AB_Testing

Reinp

2021-08-06

R Programming

Set Chunk requirements

echo=FALSE indicates that the code will not be shown in the final document (though any results/output would still be displayed).

include=FALSE to have the chunk evaluated, but neither the code nor its output displayed

warning=FALSE and message=FALSE suppress any R warnings or messages from being included in the final document

```
knitr::opts_chunk$set(echo = TRUE, message = FALSE, warning = FALSE)
```

Load relevant packages

```
library(tidyverse)
library("readxl")
#library(stats) Loaded automatically in R library

library(psych)
```

Import dataset

```
#loading the excel dataset with two sheets

setwd('F:/Documents/Reinp/GitHub Respositories/AB_Testing-with-RStudio')
ds_sd<-read_excel('data/School data.xlsx', sheet = "Data")
View(ds_sd)


ds_sd1<-read_excel('data/School data.xlsx', sheet = "District names")
View(ds_sd1)
```

Structure of the Data

```
#learn more about the dataset
help(ds_sd)
```

```
??ds_sd
str(ds_sd)
class(ds_sd)
typeof(ds_sd)
length(ds_sd)
names(ds_sd) #display variable names
#attributes(ds_sd) #names(ds_sd), class(ds_sd), row.names(ds_sd)
```

distribution of input variables

```
table(ds_sd$district_id)
```

```
## 
##   3   5   6  16  17  22  39  42  43  44  47  50  57  58  62  65  67  68  77  78 
## 253 279 256 302 218 227 274 225 248 237 222 241 294 251 239 290 260 243 260 270 
##  79  80  93  97 104 107 108 200 
## 319 288 245 247 233 254 295  14
```

```
table(ds_sd1$"DISTRICT ID")
```

```
## 
##   1   2   3   5   6  16  17  22  39  42  43  44  47  50  57  58  62  65  67  68 
##   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1 
##  77  78  79  80  93  97 104 107 108 112 
##   1   1   1   1   1   1   1   1   1   1
```

```
#unique values per column
unique(ds_sd$district_id)
```

```
##  [1]  78  79   3  80  39   5   6  16  17  22  42  43  93  44  97  47  50  57  58
## [20]  62 104  65 107 108  67  68  77 200
```

```
unique(ds_sd1$"DISTRICT ID")
```

```
##  [1]  78  79   3  80  39   5   6  16  17  22  42  43  93  44  97  47  50  57  58
## [20]  62 104  65 107 108  67  68  77 112   1   2
```

district_id 200 in (ds_sd dataframe) is not in the (ds-sd1 dataframe).

DISTRICT ID 1, DISTRICT ID 2 and DISTRICT ID 112 in (ds_sd1 dataframe) is not in the (ds-sd dataframe)

Transforming the data

```
ds_sdmerge <- merge(ds_sd, ds_sd1, by.x = "district_id", by.y = "DISTRICT ID") #N/A.
#This is default #Keep rows where there’s a match in both #innerjoin
View(ds_sdmerge)

ds_sdmerge1 <- merge(ds_sd, ds_sd1, by.x = "district_id", by.y = "DISTRICT ID", all.x = TRUE)
#Keep all rows from x, regardless of match in y #leftJoin even if there's no match in y


ds_sdmerge2 <- merge(ds_sd, ds_sd1, by.x = "district_id", by.y = "DISTRICT ID", all.y = TRUE)
#Keep all rows from y, regardless of match in x #Rightjoin even if there's no match in x
```

```
ds_sdmerge3 <- merge(ds_sd, ds_sd1, by.x = "district_id", by.y = "DISTRICT ID", all= TRUE)
#Keep all rows from x AND from y #Outerjoin
```

We select default merge for the final data. It keeps rows where there's a match in both. we get a total of 6970 schools

Get the total number of student enrolled and attended in each school.

```
#add total_enrolled column by computing the total number of student enrolled and total number
#of attended in each school


#Adding by equation
ds_sdmerge$total_enrolled=ds_sdmerge$enrolled_male_students + ds_sdmerge$enrolled_female_students
ds_sdmerge$total_attended=ds_sdmerge$attended_male + ds_sdmerge$attended_female

#transform() function
ds_sdmerge1 <- transform(ds_sdmerge1, total_enrolled = enrolled_male_students +
                    enrolled_female_students)
ds_sdmerge1 <- transform(ds_sdmerge1, total_attended = attended_male + attended_female)

#apply() function
ds_sdmerge2$total_enrolled <- apply(ds_sdmerge2[,c('enrolled_male_students',
                          'enrolled_female_students')], 1, function(x) sum(x))
ds_sdmerge2$total_attended <- apply(ds_sdmerge2[,c('attended_male', 'attended_female')], 1,
                             function(x) sum(x))

#tidyverse's dplyr
library(dplyr)
ds_sdmerge3 <- mutate(ds_sdmerge3, total_enrolled = enrolled_male_students +
                        enrolled_female_students)
ds_sdmerge3 <- mutate(ds_sdmerge3, total_attended = attended_male + attended_female)
```

Summary Statistics

```
#summary statistics
summary(ds_sdmerge) #summarizes the dataset
```

```
##   district_id     attended_male   attended_female enrolled_male_students
##  Min.   :  3.00   Min.   :  0.0   Min.   :  0.0   Min.   :-999.0
##  1st Qu.: 39.00   1st Qu.:190.0   1st Qu.:161.0   1st Qu.: 321.0
##  Median : 58.00   Median :247.0   Median :207.0   Median : 479.0
##  Mean   : 57.27   Mean   :253.3   Mean   :211.6   Mean   : 531.9
##  3rd Qu.: 79.00   3rd Qu.:308.0   3rd Qu.:257.0   3rd Qu.: 730.0
##  Max.   :108.00   Max.   :597.0   Max.   :483.0   Max.   :1194.0
##  enrolled_female_students   treatment      District Name      total_enrolled
##  Min.   :-999.0           Min.   :0.0000   Length:6970        Min.   :-1998.0
##  1st Qu.: 268.0           1st Qu.:0.0000   Class :character   1st Qu.:  592.0
##  Median : 394.0           Median :0.0000   Mode  :character   Median :  870.5
##  Mean   : 438.7           Mean   :0.4973                      Mean   :  970.7
##  3rd Qu.: 600.8           3rd Qu.:1.0000                      3rd Qu.: 1331.8
##  Max.   : 991.0           Max.   :1.0000                      Max.   : 1999.0
##   total_attended
##  Min.   :   0.0
##  1st Qu.: 353.0
##  Median : 456.0
##  Mean   : 464.9
##  3rd Qu.: 564.0
##  Max.   :1045.0
```

```
describe(ds_sdmerge)
```

```
##                          vars    n   mean     sd median trimmed    mad   min
## district_id                 1 6970  57.27  31.22   58.0   57.68  29.65     3
## attended_male               2 6970 253.31  85.78  247.0  249.84  87.47     0
## attended_female             3 6970 211.62  70.68  207.0  208.50  71.16     0
## enrolled_male_students      4 6970 531.93 266.40  479.0  518.04 276.50  -999
## enrolled_female_students    5 6970 438.73 222.13  394.0  427.54 223.87  -999
## treatment                   6 6970   0.50   0.50    0.0    0.50   0.00     0
## District Name*              7 6970  13.84   7.95   14.0   13.82  10.38     1
## total_enrolled              8 6970 970.66 485.92  870.5  946.60 496.67 -1998
## total_attended              9 6970 464.93 153.75  456.0  458.95 157.16     0
##                           max range  skew kurtosis   se
## district_id               108   105 -0.15    -0.92 0.37
## attended_male             597   597  0.39     0.09 1.03
## attended_female           483   483  0.42     0.13 0.85
## enrolled_male_students   1194  2193 -0.12     2.20 3.19
## enrolled_female_students  991  1990 -0.38     4.23 2.66
## treatment                   1     1  0.01    -2.00 0.01
## District Name*             27    26  0.01    -1.26 0.10
## total_enrolled           1999  3997 -0.26     3.07 5.82
## total_attended           1045  1045  0.36     0.03 1.84
```

Create the school_id variable by first sorting the data within each district by the total number of enrollees per school. Let the ID be 1 for the school within each district with the highest number of enrolled students, 2 for the second highest and so on……..

Adding Columns

```
ds_sdmerge <- arrange(ds_sdmerge,district_id,desc(total_enrolled))


ds_sdmerger <- ds_sdmerge %>%
  group_by(district_id) %>%
  mutate(school_id = rank(desc(total_enrolled), ties.method = "first"))

View(ds_sdmerger)
head(ds_sdmerger)
```

```
## # A tibble: 6 x 10
## # Groups:   district_id [1]
##   district_id attended_male attended_female enrolled_male_stu~ enrolled_female_~
##         <dbl>         <dbl>           <dbl>              <dbl>             <dbl>
## 1           3           212             177               1020               959
## 2           3           335             331                985               962
## 3           3           261             186               1139               807
## 4           3           208             166               1014               920
## 5           3           238             184               1050               881
## 6           3           112              75               1016               908
## # ... with 5 more variables: treatment <dbl>, District Name <chr>,
## #   total_enrolled <dbl>, total_attended <dbl>, school_id <int>
```

```r
tail(ds_sdmerger)
```

```
## # A tibble: 6 x 10
## # Groups:   district_id [1]
##   district_id attended_male attended_female enrolled_male_stu~ enrolled_female_~
##         <dbl>         <dbl>           <dbl>              <dbl>             <dbl>
## 1         108           118              97                136               110
## 2         108            73              55                126               106
## 3         108            66              64                112               108
## 4         108           242             230               -999              -999
## 5         108           156             162               -999              -999
## 6         108           239             222               -999              -999
## # ... with 5 more variables: treatment <dbl>, District Name <chr>,
## #   total_enrolled <dbl>, total_attended <dbl>, school_id <int>
```

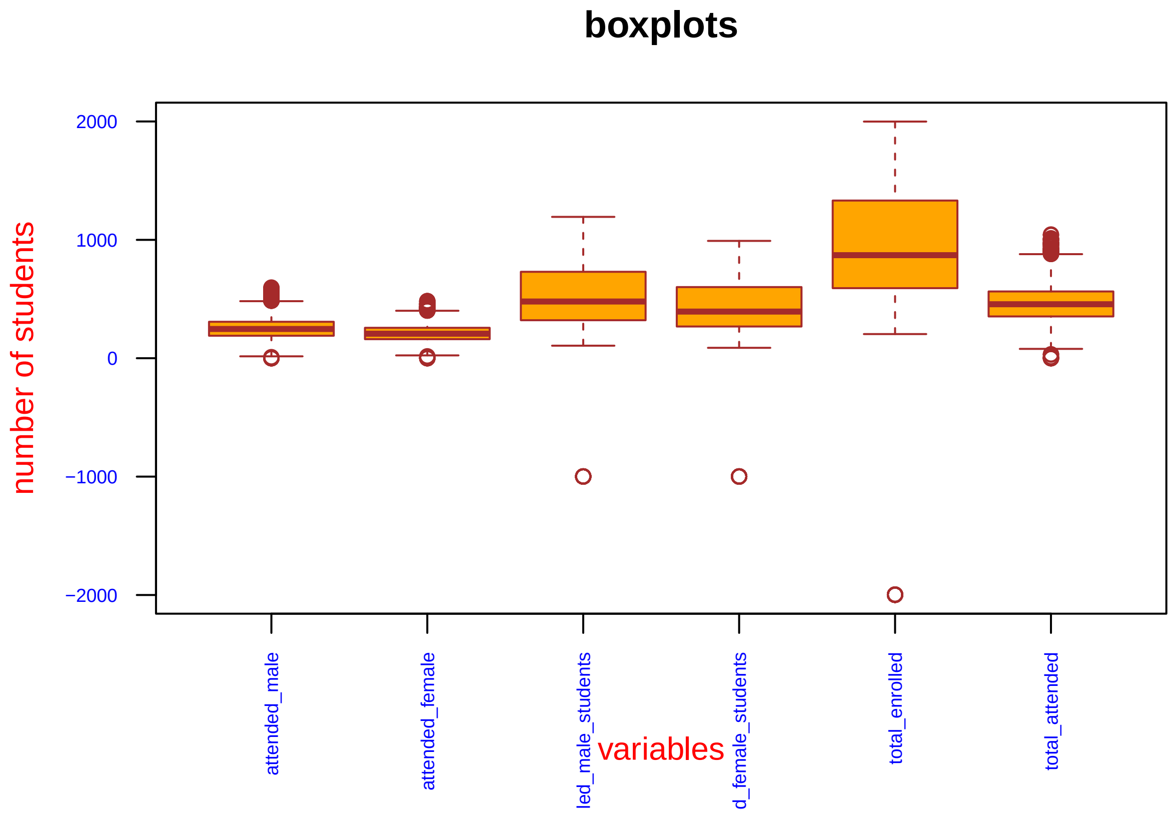
Check the numeric variables for outliers.

```r
describe(ds_sdmerger)
```

```
##                          vars    n   mean     sd median trimmed    mad   min
## district_id                 1 6970  57.27  31.22   58.0   57.68  29.65     3
## attended_male               2 6970 253.31  85.78  247.0  249.84  87.47     0
## attended_female             3 6970 211.62  70.68  207.0  208.50  71.16     0
## enrolled_male_students      4 6970 531.93 266.40  479.0  518.04 276.50  -999
## enrolled_female_students    5 6970 438.73 222.13  394.0  427.54 223.87  -999
## treatment                   6 6970   0.50   0.50    0.0    0.50   0.00     0
## District Name*              7 6970  13.84   7.95   14.0   13.82  10.38     1
## total_enrolled              8 6970 970.66 485.92  870.5  946.60 496.67 -1998
## total_attended              9 6970 464.93 153.75  456.0  458.95 157.16     0
## school_id                  10 6970 130.90  76.85  130.0  129.61  96.37     1
##                           max range  skew kurtosis   se
## district_id               108   105 -0.15    -0.92 0.37
## attended_male             597   597  0.39     0.09 1.03
## attended_female           483   483  0.42     0.13 0.85
## enrolled_male_students   1194  2193 -0.12     2.20 3.19
## enrolled_female_students  991  1990 -0.38     4.23 2.66
## treatment                   1     1  0.01    -2.00 0.01
## District Name*             27    26  0.01    -1.26 0.10
## total_enrolled           1999  3997 -0.26     3.07 5.82
## total_attended           1045  1045  0.36     0.03 1.84
## school_id                 319   318  0.11    -1.04 0.92
```

```r
## We use boxplot to visualize for any outliers

boxplot(ds_sdmerger [, c("attended_male", "attended_female", "enrolled_male_students",
      "enrolled_female_students", "total_enrolled", "total_attended")], main="boxplots",
xlab="variables",
ylab="number of students",
col="orange",
border="brown", las = 2, cex.axis = 0.6, col.axis = 'blue', col.lab = 'red')
```



From the boxplot above, outliers are present in form of negative count of students. There are negative values in enrolled_male_students and in enrolled_female_students leading to a negative total_enrolled

```
#cleaning data from the outliers
ds_sdmerger1 <- ds_sdmerger[(ds_sdmerger[,8]>0),]
View(ds_sdmerger1)
describe(ds_sdmerger1)
```

```
##                         vars    n   mean     sd median trimmed    mad min  max
## district_id                1 6948  57.27  31.22   58.0   57.67  29.65   3  108
## attended_male              2 6948 253.42  85.76  247.0  249.93  87.47   0  597
## attended_female            3 6948 211.71  70.67  207.0  208.57  71.16   0  483
## enrolled_male_students     4 6948 536.78 252.49  481.0  519.18 277.25 106 1194
## enrolled_female_students   5 6948 443.28 207.20  395.0  428.48 223.87  88  991
## treatment                  6 6948   0.50   0.50    0.0    0.50   0.00   0    1
## District Name*             7 6948  13.83   7.94   14.0   13.81  10.38   1   27
## total_enrolled             8 6948 980.06 457.02  873.5  948.68 495.93 204 1999
## total_attended             9 6948 465.13 153.72  456.0  459.11 157.16   0 1045
## school_id                 10 6948 130.49  76.62  129.0  129.21  94.89   1  319
##                         range  skew kurtosis   se
## district_id               105 -0.15    -0.92 0.37
## attended_male             597  0.40     0.08 1.03
## attended_female           483  0.42     0.12 0.85
## enrolled_male_students   1088  0.50    -0.86 3.03
## enrolled_female_students   903  0.52    -0.81 2.49
## treatment                     1  0.01    -2.00 0.01
## District Name*               26  0.02    -1.26 0.10
## total_enrolled             1795  0.49    -0.90 5.48
## total_attended             1045  0.37     0.03 1.84
## school_id                   318  0.11    -1.04 0.92
```

```
#Label values for the treatment variable appropriately (1 = Treatment, 0 = Control)
ds_sdmerger1$treatment_type <- factor(ds_sdmerger1$treatment, levels = c(0,1),
                                      labels = c("control", "treatment"))
View(ds_sdmerger1)


which(is.na(ds_sdmerger1$total_attended)) #check for missing values
```

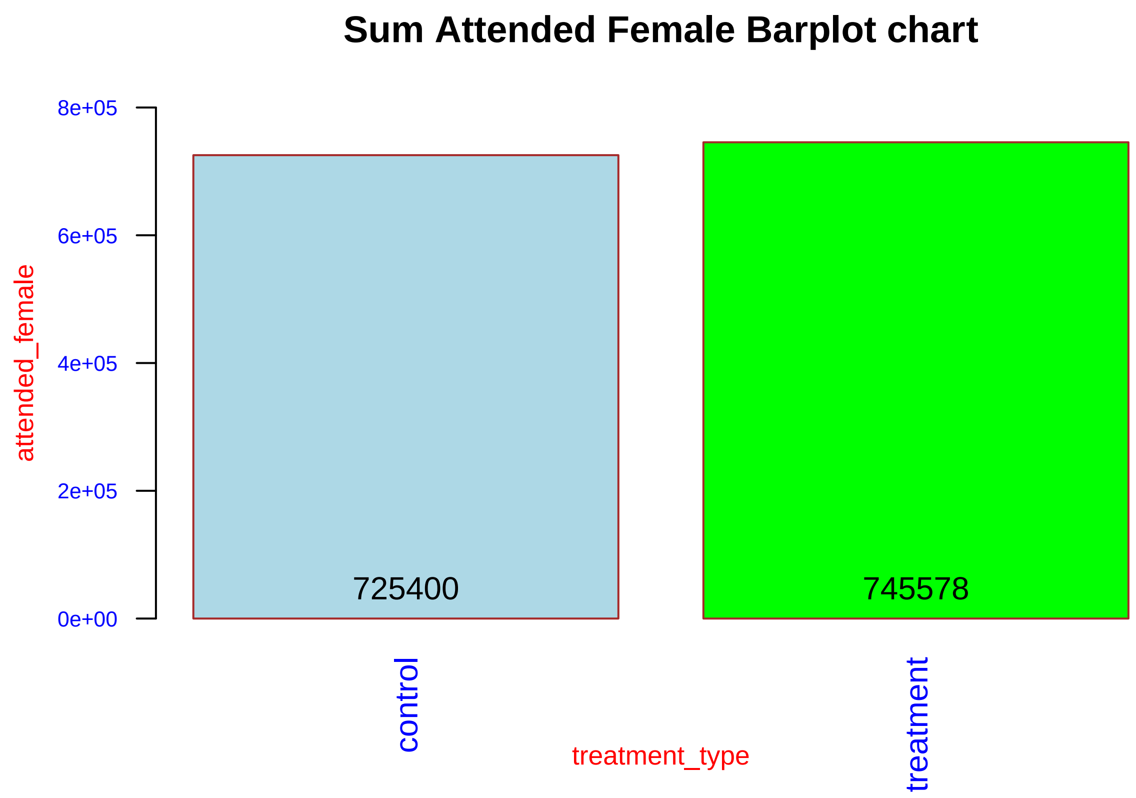
```
## integer(0)
```

```
which(!complete.cases(ds_sdmerger1))
```

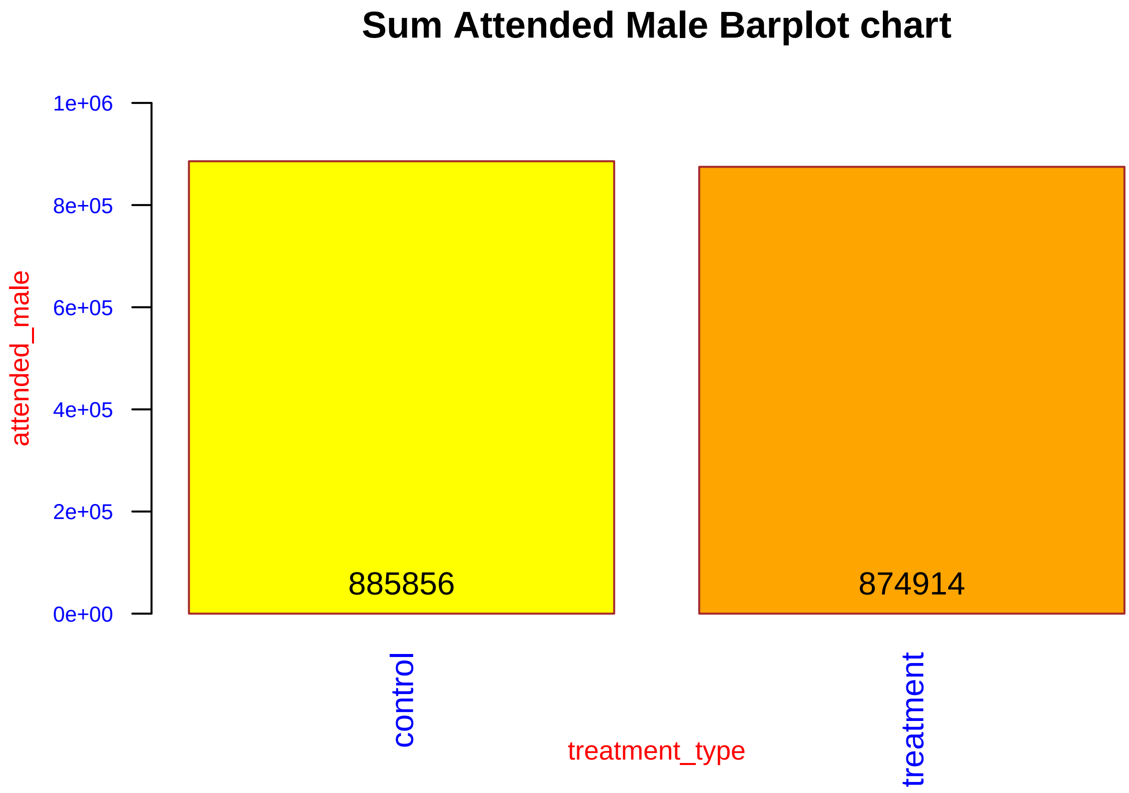
```
## integer(0)
```

Create well labelled graphs showing the difference in attendance between treatment and control schools.

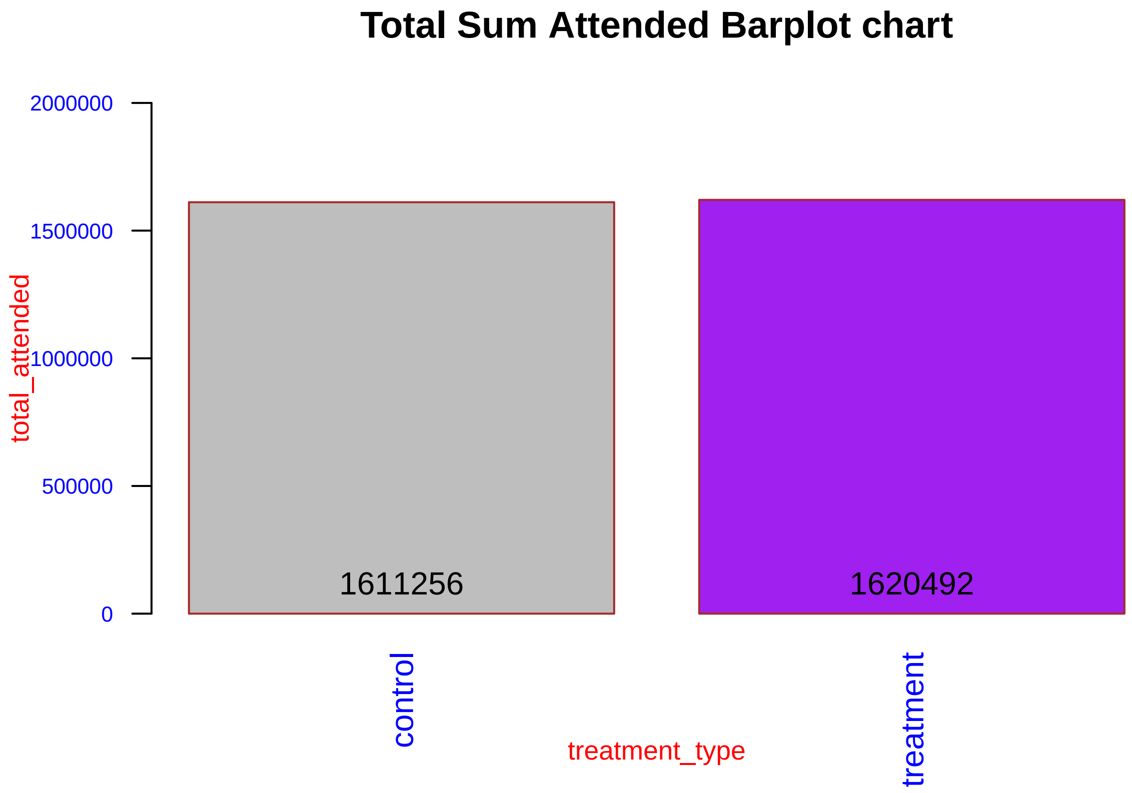
```
bp1 <- barplot(tapply(ds_sdmerger1$attended_female, ds_sdmerger1$treatment_type, FUN=sum),
    xlab="treatment_type",ylab="attended_female",col=c("lightblue", "green"),
main="Sum Attended Female Barplot chart",border="brown" , col.axis = 'blue', col.lab = 'red',
cex.axis = 0.7, cex.lab = 0.8, las = 2, ylim=c(0, 800000))
text(bp1, 0, tapply(ds_sdmerger1$attended_female, ds_sdmerger1$treatment_type, FUN=sum),
     cex=1,pos=3)
```



```
bp2 <- barplot(tapply(ds_sdmerger1$attended_male, ds_sdmerger1$treatment_type, FUN=sum),
    xlab="treatment_type",ylab="attended_male",col=c("yellow", "orange"),
    main="Sum Attended Male Barplot chart",border="brown" , col.axis = 'blue', col.lab = 'red',
    cex.axis = 0.7, cex.lab = 0.8, las = 2, ylim=c(0, 1000000))
text(bp2, 0, tapply(ds_sdmerger1$attended_male, ds_sdmerger1$treatment_type, FUN=sum),
     cex=1,pos=3)
```

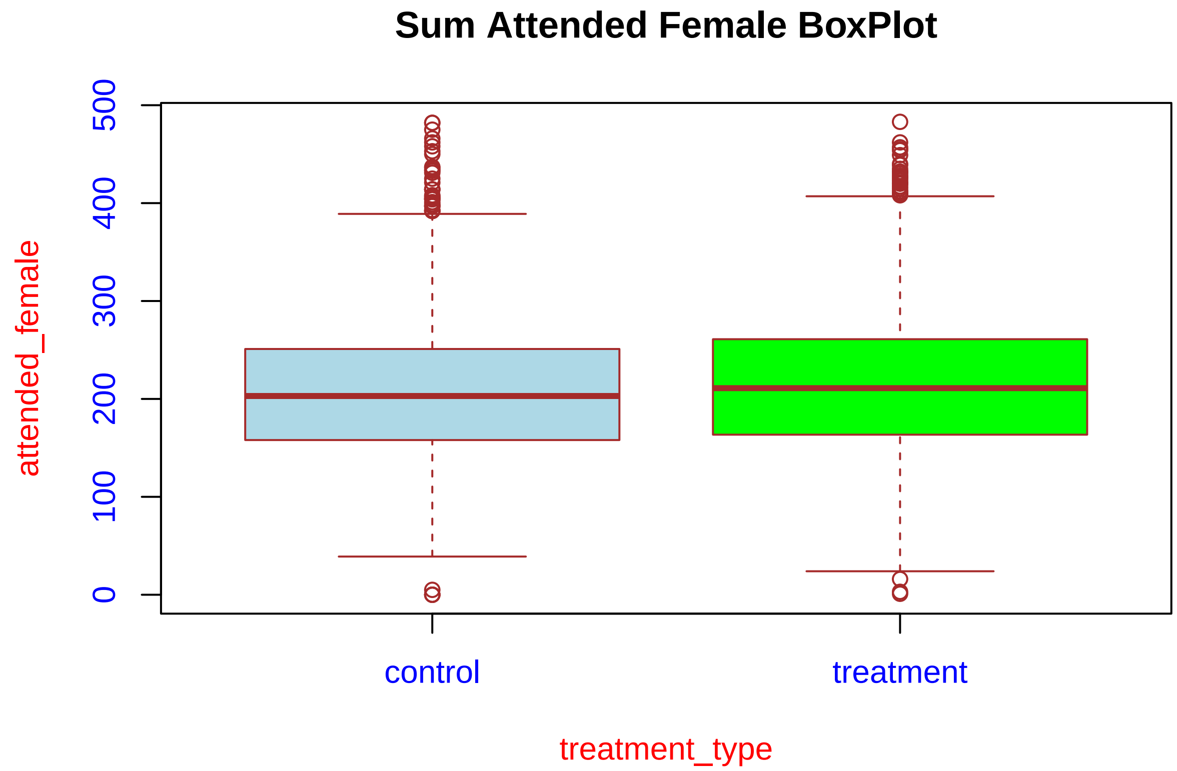


```
bp3 <- barplot(tapply(ds_sdmerger1$total_attended, ds_sdmerger1$treatment_type, FUN=sum),
      xlab="treatment_type",ylab="total_attended",col=c("grey", "purple"),
  main="Total Sum Attended Barplot chart",border="brown" , col.axis = 'blue', col.lab = 'red',
  cex.axis = 0.7, cex.lab = 0.8, las = 2, ylim=c(0, 2000000))
text(bp3, 0, tapply(ds_sdmerger1$total_attended, ds_sdmerger1$treatment_type, FUN=sum),
     cex=1,pos=3)
```

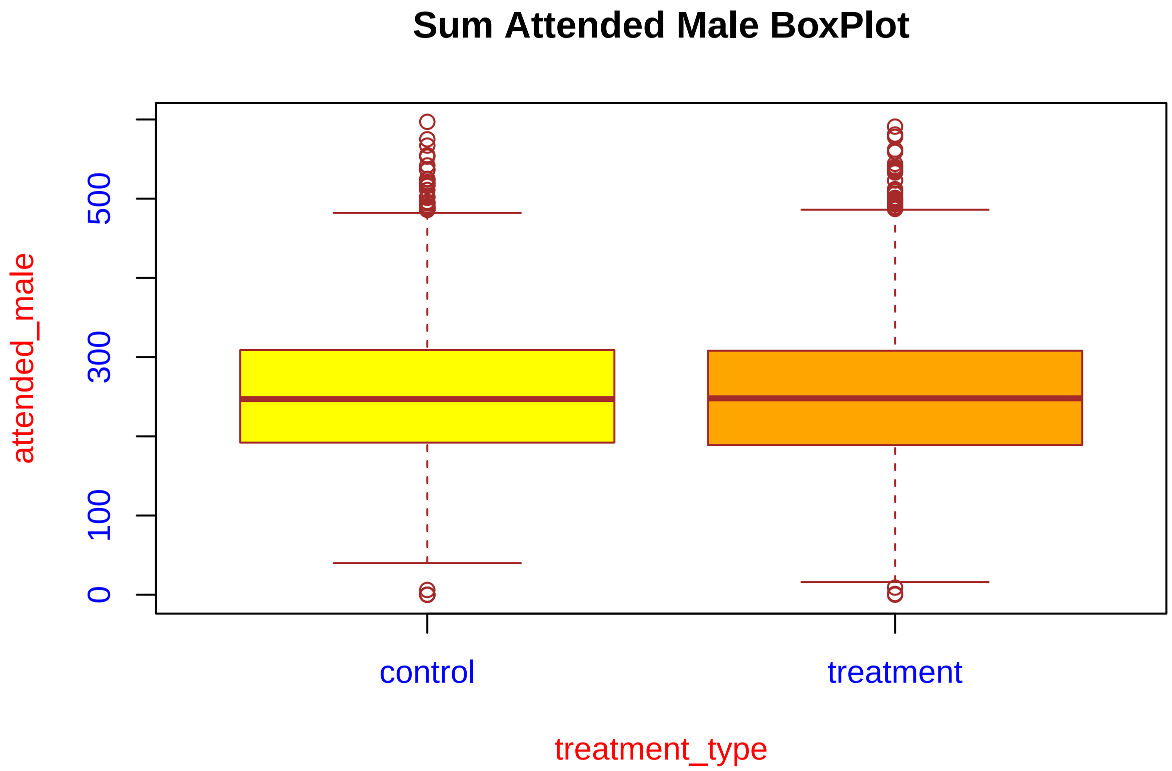


relationship between treatment_type and total_attended

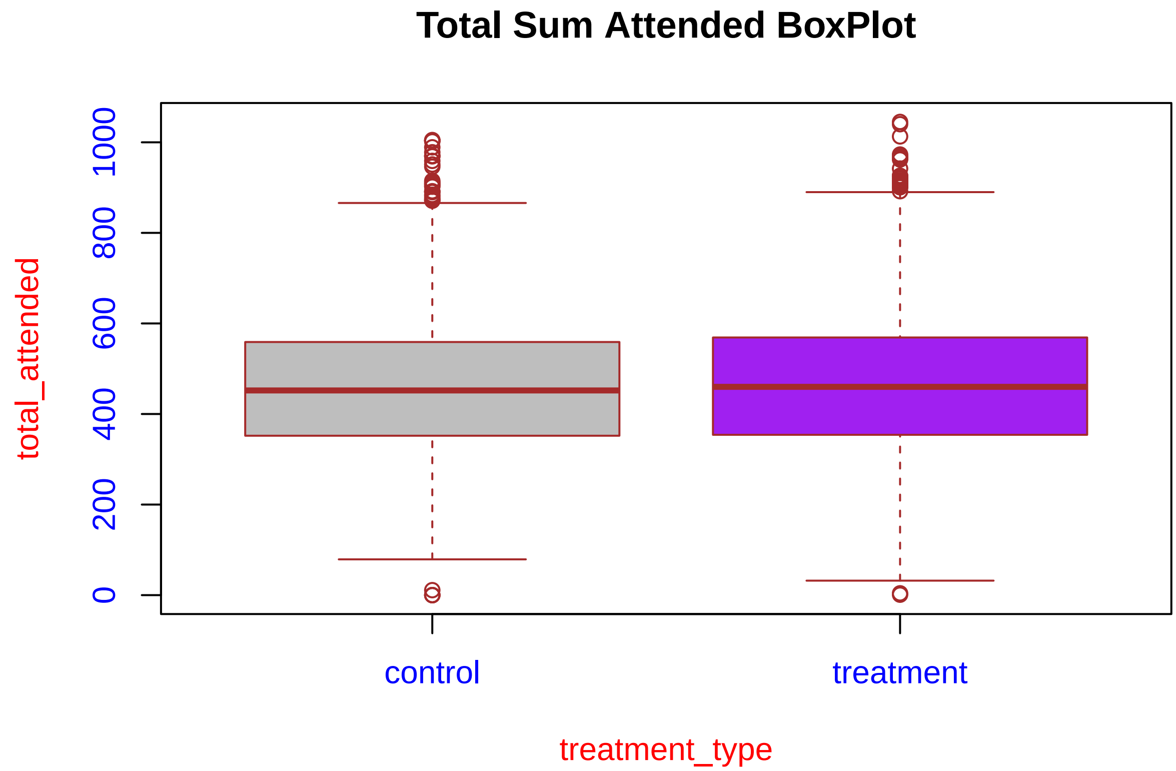
```
boxplot(attended_female ~ treatment_type,
col=c("lightblue", "green"),ds_sdmerger1,
col.axis = 'blue', col.lab = 'red', border="brown",
main="Sum Attended Female BoxPlot")
```



```
boxplot(attended_male ~ treatment_type,
col=c("yellow", "orange"),ds_sdmerger1,
col.axis = 'blue', col.lab = 'red', border="brown",
main="Sum Attended Male BoxPlot")
```



```
boxplot(total_attended ~ treatment_type,
col=c("gray","purple"),ds_sdmerger1,
col.axis = 'blue', col.lab = 'red', border="brown",
main="Total Sum Attended BoxPlot")
```



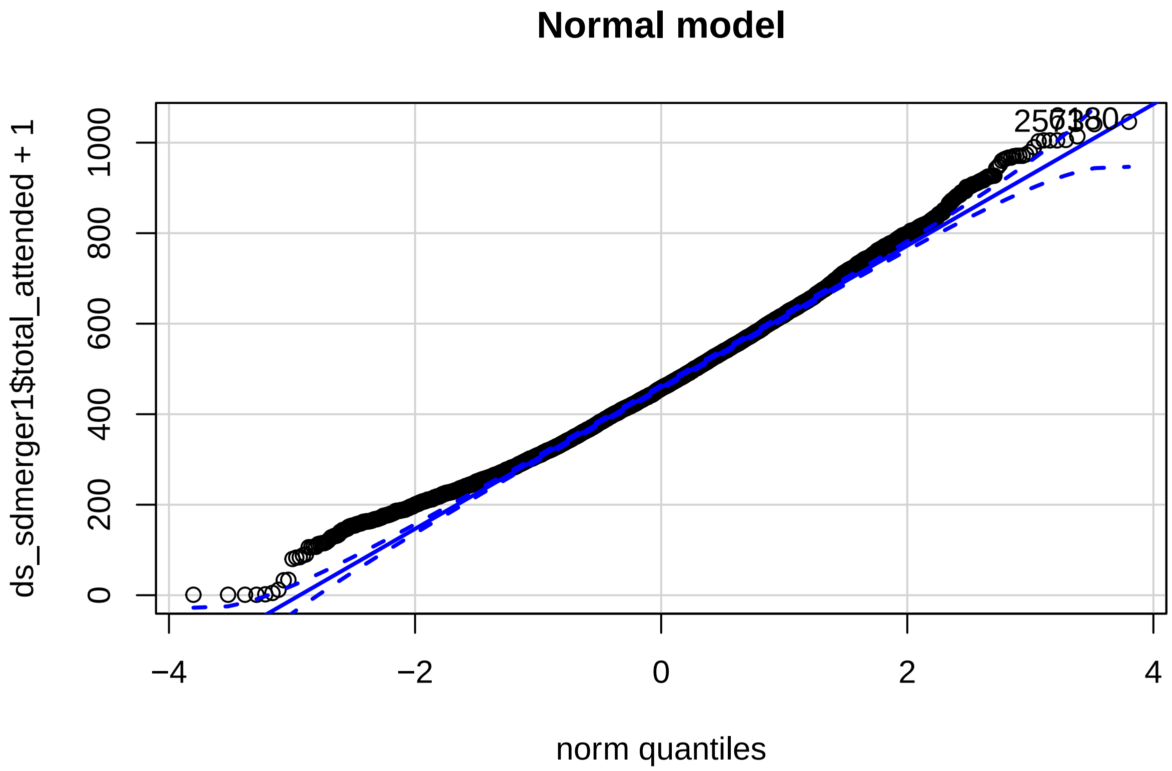
finding a fitting distribution for the total attended variable

qqp requires estimates of the parameters of the negative binomial, Poisson and gamma distributions. You can generate estimates using the fitdistr function.

Binomial and gamma distributions can only handle positive numbers. Poisson distribution can only handle positive whole numbers. Binomial and Poisson distributions are different from the others because they are discrete rather than continuous, which means they quantify distinct, countable events or the probability of these events

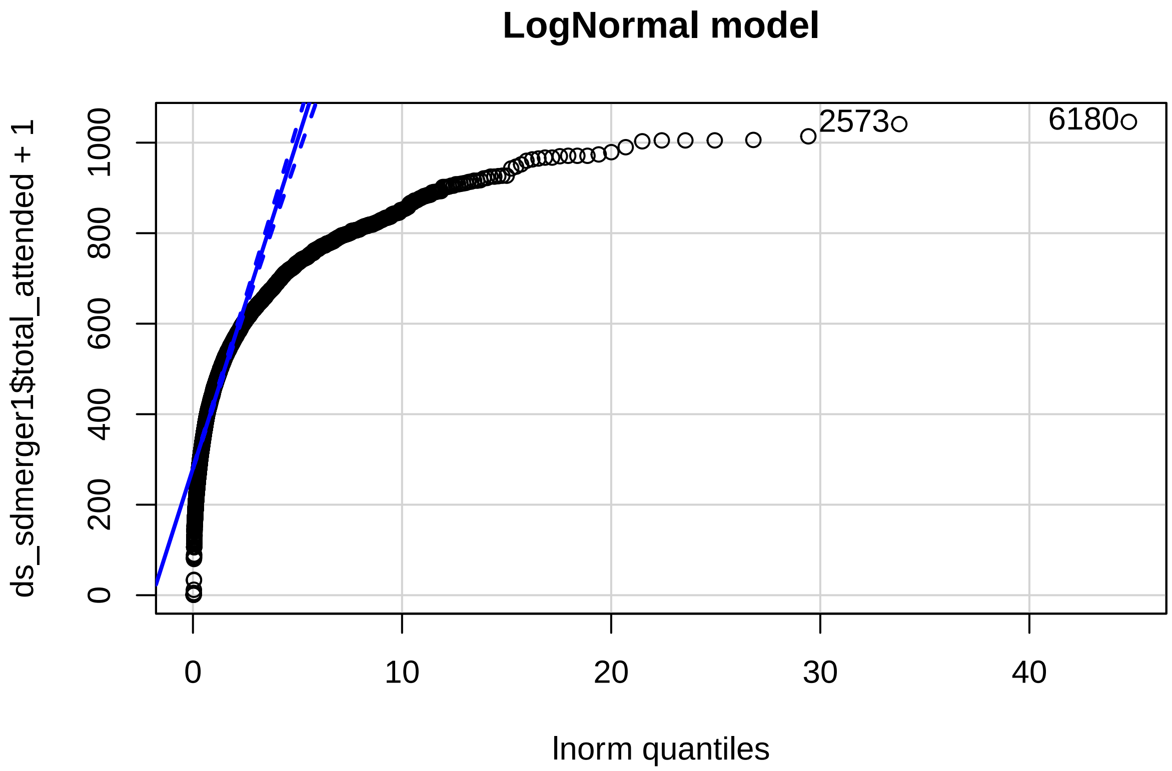
```
library(car)
library(MASS) #So that distributions that must be non-zero can make sense of my data

qqp(ds_sdmerger1$total_attended+1, "norm", main="Normal model")
```



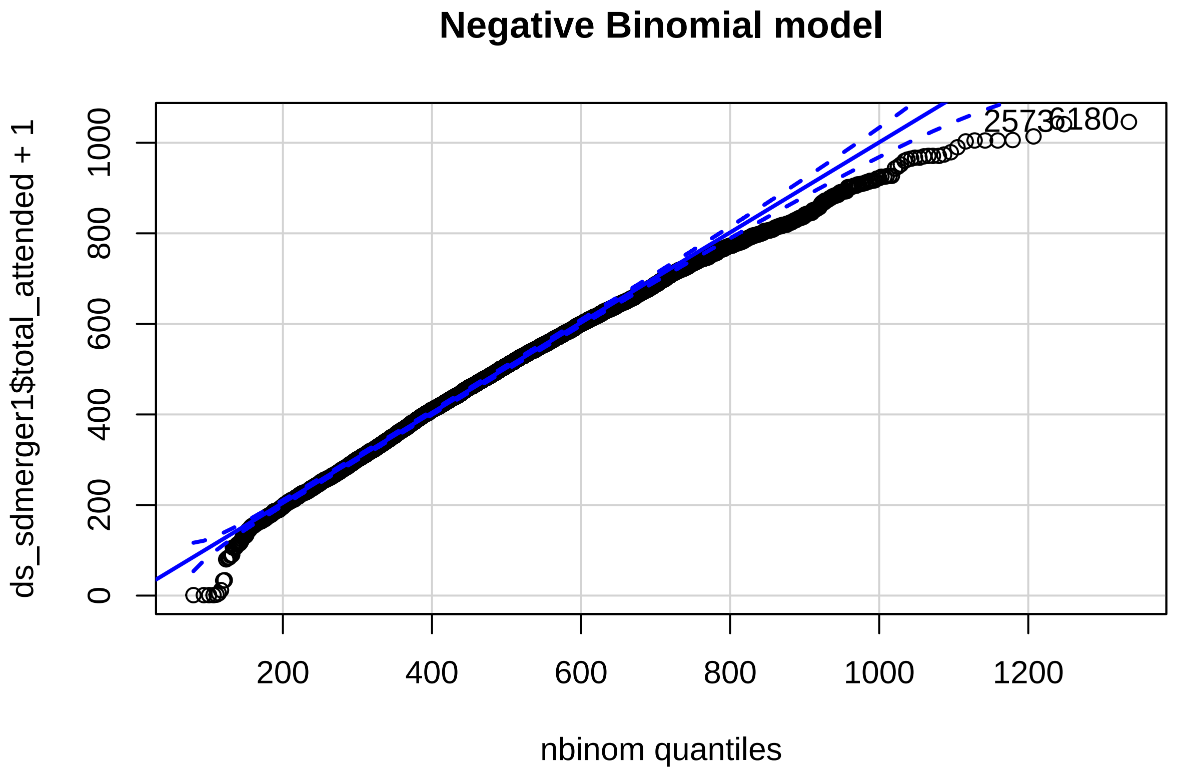
```
## [1] 6180 2573
```

```
qqp(ds_sdmerger1$total_attended+1, "lnorm", main="LogNormal model") #lnorm means lognormal
```



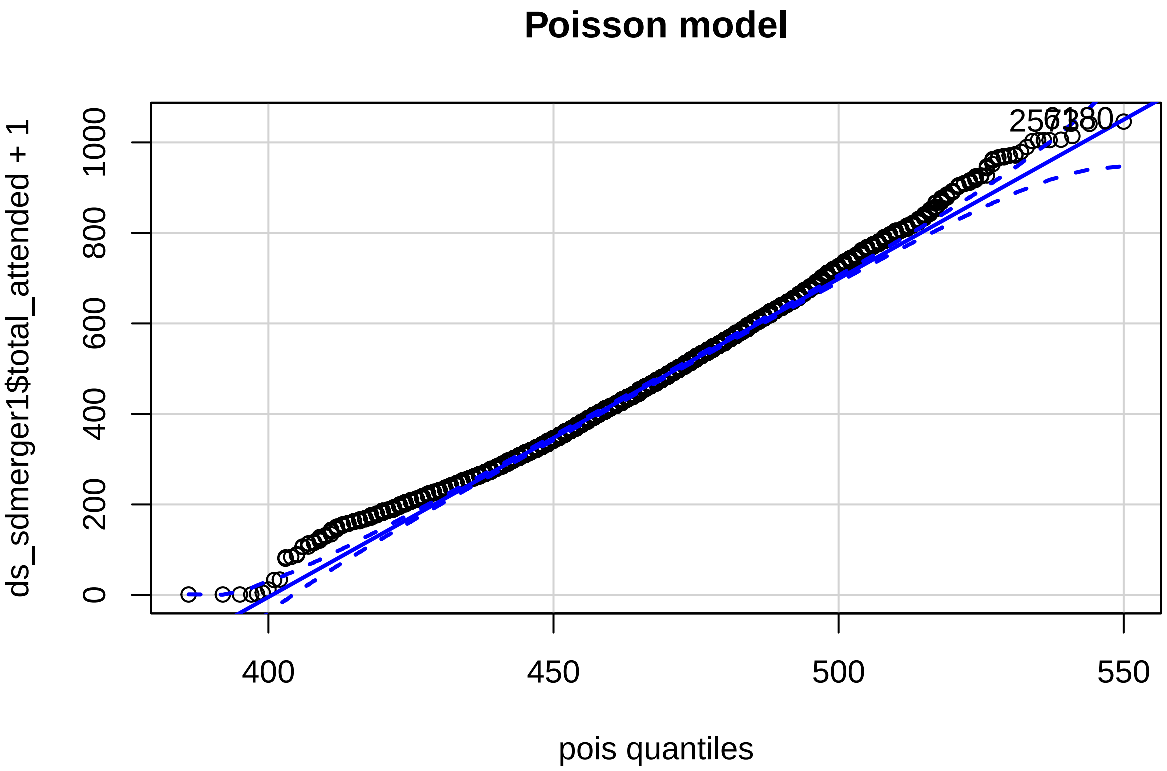
```
## [1] 6180 2573
```

```
nbinom <- fitdistr(ds_sdmerger1$total_attended+1, "Negative Binomial")
qqp(ds_sdmerger1$total_attended+1, "nbinom", size = nbinom$estimate[[1]], mu =
      nbinom$estimate[[2]], main="Negative Binomial model")
```



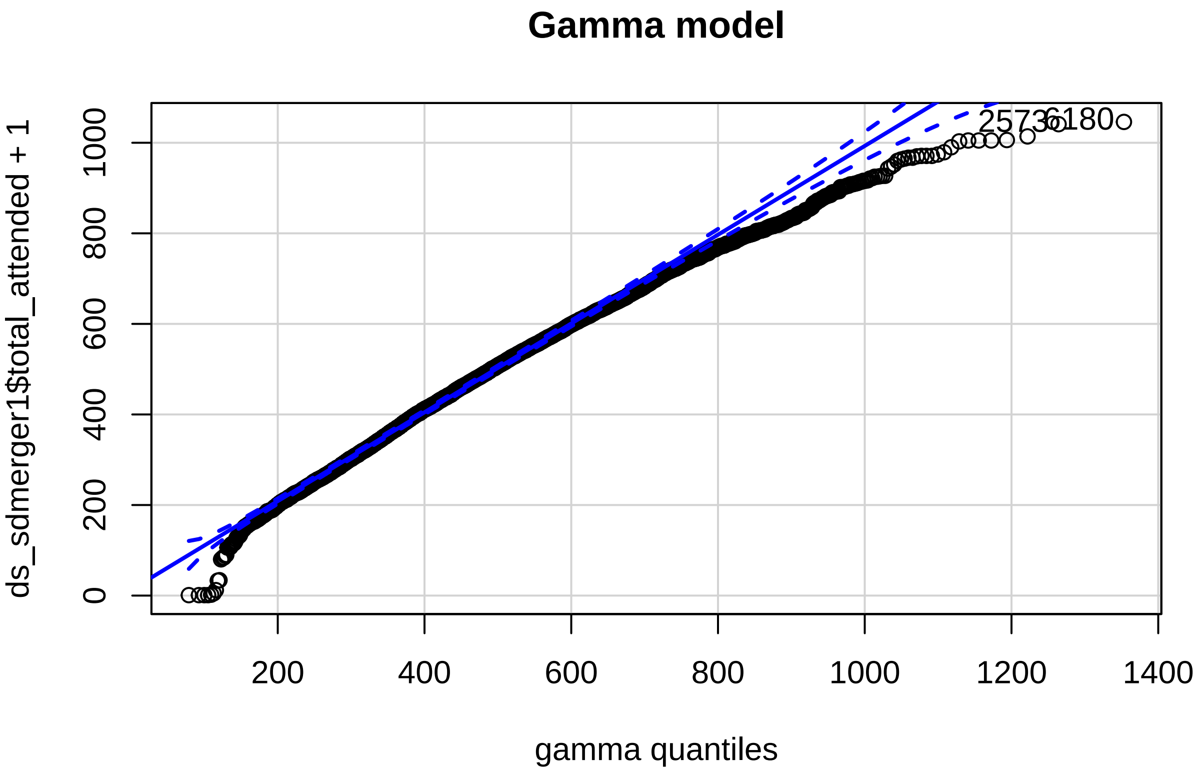
```
## [1] 6180 2573
```

```
pois <- fitdistr(ds_sdmerger1$total_attended+1, "Poisson")
qqp(ds_sdmerger1$total_attended+1, "pois", lambda=pois$estimate, main="Poisson model")
```



```
## [1] 6180 2573
```

```
gamma <- fitdistr(ds_sdmerger1$total_attended+1, "gamma")
qqp(ds_sdmerger1$total_attended+1, "gamma", shape = gamma$estimate[[1]], rate =
      gamma$estimate[[2]], main="Gamma model")
```



```
## [1] 6180 2573
```

Armed with the knowledge of which probability distribution fits best, we can try fitting a model. If data is normally distributed, we can use a linear mixed model (LMM).

linear models are "fixed-effects-only" models. They have one or more fixed effects and a general error term.

Linear Mixed Models

A mixed model is similar in many ways to a linear model. It estimates the effects of one or more explanatory variables on a response variable.

The output of a mixed model will give you a list of explanatory values, estimates and confidence intervals of their effect sizes, p-values for each effect, and at least one measure of how well the model fits.

You should use a mixed model instead of a simple linear model when you have a variable that describes your data sample as a subset of the data you could have collected.

In a mixed model, we add one or more random effects to our fixed effects. These random effects essentially give structure to the error term. this characterizes idiosyncratic variation that is due to individual differences.

load the lme4 package and make a call to the function lmer.

The first argument to the function is a formula that takes the form y ~ x1 + x2 …etc., where y is the response variable and x1, x2, etc. are explanatory variables.

Random effects are added in with the explanatory variables.

Crossed random effects take the form (1 | r1) + (1 | r2) …….while nested random effects take the form (1 | r1 / r2).

The next argument is where you designate the data frame your variables come from. This is where you can designate whether the mixed model will estimate the parameters using maximum likelihood or restricted maximum likelihood.

If your random effects are nested, or you have only one random effect, and if your data are balanced (i.e., similar sample sizes in each factor group) set REML to FALSE, because you can use maximum likelihood.

If your random effects are crossed, don't set the REML argument because it defaults to TRUE anyway.

1.We construct the null model first.

H0 (called the null hypothesis): There is no relationship between the two variables.

```
library(lme4)
library(lmerTest)

lmmtreatment.null <- lmer(total_attended ~ total_enrolled + (1 | district_id),
                          data = ds_sdmerger1, REML = FALSE)
summary(lmmtreatment.null)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: total_attended ~ total_enrolled + (1 | district_id)
##    Data: ds_sdmerger1
##
##      AIC      BIC   logLik deviance df.resid
##  88998.4  89025.8 -44495.2  88990.4     6944
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5915 -0.7191 -0.0497  0.6586  3.6938
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  district_id (Intercept)  1797     42.39
##  Residual                21121    145.33
## Number of obs: 6948, groups:  district_id, 27
##
## Fixed effects:
##                 Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    4.103e+02  9.149e+00 3.884e+01   44.84   <2e-16 ***
## total_enrolled 5.773e-02  3.825e-03 6.924e+03   15.09   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr)
## total_nrlld -0.410
```

```
anova(lmmtreatment.null)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                 Sum Sq Mean Sq NumDF DenDF F value    Pr(>F)
## total_enrolled 4811819 4811819     1  6924  227.82 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The Anova function does a Wald test, which tells us how confident we are of our estimate of the fixed effect of total enrolled on total attended, and the p-value tells us whether we should be confident or not confident at all.

```
Anova(lmmtreatment.null)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_attended
##                 Chisq Df Pr(>Chisq)
## total_enrolled 227.82  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The fixed effects for total_enrolled(0.05773, t-value=15.09) is significant, therefore, there is a linear upward trend. The average intercept is 410.3

2.we construct the full model next

H1 (called the alternative hypothesis): There exist a relationship between the two variables.

```
lmmtreatment <- lmer(total_attended ~ treatment + total_enrolled + (1 | district_id),
                          data = ds_sdmerger1, REML = FALSE)
summary(lmmtreatment)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: total_attended ~ treatment + total_enrolled + (1 | district_id)
##    Data: ds_sdmerger1
##
##      AIC      BIC   logLik deviance df.resid
##  88994.6  89028.8 -44492.3  88984.6     6943
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.6227 -0.7186 -0.0535  0.6572  3.6659
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  district_id (Intercept)  1797     42.39
##  Residual                21103    145.27
## Number of obs: 6948, groups:  district_id, 27
##
## Fixed effects:
##                 Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    4.060e+02  9.320e+00 4.184e+01  43.558   <2e-16 ***
## treatment      8.406e+00  3.486e+00 6.921e+03   2.411   0.0159 *
## total_enrolled 5.785e-02  3.823e-03 6.924e+03  15.131   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) trtmnt
## treatment   -0.191
## total_nrlld -0.405  0.014
```

```
anova(lmmtreatment)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## treatment        122696  122696     1 6920.9   5.814 0.01592 *
## total_enrolled 4831753 4831753     1 6924.0 228.955 < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(lmmtreatment)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_attended
##                  Chisq Df Pr(>Chisq)
## treatment        5.814  1     0.0159 *
## total_enrolled 228.955  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The fixed effects for total_enrolled(0.05785, t-value=15.131) and treatment(8.406, t-value=2.411) are significant, therefore, there is a linear upward trend in both. The average intercept is 406.0

```
lmmtreat <- lmer(total_attended ~ treatment + (1 | district_id),
                          data = ds_sdmerger1, REML = FALSE)
summary(lmmtreat)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: total_attended ~ treatment + (1 | district_id)
##    Data: ds_sdmerger1
##
##      AIC      BIC   logLik deviance df.resid
##  89217.8  89245.2 -44604.9  89209.8     6944
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.2597 -0.7178 -0.0352  0.6498  3.6482
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  district_id (Intercept)  1905     43.65
##  Residual                21797    147.64
## Number of obs: 6948, groups:  district_id, 27
##
## Fixed effects:
##             Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)  463.090      8.766   29.196  52.830   <2e-16 ***
## treatment      7.691      3.542 6920.905   2.171     0.03 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## treatment -0.201
```

```
anova(lmmtreat)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##           Sum Sq Mean Sq NumDF  DenDF F value  Pr(>F)
## treatment 102740  102740     1 6920.9  4.7136 0.02996 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(lmmtreat)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_attended
##            Chisq Df Pr(>Chisq)
## treatment 4.7136  1    0.02993 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The fixed effects for treatment(7.691, t-value=2.2.171) is significant, therefore, there is a linear growth trend in both. The average intercept is 463.09

The coefficient "treatment" is the slope for the categorical effect of providing meals. 7.691 means that to go from "control" to "treatment", total attendance increases by around 8 pupils. attendance is lower in control(no meals provided) than in treatment(meals provided), by about 8 pupils.

Oftentimes, model intercepts are not particularly meaningful. But this Model intercept is 463.090. If you look back at the boxplot that we constructed earlier, you can see that the value 463.090 seems to fall halfway between control and treatment(and this is indeed what this intercept represents).

It's the average of our data for the informal condition compared to the other model. With the fixed effect total enrolled added, the intercept is particularly off as we didn't inform our model that there's total enrolled in our dataset. the intercept reduces to 406. The coefficient for the effect of treatment increased to 8.406 from 7.691

If you want to interpret these results, you'll most likely need to report some kind of p-value. P-value for treatment in the models are significant(less than 0.05) and reduces from 0.02993 to 0.0159.

Unfortunately, p-values for mixed models aren't as straightforward as they are for the linear model.

Rather than getting a p-value straightforwardly from your model, we get a p-value from a comparison of two models.

3.Comparison of the models

It is useful to test whether random-effects parameters such as the variances of intercept and slope are significance or not to evaluate individual differences. This can be done by comparing the current model with a model without random intercept or slope.

Thus we focus on the Likelihood Ratio Test as a means to attain p-values. Likelihood is the probability of seeing the data you collected given your model. The logic of the likelihood ratio test is to compare the likelihood of two models with each other. First, the model without the factor that you're interested in (the null model), then the model with the factor that you're interested in.

We have two models to compare with each other: one with the effect in question, one without the effect in question. We perform the likelihood ratio test using the anova() function:

```
anova(lmmtreatment.null,lmmtreatment)
```

```
## Data: ds_sdmerger1
## Models:
## lmmtreatment.null: total_attended ~ total_enrolled + (1 | district_id)
## lmmtreatment: total_attended ~ treatment + total_enrolled + (1 | district_id)
##                    npar   AIC   BIC logLik deviance  Chisq Df Pr(>Chisq)
## lmmtreatment.null    4 88998 89026 -44495    88990
## lmmtreatment         5 88995 89029 -44492    88985 5.8116  1    0.01592 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

we compared a full model (with the fixed effects in question) against a reduced(null) model without the effects in question.

We conclude that a fixed effect treatment is significant as the difference between the likelihood of these two models is significant.

treatment(providing primary school pupils with a free meal on school days) affected total attendance (chisq.(1)=5.8116, p=0.01592), increasing it by about 8.406(8pupils) ± 3.486(3 pupils)

```
coef(lmmtreatment)
```

```
## $district_id
##     (Intercept) treatment total_enrolled
## 3      345.5238  8.405591      0.0578538
## 5      373.2582  8.405591      0.0578538
## 6      391.9255  8.405591      0.0578538
## 16     375.2961  8.405591      0.0578538
## 17     445.5645  8.405591      0.0578538
## 22     427.8311  8.405591      0.0578538
## 39     380.9146  8.405591      0.0578538
## 42     353.3708  8.405591      0.0578538
## 43     449.6900  8.405591      0.0578538
## 44     410.6224  8.405591      0.0578538
## 47     507.9889  8.405591      0.0578538
## 50     449.4153  8.405591      0.0578538
## 57     429.5080  8.405591      0.0578538
## 58     417.6187  8.405591      0.0578538
## 62     424.2424  8.405591      0.0578538
## 65     382.6116  8.405591      0.0578538
## 67     396.6649  8.405591      0.0578538
## 68     353.9196  8.405591      0.0578538
## 77     405.3434  8.405591      0.0578538
## 78     340.3057  8.405591      0.0578538
## 79     410.7081  8.405591      0.0578538
## 80     378.1203  8.405591      0.0578538
## 93     464.7975  8.405591      0.0578538
## 97     446.7653  8.405591      0.0578538
## 104    463.5627  8.405591      0.0578538
## 107    369.6693  8.405591      0.0578538
## 108    365.8604  8.405591      0.0578538
##
## attr(,"class")
## [1] "coef.mer"
```

You see that each district is assigned a different intercept given that we've told the model with "(1|district_id)" Note also that the fixed effects (treatment and total_enrolled) are all the same for all district_id. Our model is what is called a **random intercept model**.

In this model, we account for baseline-differences in total attended, but we assume that whatever the effect of treatment is, it's going to be the same for all subjects and items.

But is that a valid assumption? often times it's not – it is quite expected that some district-id would elicit more or less treatments. That is, the effect of providing meals might be different for different district-id.

4.Random slope model

Thus what we need is a random slope model, where district_id is not only allowed to have differing intercepts,but where they are also allowed to have different slopes for the effect of providing meals.

The notation "(1+treatment | district_id)" means that you tell the model to expect differing baseline-levels of (the intercept, represented by 1) as well as differing responses to the main factor which is "treatment" in this case

```
lmmtreatmentRS <- lmer(total_attended ~ treatment + total_enrolled +
        (1+treatment|district_id), data = ds_sdmerger1, REML = FALSE)
summary(lmmtreatmentRS)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use Satterthwaite's
##   method [lmerModLmerTest]
## Formula: total_attended ~ treatment + total_enrolled + (1 + treatment |
##     district_id)
##    Data: ds_sdmerger1
##
##      AIC      BIC   logLik deviance df.resid
##  88977.1  89025.0 -44481.5  88963.1     6941
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -3.5108 -0.7124 -0.0544  0.6558  3.7093
##
## Random effects:
##  Groups      Name        Variance Std.Dev. Corr
##  district_id (Intercept)  1643.7   40.54
##              treatment     578.4   24.05   0.01
##  Residual                20959.0  144.77
## Number of obs: 6948, groups:  district_id, 27
##
## Fixed effects:
##                  Estimate Std. Error        df t value Pr(>|t|)
## (Intercept)    4.061e+02  9.007e+00 3.928e+01  45.084   <2e-16 ***
## treatment      9.052e+00  5.794e+00 2.688e+01   1.562     0.13
## total_enrolled 5.743e-02  3.816e-03 6.916e+03  15.049   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) trtmnt
## treatment   -0.111
## total_nrlld -0.418  0.008
```

```
anova(lmmtreatmentRS)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##                  Sum Sq Mean Sq NumDF  DenDF  F value Pr(>F)
## treatment        51156   51156     1   26.9   2.4408 0.1299
## total_enrolled 4746576 4746576     1 6915.9 226.4700 <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Anova(lmmtreatmentRS)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: total_attended
##                   Chisq Df Pr(>Chisq)
## treatment        2.4408  1     0.1182
## total_enrolled 226.4700  1     <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The random effects for treatment is 578.4 with p-value about 0.1182. It is not significant Therefore, there is no individual difference in the (slope). This indicates that the different districts have the same treatment outcome.