Stats Exam 2016: Question 2

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Background

The good professor had developed several different kinds of traps to catch lemmings. Now he wanted to know which design was the best one. To investigate this, he puts out five traps of each kind. Every day for a whole summer, he sent out his students to empty them all and also put them in new, random, locations (to avoid catching the same lemmings all over again). At the end of the summer each trap had caught a number of lemmings, according to the data in file "lemmingtraps" (.sav and .csv). The first variable is just trap id. The variable type is the type of trap, numbered 1 through 4. Finally, catch gives the total number of caught lemmings in each trap. Note: Even though the catch data are counts, and therefore discrete, you can regard them as continuous here.

Analyses of variances ANOVA should be conducted to answer questions based on the experiment setup. In this particular case One-way ANOVA, which analyses the differences of variances between groups (for different types of traps) and within groups (for same type of trap) should be sufficient. Also this is Model I ANOVA, because factor is fixed, not randomly chosen from many other levels (types of traps).

```
traps <- read.csv('~/Documents/courses/stats/Exam/lemmingtraps.csv', sep=';')
str(traps)
```

```
## 'data.frame':    20 obs. of  3 variables:
##  $ id   : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ type : Factor w/ 4 levels "type1","type2",..: 1 1 1 1 1 2 2 2 2 2 ...
##  $ catch: int  51 45 42 41 49 32 40 38 23 30 ...
```

Data is fine - trap type is a factor, no missing data. The analyses can be started.

Sub-question a)

Is there a difference between the trap designs, in terms of catching lemmings?

One-way ANOVA, model I test

```
aov.traps <- aov(traps$catch~traps$type)
summary(aov.traps)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## traps$type   3  641.2  213.73   6.607 0.0041 **
## Residuals   16  517.6   32.35
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The difference between types of traps is significant: p-value - 0.0041

Sub-question b)

Make a suitable illustration of your result in a)

Required illustrations of results:
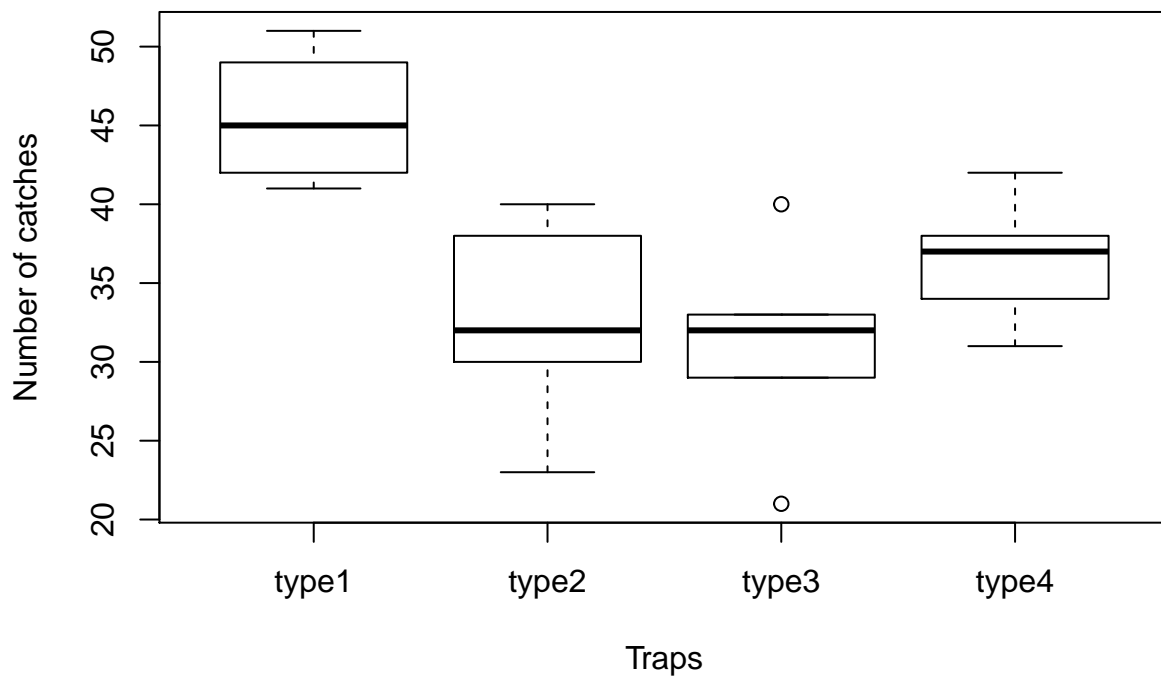
- box-plot of data
- error plot
- confidence intervals plot

```
boxplot(traps$catch~traps$type, ylab='Number of catches', xlab='Traps')

library(Rmisc)
```

```
## Loading required package: lattice
```

```
## Loading required package: plyr
```



```
mean.ci.se <- summarySE(traps, 'catch', 'type', na.rm = TRUE)
mean.ci.se
```

```
##     type N catch       sd       se       ci
## 1 type1 5  45.6 4.335897 1.939072 5.383727
## 2 type2 5  32.6 6.767570 3.026549 8.403048
## 3 type3 5  31.0 6.892024 3.082207 8.557579
## 4 type4 5  36.4 4.159327 1.860108 5.164486
```

```r
library(Hmisc)
```

```
## Loading required package: survival

## Loading required package: Formula

## Loading required package: ggplot2

##
## Attaching package: 'Hmisc'

## The following objects are masked from 'package:plyr':
##
##     is.discrete, summarize

## The following objects are masked from 'package:base':
##
##     format.pval, round.POSIXt, trunc.POSIXt, units
```
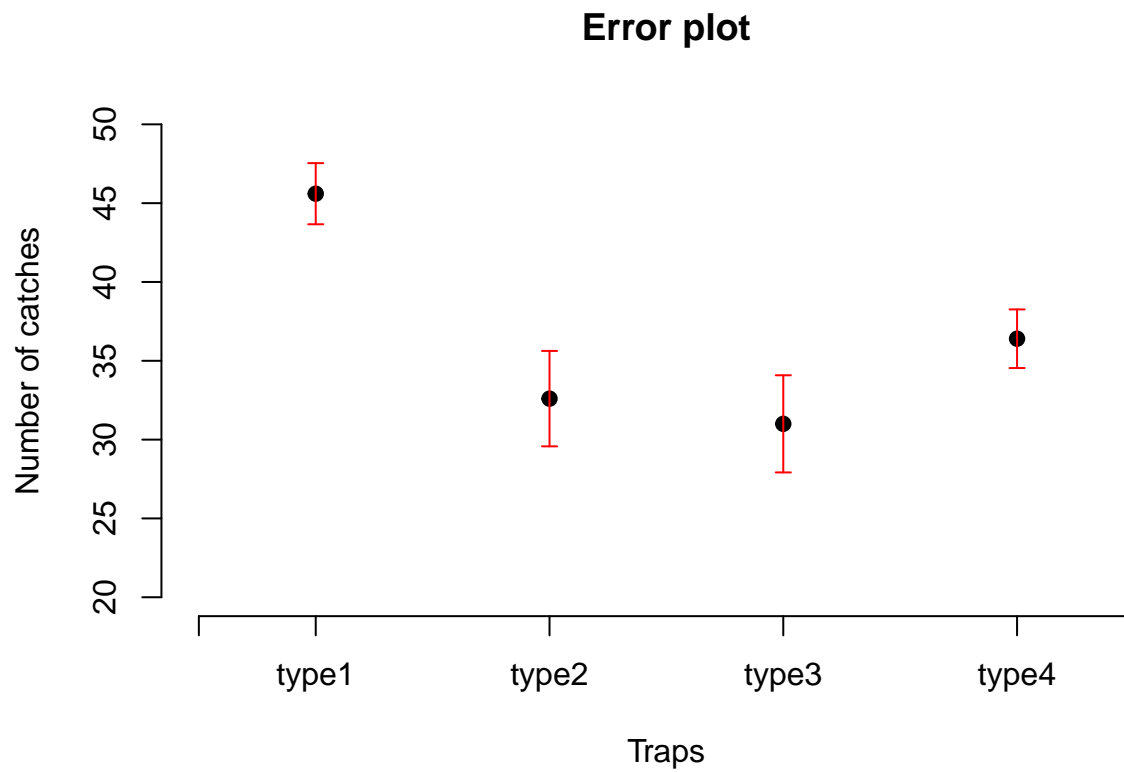
```r
x <- c(1:4)
plot(x,mean.ci.se[,3], type='p', xlim=c(0.5,4.5),
     xlab='Traps', ylim=c(20,50), main='Error plot',
     ylab='Number of catches', axes = FALSE)
axis(1, at=c(0.5,1,2,3,4,4.5), labels=c('','type1','type2','type3','type4',''))
axis(2, at=seq(20,50,5))
errbar(x, mean.ci.se[,3], mean.ci.se[,3] + mean.ci.se[,5],
       mean.ci.se[,3] - mean.ci.se[,5], add=TRUE,
       errbar.col='red')
```
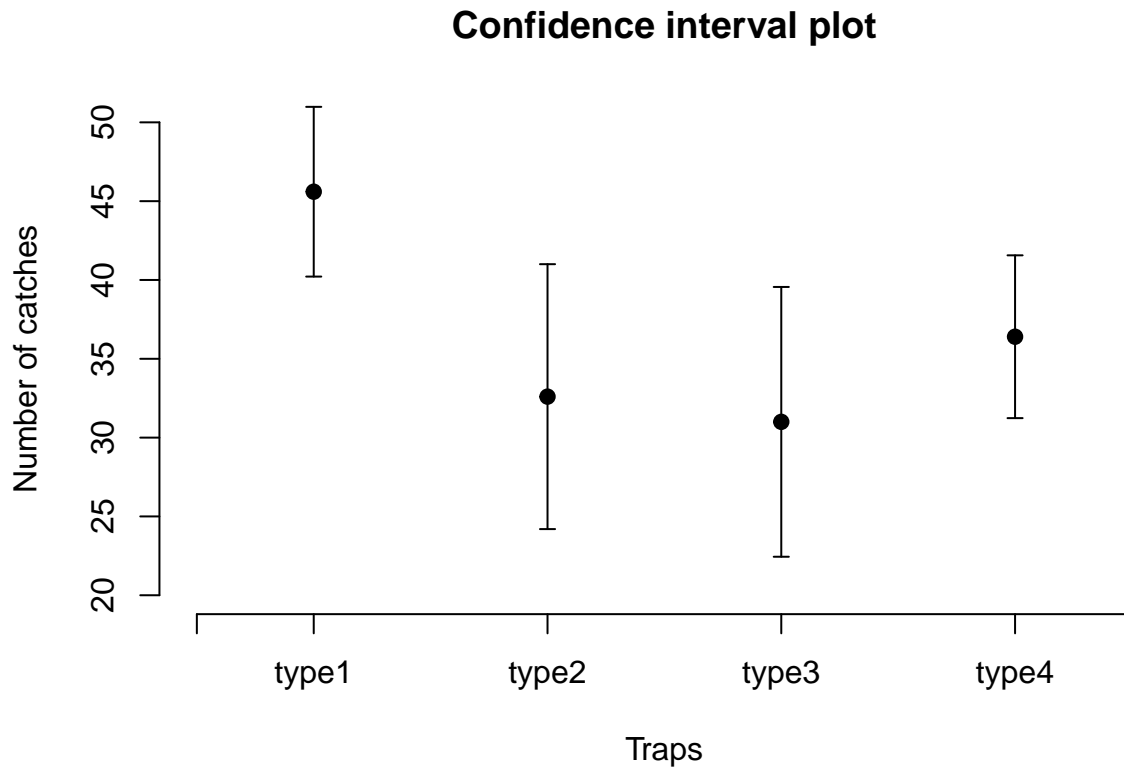
Error plot


```
plot(x,mean.ci.se[,3], type='p', xlim=c(0.5,4.5),
     xlab='Traps', ylim=c(20,50), main='Confidence interval plot',
     ylab='Number of catches', axes = FALSE)
axis(1, at=c(0.5,1,2,3,4,4.5), labels=c('','type1','type2','type3','type4',''))
axis(2, at=seq(20,50,5))
errbar(x, mean.ci.se[,3], mean.ci.se[,3] + mean.ci.se[,6],
       mean.ci.se[,3] - mean.ci.se[,6], add=TRUE)
```

Confidence interval plot

Based on the graphs built, it is seen that there are differences between trap types. The most helpful ones were error and confident intervals plots, they show that the main contributor to "between group variance" is type1. Type2 and type3 are not really different and are the worst ones. Type4 is slightly better than 2 and 4, though it is not that clear if this is significant (based on confidence interval plot).

Sub-question c)

The professor suspected beforehand that trap design number 1 was superior to the rest. Was he correct?

This hypothesis is supported based on graphs above, but numerical statistical significance of type1 traps over the others also can be calculated.

```
lm.traps <- lm(traps$catch~traps$type)
summary(lm.traps)
```

```
##
## Call:
## lm(formula = traps$catch ~ traps$type)
##
## Residuals:
##    Min    1Q Median    3Q    Max
## -10.00  -2.85   0.00   3.90   9.00
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)       45.600       2.544  17.927 5.13e-12 ***
## traps$typetype2  -13.000       3.597  -3.614 0.002330 **
## traps$typetype3  -14.600       3.597  -4.059 0.000912 ***
## traps$typetype4   -9.200       3.597  -2.558 0.021080 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 5.688 on 16 degrees of freedom
## Multiple R-squared:  0.5533, Adjusted R-squared:  0.4696
## F-statistic: 6.607 on 3 and 16 DF,  p-value: 0.004105
```

The output shows that all other 3 types in comparison to the first type are significantly different, in our case significantly worse than type1 trap. So professor was right - **trap with design 1 is superior to the rest**.

Sub-question d)

Test the assumptions of your test in a)

List of the assumptions to be tested:

- **normality**. Test either normality of residuals or normality within each group. Since size of each group is only 5 entries, it is best to go with test for normality of residuals (histogram of residuals, Shapiro-Wilk normality test, Q-Q Plot).
- **homogeneity of variances** - Levene's Test for Homogeneity of Variance
- **independence** - test of null-hypothesis that the control group is identical to all other groups. Since it is already obvious that first group is most different from other groups *planned comparison* can be used here (no need for post-hoc) based on contrasts (dummy coding procedure in R for contrasts).

```r
traps$resid <- residuals(lm.traps)
aveH <- hist(traps$resid, breaks=10, main = 'Normality of residuals')
xfit <- seq(min(traps$resid),max(traps$resid),length=100)
yfit <- dnorm(xfit,mean=mean(traps$resid),sd=sd(traps$resid))
yfit <- yfit*diff(aveH$mids[1:2])*length(traps$resid)
lines(xfit,yfit, col='blue', lwd=2)
```
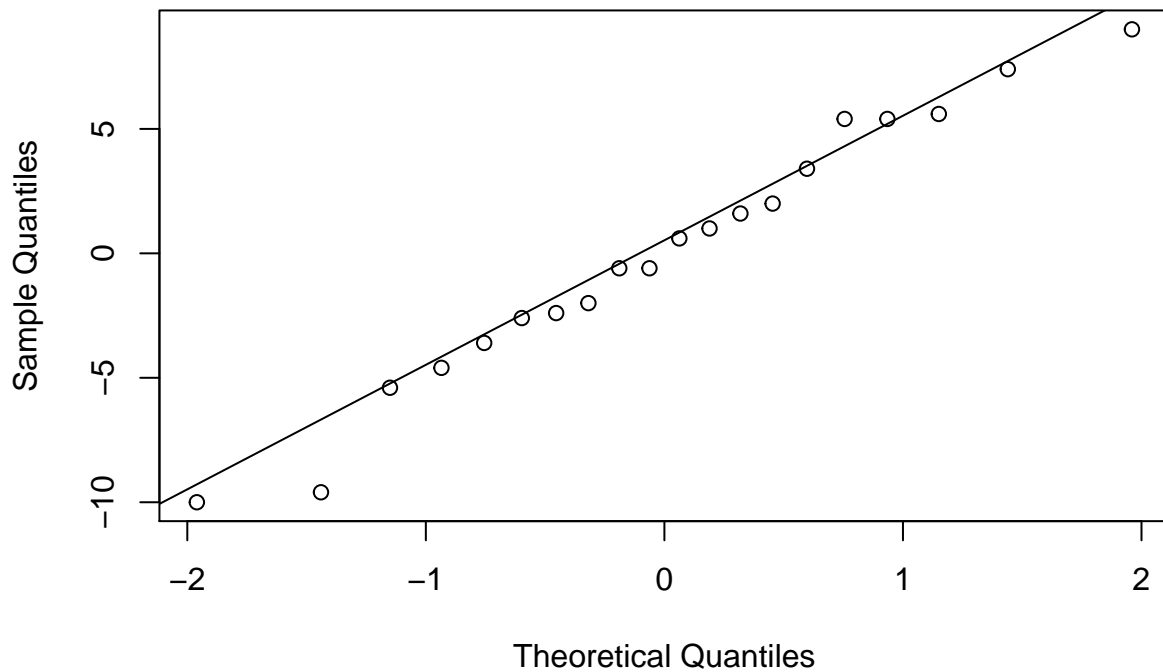
Normality of residuals
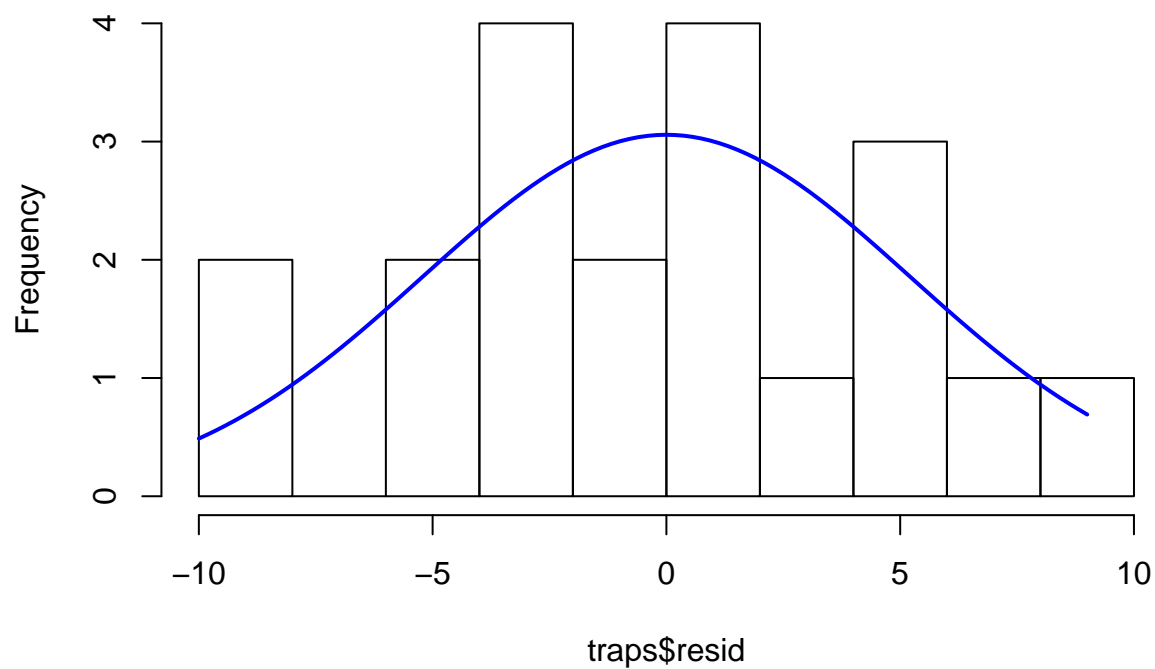

```
shapiro.test(traps$resid)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  traps$resid
## W = 0.97511, p-value = 0.8568
```

```
qqnorm(traps$resid)
qqline(traps$resid)
```

Normal Q–Q Plot


```
library(car)
leveneTest(traps$catch,traps$type)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  0.3731 0.7735
##       16
```

```
contrasts.type1 <- matrix(0, ncol=3,nrow=4)
contrasts.type1[2:4,1] <- 1
contrasts.type1
```

```
##      [,1] [,2] [,3]
## [1,]    0    0    0
## [2,]    1    0    0
## [3,]    1    0    0
## [4,]    1    0    0
```

```
contrasts(traps$type) <- contrasts.type1
summary.lm(aov(traps$catch~traps$type))
```

```
##
## Call:
## aov(formula = traps$catch ~ traps$type)
```

```
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -12.3333  -3.4000  -0.4667   4.6667   8.6667
## 
## Coefficients: (2 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    45.600      2.570  17.742 7.54e-13 ***
## traps$type1   -12.267      2.968  -4.133 0.000624 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 5.747 on 18 degrees of freedom
## Multiple R-squared:  0.4869, Adjusted R-squared:  0.4584
## F-statistic: 17.08 on 1 and 18 DF,  p-value: 0.0006243
```

Conclusions:

- Residuals are normally distributed - the histogram is not that nice, but Shapiro-Wilk normality test is not significant (p-value > 20%) so distribution or residuals is close to normal. Q-Q plot support almost-normal distribution.
- Variances are homogeneitic, since p-value in Levene's Test is very high - null-hypothesis is not rejected.
- The independence assumption was also confirmed based on tests with contrast to type1 trap. The p-value is 0.0006243 so null-hypothesis that control group is identical to all other groups should be rejected.

All ANOVA assumptions were confirmed by the set of tests, so as overall conclusion that trap with design #1 is significantly better than other designs.