CompStat/R - Paper 3

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Part I: Linear regression

In this first part of the paper, we will program a function which estimates the unknown parameters β and σ of a (ordinary) linear regression model

$$y = X\beta + \varepsilon, \qquad \varepsilon \sim N(0, \sigma^2 I)$$

by the ordinary least squares (OLS) method. For a given design matrix X and response vector y the OLS estimator is given by

$$\hat{\beta} = (X'X)^{-1}X'y \tag{1}$$

with covariance matrix

$$\mathrm{Var}(\hat{\beta}) = \sigma^2(X'X)^{-1} \tag{2}$$

where σ^2 has to be estimated via the sum of squared residuals (SSR):

$$\hat{\sigma}^2 = \frac{SSR}{df} = \frac{\sum_i (y_i - x_i'\hat{\beta})^2}{n-k}. \tag{3}$$

The term df refers to the degrees of freedom, i.e. the difference between the number of observations n and the number of coefficients k.

Raw implementation

The function `linModEst` is a raw implementation of the OLS estimator. The function takes the response vector y (`y`) and design matrix X (`x`) as arguments and returns a list with the following named elements:

- `coefficients`: the estimated coefficients $\hat{\beta}$
- `vcov`: the estimated covariance matrix $\widehat{\mathrm{Var}(\hat{\beta})}$
- `sigma`: the square root of the estimated scale parameter $\hat{\sigma}^2$
- `df`: the degrees of freedom df

We use equations (1), (2), and (3) for the implementation and compute the inverse of $X'X$ using the `solve` function, which numerically solves the equation

$$(X'X)\,A = I$$

for the matrix $A = (X'X)^{-1}$. To efficiently compute $X'X$ and $X'y$, we use the `crossprod` function.

```r
linModEst <- function(x, y) {
  # Computes the OLS estimator and sample variance assuming a (ordinary) linear
  # regression model.
  #
  # Args:
  #   x: design matrix x
  #   y: response vector y
  #
  # Returns:
  #   A list with the following named elements:
  #     $coefficients: the estimated coefficients
  #     $vcov: the estimated covariance matrix
  #     $sigma: the square root of the estimated variance
  #     $df: the degrees of freedom in the model, i.e. the difference between
  #          the number of rows and columns of x

  # Compute the inverse of (x'x) using the solve- and crossprod-function
  inv <- solve(crossprod(x), diag(nrow = ncol(x)))

  # Compute beta hat, i.e. the estimated coefficients
  coefficients <- inv %*% crossprod(x, y)

  # Compute the degrees of freedom
  df <- nrow(x) - ncol(x)

  # Compute the sample variance via the sum of squared residuals (SSR)
  SSR <- sum((y - x %*% coefficients)^2)
  sigmaSquared <- SSR / df

  # Compute the covariance matrix
  vcov <- sigmaSquared * inv

  # Create named results list to be returned
  results <- list(coefficients, vcov, sqrt(sigmaSquared), df)
  names(results) <- c("coefficients", "vcov", "sigma", "df")

  # Return results
  results
}
```

We test our implementation by computing the linear relationship between heart weight, body weight and sex for the `cats` dataset contained in the package `MASS`. In the following piece of code, `cbind` combines its arguments by columns into a matrix with the number of columns given by the number of arguments and the number of rows given by the greatest length of the given arguments. Shorter arguments are repeated, as long as the matrix number of rows is a multiple of the shorter vector lengths.

Hence, `cbind(1, cats$Bwt, as.numeric(cats$Sex) - 1)` creates a design matrix with an intercept column out of a vector of ones, the variable body weight (`bwt`), and the variable sex (`Sex`), which is converted from a factor into a dummy variable using `as.numeric`. We subtract 1 to receive dummy variable values of 0 and 1, rather than 1 and 2 from the original data. Thus, `cbind` is used to build a proper design matrix of object type `matrix` with an intercept and dummy variable, such that our implementation of `linModEst` works correctly.

```r
# Load cats dataset
data(cats, package = "MASS")

# Compute OLS using our implementation
linModEst(
  x = cbind(1, cats$Bwt, as.numeric(cats$Sex) - 1),
  y = cats$Hwt
)
```

```
## $coefficients
##             [,1]
## [1,] -0.41495263
## [2,]  4.07576892
## [3,] -0.08209684
##
## $vcov
##             [,1]        [,2]        [,3]
## [1,]  0.52900070 -0.20504763  0.06563743
## [2,] -0.20504763  0.08690026 -0.04696312
## [3,]  0.06563743 -0.04696312  0.09244480
##
## $sigma
## [1] 1.457138
##
## $df
## [1] 141
```

We verify our results by comparing them to the output of R's `lm` function:

```r
summary(lm(Hwt ~ Bwt + Sex, data = cats))
```

```
##
## Call:
## lm(formula = Hwt ~ Bwt + Sex, data = cats)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.5833 -0.9700 -0.0948  1.0432  5.1016
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.4149     0.7273  -0.571    0.569
## Bwt           4.0758     0.2948  13.826   <2e-16 ***
## SexM         -0.0821     0.3040  -0.270    0.788
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.457 on 141 degrees of freedom
## Multiple R-squared:  0.6468, Adjusted R-squared:  0.6418
## F-statistic: 129.1 on 2 and 141 DF,  p-value: < 2.2e-16
```

As we can see, our implementation is correct.

Extend implementation

In this section, we write a new function `linMod(formula, data)`, which estimates a linear regression model specified by `formula` and uses our `linModEst` function defined above to estimate the model parameters again by the OLS method. `linMod` returns a list with the following named elements:

- `coefficients`: named vector of the estimated coefficients $\hat{\beta}$
- `vcov`: named estimated covariance matrix $\widehat{\text{Var}(\hat{\beta})}$
- `sigma`: the square root of the estimated scale parameter $\hat{\sigma}^2$
- `df`: the degrees of freedom *df*
- `formula`: the formula that represents the model equation
- `call`: the arguments with which `linMod` was called

Below, we use the `model.frame`, `model.extract`, and `model.matrix` functions, which are very convenient for working with objects of the class `formula`. `model.frame` returns a `data.frame` containing only the variables from its passed `data` argument, which are used in the `formula` expression given. The returned `data.frame` from the `model.frame` function has additional attributes, but these are not needed in our application. With `model.extract`, we are able to extract the response variable from the `data.frame` created by `model.frame`. Moreover, using `model.matrix`, we can create the design matrix (of object class `matrix`) again only from `formula` and `data` arguments. By default, the matrix returned by `model.matrix` includes an intercept and converts factor variables into proper dummy variables (i.e. a factor variable with L levels results in $L - 1$ dummy variables). More precisely, the default intercept is taken over from the `formula` object, which then by default adds an intercept term to the model equation, if not specified otherwise. Finally, we use `match.call` to return the call of our function with all the specified arguments by their full names.

```r
linMod <- function(formula, data) {
  # Computes the OLS estimator and sample variance assuming a (ordinary) linear
  # regression model with model equation specified by the formula-argument.
  #
  # Args:
  #   formula: a formula specifying the linear model equation
  #   data: a data.frame, list or environment, containing the variables used in
  #         formula
  #
  # Returns:
  #   A list with the following named elements:
  #     $coefficients: named vector of the estimated coefficients
  #     $vcov: named estimated covariance matrix
  #     $sigma: the square root of the estimated variance
  #     $df: the degrees of freedom in the model
  #     $formula: the formula that represents the model equation
  #     $call: the arguments with which the function was called

  # Extract the response variable using the model.extract function on the
  # data.frame returned by model.frame
  y <- model.extract(model.frame(formula, data = data), "response")

  # Create the design matrix using model.matrix, which overtakes an intercept
  # specified in the formula argument by default and converts factor variables into proper
  # dummy variables
  x <- model.matrix(formula, data = data)

  # Use previously defined linModEst for estimation
  tmp <- linModEst(x, y)
```

```r
  # Prepare the output
  rownames(tmp$coefficients) <- colnames(x)
  colnames(tmp$vcov) <- colnames(x)
  rownames(tmp$vcov) <- colnames(x)

  # Create results list to be returned
  results <- c(tmp, formula, match.call())
  names(results) <- c("coefficients", "vcov", "sigma", "df", "formula", "call")

  # Return results
  results
}
```

Let's again test our implementation:

```r
linMod(Hwt ~ Bwt + Sex, data = cats)
```

```
## $coefficients
##                    [,1]
## (Intercept) -0.41495263
## Bwt          4.07576892
## SexM        -0.08209684
##
## $vcov
##             (Intercept)         Bwt        SexM
## (Intercept)  0.52900070 -0.20504763  0.06563743
## Bwt         -0.20504763  0.08690026 -0.04696312
## SexM         0.06563743 -0.04696312  0.09244480
##
## $sigma
## [1] 1.457138
##
## $df
## [1] 141
##
## $formula
## Hwt ~ Bwt + Sex
##
## $call
## linMod(formula = Hwt ~ Bwt + Sex, data = cats)
```

As we can see, the output has the desired format and the correct results.

Part II: S3 for linear models

In this section we will expand upon our linear model function using R's S3 class system. Our goal is to improve the function by returning a more concise output and ultimately replicating the results of the lm function. We'll start by redefining the function linMod from Part I and assigning its return a class attribute of name linMod. This means that the linMod function now is a *constructor* function. As the name implies, this function "constructs" instances of class linMod. In detail, there actually is no formal definition of the "class" in R. Instead, a list *is* of a certain class. The class of the list is assigned by a class attribute. Hence, the output of linMod is a list of class linMod. The assigned class can now be used to call class-specific methods of generic functions such as print or summary.

1. Define the class

First, we implement the constructor linMod (modified function from Part I). For some additional calculations later (in summary method), we also return the data x and the response y.

```
linMod <- function(formula, data) {
  # Extract the response variable and create the design matrix
  y <- model.extract(model.frame(formula, data = data), "response")
  x <- model.matrix(formula, data = data)

  # Calulcate model using linModEst from Part I
  tmp <- linModEst(x, y)

  # Prepare the output
  rownames(tmp$coefficients) <- colnames(x)
  colnames(tmp$vcov) <- colnames(x)
  rownames(tmp$vcov) <- colnames(x)

  # Create results list to be returned and additionally add x and y as list
  results <- c(tmp, formula, match.call(), list(x, y))
  names(results) <- c("coefficients", "vcov", "sigma", "df",
                      "formula", "call", "x", "y")

  # Redefine the results list class attribute to "linMod"
  # This makes linMod a constructor for instances of class "linMod"
  class(results) <- "linMod"

  # Return instance of class "linMod"
  results
}
```

Now we would like to have a look at the structure of our list, which is an instance of the linMod class:

```
# Call constructur function which constructs an instance of class "linMod"
# Internally it still uses the model calculations from Part I (linModEst)
modelFit <- linMod(Hwt ~ Bwt + Sex, data = cats)

# Verify the structure of modelFit
str(modelFit)
```

```
## List of 8
##  $ coefficients: num [1:3, 1] -0.415 4.0758 -0.0821
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
```

```
##   .. ..$ : NULL
##  $ vcov        : num [1:3, 1:3] 0.529 -0.205 0.0656 -0.205 0.0869 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##  $ sigma       : num 1.46
##  $ df          : int 141
##  $ formula     :Class 'formula' length 3 Hwt ~ Bwt + Sex
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##  $ call        : language linMod(formula = Hwt ~ Bwt + Sex, data = cats)
##  $ x           : num [1:144, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:144] "1" "2" "3" "4" ...
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##   ..- attr(*, "assign")= int [1:3] 0 1 2
##   ..- attr(*, "contrasts")=List of 1
##   .. ..$ Sex: chr "contr.treatment"
##  $ y           : Named num [1:144] 7 7.4 9.5 7.2 7.3 7.6 8.1 8.2 8.3 8.5 ...
##   ..- attr(*, "names")= chr [1:144] "1" "2" "3" "4" ...
##  - attr(*, "class")= chr "linMod"
```

As we can see, we successfully redefined `linMod` such that the returned list is of class `linMod`.

2. Print method

Now we'd like to define a printing method for all objects of class `linMod` so that the function returns a more readable and concise output. We want to use a style which is close to the style for printing the `lm` information. To avoid writing a function with a new name, we define a new method `print.linMod` of the generic function `print`, assigned to the class `linMod`:

```r
print.linMod <- function(x, ...)  {
  # Print the function call and coefficients for objects of class "linMod"
  #
  # Args:
  #   x: instance of class linMod
  #   ...: passed arguments from generic function to this method
  #
  # Returns:
  #   No value gets returned. The function just prints to the console.

  # Convert coefficients matrix as named vector, which is more covenient
  coefficients <- as.vector(x$coefficients)
  names(coefficients) <- rownames(x$coefficients)

  # Create the output using cat, deparse and print.default
  cat("\nCall:\n", deparse(x$call), "\n\n", "Coefficients:\n",sep="")
  print.default(format(coefficients, digits = 2),
                print.gap = 2L,
                quote = FALSE)
  cat("\n")
}
```

We simply would like to print the model to see that the output is now clear and easy to read and similar to `lm`. It is not necessary to call the defined method above explicitly. `R` will recognize the newly defined `linMod` object and then locates the `linMod` *method* that we have written for the generic `print` function. We just need to call `print` and because `R` automatically calls print if we just enter the object into the console, we just need to call:

```
# Print modelFit
modelFit
```

```
##
## Call:
## linMod(formula = Hwt ~ Bwt + Sex, data = cats)
##
## Coefficients:
## (Intercept)          Bwt         SexM
##      -0.415        4.076       -0.082
```

The output is now much clearer and user-friendly.

3. Summary method

Next, we define a function, which will add some more information to the `linMod` object. We just would like to call the `summary` function and therefore again write a method `summary.linMod` for our class `linMod`. Thereby, when calling `summary`, `R` again automatically detects the class and calls our new method.

To build the summary we need to calculate the *standard errors*, the *t values*, the *p values*, the *residuals* and the *coefficient of determination*. We first have a look at the calculation of these values.

The *standard error* $\mathrm{se}(\hat{\beta}_i)$ of the estimated coefficient $\hat{\beta}_i$ is given by its estimated standard deviation. Hence, the *standard errors* $\mathrm{se}(\hat{\beta})$ are given by the square roots of the elements on the diagonal of the estimated covariance matrix $\widehat{\mathrm{Var}(\hat{\beta})}$:

$$\mathrm{se}(\hat{\beta}) = \sqrt{\mathrm{diag}\left(\widehat{\mathrm{Var}(\hat{\beta})}\right)} \in \mathbb{R}^k, \tag{4}$$

where the square root is applied element-wise.

The *t value* t_i of each estimated coefficient $\hat{\beta}_i$ is a realization of the following t-distributed test statistic

$$T_i = \frac{\hat{\beta}_i}{\mathrm{se}(\hat{\beta}_i)} \overset{H_0}{\sim} t_{(n-k)}, \tag{5}$$

which tests if the true coefficient β_i significantly differs from zero, i.e. we test the hypothesis

$$H_0 : \beta_i = 0 \quad vs. \quad H_1 : \beta_i \neq 0. \tag{6}$$

For the calculation of the corresponding *p value* p_i, we need to calculate the propability that our test statistic T_i is larger or equal to the realization t_i given by the data. Since the t-distribution is symmetric, we have for a two-sided t-test:

$$p_i = 2 \cdot \mathbb{P}(T_i \geq t_i) \tag{7}$$

We can use the `pt` function in `R` to compute the probability for a quantile of a t-distribution.

The *residuals* $\hat{\varepsilon}$ are simply the difference between the response y and the prediction $\hat{y}$ given by the model.

$$\hat{\varepsilon} = y - \hat{y} = y - X\hat{\beta} \tag{8}$$

At last, we calculate the *coefficient of determination* R^2 (also known as R-squared), which indicates the proportion of the variance in the dependent variable y that is predictable from the independent variables X. To calculate this coefficient, we need to calculate the sum of squared residuals SSR, and the variation of y, which is usually called SST (total sum of squares):

$$R^2 = 1 - \frac{\text{SSR}}{\text{SST}}, \tag{9}$$

with

$$\text{SSR} = \sum_i \hat{\varepsilon}^2 \quad \text{and} \quad \text{SST} = \sum_i (y_i - \bar{y})^2. \tag{10}$$

In the `summary.linMod` method below, we compute all these values, combine them and assign a class attribute to the result that the method returns:

```
summary.linMod <- function(x, ...)  {
  # This summary method for objects of class linMod computes standard errors,
  # t values, p values, residuals and the R-squared of the given model.
  #
  # Args:
  #   x: instance of class linMod
  #   ...: passed arguments from generic function to this method
  #
  # Returns:
  # A list with the following named elements:
  #     $coefficients: named matrix of the estimated coefficients, their
  #       standard errors, t values and p values
  #     $vcov: named estimated covariance matrix
  #     $sigma: the square root of the estimated variance
  #     $df: the degrees of freedom in the model
  #     $formula: the formula that represents the model equation
  #     $call: the arguments with which the function was called
  #     $residuals: the residuals of the model
  #     $rSquared: coefficient of determination of the model

  # Compute extra information for coefficients and combine them
  estimates <- x$coefficients
  stdErrors <- sqrt(diag(x$vcov))
  tValues <- estimates/stdErrors
  pValues <- 2*pt(-abs(tValues), df=(nrow(x$x)-ncol(x$x)))
  x$coefficients <- cbind(estimates, stdErrors, tValues, pValues)
  colnames(x$coefficients) <- c("Estimate", "Std. Err.", "t value", "P(>|t|)")

  # Compute residuals on basis of estimated response
  residuals <- x$y - (x$x %*% estimates)

  # Compute R-squared of whole model
  # Since the mean of the residuals is zero, we can use the var function
  rSquared <- 1-(var(residuals)/var(x$y))

  # Combine all results in one list
  results <- c(x, list(residuals=as.vector(residuals), rSquared=rSquared))
```

```r
  # Redefine the results to class "summary.linMod"
  # This function has now the role of a constructor
  class(results) <- "summary.linMod"

  # Return results
  results
}
```

After the implementation, we can test the structure of our new object:

```r
# Call constructur function which constructs an
# instance of class "summary.linMod"
summaryOfModelFit <- summary(modelFit)

# Verify the structure of summaryOfMOdelFit
str(summaryOfModelFit)
```

```
## List of 10
##  $ coefficients: num [1:3, 1:4] -0.415 4.0758 -0.0821 0.7273 0.2948 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##   .. ..$ : chr [1:4] "Estimate" "Std. Err." "t value" "P(>|t|)"
##  $ vcov        : num [1:3, 1:3] 0.529 -0.205 0.0656 -0.205 0.0869 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##  $ sigma       : num 1.46
##  $ df          : int 141
##  $ formula     :Class 'formula' length 3 Hwt ~ Bwt + Sex
##   .. ..- attr(*, ".Environment")=<environment: R_GlobalEnv>
##  $ call        : language linMod(formula = Hwt ~ Bwt + Sex, data = cats)
##  $ x           : num [1:144, 1:3] 1 1 1 1 1 1 1 1 1 1 ...
##   ..- attr(*, "dimnames")=List of 2
##   .. ..$ : chr [1:144] "1" "2" "3" "4" ...
##   .. ..$ : chr [1:3] "(Intercept)" "Bwt" "SexM"
##   ..- attr(*, "assign")= int [1:3] 0 1 2
##   ..- attr(*, "contrasts")=List of 1
##   .. ..$ Sex: chr "contr.treatment"
##  $ y           : Named num [1:144] 7 7.4 9.5 7.2 7.3 7.6 8.1 8.2 8.3 8.5 ...
##   ..- attr(*, "names")= chr [1:144] "1" "2" "3" "4" ...
##  $ residuals   : num [1:144] -0.737 -0.337 1.763 -0.944 -0.844 ...
##  $ rSquared    : num [1, 1] 0.647
##  - attr(*, "class")= chr "summary.linMod"
```

We can see, that we now have a list of 10 elements, where `$residuals` and `$rSquared` are new, and additionally the coefficient vector is extended.

4. Print method for summary.linMod

In the next step we would like to have a method to print objects of class `summary.linMod` in a self defined way. For this purpose we define a new method `print.summary.linMod` which, again, bases on the generic function `print`. The goal is to have an output which is similar to the `print.summary.lm` method.

```r
print.summary.linMod <- function(x, ...)  {
  # Print the function call, the residuals, the extended coefficients,
  # and the R-squared
  #
  # Args:
  #   x: instance of class summary.linMod
  #   ...: passed arguments from generic function to this method
  #
  # Returns:
  #   No value gets returned. The function just prints to the console.

  # Prepare residuals output using the quantile and mean function
  # Combine the results in the specified order and name it
  resQuant <- quantile(x$residuals)
  resMean <- mean(x$residuals)
  residuals <- c(resQuant[1:3], resMean, resQuant[4:5])
  names(residuals) <- c("Min.", "1st Qu.", "Median", "Mean", "3rd Qu.", "Max.")

  # Print everything using cat, deparse, printCoefmat and print.default
  cat("\nCall:\n", deparse(x$call),"\n\n", "Residuals:\n", sep = "")
  print.default(format(round(residuals, 5), nsmall = 5, scientific = FALSE),
                print.gap = 2L,
                quote = FALSE)
  cat("\nCoefficients:\n", sep = "")
  printCoefmat(x$coefficients, digits = 4, dig.tst = 2, has.Pvalue = TRUE)
  cat("\nMultiple R-squared: ", x$rSquared,
      "\n",
      "More Stats ...",
      sep = "")
}
```

If we simply print the object `summaryOfModelFit` of class `summary.linMod`, `R` again automatically detects the class and chooses the correct method, defined by us.

```r
# Print summaryOfModelFit
summaryOfModelFit
```

```
##
## Call:
## linMod(formula = Hwt ~ Bwt + Sex, data = cats)
##
## Residuals:
##     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## -3.58330  -0.97004  -0.09479   0.00000   1.04322   5.10155
##
## Coefficients:
##             Estimate Std. Err. t value P(>|t|)
## (Intercept)  -0.4149    0.7273   -0.57    0.57
## Bwt           4.0758    0.2948   13.83  <2e-16 ***
## SexM         -0.0821    0.3040   -0.27    0.79
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Multiple R-squared: 0.6468035
## More Stats ...
```

As we can see, the result is beautiful and similar to the output of `print.summary.lm`.

5. Plot method

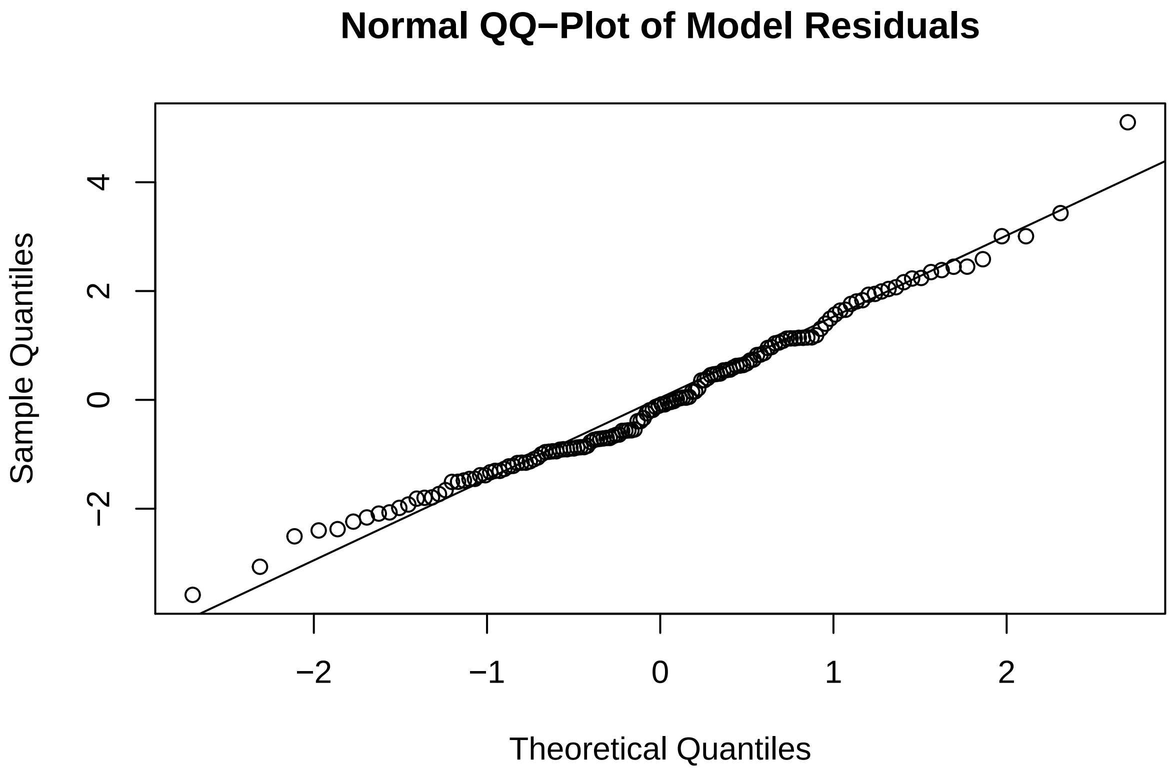
The last method will be a Q-Q plot. The Q-Q plot compares two probability distributions. In our case we would like to compare the distribution of the *residuals* $\hat{\varepsilon}$ with the theoretical quantiles of the standard normal distribution to check the normality assumption of the error terms in our model. For that purpose we can use the `qqnorm` function. Additionally we can draw a line of the ideal relation, using the `qqline` function from the `R` base package.

The method will be written for objects of class `linMod`. In this case, we have to compute the residuals again, because the residual calculation before was done for objects of class `summary.linMod`, which is not the input here.

```
plot.linMod <- function(x, ...) {
  # Plot a Q-Q plot
  #
  # Args:
  #   x: instance of class linMod
  #   ...: passed arguments from generic function to this method
  #
  # Returns:
  #   No value gets returned. The function plots a graph.

  # Compute the residuals
  residuals <- x$y - (x$x %*% x$coefficients)

  # Plot residuals against standard normal quantiles using qqnorm
  qqnorm(residuals, main="Normal QQ-Plot of Model Residuals")

  # Additionally draw a line with the ideal relation using qqline
  qqline(residuals)
}
```

If we call the generic plot function, `R` will find the correct method again, because `modelFit` is of class `linMod`.

```
# Plot modelFit
plot(modelFit)
```


Normal QQ−Plot of Model Residuals
Sample Quantiles
Theoretical Quantiles
−2
0
2
4
−2
−1
0
1
2