

Linear regression models with linear algebra and R

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1. Scatter plot and one linear predictor

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Let's consider following data set, and draw a scatter plot out of it.

The scatterplot becomes

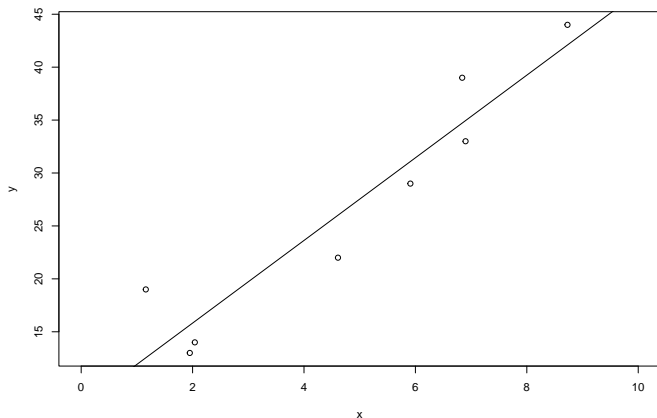


Figure 1: Scatterplot and a linear model with one predictor.

The coefficients of a linear regression fitted to that data set are $\beta_0 = 8.01$ and $\beta_1 = 3.90$.

Definition

- Importantly, a linear regression model with one variable is a statistical model which can be formulated as

$$Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i \quad (1)$$

and where $i = 1, \dots, n$ and $\varepsilon_i \sim N(0, \sigma^2)$.

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 - ▶ ε_i is an error term
 - ▶ x_i is the value of predictor aka independent aka covariate aka regressor

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- ▶ Linear model with multiple predictors X_1, X_2, \dots, X_k it can be written as

$$Y_i = \beta_0 + \beta_1 x_{i1} + \dots + \beta_k x_{ik} + \varepsilon_i \quad (2)$$

and where $i = 1, \dots, n$ and $\varepsilon_i \sim N(0, \sigma^2)$.

The fitting of linear model

- We want to minimize the sum of squares of error terms ε_i^2 , which can be written as $\varepsilon_i = Y_i - (\beta_0 + \beta_1 X_i)$. Note that error terms are in the same direction with Y -axis (and thus the same direction with Y_i).

```
m1 <- lm(y ~ x, data=dat)
m1

##
## Call:
## lm(formula = y ~ x, data = dat)
##
## Coefficients:
## (Intercept)          x
##      8.01      3.90
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- ▶ We will not go into technical details of minimization here.
- ▶ Using R we can fit the above model as follows. Assume that we have already read in data into object `dat`. We use `lm` function to fit the **linear model**. The resulting calculation we store into object named `m1`. The data object `dat` has columns named `x` and `y` but the names could be something else as well. The first argument of `lm` is formula, which is special type in R. Formula is handy for fitting many types of models. On the left hand side of the formula one writes the dependent (e.g. what is Y_i), then tilde (`~`) and then predictor variable(s). For multiple predictors one need to put a plus sign (`+`) between the predictors.

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## Call:
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```

2. Properties of linear models and interpretation

Properties of linear models

To have an interpretation for β_0 and β_1 we note that:

Expected value of Y_i is if we consider x_i being known and fixed:

$$\begin{aligned}E(Y_i|x_i) &= E(\beta_0 + \beta_1 x_i + \varepsilon_i) \\&= E(\beta_0) + E(\beta_1 x_i) + E(\varepsilon_i) \\&= E(\beta_0) + x_i E(\beta_1) + E(\varepsilon_i) \\&= \beta_0 + \beta_1 x_i\end{aligned}$$

because x_i is constant and $E(\varepsilon_i) = 0$.

Shortly put, the above calculation gives $E(Y_i|x_i) = \beta_0 + \beta_1 x_i$, which is called a systematic part of linear model.

- If we replace the β -notation with their estimates, then we can use that equation to calculate fitted values:

$$\hat{Y}_i = \hat{\beta}_0 + \hat{\beta}_1 x_i$$

Fitted values are calculated for the same x_i values which were in the original data.

```
fitted(m1)
```

```
##      1      2      3      4      5      6      7      8
## 34.716 42.095 34.951 12.541 15.625 26.010 15.976 31.085
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- Prediction can be obtained by the same equation but using any value. Here we predict new values using $x=10$ and $x=11$.

```
predict(m1,newdata = data.frame(x=c(10,11)))
```

```
##      1      2
## 47.053 50.958
```

Interpretation

- We want to interpret what happens in the population of our study. That is why we use equation of expected value of Y_i , that is $E(Y_i|x_i) = \beta_0 + \beta_1 x_i$ to give interpretation.

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- ▶ An interpretation of β_1 becomes available as

$$\begin{aligned} E(Y_i|x_i + 1) - E(Y_i|x_i) &= (\beta_0 + \beta_1(x_i + 1)) - (\beta_0 + \beta_1 x_i) \\ &= \beta_1(x_i + 1) - \beta_1 x_i \\ &= \beta_1 x_i + \beta_1 \cdot 1 - \beta_1 x_i \\ &= \beta_1 \end{aligned}$$

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- ▶ Thus, if e.g. $\beta_1 = 3.90415$ then the expected value of Y_i increases by 3.90415 units of y if x_i becomes increased with 1 unit of x .
- ▶ An interpretation of intercept term β_0 becomes available if we set $x_i = 0$ since that removes β_1 from the equation. Thus $E(Y_i|x_i = 0) = \beta_0 + \beta_1 \cdot 0 = \beta_0$.

3. Categorical predictors

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The predictors may as well be categorical ones. For example, we can model the mice weights where mice have two groups in a study. We are used to do that with a t-test but here we formulate it using linear regression. The results are the very same as with t-test!

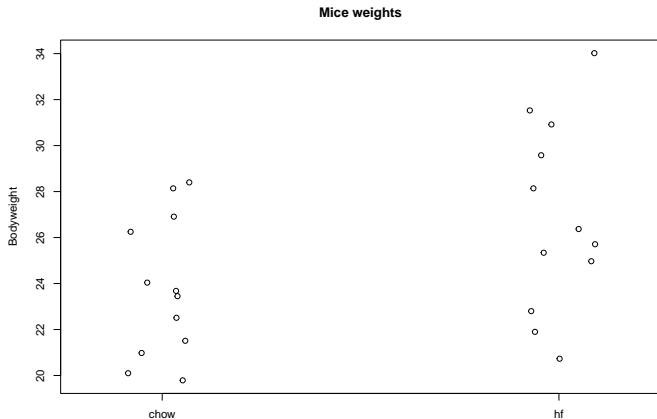


Figure 2: Mice weight with jitter. Example borrowed from Mike Love.

```
m1 <- lm(Bodyweight ~ Diet, data=dat)
```

```
summary(m1)
```

Dummy variables and indicator function

- ▶ Let's familiarise ourselves with dummy variables. Dummy variable is a variable which can have either value 0 or 1. For the example above, the dummy variable can be used to indicate that diet of a mouse is hf instead of chow. Thus, let's create a dummy variable so that it takes a value 1 if diet is hf and value 0 if diet is chow.

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- ▶ In mathematical formulations, a useful way of reminding ourselves that a predictor is a dummy variable is to use an indicator function. Indicator function $\mathbf{1}(x)$ takes value 1 if the condition x is true, and value 0 otherwise. The notation of indicator variable nicely reminds us that it will give value 1 or 0.

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$$Y_i = \beta_0 + \beta_1 \mathbf{1}(X_i = \text{hf}) + \varepsilon_i$$

where Y_i and x_i stand for values of Bodyweight and Diet respectively, and $i = 1, \dots, n$ and $\varepsilon_i \sim N(0, \sigma^2)$. In the above, the $\mathbf{1}(X_i = \text{hf})$ gives a value 1 if Diet is hf. Otherwise it gives 0.

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- ▶ Thus, the expected value of Y_i is β_0 if diet is chow. If the diet is hf, the expected values of Y_i is $\beta_0 + \beta_1$.

4. Basics of linear algebra

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Linear algebra is a branch of mathematics where instead of numbers (aka scalars) we operate on vectors and matrices. Linear algebra is a useful tool for solving systems of linear equations, and thus suitable for handling mathematics behind linear regression. Next, we go through some of the key concepts so that we can move forward to understand how linear regression can be solved.

Transpose

- ▶ Transpose of matrix \mathbf{A} is denoted as \mathbf{A}^T

$$\mathbf{A} = \begin{pmatrix} 1 & 2 \\ 3 & 4 \\ 5 & 6 \end{pmatrix} \implies \mathbf{A}^T = \begin{pmatrix} 1 & 3 & 5 \\ 2 & 4 & 6 \end{pmatrix}$$

Above matrix A is n times p matrix, where $n = 2, p = 3$.

```
A <- matrix(c(1,2,
              3,4,
              5,6),nrow=3,ncol=2,byrow=T)
```

A

```
##      [,1] [,2]
## [1,]    1    2
## [2,]    3    4
## [3,]    5    6
```

t(A)

```
##      [,1] [,2] [,3]
## [1,]    1    3    5
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- ▶ The above in R

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t(A)

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Vector

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Vector

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$$d = \begin{pmatrix} 1 \\ 3 \\ 5 \end{pmatrix}$$

- ▶ A transpose of a vector is a row vector.

$$d^T = \begin{bmatrix} 1 & 3 & 5 \end{bmatrix}$$

Cross product

- A cross product (aka matrix multiplication) of row vector with a column vector is

$$\begin{bmatrix} 1 & 2 & 3 \end{bmatrix} \begin{pmatrix} 4 \\ 5 \\ 6 \end{pmatrix} = \begin{bmatrix} 1 \cdot 4 + 2 \cdot 5 + 3 \cdot 6 \end{bmatrix} = \begin{bmatrix} 32 \end{bmatrix}$$

```
d <- c(4,5,6)
d
```

```
## [1] 4 5 6
```

```
t(d)
```

```
##      [,1] [,2] [,3]
## [1,]    4    5    6
```

```
t(t(d))
```

```
##      [,1]
## [1,]    4
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- ▶ Example with R

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Identity matrix

- Identity matrix is **I** has 1 on diagonal and 0 elsewhere. E.g.

$$\mathbf{I}_3 = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

```
diag(3)
```

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

Square matrix and inverse of a matrix

- If matrix has the same number of rows and columns, it is called a square matrix.

```
# Let's create a square matrix
```

```
B <- t(A) %*% A
```

```
B
```

```
##      [,1] [,2]
```

```
## [1,]   35   44
```

```
## [2,]   44   56
```

```
det(B) #determinant is not zero => invertible
```

```
## [1] 24
```

```
solve(B)
```

```
##      [,1] [,2]
```

```
## [1,]  2.3333 -1.8333
```

```
## [2,] -1.8333  1.4583
```

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- ▶ If matrix has the same number of rows and columns, it is called a square matrix.
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```

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```

- ▶ For invertible matrix **B** it follows that $\mathbf{B}\mathbf{B}^{-1} = \mathbf{I}$ and also $\mathbf{B}^{-1}\mathbf{B} = \mathbf{I}$.

Solving systems of equations using linear algebra

Matrices can be used to represent a systems of equations. To understand the basic concepts, let's have a look at following system of equations:

$$a + b + c = 6$$

$$3a - 2b + c = 2$$

$$2a + b - c = 1$$

$$\begin{pmatrix} 1 & 1 & 1 \\ 3 & -2 & 1 \\ 2 & 1 & -1 \end{pmatrix} \begin{pmatrix} a \\ b \\ c \end{pmatrix} = \begin{pmatrix} 6 \\ 2 \\ 1 \end{pmatrix}$$

Taking the inverse of square matrix and multiplying the equation from the left hand side with that solves the system.

$$\Rightarrow \begin{pmatrix} a \\ b \\ c \end{pmatrix} = \begin{pmatrix} 1 & 1 & 1 \\ 3 & -2 & 1 \\ 2 & 1 & -1 \end{pmatrix}^{-1} \begin{pmatrix} 6 \\ 2 \\ 1 \end{pmatrix}$$

The same as above with R

```
A <- matrix(c(1, 1, 1,
              3,-2, 1,
              2, 1,-1),nrow=3,ncol=3,byrow=T)
d <- c(6,2,1)
solve(A) %*% d
```

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

5. Linear models formulated with linear algebra

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Let's consider the previous example of two mice populations in Chapter 3. We have already seen how linear regression connects nicely with t-tests. We will now go through how it can be formulated using linear algebra.

Let $x_i = \mathbf{1}(\text{Diet} = \text{hf})$ which means that $x_i = 1$ if diet is hf, and $x_i = 0$ if diet is chow.

Lets define notation of matrices and vectors

$$\mathbf{Y} = \begin{pmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{pmatrix}, \mathbf{X} = \begin{pmatrix} 1 & x_1 \\ 1 & x_2 \\ \vdots & \vdots \\ 1 & x_n \end{pmatrix}, \beta = \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix} \text{ and } \varepsilon = \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{pmatrix}$$

So we can write linear regression using the notation above as

$$\begin{pmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{pmatrix} = \begin{pmatrix} 1 & x_1 \\ 1 & x_2 \\ \vdots & \vdots \\ 1 & x_n \end{pmatrix} \begin{pmatrix} \beta_0 \\ \beta_1 \end{pmatrix} + \begin{pmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{pmatrix}$$

and we can use matrix notation, so the above can be written as

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon$$

$$\mathbf{Y} = \mathbf{X}\beta + \varepsilon$$

The \mathbf{X} is what we call a design matrix. We can show design matrix in R from an object of `lm` by:

```
model.matrix(~ Diet, data=dat)
# or
model.matrix(m1)
```

6. Contrasts

6. Contrasts

As a running example to learn about more complex linear models, we will be using a dataset which compares the different frictional coefficients on the different legs of a spider. Specifically, we will be determining whether more friction comes from a pushing or pulling motion of the leg.

```
spider <- read.csv("spider_wolff_gorb_2013.csv", skip=1)
```

Initial visual inspection of the data

Each measurement comes from one of our legs while it is either pushing or pulling. So we have two variables. In RStudio we may view the data as

```
View(spider)
```

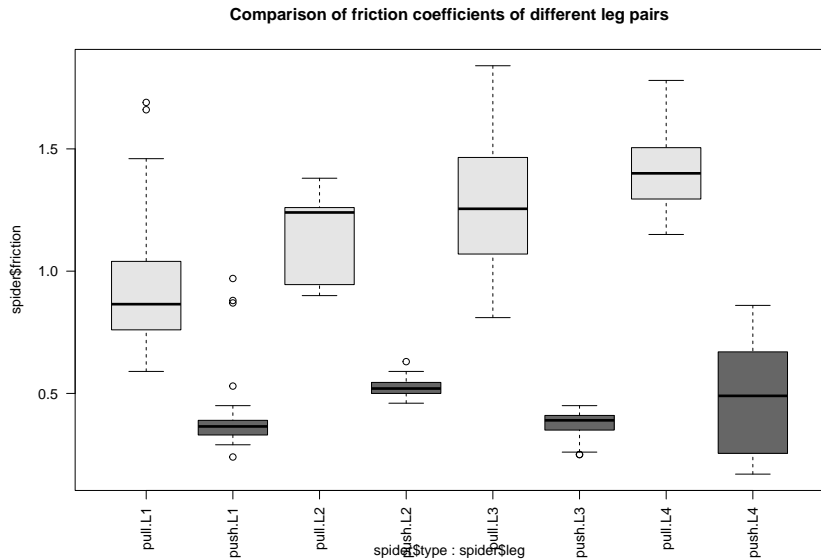
or just print it to console using `spider` or have a glimpse of first 6 rows

```
head(spider)
```

```
##   leg type friction
## 1  L1 pull    0.90
## 2  L1 pull    0.91
## 3  L1 pull    0.86
## 4  L1 pull    0.85
## 5  L1 pull    0.80
## 6  L1 pull    0.87
```

We can make a boxplot

```
boxplot(spider$friction ~ spider$type * spider$leg,  
        col=c("grey90","grey40"), las=2,  
        main="Comparison of friction coefficients of different leg pairs")
```



A linear model with two variables

In order to model both the leg pair differences (L1, L2, L3, L4) and the push vs. pull difference, we need to include both terms in the R formula. Let's see what kind of design matrix will be formed with two variables in the formula:

```
X <- model.matrix(~ type + leg, data=spider)
```

```
View(X)
```

To estimate coefficients for this model, we use `lm` with the formula `~ type + leg`. We'll save the linear model to `fitTL` standing for a *fit* with *Type* and *Leg*.

```
fitTL <- lm(friction ~ type + leg, data=spider)
fitTL
```

```
##
```

```
## Call:
```

```
## lm(formula = friction ~ type + leg, data = spider)
```

```
##
```

```
## Coefficients:
```

## (Intercept)	typepush	legL2	legL3	legL4
## 1.054	-0.779	0.172	0.160	0.281

```
coefs <- coef(fitTL)
coefs
```

## (Intercept)	typepush	legL2	legL3	legL4
## 1.05392	-0.77901	0.17192	0.16049	0.28134

R uses the name `Coefficients` to denote the component containing the least squares **estimates**. It is important to remember that the coefficients are parameters that we do not observe, but only estimate.

Mathematical representation

- The model we are fitting above can be written as

$$Y_i = \beta_0 + \beta_1 x_{i,1} + \beta_2 x_{i,2} + \beta_3 x_{i,3} + \beta_4 x_{i,4} + \varepsilon_i, i = 1, \dots, n$$

```
Y <- spider$friction
X <- model.matrix(~ type + leg, data=spider)
beta.hat <- solve(t(X) %*% X) %*% t(X) %*% Y
t(beta.hat)
```

```
##      (Intercept) typepush  legL2  legL3  legL4
## [1,]      1.0539 -0.77901 0.17192 0.16049 0.28134
```

We can see that these values agree with the output of `lm`.

Mathematical representation

- The model we are fitting above can be written as

$$Y_i = \beta_0 + \beta_1 x_{i,1} + \beta_2 x_{i,2} + \beta_3 x_{i,3} + \beta_4 x_{i,4} + \varepsilon_i, i = 1, \dots, n$$

- or consider the indicator variable style

$$\text{friction} = \beta_0 + \beta_1 \mathbf{1}(\text{type}=\text{push}) + \beta_2 \mathbf{1}(\text{leg}=\text{L2}) + \beta_3 \mathbf{1}(\text{leg}=\text{L3}) + \beta_4 \mathbf{1}(\text{leg}=\text{L4}) + \varepsilon_i,$$

where $i = 1, \dots, n$

```
Y <- spider$friction
X <- model.matrix(~ type + leg, data=spider)
beta.hat <- solve(t(X) %*% X) %*% t(X) %*% Y
t(beta.hat)
```

```
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where $i = 1, \dots, n$

- We can now form the matrix \mathbf{X} depicted above and obtain the least square estimates with:

$$\hat{\beta} = (\mathbf{X}^\top \mathbf{X})^{-1} \mathbf{X}^\top \mathbf{Y}$$

```
Y <- spider$friction
X <- model.matrix(~ type + leg, data=spider)
beta.hat <- solve(t(X) %*% X) %*% t(X) %*% Y
t(beta.hat)
```

```
##      (Intercept) typepush  legL2  legL3  legL4
## [1,]      1.0539 -0.77901 0.17192 0.16049 0.28134
```

We can see that these values agree with the output of `lm`.

Examining the estimated coefficients

We can make the same plot as before, with arrows for each of the estimated coefficients in the model (code not shown).

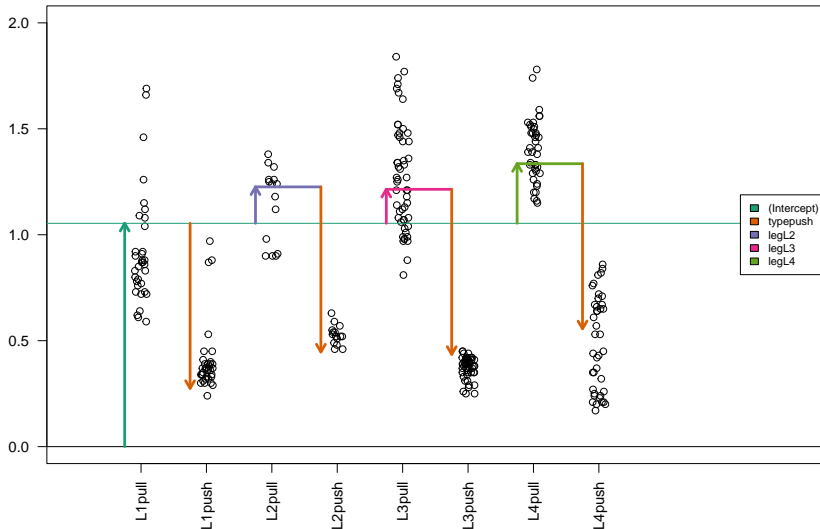


Figure 4: Diagram of the estimated coefficients in the linear model.

Contrasting coefficients

Sometimes, the comparison we are interested in is represented directly by a single coefficient in the model, such as the push vs. pull difference, which was `coefs[2]` above. However, sometimes, we want to make a comparison which is not a single coefficient, but a combination of coefficients, which is called a *contrast*. To introduce the concept of *contrasts*, first consider the comparisons which we can read off from the linear model summary:

```
coef(fitTL)
```

## (Intercept)	typepush	legL2	legL3	legL4	
##	1.05392	-0.77901	0.17192	0.16049	0.28134

Here we have the intercept estimate, the push vs. pull estimated effect across all leg pairs, and the estimates for the L2 vs. L1 effect, the L3 vs. L1 effect, and the L4 vs. L1 effect. What if we want to compare two groups and one of those groups is not L1? The solution to this question is to use *contrasts*.

A *contrast* is a combination of estimated coefficient: $\mathbf{c}^\top \hat{\beta}$, where \mathbf{c} is a column vector with as many rows as the number of coefficients in the linear model. If \mathbf{c} has a 0 for one or more of its rows, then the corresponding estimated coefficients in $\hat{\beta}$ are not involved in the contrast.

If we want to compare leg pairs L3 and L2, this is equivalent to contrasting two coefficients from the linear model because, in this contrast, the comparison to the reference level *L1* cancels out:

$$(L3 - L1) - (L2 - L1) = L3 - L2$$

An easy way to make these contrasts of two groups is to use the `contrast` function from the *contrast* package. We just need to specify which groups we want to compare. We have to pick one of *pull* or *push* types, although the answer will not differ, as we will see below.

```
library(contrast) #Available from CRAN
L3vsL2 <- contrast(fitTL,list(leg="L3",type="pull"),list(leg="L2",type="pull"))
L3vsL2
```

```
## lm model parameter contrast
```

```
##
```

##	Contrast	S.E.	Lower	Upper	t	df	Pr(> t)
##	-0.011429	0.043197	-0.096465	0.073606	-0.26	277	0.7915

The first column Contrast gives the L3 vs. L2 estimate from the model we fit above.

We can show that the least squares estimates of a linear combination of coefficients is the same linear combination of the estimates. Therefore, the effect size estimate is just the difference between two estimated coefficients. The contrast vector used by contrast is stored as a variable called X within the resulting object (not to be confused with our original **X**, the design matrix).

```
coefs[4] - coefs[3]
```

```
##      legL3
```

```
## -0.011429
```

```
(cT <- L3vsL2$X)
```

```
## (Intercept) typepush legL2 legL3 legL4
```

```
## 1          0          0      -1       1       0
```

```
## attr("assign")
```

```
## [1] 0 1 2 2 2
```

```
## attr("contrasts")
```

```
## attr("contrasts")$type
```

```
## [1] "contr.treatment"
```

```
##
```

```
## attr("contrasts")$leg
```

```
## [1] "contr.treatment"
```

```
cT %*% coefs
```

```
##      [,1]
```

```
## 1 -0.011429
```


Remarks

There will be an update on exercises:

- ▶ Topic of confounding is noted not needed to be completed.