

PSC 103B - Lab 4 Assignment

Answer Key

The data

This week, we will be moving away from the NPAS dataset and using the version of the penguins dataset that we have been using in lab. Download this dataset from the Homework 5 assignment page on Canvas.

The variables we will be using today are:

- **species**: The species of the penguin (Adelie, Chinstrap, or Gentoo)
- **sex**: The sex of the penguin (male or female)
- **bill_length_mm**: The bill length of the penguin, measured in mm

```
hw_data <- read.csv("../lab/data/penguins_103b.csv")
```

Question 1

Suppose we were interested in conducting a factorial ANOVA with species and sex as our grouping variables, and bill length as the outcome.

Write out the 3 sets of null and alternative hypotheses for the factorial ANOVA – one for each main effect and one for the interaction. (3 points)

Hypotheses for Main Effect of Species

$$H_0 : \mu_{Adelie} = \mu_{Chinstrap} = \mu_{Gentoo} \quad H_1 : \text{At least one mean is not equal to the rest}$$

Where μ represents the average bill length

Hypotheses for Main Effect of Sex

$$H_0 : \mu_{Female} = \mu_{Male} \quad H_1 : \mu_{Female} \neq \mu_{Male}$$

Where μ represents the average bill length (note that our alternative hypothesis can be so specific because we only have 2 groups).

Hypotheses for the Interaction

H_0 : There is no interaction between species and sex on bill length
 H_1 : There is an interaction between species

Question 2

Conduct the factorial ANOVA. Show your code and output. (1 point)

```
fact_anova <- aov(bill_length_mm ~ species*sex, data = hw_data)
summary(fact_anova)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
species	2	4376	2187.8	399.792	<2e-16 ***
sex	1	752	752.0	137.424	<2e-16 ***
species:sex	2	18	9.1	1.669	0.191
Residuals	196	1073	5.5		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
2 observations deleted due to missingness

Question 3

If the main effect of dose is significant: Conduct the Tukey Honest Significant Difference post-hoc test. Show your code.

If the main effect of dose is not significant: State “The main effect of species was not significant”. (1 point)

```
TukeyHSD(fact_anova, which = "species")
```

Tukey multiple comparisons of means
95% family-wise confidence level

```
Fit: aov(formula = bill_length_mm ~ species * sex, data = hw_data)
```

\$species		diff	lwr	upr	p adj
Chinstrap-Adelie	10.435316	9.484314	11.3863184	0.000000	
Gentoo-Adelie	9.211940	8.257422	10.1664584	0.000000	
Gentoo-Chinstrap	-1.223376	-2.174378	-0.2723734	0.007592	

Question 4

If you conducted the Tukey HSD test in the previous question: Which groups were significantly different from each other? What was the difference (e.g., which group had the larger/smaller bill length)? (1 point)

Adelie penguins had significantly smaller bill lengths than both Chinstrap and Gentoo penguins, and Gentoo penguins had significantly smaller bill lengths than Chinstrap penguins.

Question 5

If the main effect of sex is significant: Calculate the means for each group. Show your code and output.

If the main effect of sex is not significant: State “The main effect of sex was not significant”. (1 point)

The mean bill length for female penguins was 42.61 mm, whereas the mean bill length for male penguins was 47.47 mm.

```
tapply(hw_data$bill_length_mm, hw_data$sex, mean)
```

female	male
42.60865	47.46939

Question 6

If you calculated the means in the previous question: Which group (males or females) had the longer bill length? (1 point)

Question 7

Was the interaction significant? What does this tell us (e.g., does the main effect of species depend on sex)? (1 point)

The interaction was not significant ($p = .19$), which means that the main effect of sex does not depend on species (or, that the main effect of species does not depend on the penguin's sex).

Question 8

```
interaction.plot(hw_data$species,  
                hw_data$sex,  
                hw_data$bill_length_mm,  
                type = "l",  
                xlab = "Species",  
                ylab = "Mean Bill Length",  
                trace.label = "Sex")
```

