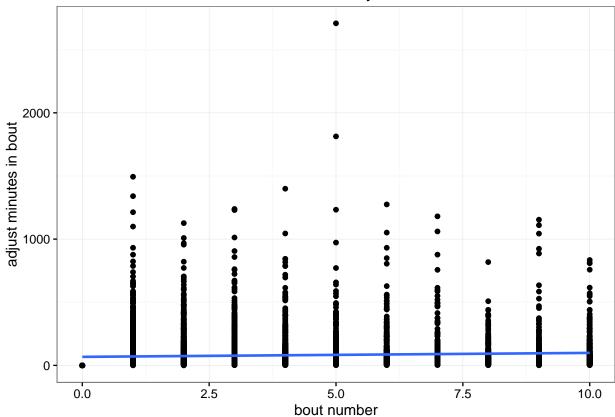


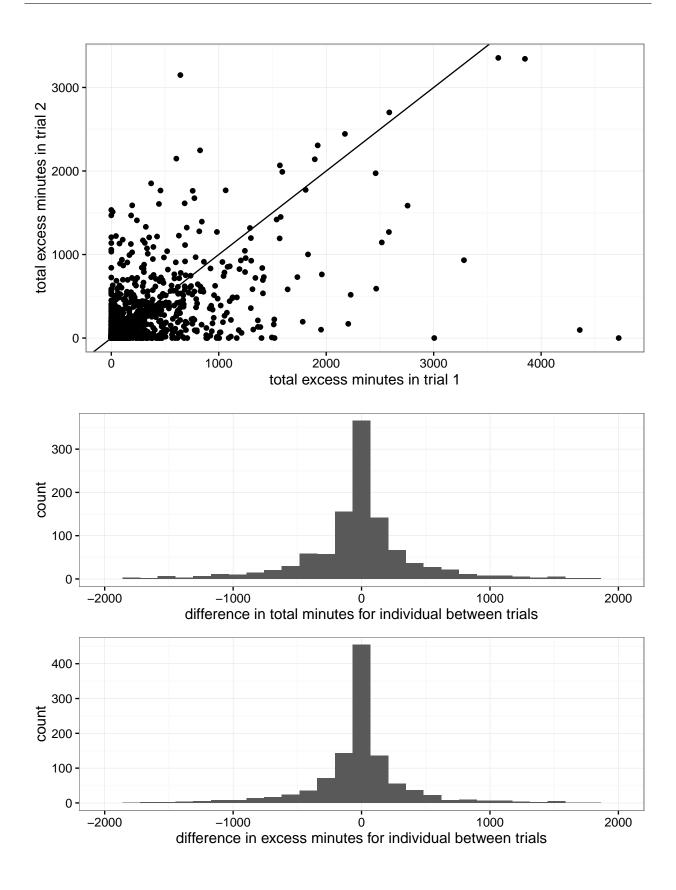


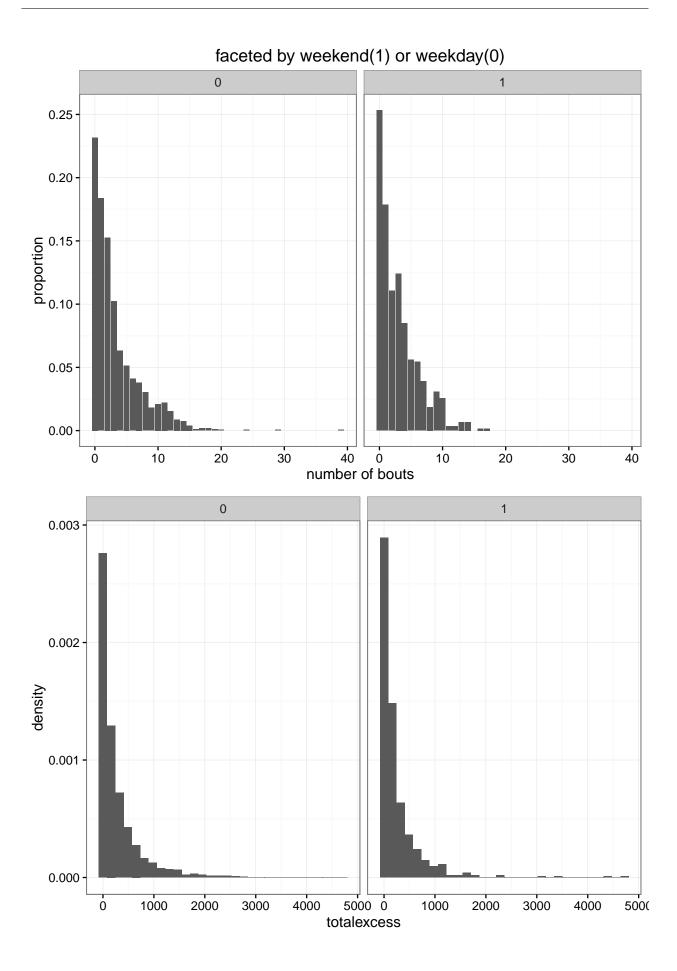




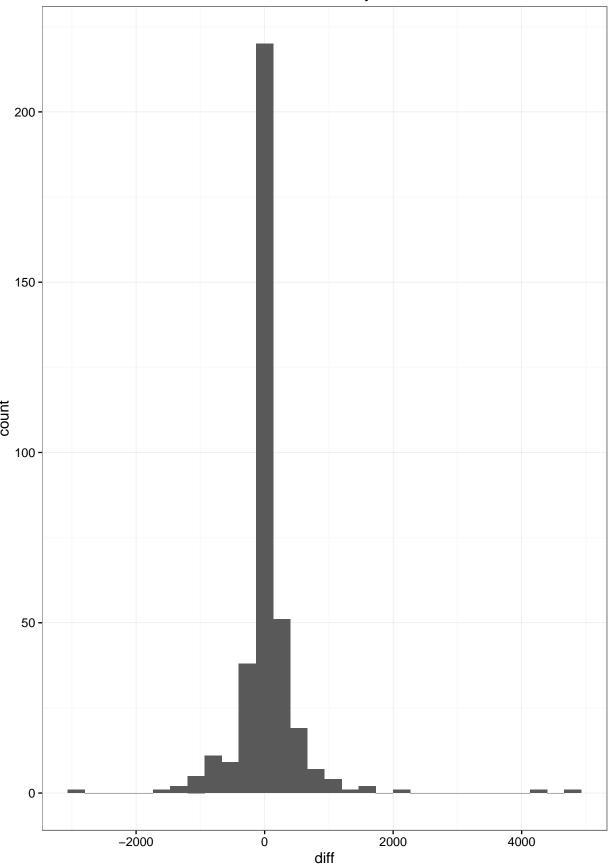
total excess minutes by bout number











```
#test difference in mean totalexcess min from trial 1 to trial 2 paired by individual
trial1 <- bouts %>% group_by(id) %>% filter(length((id))==2, rep==1)
trial2 <- bouts %>% group_by(id) %>% filter(length((id))==2, rep==2)

wilcox.test(trial1$totalexcess,trial2$totalexcess,paired=TRUE)

##
## Wilcoxon signed rank test with continuity correction
##
## data: trial1$totalexcess and trial2$totalexcess
## V = 245710, p-value = 0.07001
## alternative hypothesis: true location shift is not equal to 0
```

```
#test difference in distribution of totalexcess min from trial 1 to trial 2
ks.test(bouts$totalexcess[bouts$rep==1],bouts$totalexcess[bouts$rep==2])

##
## Two-sample Kolmogorov-Smirnov test
##
## data: bouts$totalexcess[bouts$rep == 1] and bouts$totalexcess[bouts$rep == 2]
## D = 0.034009, p-value = 0.5031
## alternative hypothesis: two-sided
```

```
#test difference in distribution of differenced totalexcess min from trial 1 to trial 2 compar
a1 <- (trial2$totalexcess-trial1$totalexcess)
a2 <- (trial1$totalexcess-trial2$totalexcess)
ks.test(a1,a2)
##
## Two-sample Kolmogorov-Smirnov test
##
```

```
## data: a1 and a2
## D = 0.04977, p-value = 0.1361
## alternative hypothesis: two-sided
```

```
#difference in mean nbouts min from trial 1 to trial 2
wilcox.test(trial1$nbouts,trial2$nbouts,paired=TRUE)

##
## Wilcoxon signed rank test with continuity correction
##
## data: trial1$nbouts and trial2$nbouts
## V = 187960, p-value = 0.06021
## alternative hypothesis: true location shift is not equal to 0
```

```
#test marginal distributional differences in nbouts from trial 1 to trial 2
ks.test(bouts$nbouts[bouts$rep==1],bouts$nbouts[bouts$rep==2])

##
## Two-sample Kolmogorov-Smirnov test
##
## data: bouts$nbouts[bouts$rep == 1] and bouts$nbouts[bouts$rep == 2]

## D = 0.024617, p-value = 0.8674

## alternative hypothesis: two-sided
```

```
#nbouts of weekday vs weekend
ks.test(bouts$nbouts[bouts$Weekend==0],bouts$nbouts[bouts$Weekend==1])

##

##

## Two-sample Kolmogorov-Smirnov test

##

## data: bouts$nbouts[bouts$Weekend == 0] and bouts$nbouts[bouts$Weekend == 1]
```

```
## D = 0.042311, p-value = 0.4138
## alternative hypothesis: two-sided
#excess minutes of weekday vs weekend
ks.test(bouts$totalexcess[bouts$Weekend==0],bouts$totalexcess[bouts$Weekend==1])
##
   Two-sample Kolmogorov-Smirnov test
##
##
## data: bouts$totalexcess[bouts$Weekend == 0] and bouts$totalexcess[bouts$Weekend == 1]
## D = 0.062531, p-value = 0.06534
## alternative hypothesis: two-sided
#test difference in means of total excess in weekday vs weekend for those with both
week1weekend1 <- bouts %>% group_by(id) %>% filter(length((id))==2, sum(Weekend)==1, rep==1)
week1weekend2 <- bouts %>% group_by(id) %>% filter(length((id))==2, sum(Weekend)==1, rep==2)
wilcox.test(week1weekend1$totalexcess, week1weekend2$totalexcess, paired=TRUE)
##
   Wilcoxon signed rank test with continuity correction
##
## data: week1weekend1$totalexcess and week1weekend2$totalexcess
## V = 30118, p-value = 0.3099
## alternative hypothesis: true location shift is not equal to 0
#test difference in means of nbouts in weekday vs weekend for those with both
wilcox.test(week1weekend1$nbouts, week1weekend2$nbouts, paired=TRUE)
##
   Wilcoxon signed rank test with continuity correction
##
```

```
## data: week1weekend1$nbouts and week1weekend2$nbouts
## V = 22398, p-value = 0.3595
## alternative hypothesis: true location shift is not equal to 0
```

```
#test for difference in any total excess mins by number of bouts
#nonparametric test since normality doesn't hold
kruskal.test(anytotalexcess nbouts, data=subset(bouts, nbouts>0))

##
## Kruskal-Wallis rank sum test
##
## data: anytotalexcess by nbouts
## Kruskal-Wallis chi-squared = 136.9, df = 23, p-value < 2.2e-16

kruskal.test(anytotalexcess nbouts, data=subset(bouts, nbouts>0&nbouts<11))

##
## Kruskal-Wallis rank sum test
##
## data: anytotalexcess by nbouts
## Kruskal-Wallis chi-squared = 101.37, df = 9, p-value < 2.2e-16</pre>
```

```
#linear trend on avgtotalexcess minutes with nbouts as covariate
m1lm <- lm((avgtotalexcess)~(nbouts),data=subset(bouts,nbouts>0))
summary(m1lm)

##
## Call:
## lm(formula = (avgtotalexcess)~ (nbouts), data = subset(bouts,
## nbouts > 0))
##
```

```
## Residuals:
    Min 1Q Median 3Q
                              Max
## -76.60 -50.48 -27.62 20.02 591.14
##
## Coefficients:
             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 76.2126 2.9927 25.466 <2e-16 ***
## nbouts
         1.1982 0.5323 2.251 0.0245 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 83.13 on 1808 degrees of freedom
## Multiple R-squared: 0.002795, Adjusted R-squared: 0.002243
## F-statistic: 5.067 on 1 and 1808 DF, p-value: 0.02451
m1lmb <- lm((avgtotalexcess)~(nbouts),data=subset(bouts,nbouts>0&nbouts<11))
summary(m1lmb)
##
## Call:
## lm(formula = (avgtotalexcess) ~ (nbouts), data = subset(bouts,
     nbouts > 0 & nbouts < 11))
##
##
## Residuals:
     Min 1Q Median 3Q Max
## -75.86 -51.23 -29.87 19.85 591.88
##
## Coefficients:
            Estimate Std. Error t value Pr(>|t|)
##
## (Intercept) 75.1162
                        3.5804 20.980 <2e-16 ***
## nbouts 1.5505 0.8238 1.882 0.06
```

```
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 85.28 on 1675 degrees of freedom
## Multiple R-squared: 0.00211, Adjusted R-squared: 0.001515
## F-statistic: 3.542 on 1 and 1675 DF, p-value: 0.05999
```

```
#test for diff in total excess mins by bout number
#nonparametric test since normality doesn't hold
kruskal.test(totalpadj~bout,data=subset(bybout,bout>0))

##
## Kruskal-Wallis rank sum test
##
## data: totalpadj by bout
## Kruskal-Wallis chi-squared = 50.569, df = 38, p-value = 0.08341
kruskal.test(totalpadj~bout,data=subset(bybout,bout>0&bout<11))

##
## Kruskal-Wallis rank sum test
##
## data: totalpadj by bout
## Kruskal-Wallis chi-squared = 23.959, df = 9, p-value = 0.004367</pre>
```

```
#linear trend on total excess minutes with bout number as covariate
m2lm <- lm(totalpadj~(bout),data=subset(bybout,bout>0))
summary(m2lm)
##
## Call:
```

```
## lm(formula = totalpadj ~ (bout), data = subset(bybout, bout >
      0))
##
## Residuals:
              1Q Median 3Q
##
      Min
   -84.41 -64.84 -43.49 7.63 2623.50
##
##
## Coefficients:
              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 84.4900 2.2689 37.238 <2e-16 ***
## bout
              0.1463 0.4078 0.359
                                           0.72
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 130.2 on 7706 degrees of freedom
## Multiple R-squared: 1.671e-05, Adjusted R-squared: -0.0001131
## F-statistic: 0.1287 on 1 and 7706 DF, p-value: 0.7197
m2lmb <- lm(totalpadj~(bout),data=subset(bybout,bout>0&bout<11))</pre>
summary(m2lmb)
##
## Call:
## lm(formula = totalpadj ~ (bout), data = subset(bybout, bout >
      0 & bout < 11))
##
## Residuals:
          1Q Median 3Q
##
      Min
                                     Max
   -90.87 -65.00 -43.91 7.54 2621.49
##
## Coefficients:
```

```
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 80.8104   2.7105   29.814   <2e-16 ***
## bout    1.2850   0.6189   2.076   0.0379 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 131.7 on 7257 degrees of freedom
## Multiple R-squared: 0.0005938,Adjusted R-squared: 0.0004561
## F-statistic: 4.312 on 1 and 7257 DF, p-value: 0.03789</pre>
```

```
#testing marginal homogeneity of 2 way table of nbouts
ct1 <- matrix(table(trial1$nbouts,trial2$nbouts)[1:10,1:10],nrow=10,byrow=T)</pre>
stuart.maxwell.mh(ct1[1:6,1:6])
   Stuart-Maxwell marginal homogeneity
##
  Subjects = 584
##
      Raters = 2
##
       Chisq = 1.39
##
##
   Chisq(4) = 1.39
##
     p-value = 0.845
stuart.maxwell.mh(ct1)
   Stuart-Maxwell marginal homogeneity
##
##
   Subjects = 845
      Raters = 2
##
       Chisq = 4.54
##
##
```

```
## Chisq(8) = 4.54
## p-value = 0.805
```

```
#Bowker's test of symmetry, ie. generalization of McNemar's test
mcnemar.test(ct1[1:6,1:6])

##

## McNemar's Chi-squared test
##

## data: ct1[1:6, 1:6]

## McNemar's chi-squared = 20.679, df = 15, p-value = 0.1474

mcnemar.test(ct1)

##

## McNemar's Chi-squared test
##

## data: ct1

## McNemar's chi-squared = 52.875, df = 45, p-value = 0.1961
```

```
#permutation test
#H_0 : sum |lower.tri-upper.tri| = 0, ie. trial 1 and trial 2 exchangeable
# H_a : sum > 0, not exchangeable

obs <- sum(abs(ct1[lower.tri(ct1)]-ct1[upper.tri(ct1)]))

nsim <- 10000

permutei <- rep(0,nsim)

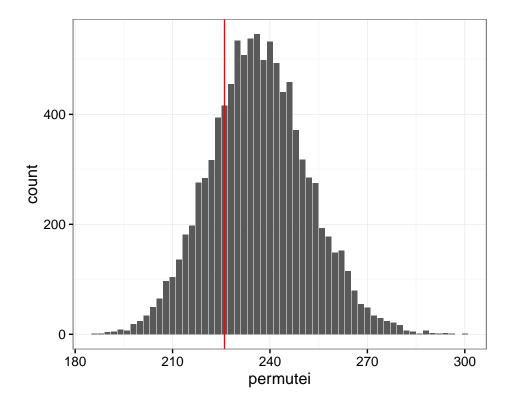
nboutmat <- cbind(trial1$nbouts,trial2$nbouts)

newmat <- matrix(0,nrow=nrow(nboutmat),ncol=ncol(nboutmat)))

for(i in 1:nsim){
    for(j in 1:nrow(nboutmat)){
        s <- sample(1:2,2)</pre>
```

```
newmat[j,s[1]] <- nboutmat[j,1]
newmat[j,s[2]] <- nboutmat[j,2]
}
cti <- matrix(table(newmat[,1],newmat[,2])[1:10,1:10],ncol=10,byrow=T)
#mat <- ct1[sample(nrow(ct1)),sample(ncol(ct1))]
permutei[i] <- sum(abs(cti[lower.tri(cti)]-cti[upper.tri(cti)]))
}

qplot(x=permutei,geom="bar") + geom_vline(xintercept=obs,col="red") + theme_bw()</pre>
```



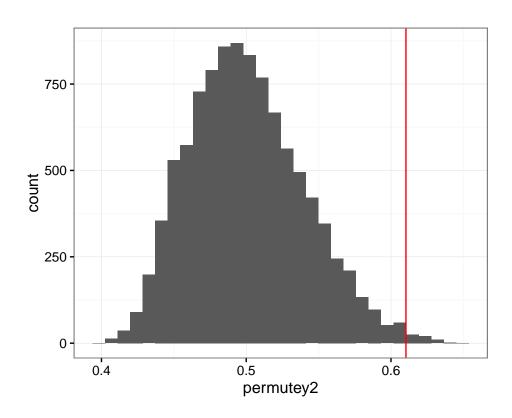
```
#checking exchangeability for y2 total excess minutes
#or like this? instead permute obs from trial 1 and trial 2?
#obsy2 <- sum(trial1ftotalexcess-trial2ftotalexcess)#cor(trial1ftotalexcess, trial2ftotalexcess)
obsy2 <- coef(lm(trial1$totalexcess~trial2$totalexcess))[2]
nsim <- 10000
permutey2 <- rep(0,nsim)
nboutmaty2 <- cbind(trial1$totalexcess,trial2$totalexcess)</pre>
```

```
newmaty2 <- matrix(0,nrow=nrow(nboutmaty2),ncol=ncol(nboutmaty2))
for(i in 1:nsim){
  for(j in 1:nrow(nboutmaty2)){
    s <- sample(1:2,2)
    newmaty2[j,s[1]] <- nboutmaty2[j,1]
    newmaty2[j,s[2]] <- nboutmaty2[j,2]
}

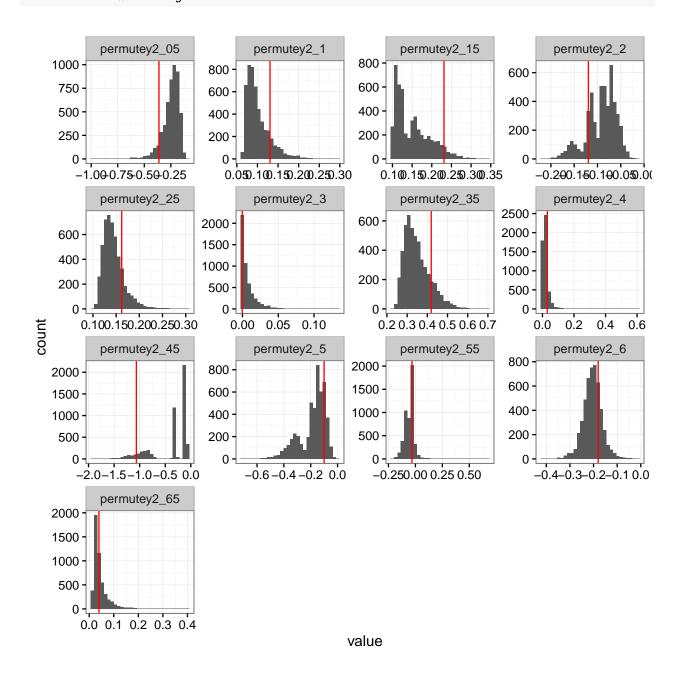
#permutey2[i] <- sum(newmaty2[,1]-newmaty2[,2])#cor(newmaty2)[1,2]
permutey2[i] <- coef(lm(newmaty2[,1]~newmaty2[,2]))[2]#cor(newmaty2)[1,2]
}

qplot(x=permutey2) + geom_vline(xintercept=obsy2,col="red") + theme_bw()

## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.</pre>
```



'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.



[1] 0.0800 0.8566 0.9380 0.1660 0.8268 0.1682 0.8546 0.8466 0.0844 0.8180 ## [11] 0.7664 0.7506 0.5918