Applied Statistical Methods - Solution 5

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Problem 1: Helmert Contrasts

Use the dataset of Body Weight and Breed to fit a linear model of Body Weight on Breed. The aim of this exercise is to use the Helmert-contrasts instead of the defautl Treatment contrasts. What are the estimable functions used in the Helmert-Contrasts and what are the effects that are reported for the different levels of the factor Breed? Verify your answer by comparing estimable functions of solutions of the least squares normal equations to the effects of lm().

The dataset is available under

https://charlotte-ngs.github.io/asmss2022/data/asm_bw_flem.csv

Hint

• Use options(contrasts = c("contr.helmert", "contr.helmert")) to change the default contrasts to the desired Helmert-Contrasts

Solution

• Compute solutions to least squares normal equation. First the data is read from the given file

## # A tibble: 10 x 6											
##		Animal	`Breast	Circumference`	`Body	Weight`	BCS	HEI	Breed		
##		<dbl></dbl>		<dbl></dbl>		<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<chr></chr>		
##	1	1		176		471	5	161	Angus		
##	2	2		177		463	4.2	121	Angus		
##	3	4		179		470	3	165	Angus		
##	4	7		181		518	4.4	163	Limousin		
##	5	8		182		511	4.4	149	Limousin		

##	6	9	183	510	3.5	143 Limousin
##	7	10	184	541	4.7	130 Limousin
##	8	3	178	481	4.9	157 Simmental
##	9	5	179	496	6.8	136 Simmental
##	10	6	180	491	4.9	123 Simmental

A solution vector depends on the matrix X and on the vector y. The vector y is directly obtained from the column Body Weight of the dataframe.

```
vec_y <- tbl_e05p01$`Body Weight`</pre>
```

The matrix X can be obtained from the function model.matrix().

```
mat_X <- model.matrix(lm(`Body Weight` ~ 0 + Breed, data = tbl_e05p01))
mat_X <- cbind(matrix(1, nrow = nrow(mat_X), ncol = 1), mat_X)
mat_X</pre>
```

```
##
       BreedAngus BreedLimousin BreedSimmental
## 1
                1
     1
                                             0
## 2 1
## 3 1
                                             0
                1
                0
## 4 1
## 5 1
                0
                                             0
## 6 1
## 7 1
## 8 1
## 9 1
                                             1
## 10 1
```

A solution for the least squares normal equations is obtained by

```
mat_xtx_ginv <- MASS::ginv(crossprod(mat_X))
mat_xty <- crossprod(mat_X, vec_y)
mat_b0 <- crossprod(mat_xtx_ginv, mat_xty)
mat_b0</pre>
```

```
## [,1]
## [1,] 369.33333
## [2,] 98.66667
## [3,] 150.66667
## [4,] 120.00000
```

The solutions correspond to the vector b^0 with the components

$$b^0 = \begin{bmatrix} \mu \\ \alpha_1 \\ \alpha_2 \\ \alpha_3 \end{bmatrix} = \begin{bmatrix} 369.333 \\ 98.667 \\ 150.667 \\ 120 \end{bmatrix}$$

• Change contrasts from default to Helmert. Start by saving away the existing options

```
opts <- options()
```

Change contrasts

```
options(contrasts = c("contr.helmert", "contr.helmert"))
getOption("contrasts")
```

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

• Find estimable functions associated to Helmert contrasts. Estimable functions are derived from the contrasts matrix. First the Breed column must be converted to a factor.

```
tbl_e05p01$Breed <- as.factor(tbl_e05p01$Breed)
c_mat_helmert <- contrasts(tbl_e05p01$Breed)
c_mat_helmert</pre>
```

```
## [,1] [,2]
## Angus -1 -1
## Limousin 1 -1
## Simmental 0 2
```

Add a columns of all ones to c_mat_helmert.

```
c_mat_helmert <- cbind(matrix(1, nrow = nrow(c_mat_helmert), ncol = 1), c_mat_helmert)
c_mat_helmert</pre>
```

```
## [,1] [,2] [,3]
## Angus 1 -1 -1
## Limousin 1 1 -1
## Simmental 1 0 2
```

Compute the inverse of c mat helmert

```
est_mat_helmert <- solve(c_mat_helmert)
est_mat_helmert</pre>
```

```
## Angus Limousin Simmental
## [1,] 0.3333333 0.3333333 0.3333333
## [2,] -0.5000000 0.5000000 0.0000000
## [3,] -0.1666667 -0.1666667 0.3333333
```

The first row tells us how the intercept is computed. The intercept (\hat{b}_0) here corresponds to

$$\hat{b}_0 = \frac{1}{3} \left(E(y_{1.}) + E(y_{2.}) + E(y_{3.}) \right)$$

where $E(y_1)$, $E(y_2)$ and $E(y_3)$ are the mean values of Body Weight for Angus, Limousin and Simmental animals, respectively.

```
n_mean_angus <- mean(tbl_e05p01[tbl_e05p01$Breed == "Angus", ]$`Body Weight`)
n_mean_limousin <- mean(tbl_e05p01[tbl_e05p01$Breed == "Limousin", ]$`Body Weight`)
n_mean_simmental <- mean(tbl_e05p01[tbl_e05p01$Breed == "Simmental", ]$`Body Weight`)
mean(c(n_mean_angus, n_mean_limousin,n_mean_simmental))</pre>
```

```
## [1] 492.4444
```

The second row of est_mat_helmert shows the first estimable function that is used. It corresponds to

$$\hat{b}_1 = \frac{1}{2}(\alpha_2 - \alpha_1)$$

where \hat{b}_1 measures the difference between the breeds Limousin and Angus corresponding to

```
1/2*(mat_b0[3] - mat_b0[2])
```

```
## [1] 26
```

The third row of est_mat_helmert shows how the Body Weight of the breed Simmental is compared to the two other breeds. It is

$$\hat{b}_2 = \frac{1}{6}(2\alpha_3 - \alpha_2 - \alpha_1)$$

which measures the difference between Simmental and Limousin and Angus together.

```
1/6 * (2*mat_b0[4] - mat_b0[3] - mat_b0[2])
```

```
## [1] -1.555556
```

 \bullet Check back with effects of lm(). The estimate for the intercept is

```
lm_helmert <- lm(`Body Weight` ~ Breed, data = tbl_e05p01)
coefficients(lm_helmert)["(Intercept)"]</pre>
```

```
## (Intercept)
## 492.4444
```

The estimates for the Breed effects can be seen from the list of all coefficients.

```
coefficients(lm_helmert)
```

```
## (Intercept) Breed1 Breed2
## 492.444444 26.00000 -1.555556
```

• Restore original options

```
options(opts)
```

Problem 2: Simulation

Use the results of the regression of Body Weight on Breast Circumference and simulate three datasets with 10, 30 and 100 observations respectively. What is the number of observations required to obtain the same regression results from the simulated dataset that you used in the simulation?

The original dataset is available under:

```
## https://charlotte-ngs.github.io/asmss2022/data/asm_bw_flem.csv
```

Solution