

Statistical Computing with R - Assignment 3

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Exercise 1

Formatting and output config.

```
library(knitr)
library(formatR)
library(palmerpenguins)
library(dplyr)

##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##   filter, lag

## The following objects are masked from 'package:base':
##
##   intersect, setdiff, setequal, union

library(ggplot2)
knitr::opts_chunk$set(echo = TRUE)
knitr::opts_chunk$set(tidy.opts = list(width.cutoff = 80))
```

Q1

```
# Read in penguins
penguins_data <- palmerpenguins::penguins
# Print penguins to inspect
print(penguins_data)

## # A tibble: 344 x 8
##   species island   bill_length_mm bill_depth_mm flipper_length_mm body_mass_g
##   <fct>   <fct>         <dbl>         <dbl>         <int>         <int>
## 1 Adelie Torgersen     39.1           18.7           181           3750
## 2 Adelie Torgersen     39.5           17.4           186           3800
## 3 Adelie Torgersen     40.3            18           195           3250
## 4 Adelie Torgersen      NA            NA            NA            NA
## 5 Adelie Torgersen     36.7           19.3           193           3450
## 6 Adelie Torgersen     39.3           20.6           190           3650
## 7 Adelie Torgersen     38.9           17.8           181           3625
## 8 Adelie Torgersen     39.2           19.6           195           4675
## 9 Adelie Torgersen     34.1           18.1           193           3475
## 10 Adelie Torgersen     42            20.2           190           4250
## # i 334 more rows
## # i 2 more variables: sex <fct>, year <int>
```

```

# Convert penguins to a dataframe
penguins_df <- as.data.frame(penguins_data)

penguins is a tibble. ### Q2

# Count penguins by species and island
penguins_frequency_dist <- penguins_df %>%
  group_by(species, island) %>%
  count()
# Convert to DF
penguins_frequency_dist_df <- as.data.frame(penguins_frequency_dist)
# Print results
knitr::kable(penguins_frequency_dist_df,
  caption = "Distribution Frequency of Penguins by Species and Island"
)

```

Table 1: Distribution Frequency of Penguins by Species and Island

species	island	n
Adelie	Biscoe	44
Adelie	Dream	56
Adelie	Torgersen	52
Chinstrap	Dream	68
Gentoo	Biscoe	124

There are 3 different species in this dataset. The following are the species found on each island.

```

# Get unique penguin categories by island
species_by_island_df <- penguins_df %>%
  group_by(island) %>%
  summarise(species = unique(species))

## Warning: Returning more (or less) than 1 row per 'summarise()' group was deprecated in
## dplyr 1.1.0.
## i Please use 'reframe()' instead.
## i When switching from 'summarise()' to 'reframe()', remember that 'reframe()'
## always returns an ungrouped data frame and adjust accordingly.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.

## 'summarise()' has grouped output by 'island'. You can override using the
## '.groups' argument.

# Print results
knitr::kable(species_by_island_df,
  caption = "Penguin Species by Island"
)

```

Table 2: Penguin Species by Island

island	species
Biscoe	Adelie
Biscoe	Gentoo
Dream	Adelie

island	species
Dream	Chinstrap
Torgersen	Adelie

Q3

```
# Filter for Gentoo penguins and get bill length values
gentoo_idx <- which(penguins_df$species == "Gentoo")
gentoo_bill_lengths <- penguins_df[gentoo_idx, ]$bill_length_mm

# Filter for Chinstrap penguins and get bill length values
chinstrap_idx <- which(penguins_df$species == "Chinstrap")
chinstrap_bill_lengths <- penguins_df[chinstrap_idx, ]$bill_length_mm

# Define significance value
alpha <- 0.05

# Do t test to evaluate if chinstrap average length
# is greater than gentoo average length
t_test_results <- t.test(
  x = chinstrap_bill_lengths,
  y = gentoo_bill_lengths,
  alternative = "greater",
  var.equal = F
)
t_test_pvalue <- t_test_results$p.value
# Evaluate if p-value of t test is greater than signif. value
if (t_test_pvalue < alpha) {
  print("p-value of t-test is less than alpha, so we reject H0")
} else {
  print("p-value of t-test is greater than alpha, so we do not reject H0")
}
```

```
## [1] "p-value of t-test is less than alpha, so we reject H0"
```

Since a p-value of 0.0038652 is less than $\alpha = 0.05$, we reject H_0 that $\mu_C \geq \mu_G$, and conclude that the expected value of bill lengths of Chinstrap penguins is greater than that of Gentoo penguins.

Exercise 2

Q1

```
species_na_bool_idx <- is.na(penguins_df$species)
body_mass_na_bool_idx <- is.na(penguins_df$body_mass_g)
combined_bool_idx <- !species_na_bool_idx & !body_mass_na_bool_idx

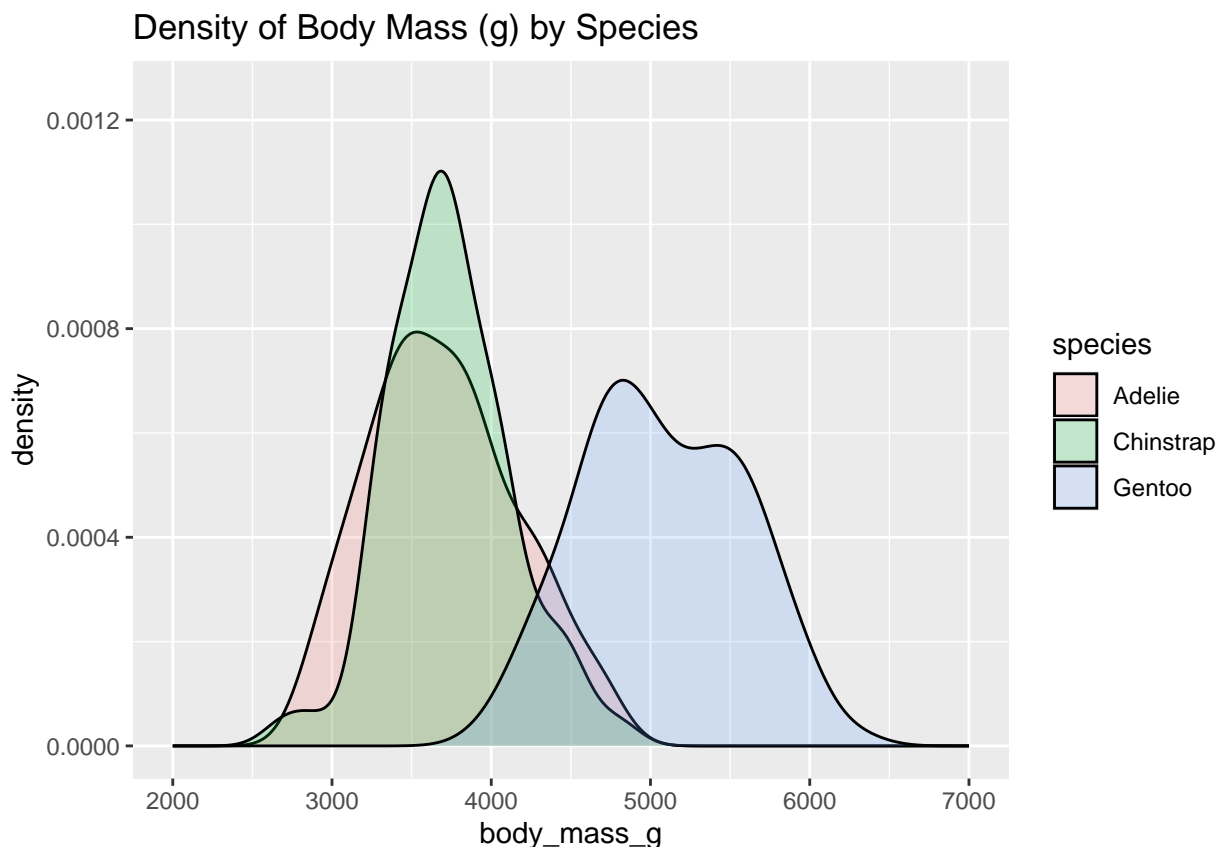
filtered_penguins_df <- penguins_df[combined_bool_idx, ]
rows_removed_num <- nrow(penguins_df) - nrow(filtered_penguins_df)
```

There are 2 rows removed due to missing species or body_mass values.

Q2

```
species <- unique(filtered_penguins_df$species)
species_color_list <- c("red", "blue", "green")
combined_species_df <- data.frame()
for (species_i in species) {
  species_idx <- filtered_penguins_df$species == species_i
  species_df <- filtered_penguins_df[species_idx, ]
  species_df_slice <- species_df[c("species", "body_mass_g")]
  combined_species_df <- rbind(combined_species_df, species_df_slice)
}

ggplot(combined_species_df, aes(body_mass_g, fill = species)) +
  geom_density(alpha = 0.2) +
  xlim(2000, 7000) +
  ylim(0, 1.25e-3) +
  ggtitle("Density of Body Mass (g) by Species")
```



It appears that Chinstrap and Adelie penguins have a similar average weight, which is lower than that of Gentoo penguins. Adelie and Gentoo penguins also have wider variance in weight than Chinstrap penguins.

Q3

```
filtered_penguins_df$body_mass_kg <- filtered_penguins_df$body_mass_g / 1000
neg.logl <- function(theta, pi1, pi2, pi3, w1, w2, w3, x) {
  mu1 <- theta[1]
  mu2 <- theta[2]
  mu3 <- theta[3]

  sigma_1 <- exp(theta[4])
```

```

sigma_2 <- exp(theta[5])
sigma_3 <- exp(theta[6])
# density of the mixture model:
f.x1 <- pi1 * dnorm(x, mu1, sd = sigma_1)
f.x2 <- pi2 * dnorm(x, mu2, sd = sigma_2)
f.x3 <- pi3 * dnorm(x, mu3, sd = sigma_3)
# negative log-likelihood:
-sum(w1 * log(f.x1) + w2 * log(f.x2) + w3 * log(f.x3))
}

```

Q4

```

set.seed(3953629)

em_algo <- function(x, pi1hat_init, pi2hat_init, pi3hat_init, n.iter) {
  n <- length(x)

  pi1hat <- rep(NA, n.iter)
  pi2hat <- rep(NA, n.iter)
  pi3hat <- rep(NA, n.iter)

  p1hat <- matrix(NA, n.iter, n)
  p2hat <- matrix(NA, n.iter, n)
  p3hat <- matrix(NA, n.iter, n)

  pi1hat_range <- pi1hat_init * 0.8
  pi2hat_range <- pi2hat_init * 0.8
  pi3hat_range <- pi3hat_init * 0.8

  pi1hat[1] <- pi1hat_init
  pi2hat[1] <- pi2hat_init
  pi3hat[1] <- pi3hat_init

  p1hat[1, ] <- runif(n, pi1hat_init - pi1hat_range, pi1hat_init + pi1hat_range)
  p2hat[1, ] <- runif(n, pi2hat_init - pi2hat_range, pi2hat_init + pi2hat_range)
  p3hat[1, ] <- runif(n, pi3hat_init - pi3hat_range, pi3hat_init + pi3hat_range)

  thetahat <- matrix(NA, n.iter, 6)
  theta_init_guesses <- c(
    rep(mean(x), 3),
    rep(sd(x), 3)
  )

  thetahat[1, ] <- optim(
    theta_init_guesses,
    function(theta) {
      neg.logl(theta, pi1hat[1], pi2hat[1], pi3hat[1],
        p1hat[1, ], p2hat[1, ], p3hat[1, ], x)
    }
  )$par

  for (t in 2:n.iter) {
    # modify to account for additional pi2
    # E step: update individual probability memberships
    #p1.temp <- cbind(
    #  pi1hat[t - 1] * dnorm(x, thetahat[t - 1, 1], exp(thetahat[t - 1, 4])),
    #  (1 - pi1hat[t - 1]) * dnorm(x, thetahat[t - 1, 2], exp(thetahat[t - 1, 5]))
    # )
  }
}

```

```

phat_numer.temp <- cbind(
  pi1hat[t - 1] * dnorm(x, thetahat[t - 1, 1], exp(thetahat[t - 1, 4])),
  pi2hat[t - 1] * dnorm(x, thetahat[t - 1, 2], exp(thetahat[t - 1, 5])),
  pi3hat[t - 1] * dnorm(x, thetahat[t - 1, 3], exp(thetahat[t - 1, 6]))
)
p1hat[t, ] <- phat_numer.temp[, 1]/rowSums(phat_numer.temp)
p2hat[t, ] <- phat_numer.temp[, 2]/rowSums(phat_numer.temp)
p3hat[t, ] <- phat_numer.temp[, 3]/rowSums(phat_numer.temp)
# M step: update parameter estimates
pi1hat[t] <- mean(p1hat[t, ])
pi2hat[t] <- mean(p2hat[t, ])
pi3hat[t] <- mean(p3hat[t, ])
thetahat[t, ] <- optim(thetahat[t-1, ], function(theta) {
  neg.logl(theta, pi1hat[t], pi2hat[t], pi3hat[t],
    p1hat[t, ], p2hat[t, ], p3hat[t, ], x)
})
)$par
}
final_theta <- thetahat[n.iter, ]
final_pi <- c(pi1hat[n.iter], pi2hat[n.iter], pi3hat[n.iter])
return(list(theta = final_theta, pi = final_pi))
}

n <- nrow(filtered_penguins_df)
peng_species_prop <- filtered_penguins_df %>%
  group_by(species) %>%
  count()
peng_species_prop$prop <- peng_species_prop$n / n

pi1hat_1 <- 1 / 3
pi2hat_1 <- 1 / 3
pi3hat_1 <- 1 / 3
# pihat_1 <- c(pi1hat_1, pi2hat_1)

pi1hat_2 <- c(peng_species_prop$prop)[1]
pi2hat_2 <- c(peng_species_prop$prop)[2]
pi3hat_2 <- c(peng_species_prop$prop)[3]
# pihat_2 <- c(pi1hat_2, pi2hat_2)

pi1hat_3 <- runif(1, 0, 0.45)
pi2hat_3 <- runif(1, 0, 0.45)
pi3hat_3 <- 1 - pi1hat_3 - pi2hat_3
# pihat_3 <- c(pi1hat_3, pi2hat_3)
# pihat_inits <- c(pihat_1, pihat_2, pihat_3)

n.iter <- 500

run_1 <- em_algo(filtered_penguins_df$body_mass_kg,
  pi1hat_1,
  pi2hat_1,
  pi3hat_1,
  n.iter)
run_2 <- em_algo(filtered_penguins_df$body_mass_kg,
  pi1hat_2,
  pi2hat_2,
  pi3hat_2,
  n.iter)
run_3 <- em_algo(filtered_penguins_df$body_mass_kg,
  pi1hat_3,

```

```
pi2hat_3,  
pi3hat_3,  
n.iter)
```

The starting points for `run_1` assume even probability across all three penguin distributions.

The starting points for `run_2` follows the empirical frequency distribution in the data.

The starting points for `run_3` are randomized, ensuring all three π still add to 1.