Assignment 4

Tommy Maaiveld, Krishnakanth Sasi, Halil Kaan Kara, Group 6

Introduction

Question 1

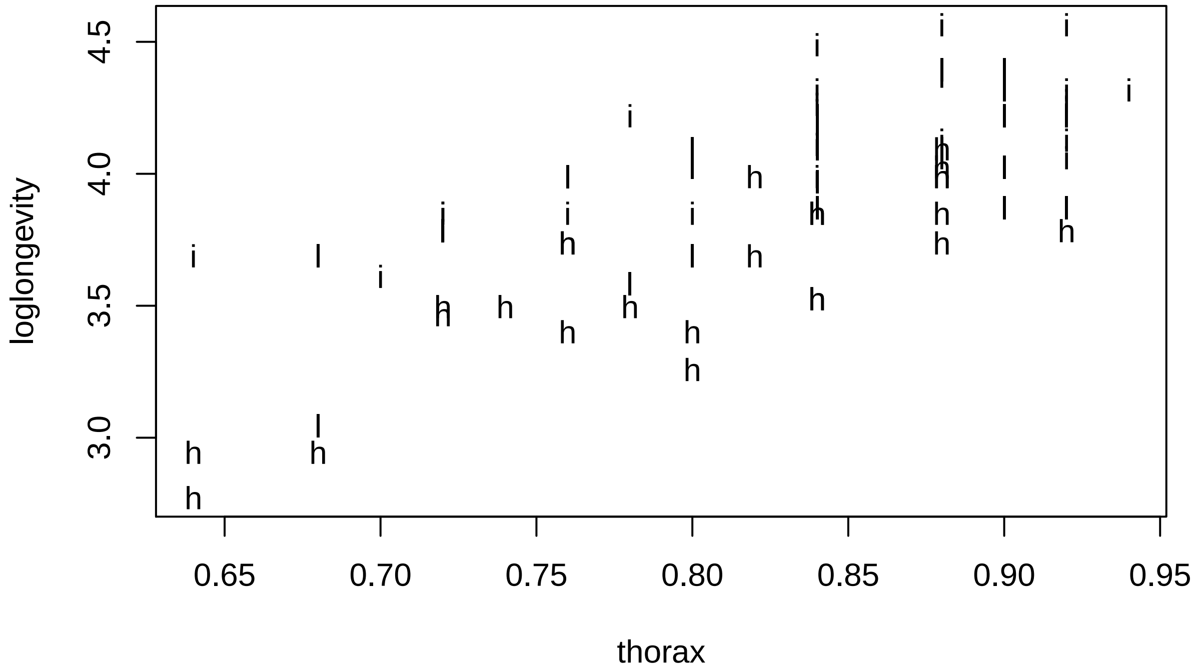
Section 1

```
fruitflies = read.table(file="data/fruitflies.txt", header=TRUE)
fruitflies = cbind(fruitflies, log(fruitflies[,2]))
names(fruitflies)[4] = "loglongevity"
head(fruitflies,6) # some output deleted
```

```
##   thorax longevity activity loglongevity
## 1   0.64        40 isolated     3.688879
## 2   0.70        37 isolated     3.610918
## 3   0.72        44 isolated     3.784190
## 4   0.72        47 isolated     3.850148
## 5   0.72        47 isolated     3.850148
## 6   0.76        47 isolated     3.850148
```

Section 2

```
attach(fruitflies)
plot(loglongevity~thorax,pch=as.character(activity))
```



The plot shows a linear correlation between thoractic length (`thorax`) and log longevity. It seems to indicate that flies with the `activity` factor set to `high` live shorter than those with `low`, which in turn score lower than those with `isolated`, assuming equal thoractic length between specimens.

Section 3

```
fruitfliesaov = lm(loglongevity~activity, data=fruitflies)
attach(fruitfliesaov)
anova(fruitfliesaov)
```

```
## Analysis of Variance Table
##
## Response: loglongevity
##           Df Sum Sq Mean Sq F value    Pr(>F)
## activity   2 3.6665  1.8333  19.421 1.798e-07 ***
## Residuals 72 6.7966  0.0944
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

According to this analysis, `activity` seems likely to have an effect on `loglongevity`, since the p-value < 0.05 (p-value $\approx 1.8 \times 10^{-7}$). Thus, sexual activity seems to influence longevity.

Section 4

the analysis shows that sexual activity decreases longevity in fruitflies, since the `activity` factor affects `loglongevity`.

```r
summary(fruitfliesaov)
```

```
##
## Call:
## lm(formula = loglongevity ~ activity, data = fruitflies)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.95531 -0.13338  0.02552  0.20891  0.49222
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)        3.60212    0.06145  58.621  < 2e-16 ***
## activityisolated   0.51722    0.08690   5.952 8.82e-08 ***
## activitylow        0.39771    0.08690   4.577 1.93e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3072 on 72 degrees of freedom
## Multiple R-squared:  0.3504, Adjusted R-squared:  0.3324
## F-statistic: 19.42 on 2 and 72 DF,  p-value: 1.798e-07
```

could recheck these means by doing visual to check if they are valid... Not sure if I interpreted estimates right from the slide

the longevity estimates for each level of the factor `activity` are 3.6021243 for fruitflies of level `high`, 3.9998359 for fruitflies of level `low`, and 4.1193489 for fruitflies of level `isolated`. As sexual activity increases, lifespan decreases.

Section 5

```r
fruitfliesfullaov = lm(loglongevity~thorax+activity, data=fruitflies)
attach(fruitfliesfullaov)
```

```
## The following objects are masked from fruitfliesaov:
##
##     assign, call, coefficients, contrasts, df.residual, effects,
##     fitted.values, model, qr, rank, residuals, terms, xlevels
```

```r
anova(fruitfliesfullaov)
```

```
## Analysis of Variance Table
##
```

```
## Response: loglongevity
##           Df Sum Sq Mean Sq F value Pr(>F)
## thorax     1 5.4322  5.4322 132.175 <2e-16 ***
## activity   2 2.1129  1.0565  25.705  4e-09 ***
## Residuals 71 2.9180  0.0411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(fruitfliesfullaov)$coef
```

```
##                   Estimate Std. Error  t value     Pr(>|t|)
## (Intercept)      1.2189341 0.24864843 4.902239 5.787723e-06
## thorax           2.9789877 0.30665052 9.714602 1.138552e-14
## activityisolated 0.4099810 0.05839296 7.021070 1.074333e-09
## activitylow      0.2857017 0.05848770 4.884817 6.183669e-06
```

The output gives the following rounded estimates for the model coefficients μ, β α_1 and α_2:
$\mu = 1.219$
$\beta = 2.979$
$\alpha_1 = 0.286$
$\alpha_2 = 0.41$
Where mu is the estimate for an average fly with high sexual activity, beta is the parameters The p-values are all virtually zero, meaning there is almost no risk of a type I error. Sexual activity is very likely to influence longevity, regardless of whether thorax length is taken into account.

Section 6

Sexual activity decreases longevity, since the estimate is lowest for flies with high sexual activity, and highest for isolated flies.

```
mean(fruitflies[,1])
```

```
## [1] 0.8245333
```

```
min(fruitflies[,1])
```

```
## [1] 0.64
```

For an average fly with a thorax length ≈ 0.82, the value for parameter β given above can be used in a sum to compute all three estimates for loglongevity based on variable X_{avg}:

$\mu + \beta * X_{avg} = 1.219 + 2.979 * 0.82 = 3.675$ (high sexual activity)

$\mu + \beta * X_{avg} + \alpha_1 = 1.219 + 2.979 * 0.82 + 0.286 = 3.961$ (low sexual activity)

$\mu + \beta * X_{avg} + \alpha_2 = 1.219 + 2.979 * 0.82 + 0.41 = 4.085$ (isolated specimen)

In order to compute the estimates for a fly as small as the smallest fly in the dataset, the term X is substituted with X_{min}, the thorax size of the smallest fly in the dataset (0.64).

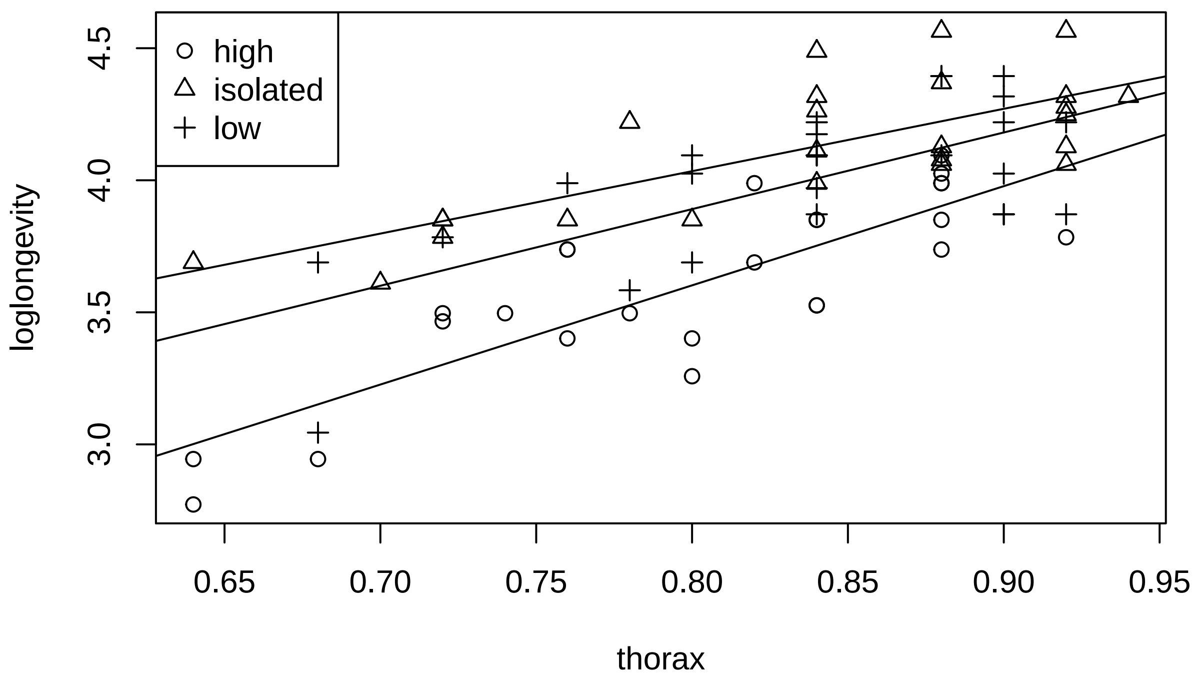
$\mu + \beta * X_{min} = 1.219 + 2.979 * 0.64 = 3.125$ (high sexual activity)

$\mu + \beta * X_{min} + \alpha_1 = 1.219 + 2.979 * 0.64 + 0.286 = 3.411$ (low sexual activity)

$\mu + \beta * X_{min} + \alpha_2 = 1.219 + 2.979 * 0.64 + 0.41 = 3.535$ (isolated specimen)

Section 7

```
plot(loglongevity~thorax,pch=unclass(activity))
for (i in c("high", "low", "isolated")) abline(lm(loglongevity~thorax,data=fruitflies[fruitflies$activi
legend('topleft',legend=levels(fruitflies$activity),pch=1:3)
```



The given plot shows fit lines for each level of the `activity` factor. Thorax length correlates positively with longevity (bigger flies live longer), meaning β is expected to be nonzero. The fit lines in the plot converge slightly, although the true lines could still be parallel. In other words, the parameter β is similar for each factor level, meaning the dependence on thorax length is similar on each level. This means that the lifespan of a given fruitfly is affected by its sexual activity, regardless of its size, and bigger flies live longer within each factor level. The slight convergence could be interpreted as bigger flies being more 'resistant' to the detrimental effect of sexual activity on longevity, since there is a more pronounced difference in `loglongevity` for small flies compared to large ones visible in the plot.

Section 8

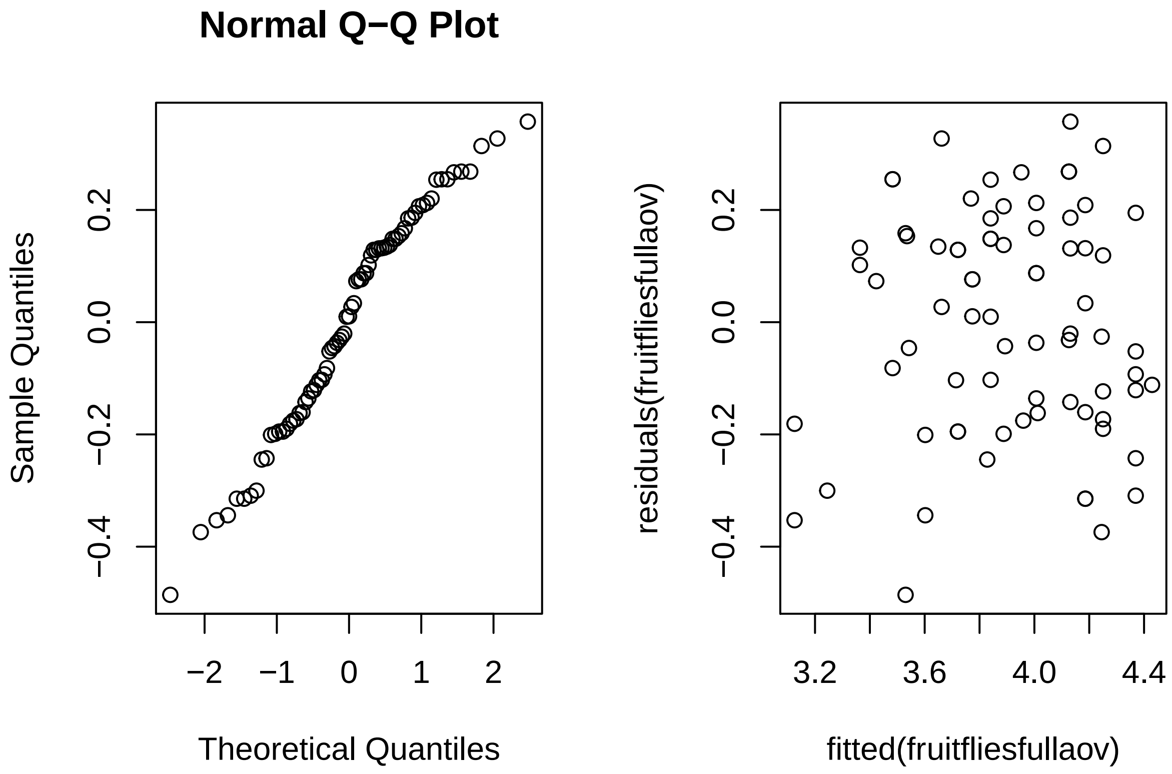
```
drop1(fruitfliesfullaov,test="F")
```

```
## Single term deletions
##
## Model:
```

```
## loglongevity ~ thorax + activity
##          Df Sum of Sq    RSS     AIC F value    Pr(>F)
## <none>                2.9180 -235.50
## thorax    1    3.8786 6.7966 -174.08  94.374 1.139e-14 ***
## activity  2    2.1129 5.0309 -198.64  25.705 4.000e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Section 9

```
par(mfrow=c(1,2))
qqnorm(residuals(fruitfliesfullaov))
plot(fitted(fruitfliesfullaov),residuals(fruitfliesfullaov))
```



The assumption of normality does not seem to be violated, and the data appears reasonably homoskedastic - the variance of the residuals does not increase greatly for higher fitted values.

Section 10

```
ffnonlogaov = lm(longevity~thorax+activity, data=fruitflies)
attach(ffnonlogaov)
```

```
## The following objects are masked from fruitfliesfullaov:
##
##     assign, call, coefficients, contrasts, df.residual, effects,
##     fitted.values, model, qr, rank, residuals, terms, xlevels

## The following objects are masked from fruitfliesaov:
##
##     assign, call, coefficients, contrasts, df.residual, effects,
##     fitted.values, model, qr, rank, residuals, terms, xlevels
```

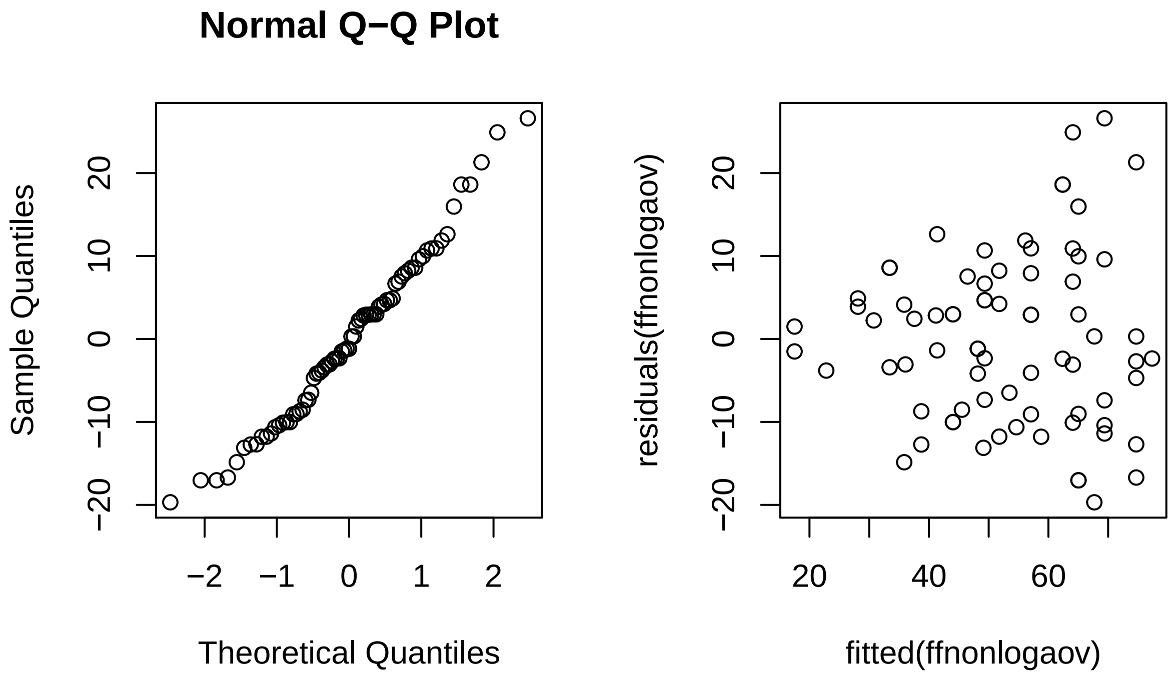
```
anova(ffnonlogaov)
```

```
## Analysis of Variance Table
##
## Response: longevity
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## thorax     1 10959.3 10959.3 101.409 2.557e-15 ***
## activity   2  4966.7  2483.4  22.979 2.016e-08 ***
## Residuals 71  7673.0   108.1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(ffnonlogaov)$coef
```

```
##                   Estimate Std. Error   t value     Pr(>|t|)
## (Intercept)      -67.37460  12.750486 -5.284081 1.325213e-06
## thorax           132.61825  15.724785  8.433708 2.623943e-12
## activityisolated  20.06574   2.994343  6.701218 4.126605e-09
## activitylow       13.05355   2.999201  4.352344 4.434649e-05
```

```
par(mfrow=c(1,2))
qqnorm(residuals(ffnonlogaov))
plot(fitted(ffnonlogaov),residuals(ffnonlogaov))
```



In the plot on the right, the residuals appear more heteroskedastic as the fitted Log transforming the `longevity` variable improves the homoskedasticity of the data and decreases the variance in residuals for increasingly large fitted values. Normality does not seem significantly affected by the log transformation.

Question 2

Section 1

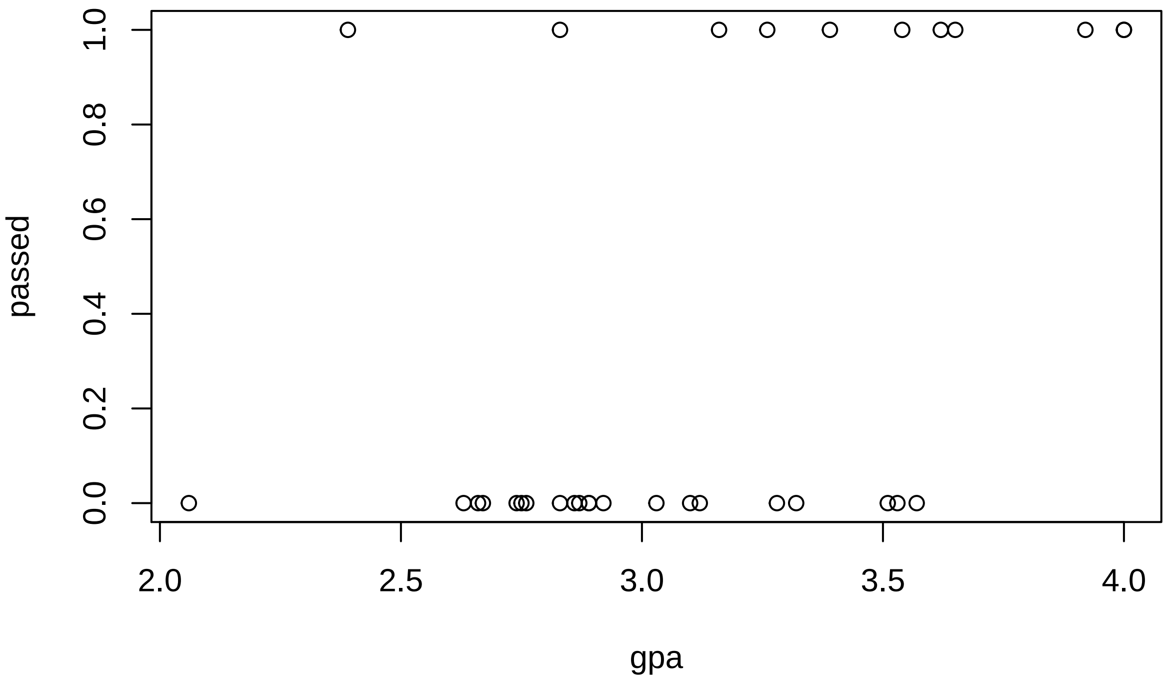
Given data set for this question consists of one binary response and two explanatory variables which one of them is also a binary variable. Scatter plot of passed and gpa can be seen below. It can be seen that a linear line cannot be fitted to this data set.

```
psiData = read.table("./data/psi.txt", header = TRUE)
psiDataNonFactor = data.frame(psiData)

psiData$passed = ifelse(test=psiData$passed == 1, yes="Pass", no="Fail")
psiData$passed = as.factor(psiData$passed)

psiData$psi = ifelse(test=psiData$psi == 1, yes="Yes", no="No")
psiData$psi = as.factor(psiData$psi)

par(mfrow=c(1,1))
plot(passed ~ gpa, data = psiDataNonFactor)
```



The numeric variable; gpa seems to be from a standart normal distribution and its histogram and QQ-Plot can be seen below. As a first step, binary variables are converted into factors.

```
par(mfrow=c(1,2))
hist(psiData$gpa, freq = FALSE)
qqnorm(psiData$gpa)
```

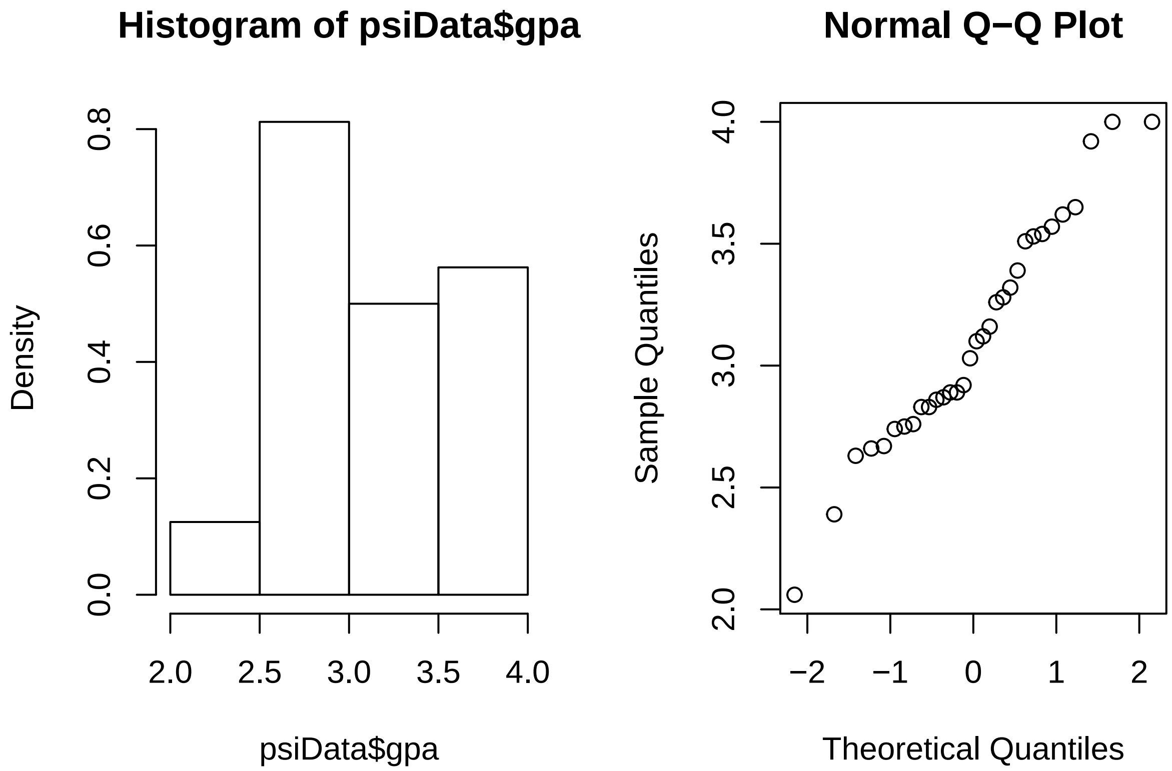


Table of combination of two binary variables can be seen in the table below. From this table we can say that psi is looking promising since more students have passed upon receiving psi.

```
str(psiData)
```

```
## 'data.frame':    32 obs. of  3 variables:
##  $ passed: Factor w/ 2 levels "Fail","Pass": 1 1 1 1 2 1 1 1 1 2 ...
##  $ psi   : Factor w/ 2 levels "No","Yes": 1 1 1 1 1 1 1 1 1 1 ...
##  $ gpa   : num  2.66 2.89 3.28 2.92 4 2.86 2.76 2.87 3.03 3.92 ...
```

```
xtabs(~passed + psi, data = psiData)
```

```
##       psi
## passed No Yes
##   Fail 15   6
##   Pass  3   8
```

Section 2

The output of the basic logistic regression model fitted with glm command using both numeric and binary variables can be seen below. The model is trained on training data set and validated on test data set as can be seen below. The test data set uses 10% of the whole data set without replacement.

```r
# Fit the model
logRegModel = glm(passed ~ psi + gpa, data = psiData, family = "binomial")
logSummary = summary(logRegModel)
logSummary
```

```
##
## Call:
## glm(formula = passed ~ psi + gpa, family = "binomial", data = psiData)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.8396  -0.6282  -0.3045   0.5629   2.0378
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -11.602      4.213  -2.754  0.00589 **
## psiYes         2.338      1.041   2.246  0.02470 *
## gpa            3.063      1.223   2.505  0.01224 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 41.183  on 31  degrees of freedom
## Residual deviance: 26.253  on 29  degrees of freedom
## AIC: 32.253
##
## Number of Fisher Scoring iterations: 5
```

From the output, this model corresponds to the equation given below.

$P(Y) = \Psi(-11.6015646 + (2.3377756) * psi + (3.0633672) * gpa)$

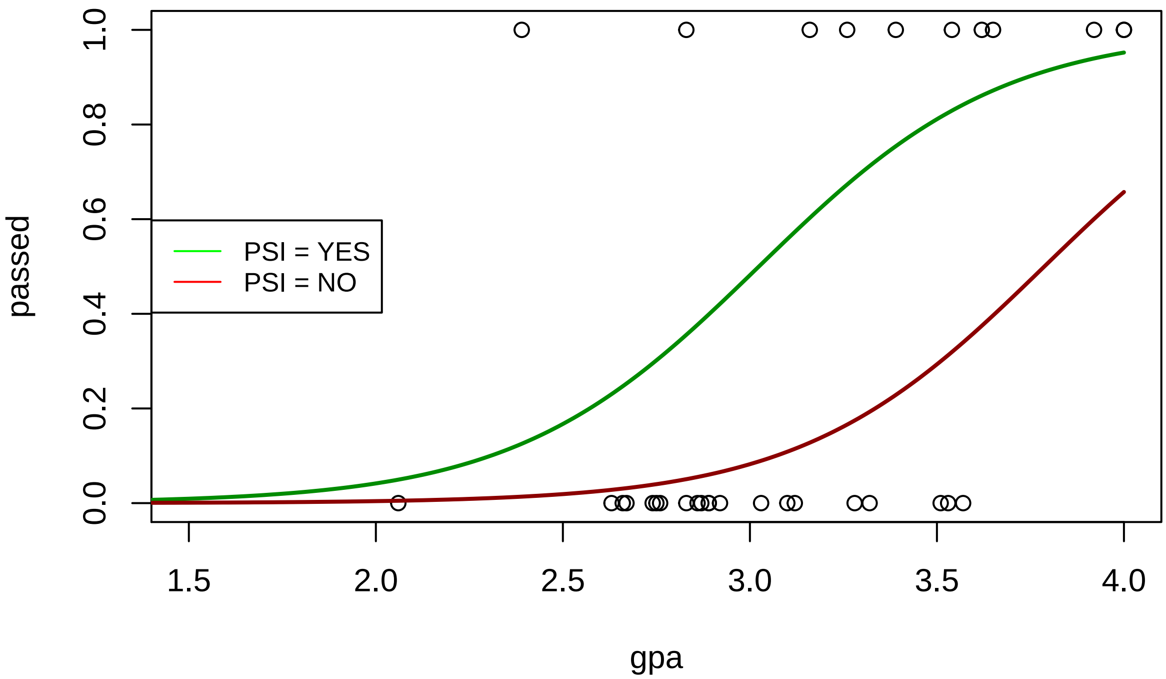
Graph of this equations predictions can be seen below.

```r
newdat1 = data.frame(gpa=seq(0, 4, len=300))
newdat2 = data.frame(gpa=seq(0, 4, len=300))

newdat1$psi = 1
newdat1$psi = ifelse(test=newdat1$psi == 1, yes="Yes", no="No")
newdat1$psi = as.factor(newdat1$psi)
newdat2$psi = 0
newdat2$psi = ifelse(test=newdat2$psi == 1, yes="Yes", no="No")
newdat2$psi = as.factor(newdat2$psi)

newdat1$passed = predict(logRegModel, newdata=newdat1, type="response")
newdat2$passed = predict(logRegModel, newdata=newdat2, type="response")

par(mfrow=c(1,1))
plot(passed ~ gpa, data = psiDataNonFactor, xlim = c(1.5 ,4))
lines(passed ~ gpa, data = newdat1, col="green4", lwd=2)
lines(passed ~ gpa, data = newdat2, col="red4", lwd=2)
legend(x = "left", legend=c("PSI = YES", "PSI = NO"),
       col=c("green", "red"), lty=1:1, cex=0.8)
```



Section 3

From the table given in Section 1, we can calculate the probability of a student passing the assignment given he or she received psi is $P(Passed = TRUE|PSI = TRUE) = 0.5714286$. From the predictions made with the model given in Section 2, we see higher probabilities for students which received psi. Also, the graph for logistic curve given in Section 2 clearly demonstrates the effect of psi in a positive way. Finally, we can check the coefficient of the equation for psi which is 2.3377756. All these information point that psi works.

Section 4

Probabilities for one student having gpa of 3 and receiving psi and one student having gpa of 3 and not receiving psi is given below.

```
testSec4 = read.table("./data/psi-Section4.txt", header = TRUE)
testSec4$passed = ifelse(test=testSec4$passed == 1, yes="Pass", no="Fail")
testSec4$passed = as.factor(testSec4$passed)
testSec4$psi = ifelse(test=testSec4$psi == 1, yes="Yes", no="No")
testSec4$psi = as.factor(testSec4$psi)

testSec4 # Passed column is irrelevant in this case
```

```
##   passed psi gpa
## 1   Fail Yes   3
## 2   Fail  No   3
```

```
predicted = predict(logRegModel, testSec4, type = "response")
predicted
```

```
##          1          2
## 0.48158645 0.08230274
```

Section 5

Estimation of relative change in odds can be seen below with the command. This command yields two numbers for each explanatory variable.

```
odds = round(exp(logRegModel$coefficients), 3)
odds
```

```
## (Intercept)      psiYes         gpa
##       0.000      10.358      21.399
```

From the output of the command, we can say that if the student has received psi, the odds of that student passing increase by a factor of 10.358. So it can be said that psi works better than the standard teaching method since odds of a student increases upon receiving psi regardless of the student's gpa. Also, we can say for a one unit increase in gpa of a student, the odds of that student passing increase by a factor of 21.399 of the teaching method.

Section 6

The table of the alternate analysis can be seen below. This table looks familiar with the table shown in Section 1. With the table from Section 1 in mind, we can assume numbers 15 and 6 are the students failed regardles of the teaching method. So this is a table which is showing the combinations of the binary response variable and the binary explanatory variable.

```
x = matrix(c(3, 15, 8, 6), 2, 2)
x
```

```
##      [,1] [,2]
## [1,]    3    8
## [2,]   15    6
```

```
fisher.test(x)
```

```
## 
##  Fisher's Exact Test for Count Data
## 
## data:  x
## p-value = 0.0265
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.02016297 0.95505763
## sample estimates:
## odds ratio 
##  0.1605805
```

The outcome of Fisher's Exact Test with the p-value of 0.0265, describes that the difference of the probabilities of the matrix are statistically significant. This means that the proportions at one variable are not the same for different values of the second variable thus the variables are not independent of each other.

Section 7

Fisher's Exact Test yields whether the proportions of two nominal variables are different depending on the value of the other variable. So it is a test of independency. This test is not appropriate for this case since we are after the probabilities of students passing or failing based on the teaching method and gpa.

Section 8

Fisher's Exact Test

```
- Advantage: Identifies the significance of a relationship.
- Disadvantage: It fits for small data sets but computationally expensive for large data sets.
```

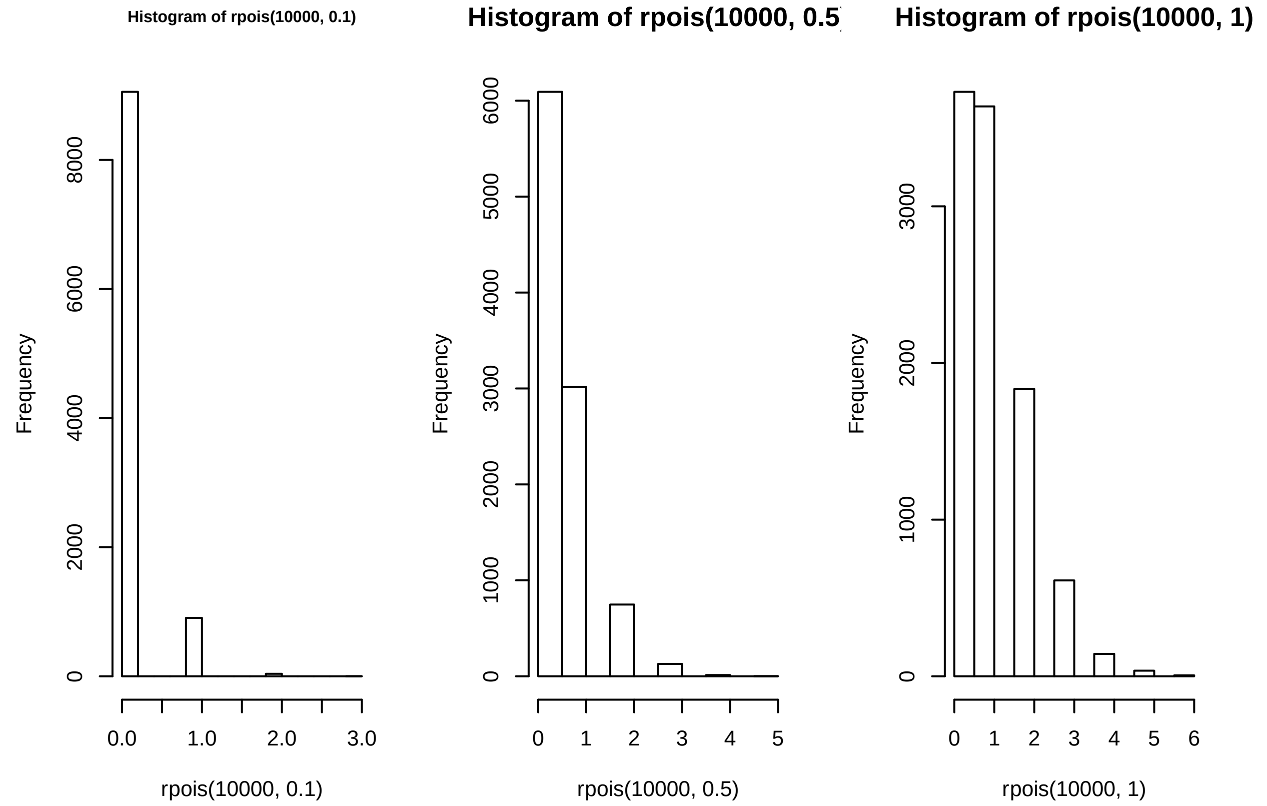
Logistic Regression

```
- Advantage: Constructs a model that measure the relationship between the dependent variable and the ind
- Disadvantage: Logistic Regression will not work if there is a feature that completely separates the tw
```

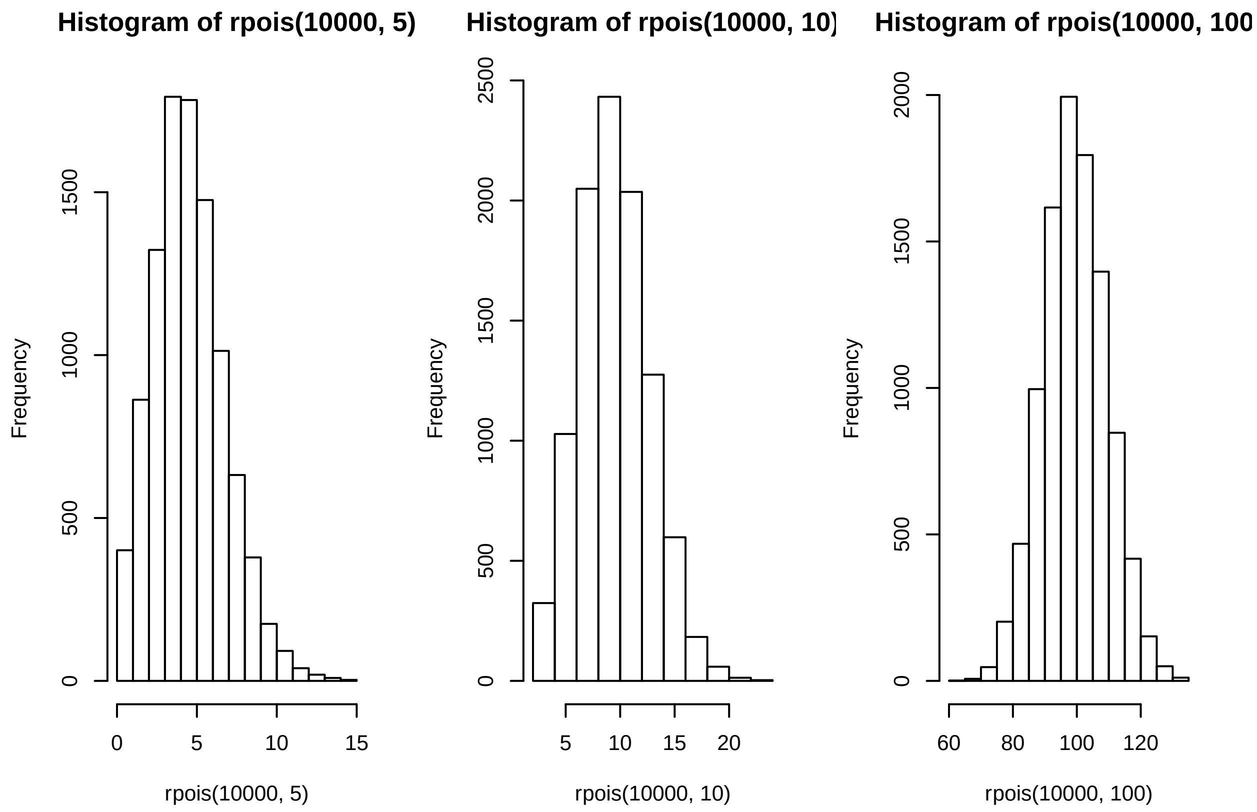
Question 3

Section 1

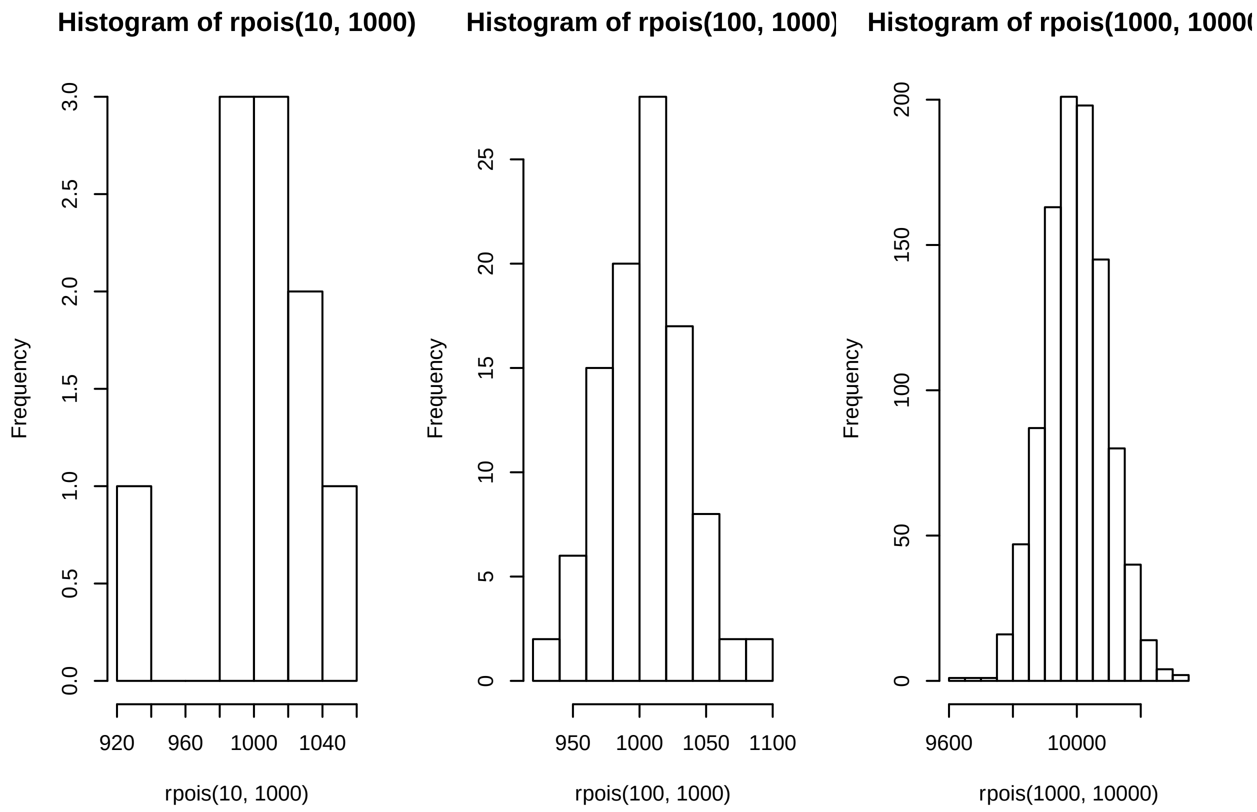
```r
par(mfrow=c(1,3))
hist(rpois(10000,.1), cex.main=.8); hist(rpois(10000,.5)); hist(rpois(10000,1))
```



```
hist(rpois(10000,5)); hist(rpois(10000,10)); hist(rpois(10000,100))
```



```r
hist(rpois(10,1000)); hist(rpois(100,1000)); hist(rpois(1000,10000))
```



For larger values of λ, the distribution is similar to a normal distribution with the mean and variance both equal to λ. Parameter n is of limited influence - it merely determines the amount of values to be sampled from the Poisson distribution. So long as a reasonable amount of points are sampled, the same distribution should emerge for equal λ.

Section 2

In order for the distribution of a randomly distributed variable Y to be in a location-scale family as a given random variable X, Y must have the same distribution as $a + bX$ for some parameters a and b (in other words, $Y \overset{d}{=} a + bX$, where $Y \overset{d}{=}$ means ‘equal in distribution’.

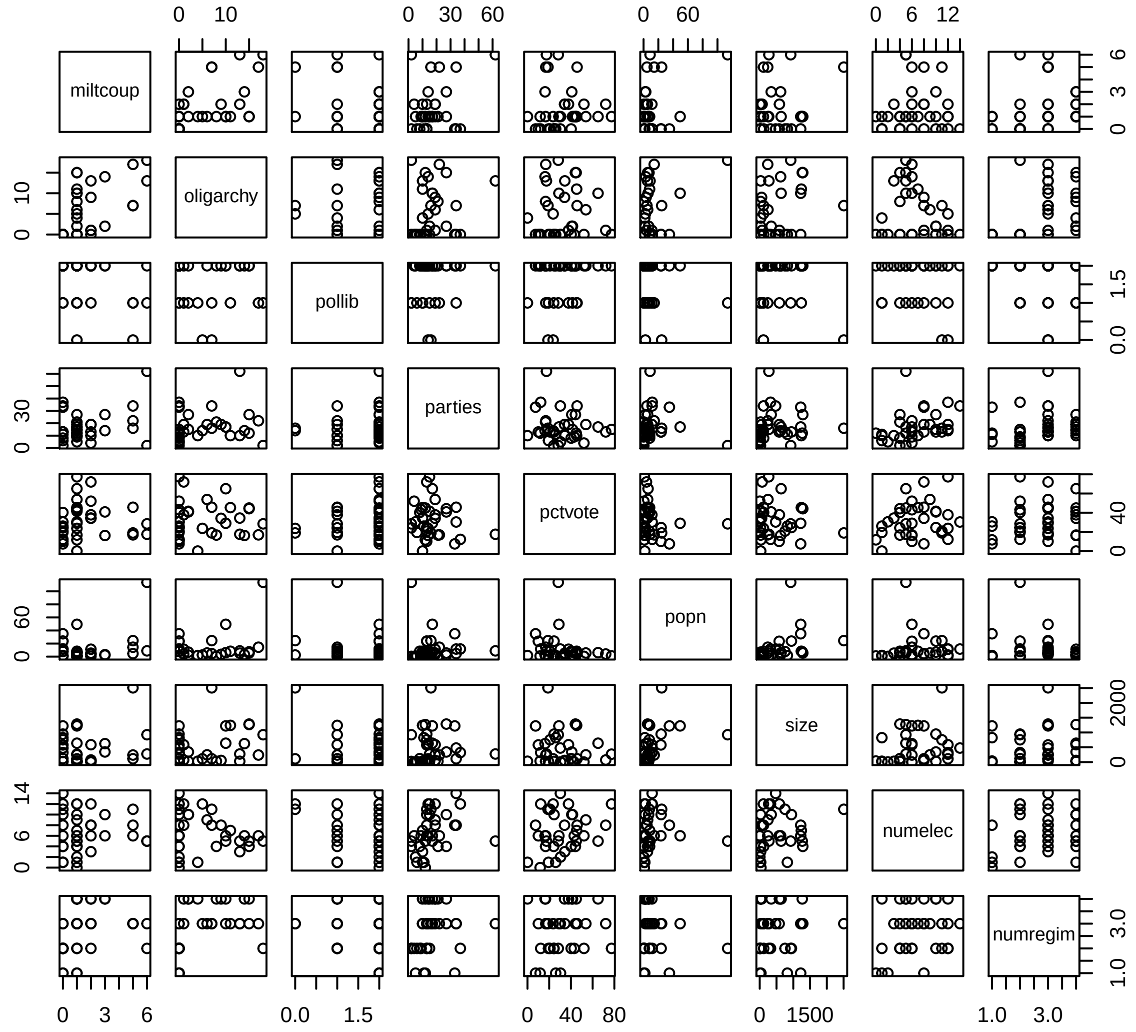
In the case of the Poisson distribution, the distribution is both scaled by parameter λ, since the mean and variance are both equal to λ. Thus, it can be said that, given a variable Y and a variable X that follow a Poisson distribution, $Y \overset{d}{=} \lambda X$, which satisfies the above condition for location-scale families.

However, for very small values of lambda ($\lambda < 1$),where the distribution looks less similar to a normal distribution, it may prove difficult to produce Poisson distributions with larger λ values via a linear transformation, as a scaling transformation may not be able to fit a normal distribution.

Section 3

```
africa = read.table("data/africa.txt",header=TRUE)
africaglm=glm(miltcoup~oligarchy+pollib+parties+pctvote+popn+size+numelec+numregim,
               family=poisson,data=africa)

plot(africa)
```



```
summary(africaglm)
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote +
##     popn + size + numelec + numregim, family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3443  -0.9542  -0.2587   0.3905   1.6953
##
```

```
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.5102693  0.9053301  -0.564  0.57301
## oligarchy    0.0730814  0.0345958   2.112  0.03465 *
## pollib      -0.7129779  0.2725635  -2.616  0.00890 **
## parties      0.0307739  0.0111873   2.751  0.00595 **
## pctvote      0.0138722  0.0097526   1.422  0.15491
## popn         0.0093429  0.0065950   1.417  0.15658
## size        -0.0001900  0.0002485  -0.765  0.44447
## numelec     -0.0160783  0.0654842  -0.246  0.80605
## numregim     0.1917349  0.2292890   0.836  0.40303
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 28.668  on 27  degrees of freedom
## AIC: 111.48
##
## Number of Fisher Scoring iterations: 6
```

```
confint(africaglm)
```

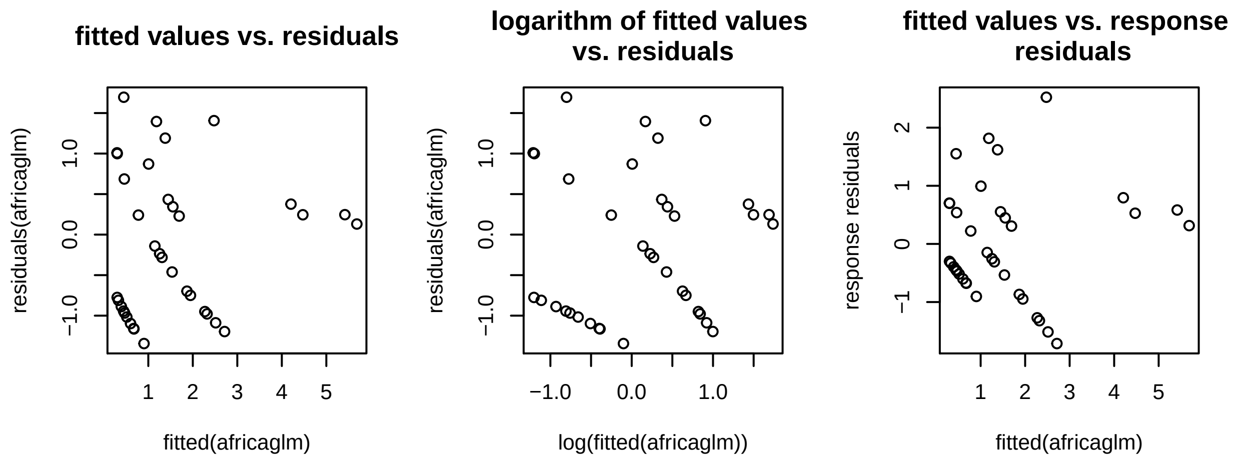
```
## Waiting for profiling to be done...
```

```
##                     2.5 %       97.5 %
## (Intercept) -2.4335049109  1.148089620
## oligarchy    0.0045915288  0.141483576
## pollib      -1.2570629668 -0.182012570
## parties      0.0080568606  0.052321186
## pctvote     -0.0054171503  0.032940743
## popn        -0.0038404317  0.022244262
## size        -0.0007146351  0.000272539
## numelec     -0.1438197483  0.114689702
## numregim    -0.2632334399  0.643070807
```

```
coef(africaglm)
```

```
##   (Intercept)     oligarchy        pollib       parties       pctvote
## -0.5102692854  0.0730813725 -0.7129778804  0.0307739289  0.0138722128
##          popn          size       numelec      numregim
##  0.0093429334 -0.0001899975 -0.0160783349  0.1917349158
```

```
# Assumption checks:
par(mfrow=c(1,3))
plot(fitted(africaglm),residuals(africaglm), main='fitted values vs. residuals')
plot(log(fitted(africaglm)),residuals(africaglm), main='logarithm of fitted values \nvs. residuals')
plot(fitted(africaglm),residuals(africaglm,type="response"), main='fitted values vs. response \n residu
```



Performing visual checks on the residuals of the model shows some odd relationships between the relationships and the fitted values, as the variance of the residuals doesn't seem to increase for higher fitted values. This is expected under a Poisson distribution, as higher fitted values correspond to higher variances as lambda is modeled differently for each observation. The first plot also shows some collinearity between variables such as `popn` and `pollib`.

Section 4

```r
summary(glm(miltcoup~oligarchy+pollib+parties+pctvote+popn+size+numelec+numregim,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote +
##     popn + size + numelec + numregim, family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3443  -0.9542  -0.2587   0.3905   1.6953
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.5102693  0.9053301  -0.564  0.57301
## oligarchy    0.0730814  0.0345958   2.112  0.03465 *
## pollib      -0.7129779  0.2725635  -2.616  0.00890 **
## parties      0.0307739  0.0111873   2.751  0.00595 **
## pctvote      0.0138722  0.0097526   1.422  0.15491
## popn         0.0093429  0.0065950   1.417  0.15658
## size        -0.0001900  0.0002485  -0.765  0.44447
## numelec     -0.0160783  0.0654842  -0.246  0.80605
## numregim     0.1917349  0.2292890   0.836  0.40303
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
```

```
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 28.668  on 27  degrees of freedom
## AIC: 111.48
##
## Number of Fisher Scoring iterations: 6
```

```
# `numelec` has the highest p-value, and is removed.
summary(glm(miltcoup~oligarchy+pollib+parties+pctvote+popn+size+numregim,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote +
##     popn + size + numregim, family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3997  -0.9381  -0.2666   0.4220   1.6998
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.6078028  0.8239267  -0.738  0.46070
## oligarchy    0.0781368  0.0277656   2.814  0.00489 **
## pollib      -0.6773897  0.2290130  -2.958  0.00310 **
## parties      0.0296786  0.0102888   2.885  0.00392 **
## pctvote      0.0131290  0.0092895   1.413  0.15756
## popn         0.0089313  0.0063746   1.401  0.16120
## size        -0.0002021  0.0002436  -0.830  0.40682
## numregim     0.1758198  0.2210498   0.795  0.42639
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 28.728  on 28  degrees of freedom
## AIC: 109.54
##
## Number of Fisher Scoring iterations: 5
```

```
# `numregim` is removed next.
summary(glm(miltcoup~oligarchy+pollib+parties+pctvote+popn+size,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote +
##     popn + size, family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3522  -0.9651  -0.1945   0.4833   1.6179
```

```
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.1126871  0.5163030  -0.218 0.827228
## oligarchy    0.0859620  0.0259100   3.318 0.000908 ***
## pollib      -0.6894029  0.2278572  -3.026 0.002481 **
## parties      0.0291944  0.0101954   2.863 0.004190 **
## pctvote      0.0141588  0.0091980   1.539 0.123723
## popn         0.0062736  0.0053994   1.162 0.245272
## size        -0.0001950  0.0002425  -0.804 0.421378
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 29.363  on 29  degrees of freedom
## AIC: 108.17
##
## Number of Fisher Scoring iterations: 5
```

```
# removing `size`
summary(glm(miltcoup~oligarchy+pollib+parties+pctvote+popn,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote +
##     popn, family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.4109  -0.9943  -0.1399   0.5516   1.6125
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.244466   0.495708  -0.493  0.62190
## oligarchy    0.083168   0.025437   3.270  0.00108 **
## pollib      -0.652830   0.221234  -2.951  0.00317 **
## parties      0.029800   0.010294   2.895  0.00379 **
## pctvote      0.013842   0.009282   1.491  0.13591
## popn         0.005587   0.005378   1.039  0.29883
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 30.044  on 30  degrees of freedom
## AIC: 106.85
##
## Number of Fisher Scoring iterations: 5
```

```
# removing `popn`
summary(glm(miltcoup~oligarchy+pollib+parties+pctvote,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties + pctvote,
##     family = poisson, data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5456  -0.9841  -0.1881   0.5948   1.6705
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.093657   0.463279  -0.202  0.83979
## oligarchy    0.095358   0.022421   4.253 2.11e-05 ***
## pollib      -0.666615   0.217564  -3.064  0.00218 **
## parties      0.025630   0.009502   2.697  0.00699 **
## pctvote      0.012134   0.009056   1.340  0.18031
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 31.081  on 31  degrees of freedom
## AIC: 105.89
##
## Number of Fisher Scoring iterations: 5
```

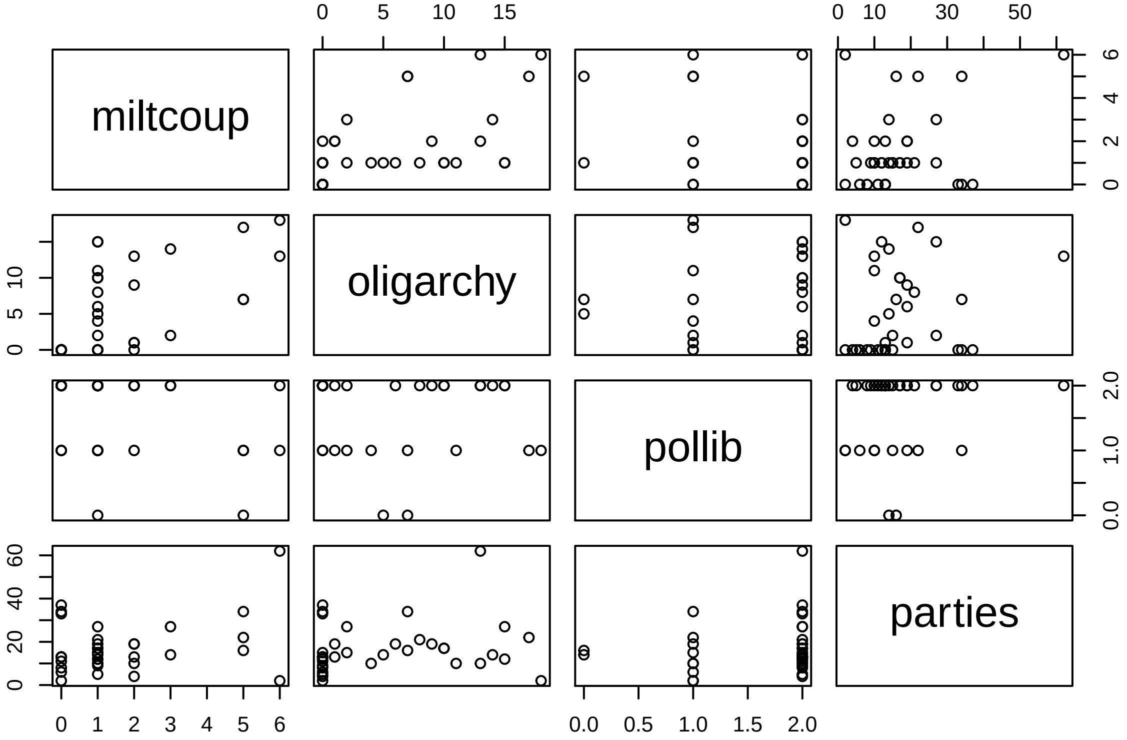
```
# removing `pctvote`
summary(glm(miltcoup~oligarchy+pollib+parties,
            family=poisson,data=africa))
```

```
##
## Call:
## glm(formula = miltcoup ~ oligarchy + pollib + parties, family = poisson,
##     data = africa)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.3583  -1.0424  -0.2863   0.6278   1.7517
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.251377   0.372689   0.674  0.50000
## oligarchy    0.092622   0.021779   4.253 2.11e-05 ***
## pollib      -0.574103   0.204383  -2.809  0.00497 **
## parties      0.022059   0.008955   2.463  0.01377 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 65.945  on 35  degrees of freedom
## Residual deviance: 32.856  on 32  degrees of freedom
## AIC: 105.66
##
## Number of Fisher Scoring iterations: 5
```

The remaining parameters appear significant, as their p-value is lower than 0.05. By examining the collinearity of the remaining variables using the plot below, it appears that none of the remaining variables are excessively collinear.

```
plot(africa[,1:4])
```


miltcoup
oligarchy
pollib
parties