Assignment 2

Group 47: Luca Cavellini, Paul Hosek, Robert Satzger

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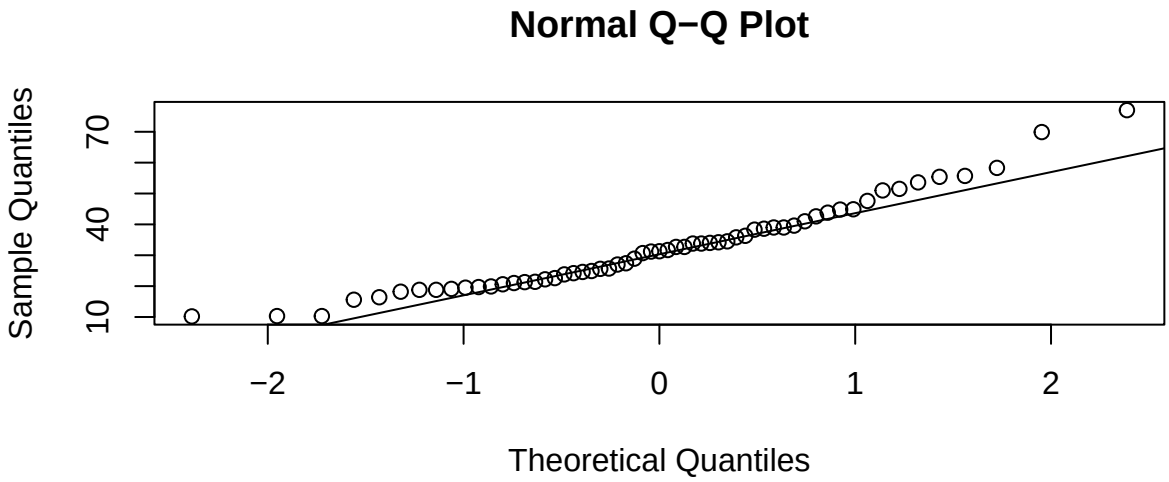
Exercise 1. Trees

a)

First, we test the normality assumption of the ANOVA.

```
trees = read.table("data/treeVolume.txt", header = T)
trees$type <- as.factor(trees$type)
qqnorm(trees$volume); qqline(trees$volume)
```



The QQ-plot suggests that the data may deviate from the normality assumption. However, the ANOVA is generally robust against such violations when there are more than ten observations per condition. Therefore, we will proceed with the analysis.

```
trees_lm1 <- lm(volume ~ type, data = trees)
summary(trees_lm1)
```

```
##
## Call:
## lm(formula = volume ~ type, data = trees)
##
## Residuals:
```

```
##    Min     1Q Median     3Q    Max
## -19.97  -9.96  -2.77   5.94  46.83
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)    30.17       2.54   11.88   <2e-16 ***
## typeoak         5.08       3.69    1.38     0.17
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.1 on 57 degrees of freedom
## Multiple R-squared:  0.0322, Adjusted R-squared:  0.0153
## F-statistic:  1.9 on 1 and 57 DF,  p-value: 0.174
```

```
trees_aov <- anova(trees_lm1)
print(trees_aov)
```

```
## Analysis of Variance Table
##
## Response: volume
##           Df Sum Sq Mean Sq F value Pr(>F)
## type       1    380     380     1.9   0.17
## Residuals 57  11395     200
```

The one-way ANOVA returned a p-value of $p = 0.17$. Therefore, we cannot refute the null hypothesis that there is no influence of tree type on volume. It is noteworthy that a one-way ANOVA is generally endorsed in situations with a factor of more than two levels. In this case, the factor has two levels only. Thus, the result is equal to the result of a t-test (shown in the summary of the linear model). Based on our results, the estimated volume for the beech trees is 30.17, while for the oak trees it is 35.25.

b)

```
trees_lm2 <- lm(volume ~ type * diameter + height, data = trees)
anova(trees_lm2)
```

```
## Analysis of Variance Table
##
## Response: volume
##               Df Sum Sq Mean Sq F value  Pr(>F)
## type           1    380     380   35.77 1.8e-07 ***
## diameter       1  10492   10492  989.02 < 2e-16 ***
## height         1    324     324   30.56 9.6e-07 ***
## type:diameter  1      6       6    0.52    0.47
## Residuals     54    573      11
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
trees_lm3 <- lm(volume ~ type * height + diameter, data = trees)
anova(trees_lm3)
```

```
## Analysis of Variance Table
##
## Response: volume
##             Df Sum Sq Mean Sq F value  Pr(>F)
## type         1    380     380   36.67 1.4e-07 ***
## height       1   2239    2239  216.34 < 2e-16 ***
## diameter     1   8577    8577  828.64 < 2e-16 ***
## type:height  1     19      19    1.88    0.18
## Residuals   54    559      10
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

In order to check whether diameter and height have the same influence on the volume for both tree types, we fit two models. The p-values returned from our tests do not support an interaction effect of tree type with either diameter or height on volume. Therefore, we can conclude that the effects of both height and diameter on volume are similar for both tree types.

c) Based on the results in **b**, we continue with an exclusively additive model.

```
trees_lm4 <- lm(volume ~ diameter + height + type, data = trees)
summary(trees_lm4)
```

```
##
## Call:
## lm(formula = volume ~ diameter + height + type, data = trees)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -7.186 -2.140 -0.087  1.721  7.701
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -63.7814     5.5129  -11.57  2.3e-16 ***
## diameter      4.6981     0.1645   28.56  < 2e-16 ***
## height        0.4172     0.0752    5.55  8.4e-07 ***
## typeoak      -1.3046     0.8779   -1.49     0.14
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.24 on 55 degrees of freedom
## Multiple R-squared:  0.951,  Adjusted R-squared:  0.948
## F-statistic:  355 on 3 and 55 DF,  p-value: <2e-16
```

```
drop1(trees_lm4, test='F')
```

```
## Single term deletions
##
## Model:
## volume ~ diameter + height + type
##          Df Sum of Sq  RSS AIC F value  Pr(>F)
```

```
## <none>                  578 143
## diameter  1      8577 9155 304  815.61 < 2e-16 ***
## height    1       324  903 167   30.82 8.4e-07 ***
## type      1        23  602 143    2.21    0.14
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The results suggest that tree type is not a significant factor in this model. Thus, we further reduce the linear model to only contain the predictors diameter and height.

```
tree_lm5 <- lm(volume ~ diameter + height, data = trees)
smry <- summary(tree_lm5)
smry
```

```
##
## Call:
## lm(formula = volume ~ diameter + height, data = trees)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.724 -2.278 -0.034  1.820  8.629
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -64.3697     5.5577  -11.58  < 2e-16 ***
## diameter      4.6325     0.1602   28.92  < 2e-16 ***
## height        0.4289     0.0755    5.68  5.1e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 3.28 on 56 degrees of freedom
## Multiple R-squared:  0.949,  Adjusted R-squared:  0.947
## F-statistic:  520 on 2 and 56 DF,  p-value: <2e-16
```

```
smry$coefficient["(Intercept)","Estimate"]+
  smry$coefficient["diameter","Estimate"]*mean(trees$diameter)+
  smry$coefficient["height","Estimate"]*mean(trees$height)
```

```
## [1] 32.6
```

To predict the volume of a tree based on the diameter and the height we followed the formula $\hat{Y} = \hat{\mu} + \hat{\beta}_{diameter}\bar{X}_{diameter} + \hat{\beta}_{height}\bar{X}_{height}$, by which we obtained a value of 32.58.

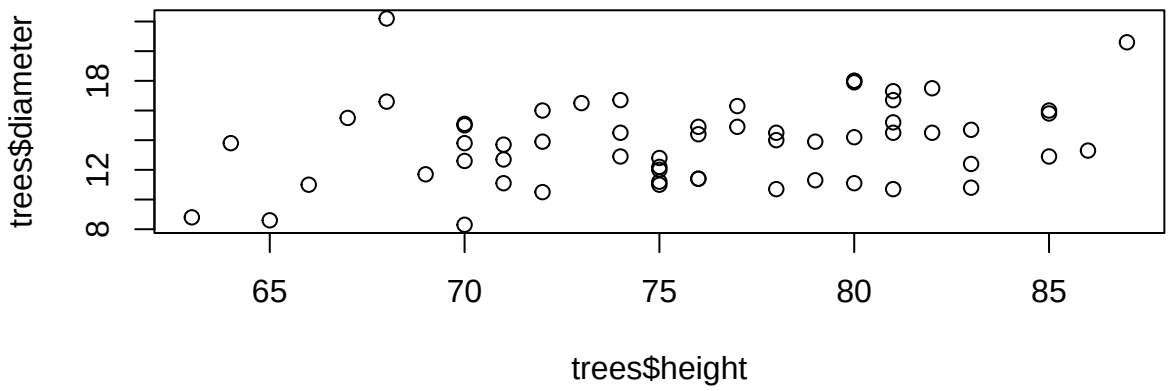
d) A cylinder's volume is given by $V = \pi * (d/2)^2 * h$. So, the most logical explanatory variable would be to calculate the volume using this formula.

```
trees$transform <- pi * (trees$diameter/2)^2 * trees$height
trees_lm5 <- lm(volume ~ transform, data = trees)
summary(trees_lm5)
```

```
##
```

```
## Call:
## lm(formula = volume ~ transform, data = trees)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -4.846 -1.343 -0.245  1.533  5.532
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -3.79e-01   7.63e-01    -0.5     0.62
## transform    2.73e-03   5.82e-05    46.9   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.28 on 57 degrees of freedom
## Multiple R-squared:  0.975,  Adjusted R-squared:  0.974
## F-statistic: 2.2e+03 on 1 and 57 DF,  p-value: <2e-16
```

```
plot(trees$height, trees$diameter)
```

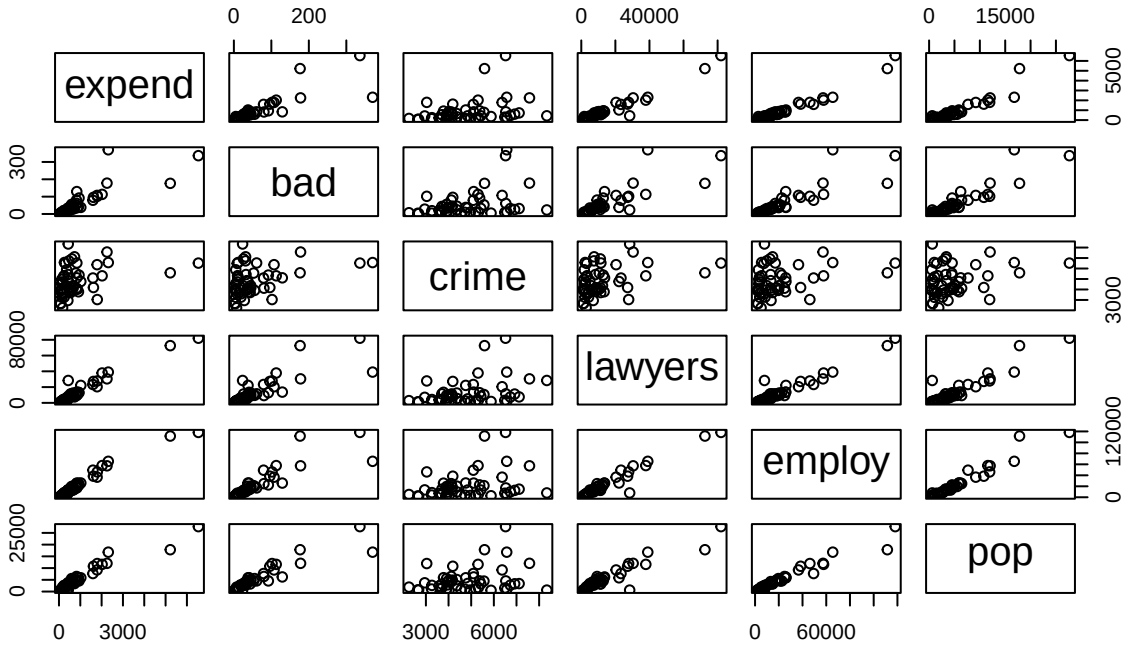


The transformation increases R-squared from .949 to .975. This shows the utility of using the correct mathematical formula in creating a new explanatory variable. It is noteworthy, however, that the fitness may be further improved by scaling the original predictors according to their units. As we are unaware of the units, we proceeded with the unscaled measures.

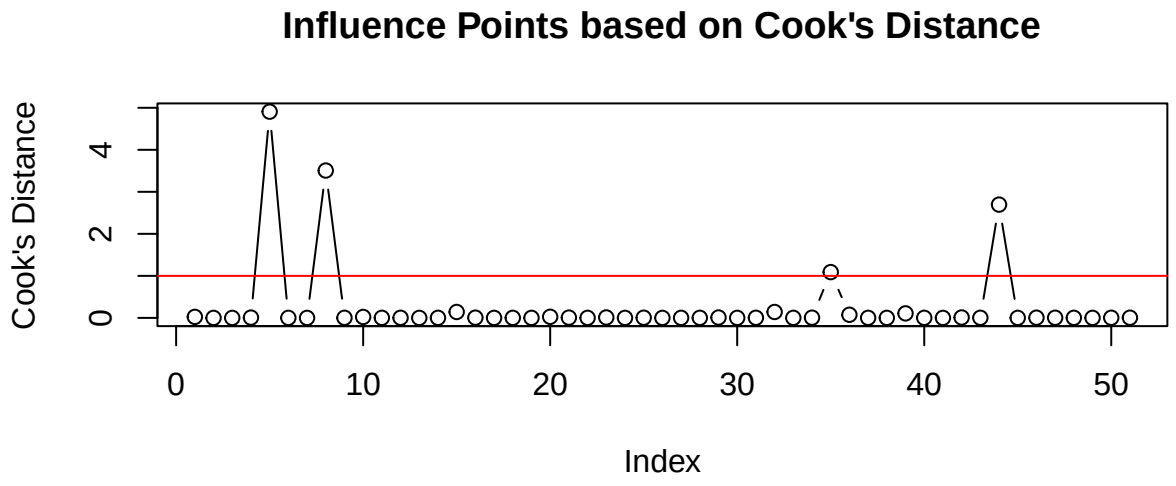
Exercise 2. Expenditure on criminal activities

a)

```
data <- read.table("data/expensescrime.txt", header = TRUE);
pairs(data[,2:7])
```




```
# Influence points
full_model <- lm(expend ~ bad + crime + lawyers + employ + pop, data = data)
cdist <- cooks.distance(full_model)
plot(1:length(cdist), cdist, xlab = "Index", ylab = "Cook's Distance",
     main = "Influence Points based on Cook's Distance", type="b")
abline(h=1, col="red")
```




```
# Collinearity
print(vif(full_model))
```

Table 1: VIF Values by term dropped from full model and Variable

	vif.bad	vif.crime	vif.lawyers	vif.employ	vif.pop
Population	4.46	1.30	16.8	21.1	NA
Employment	8.24	1.49	10.1	NA	20.7
Lawyers	8.07	1.31	NA	20.0	32.5
Crime Rate	NA	1.23	16.4	33.1	17.6

```
##     bad   crime lawyers  employ     pop
##    8.36    1.49   16.97   33.59   32.94
```

Our graphical summary of the data shows that the crime rate, lawyers, employment and population are most notably related with expenditure. "Crime" shows random variation with all other variables.

Analyses of Influence points based on Cook's distance indicates that 4 observations with disproportionate influence on the model, with one marginally outside the cutoff of one. All four observations must undergo further inspection and potentially dropped from the model.

Concerning Colliniarity, our rule of thumb dicatates that a VIF > 5 is concerning, indicating $R^2 > .8$. In our dataset, all variables besides "crime" were found with VIF >5, further "Pop" and "Employ" show extreme VIF values with VIF >30. This indicates that at least one variable is a linear combination of the others. This corroborates the inpection of the scatter-matrix from before, indicating close relationships between the variables. We can try to drop a single term from the model, but may need to drop more.

Table 1 shows that dropping the term with the highest VIF did not reduce all VIFs to under five, as such we should use the step-down or step-up method to select the correct model.

b)

The step-up method can be summarized in 4 steps:

1. Build model with constant predictor (background model).
2. Find term that, if added to the model would maximise R^2.
3. If the variable is significant, add it to the model.
4. Go to 2 until 3 does not occur.

```
# find the next best term that significantly improves model fit
find_best_term <- function(formula, data) {
  best_fit <- summary(lm(formula, data))$adj.r.squared
  best_term <- 1
  # maximize r^2
  for (term in names(data[,-c(1:2)])) {
    if (!term %in% attr(formula, "term.labels")) {
      cur_formula <- paste(formula, term, sep="+")
      cur_model <- lm(cur_formula, data = data)
      cur_fit <- summary(cur_model)$r.squared
      if (cur_fit > best_fit) {
```

```
        best_fit <- cur_fit
        best_term <- term
        best_coef_pval <- summary(cur_model)$coefficients[
          nrow(summary(cur_model)$coefficients), "Pr(>|t|)"]

      }
    }
  }
  # test if increase is significant and return new formula
  if (best_coef_pval<0.05){
    return(best_term)
  } else {
    return(1)
  }
}
# recursively add terms
step_up <- function(formula, data){
  new_term <- find_best_term(formula,data)
  if (new_term == 1){
    return(formula)}
  step_up(paste(formula, new_term, sep="+"), data)
}

best_formula <- step_up("expend~1", data)
best_model <- lm(best_formula, data=data)
print(summary(best_model))
```

```
##
## Call:
## lm(formula = best_formula, data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -599.5  -94.4   36.0   92.0  936.5
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.11e+02   4.26e+01   -2.60   0.0124 *
## employ       2.97e-02   5.11e-03    5.81  4.9e-07 ***
## lawyers      2.69e-02   7.76e-03    3.46   0.0011 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 233 on 48 degrees of freedom
## Multiple R-squared:  0.963,  Adjusted R-squared:  0.962
## F-statistic:  628 on 2 and 48 DF,  p-value: <2e-16
```

```
print(vif(best_model))
```

```
##  employ lawyers
##    14.8    14.8
```

The model found includes only "employ" and "lawyers". It explains a high proportion of the variance ($R^2 = 0.963$). Analysis of collinearity found all VIF values larger than five. This model may not be the most suitable model as factors linearly depend on another.

c)

```
hypo_state <- data.frame(
  bad = 50, crime = 5000, lawyers = 5000, employ = 5000, pop = 5000)
pred_interv_b <- predict(best_model,hypo_state,interval="prediction",level=0.95)
pred_interv_b
```

```
##   fit  lwr upr
## 1 172 -303 647
```

Given this model, we predict $p = 172.21$ for "expend". 95% and lower bounds are: $[-302.93, 647.35]$. We could improve this prediction by trying out different models (e.g., add more terms) and examine if the prediction interval becomes smaller. For example, we could try the full model from earlier:

```
pred_interv_f <- predict(full_model,hypo_state,interval="prediction",level=0.95)
```

The prediction interval of the full model is larger (1003.18) than using the model found with the step-up method (950.28). Alternatively, assuming "improving" the interval means making it smaller, we could lower the confidence level.

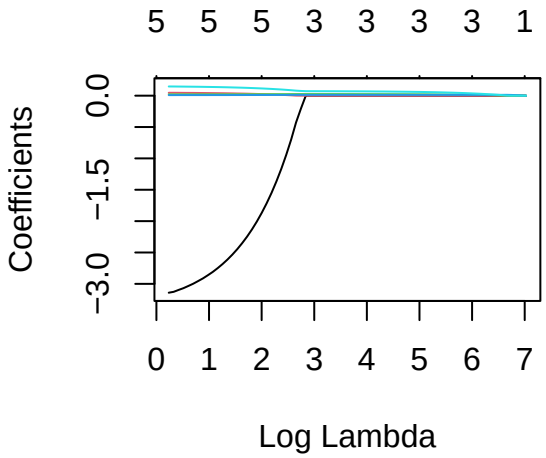
d)

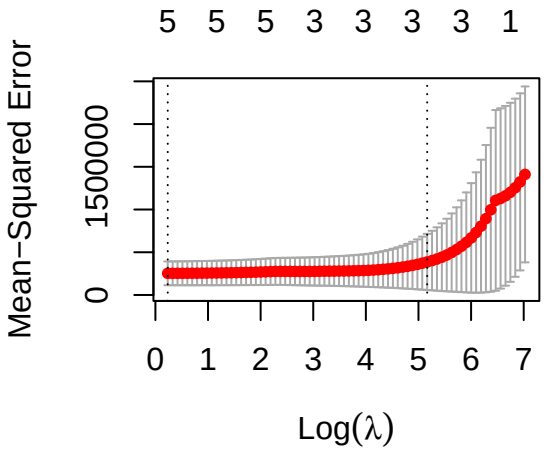
```
set.seed(42)
x <- as.matrix(data[,-2:-1]) # remove expend and state
y <- as.double(as.matrix(data[,2])) # expend is response

train=sample(1:nrow(x),0.67*nrow(x))
x.train=x[train,]; y.train=y[train]
x.test=x[-train,]; y.test=y[-train]

lasso.mod=glmnet(x.train,y.train,alpha=1)
lasso.cv=cv.glmnet(x.train,y.train,alpha=1,type.measure="mse")
par(mfrow=c(1,2))

lambda.min=lasso.cv$lambda.min; lambda.1se=lasso.cv$lambda.1se
coef(lasso.mod,lasso.cv$lambda.1se) #beta's for the best lambda
```

```
## 6 x 1 sparse Matrix of class "dgCMatrix"
##                    s1
## (Intercept) 5.9559
```

```
## bad          .
## crime        .
## lawyers      0.0214
## employ       0.0132
## pop          0.0569
```

```
y.pred=predict(lasso.mod,s=lambda.1se,newx=x.test) #predict for test
mse.lasso=mean((y.test-y.pred)^2) #mse for the predicted test rows

plot(lasso.mod,label=T,xvar="lambda")
plot(lasso.cv) # the best lambda by cross-validation
```






```
print(mse.lasso)
```

```
## [1] 93665
```

```
lass_model = lm("expend~lawyers+employ+pop", data=data)
summary(lass_model)
```

```
##
## Call:
## lm(formula = "expend~lawyers+employ+pop", data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -633.8  -91.8   34.5  100.2  866.9
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.23e+02   4.52e+01   -2.73   0.0089 **
## lawyers      2.72e-02   7.79e-03    3.49   0.0010 **
## employ       2.49e-02   7.64e-03    3.26   0.0021 **
## pop          2.25e-02   2.64e-02    0.85   0.3994
```

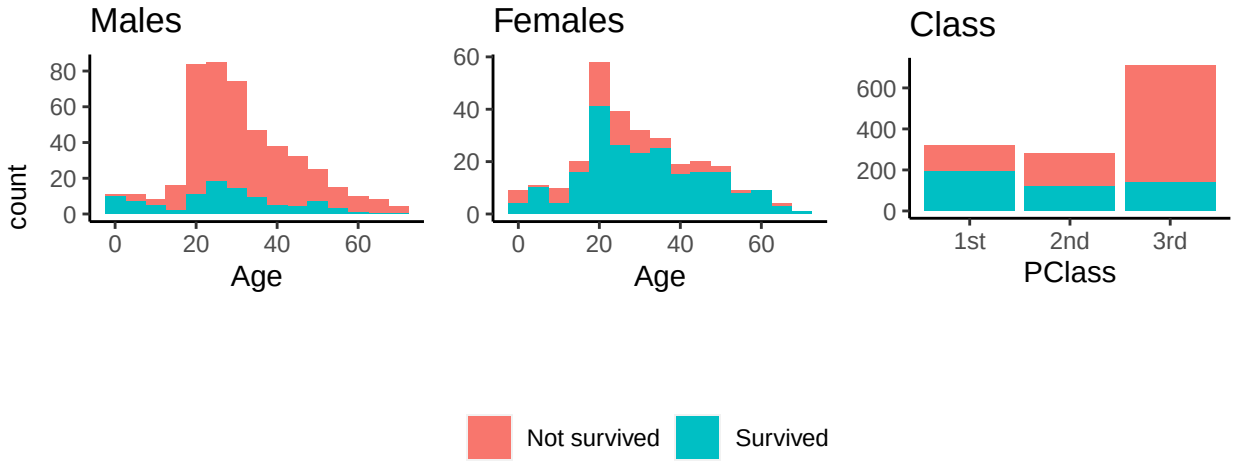
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 233 on 47 degrees of freedom
## Multiple R-squared:  0.964,  Adjusted R-squared:  0.961
## F-statistic:  416 on 3 and 47 DF,  p-value: <2e-16
```

The model chosen by the LASSO method includes lawyers, employ, and pop as predictors. This model is more complex than the model chosen in b, as that model only contained the predictors of lawyers and employ. Interestingly, both models lead to a similar R-squared with $R^2 = 0.964$ (LASSO model) and $R^2 = 0.963$ (step-down model), respectively. Given a similar model fitness, the more parsimonious model should be favored. The adjusted R-squared reflects this with $R^2_{adj} = 0.961$ (LASSO model) and $R^2_{adj} = 0.962$ (step-down model). Therefore, the model based on the step-down approach should be slightly favored.

Exercise 3. Titanic

a)

```
data_titanic <- read.table("data/titanic.txt", header=TRUE)
data_titanic$PClass <- as.factor(data_titanic$PClass)
data_titanic$Sex <- as.factor(data_titanic$Sex)
data_titanic$Survived <- as.factor(data_titanic$Survived)
```




```
model_log1 <- glm(Survived ~ PClass + Age + Sex, data = data_titanic, family = binomial())
drop1(model_log1, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Survived ~ PClass + Age + Sex
##        Df Deviance AIC    LRT Pr(>Chi)
```

```
## <none>         695 705
## PClass  2      796 802 100.4  < 2e-16 ***
## Age     1      724 732  28.5  9.6e-08 ***
## Sex     1      910 918 214.8  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(model_log1)$coef
```

```
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   3.7597    0.39757    9.46 3.18e-21
## PClass2nd    -1.2920    0.26008   -4.97 6.78e-07
## PClass3rd    -2.5214    0.27666   -9.11 7.95e-20
## Age          -0.0392    0.00762   -5.14 2.69e-07
## Sexmale      -2.6314    0.20151  -13.06 5.68e-39
```

We find that all factors PClass, Age and Sex are significant. Further, excluding interaction effects, we find that being a female or a first class passengers or young increases your odds of survival.

To obtain the odds from the estimated coefficients in the output, we can use the following formula: $e^{\mu+\alpha_i+\beta X_{in}}$. Consequently, we can calculate the relative change in odds by $e^{\alpha_i'-\alpha_i}$ or e^{β} for categorical versus continuous variables, respectively. From the main effects we can conclude: Males are 13.89 more likely to die compared to females. 2nd-class passengers are 3.64 and third-class passengers are 12.45 as likely to die than passengers in other classes. Further, for each year a person is older, odds decrease by a factor of 0.96: younger passengers are more likely to survive. All these main effects are statistically significantly associated with survival.

b)

Based on the previous analyses, we know that Sex, Age and PClass are significantly related to the chance of survival. However, there may be interaction effects. It could be, that children are all treated equally independent of their Sex, but with higher ages, females are more likely to survive. The same may be true for Class. For this, we compare the model used in a) with a model that adds an interactions between Age with Sex and Age with Class.

```
model_log2 <- glm(Survived ~ PClass + Age + Sex + PClass:Age + Age:Sex,
                  data = data_titanic, family = binomial)
summary(model_log2)
```

```
##
## Call:
## glm(formula = Survived ~ PClass + Age + Sex + PClass:Age + Age:Sex,
##     family = binomial, data = data_titanic)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -2.686  -0.646  -0.339   0.675   2.727
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
```

```
## (Intercept)     2.0299     0.6598    3.08   0.0021 **
## PClass2nd      -0.2115     0.7101   -0.30   0.7658
## PClass3rd      -2.0811     0.6658   -3.13   0.0018 **
## Age             0.0246     0.0198    1.25   0.2131
## Sexmale        -0.3889     0.4803   -0.81   0.4180
## PClass2nd:Age  -0.0451     0.0220   -2.05   0.0401 *
## PClass3rd:Age  -0.0148     0.0211   -0.70   0.4834
## Age:Sexmale    -0.0821     0.0171   -4.81  1.5e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1025.57  on 755  degrees of freedom
## Residual deviance:  662.45  on 748  degrees of freedom
##   (557 observations deleted due to missingness)
## AIC: 678.4
##
## Number of Fisher Scoring iterations: 5
```

We find, that the interaction in the second model of Age and being Male is significant. However, the interaction of Age and Class is not. Ideally we would choose the best model depending on results of fit to a validation set. Since we do not have the resources for this, we instead reason that the model with the interaction between Age and Sex should be kept. Theoretically, it is possible that the effect of being a child is larger than being a female. If this was the case, then we would expect an interaction between both variables, were at young age being a child improves survival odds most and at higher ages this effect is less strong. Here, it then matters what sex we are instead.

```
all_comb_55 <- expand.grid(PClass = levels(data_titanic$PClass), Sex = levels(data_titanic$Sex)
all_comb_55$Survival_Probability <- predict(model_log2, all_comb_55, type = "response") # resp
kable(all_comb_55, format = "markdown",
      caption = "Survival probability for 55 year olds.")
```

Table 2: Survival probability for 55 year olds.

PClass	Sex	Age	Survival_Probability
1st	female	55	0.967
2nd	female	55	0.667
3rd	female	55	0.619
1st	male	55	0.179
2nd	male	55	0.015
3rd	male	55	0.012

As shown in Table 2, we observe that being female has the largest influence on survival. Independent of gender, more expensive classes have larger survival probability. We observe that females in the first class have a extremely high survival probability of 0.97.

c)

We can use the estimated logistic regression model to predict the probability of survival for a new observation, and then apply a threashold to classify the observation as either a survivor (1) or a non-survivor (0).

Here, we first fit the logistic regression model to the observed data to estimate $\hat{\theta}$ in $P(Y_k = 1) = \frac{1}{1+e^{-x_k^T\theta}}, \quad k = 1, \ldots, N$. Then, we use this estimate to predict the probability of survival for a new passenger with predictor values X_{new}. We then apply a threshold p_0 to classify the new passenger into survivor (1) or a non-survivor (0). Specifically, whether the predicted probability $\hat{P}_{new}$ is above or below the threshold is used to classify a new passenger.

The threshold p_0 determines the trade-off between sensitivity and specificity of our model. We may choose a validation set and some quality measure (e.g., accuracy: predictions correct) to maximize on this data set. Note, however, that this quality measure should be chosen depending on what our goal is, if we want high sensitivity or high specificicity, maximizing these may also guide the threshold.

d)

```
ct_class <- xtabs(~ PClass + Survived, data = data_titanic)
ct_class
```

```
##       Survived
## PClass   0   1
##    1st 129 193
##    2nd 161 119
##    3rd 573 138
```

```
xtest_class <- chisq.test(ct_class)
xtest_class
```

```
##
##  Pearson's Chi-squared test
##
## data:  ct_class
## X-squared = 172, df = 2, p-value <2e-16
```

```
ct_sex <- xtabs(~ Sex + Survived, data = data_titanic)
ct_sex
```

```
##         Survived
## Sex        0   1
##   female 154 308
##   male   709 142
```

```
xtest_sex <- fisher.test(ct_sex)
xtest_sex
```

```
##
##  Fisher's Exact Test for Count Data
```

```
##
## data:  ct_sex
## p-value <2e-16
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.0762 0.1316
## sample estimates:
## odds ratio
##        0.1
```

Here, we find that both class and sex have significant p-values. This indicates, that survival odds are not independent of neither sex nor class. The tables of residuals below show that the higher the class, relatively more people survive. The same is true for females compared to males.

```
residuals(xtest_class)
```

```
##       Survived
## PClass     0     1
##    1st -5.68  7.87
##    2nd -1.70  2.35
##    3rd  4.89 -6.77
```

```
residuals(chisq.test(ct_sex))
```

```
##         Survived
## Sex          0     1
##   female -8.59 11.89
##   male    6.33 -8.76
```

e)

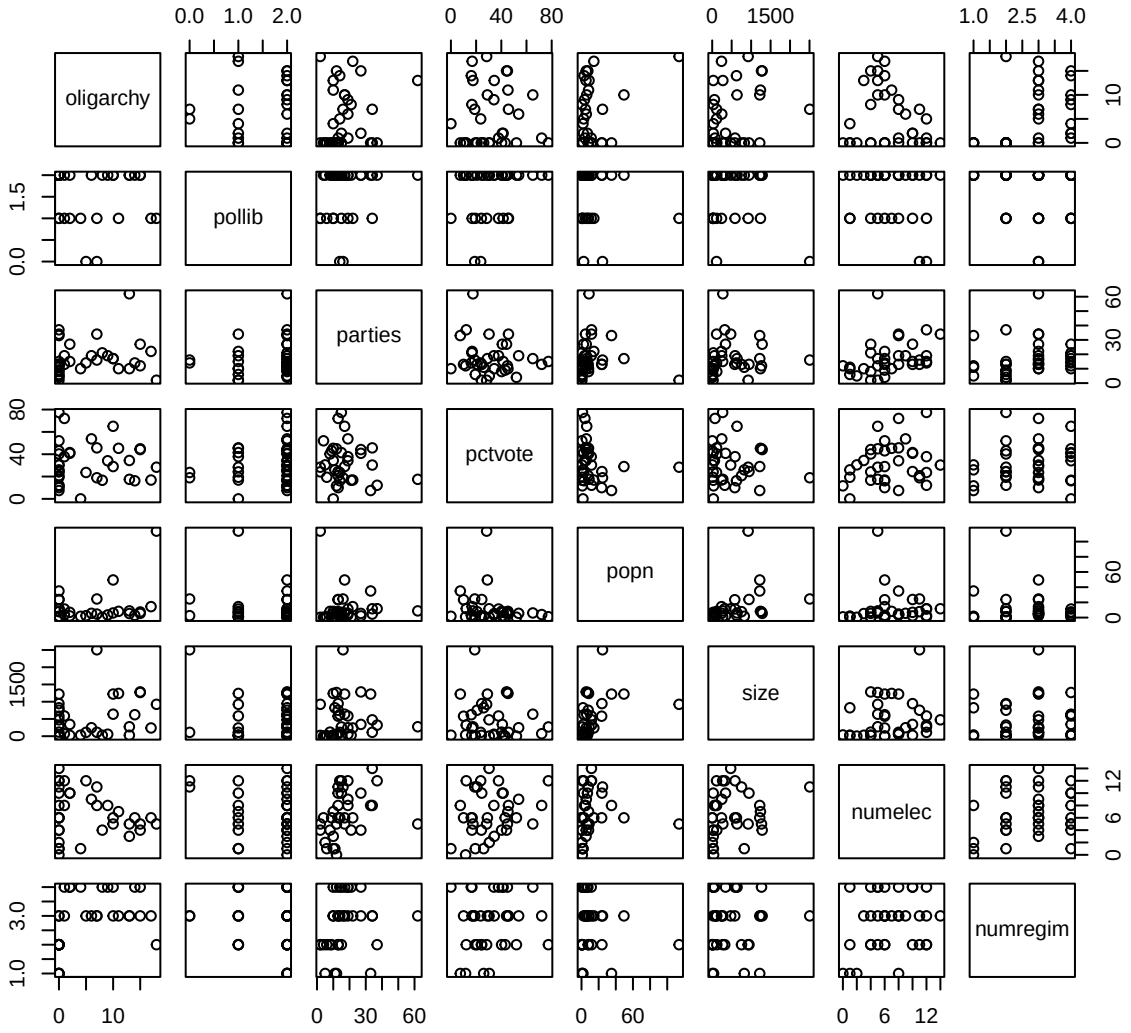
The approach in d) is not wrong, but has limited interpretability. Specifically, the contingency table is limited by its simplicity. It does not account for confounding variables (e.g., age in this case), leading to potentially false conclusions. This is related to the fact that no continuous predictors can be added to this model. Further, this approach does not provide us with a strength of the association between predictor and outcome. Logistic regression on the other hand, is able to account for multiple predictors simultaneously and estimate the magnitude and direction of predictor-outcome relationships. This may be further built upon to predict new data using a machine learning based on some quality criterion. However, logistic regression is more complex and less intuitive than a contingency table, so to guide hypothesis, it may be better to use a contingency table.

Exercise 4. Military Coups

a)

First, we test for collinearity between the explanatory variables in the dataset.

```
coups <- read.table("data/coups.txt", header = T)
pairs(coups[,-1])
```



There is no clear relationship between any of the explanatory variables. Thus, we can assume there is no issue with collinearity and we include all explanatory variables in the Poisson regression.

For simplicity, we treat all discrete numerical variables as continuous. However, we convert the categorical variable pollib to a factor.

```
coups$pollib <- as.factor(coups$pollib)
coupsglm <- glm(miltcoup~., family = poisson, data = coups)
drop1(coupsglm, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## miltcoup ~ oligarchy + pollib + parties + pctvote + popn + size +
##     numelec + numregim
##           Df Deviance AIC  LRT Pr(>Chi)
## <none>           28.2 113
```

```
## oligarchy  1     32.4 115 4.10   0.0428 *
## pollib     2     35.6 116 7.33   0.0256 *
## parties    1     35.3 118 7.06   0.0079 **
## pctvote    1     30.6 113 2.32   0.1275
## popn       1     30.6 113 2.35   0.1252
## size       1     29.2 112 0.99   0.3202
## numelec    1     28.4 111 0.18   0.6705
## numregim   1     29.1 112 0.81   0.3681
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The poisson regression suggests that only the explanatory variables of oligarchy, pollib, and parties significantly influence the odds of a successful military coup. As shown by the positive signs of the coefficients below, oligarchy and parties are both estimated to increase the odds of successful military coups. Compared to no civil rights ("pollib0"), having limited ("pollib1") or full ("pollib2") civil rights decreases the odds of coups.

```
summary(coupsglm)$coefficient[
  c("(Intercept)","oligarchy","pollib1", "pollib2","parties"),"Estimate"]
```

```
## (Intercept)   oligarchy     pollib1     pollib2     parties
##     -0.2334      0.0726     -1.1032     -1.6903      0.0312
```

b)

To ensure interpretability of the summary output, we treat the variable pollib as continuous during the step-down procedure. This is possible as pollib is an ordinal variable: Increasing levels of pollib correspond to increasing levels of political liberalization of a country. Once the step-down procedure is completed, we treat pollib categorically again to compare model fit.

```
model_df <- coups # create copy for step-down selection
model_df$pollib <- as.numeric(model_df$pollib)

done <- F
while (!done){
  model <- glm(miltcoup ~ ., family = poisson, data = model_df)
  model_smry <- summary(model)
  print(model_smry$coefficients)

  model_smry_coefs <- model_smry$coefficient[-1,"Pr(>|z|)"] # ignore intercept
  is_insignificant <- model_smry_coefs > .05
  if (sum(is_insignificant) == 0) done = T
  else {
    excl_var <- model_smry_coefs[which.max(model_smry_coefs)]
    # if (substr(names(excl_var), 1, 6) == "pollib"){
    #   names(excl_var) <- "pollib"
    #   print("WARNING POLLIB")
    # }
    writeLines(paste("\nExcluding variable:", names(excl_var), "\n"))
    model_df <- model_df[, -which(names(model_df) == names(excl_var))]
```

```
  }
}
```

```
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.20271   1.049314   0.193  0.84682
## oligarchy    0.07308   0.034596   2.112  0.03465
## pollib      -0.71298   0.272563  -2.616  0.00890
## parties      0.03077   0.011187   2.751  0.00595
## pctvote      0.01387   0.009753   1.422  0.15491
## popn         0.00934   0.006595   1.417  0.15658
## size        -0.00019   0.000248  -0.765  0.44447
## numelec     -0.01608   0.065484  -0.246  0.80605
## numregim     0.19173   0.229289   0.836  0.40303
##
## Excluding variable: numelec
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.069587   0.906928  0.0767  0.93884
## oligarchy    0.078137   0.027766  2.8142  0.00489
## pollib      -0.677390   0.229013 -2.9579  0.00310
## parties      0.029679   0.010289  2.8846  0.00392
## pctvote      0.013129   0.009289  1.4133  0.15756
## popn         0.008931   0.006375  1.4011  0.16120
## size        -0.000202   0.000244 -0.8295  0.40682
## numregim     0.175820   0.221050  0.7954  0.42639
##
## Excluding variable: numregim
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.576716   0.632427   0.912 0.361817
## oligarchy    0.085962   0.025910   3.318 0.000908
## pollib      -0.689403   0.227857  -3.026 0.002481
## parties      0.029194   0.010195   2.863 0.004190
## pctvote      0.014159   0.009198   1.539 0.123723
## popn         0.006274   0.005399   1.162 0.245272
## size        -0.000195   0.000242  -0.804 0.421378
##
## Excluding variable: size
##
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.40836    0.59923   0.681  0.49557
## oligarchy    0.08317    0.02544   3.270  0.00108
## pollib      -0.65283    0.22123  -2.951  0.00317
## parties      0.02980    0.01029   2.895  0.00379
## pctvote      0.01384    0.00928   1.491  0.13591
## popn         0.00559    0.00538   1.039  0.29883
##
```

```
## Excluding variable: popn
##
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.5730    0.56352    1.02 3.09e-01
## oligarchy     0.0954    0.02242    4.25 2.11e-05
## pollib       -0.6666    0.21756   -3.06 2.18e-03
## parties       0.0256    0.00950    2.70 6.99e-03
## pctvote       0.0121    0.00906    1.34 1.80e-01
##
## Excluding variable: pctvote
##
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   0.8255    0.52763    1.56 1.18e-01
## oligarchy     0.0926    0.02178    4.25 2.11e-05
## pollib       -0.5741    0.20438   -2.81 4.97e-03
## parties       0.0221    0.00896    2.46 1.38e-02
```

The step-down procedure corroborates our findings from a. Both approaches suggest that the most sensible additive model would contain only the three variables of oligarchy, pollib, and parties.

We can compare this reduced model to the model full model from **a**. Here we treat pollib categorically again.

```
coupsglm_reduced <- glm(miltcoup~oligarchy+pollib+parties, family = poisson, data = coups)
comparison <- anova(coupsglm_reduced, coupsglm, test = "Chisq")
comparison
```

```
## Analysis of Deviance Table
##
## Model 1: miltcoup ~ oligarchy + pollib + parties
## Model 2: miltcoup ~ oligarchy + pollib + parties + pctvote + popn + size +
##     numelec + numregim
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1        31       32.8
## 2        26       28.2  5     4.57     0.47
```

Excluding five of the eight explanatory variables from the model did not yield a significant drop in model fitness with $p = 0.47$. This shows that we have successfully reduced model complexity without significantly sacrificing fitness.

c)

```
obs <- data.frame(pollib = factor(0:2), oligarchy = mean(coups$oligarchy), parties = mean(coups
y_hat <- predict(coupsglm_reduced, obs, type="response")
names(y_hat) <- c("0", "1", "2")
print(y_hat)
```

```
##     0     1     2
## 2.908 1.772 0.956
```

As could be expected, the number of successful military coups seems to be negatively associated with the level of political liberalization. For a country with an average duration of oligarchy rule and an average number of political parties, the **expected number** of military coups is 2.91, 1.77, and 0.96 for levels 0,1, and 2, of political liberalization, respectively.