# Assignment 9

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```
library(tidyverse)
                                        ----- tidyverse 1.3.2 --
## -- Attaching packages -----
## v ggplot2 3.3.6 v purrr 0.3.5
## v tibble 3.1.8
                   v dplyr 1.0.10
## v tidyr 1.2.1
                   v stringr 1.4.1
## v readr 2.1.3 v forcats 0.5.2
## -- Conflicts ----- tidyverse conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
library(ggplot2)
library(Stat2Data)
library(palmerpenguins)
## Warning: package 'palmerpenguins' was built under R version 4.2.2
data(package = 'palmerpenguins')
```

#### 1. Basic concepts in classification

 $http://ianmadd.github.io/pages/Confidence\_Intervals\_Part4.html$ 

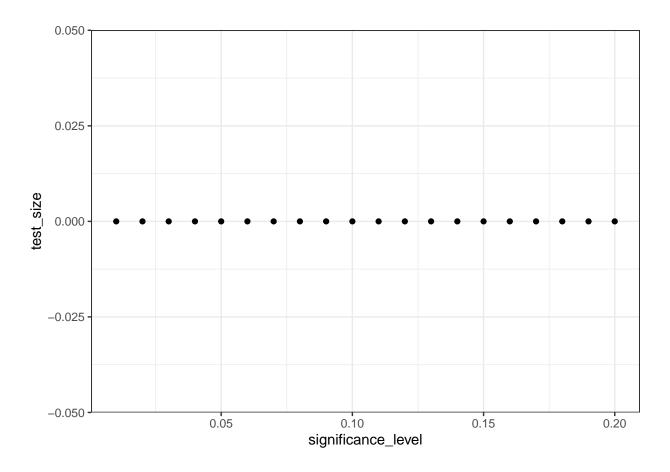
### 2. A chi-squared test of populatinn variance

#### 2 (Q1)

data("Hawks")

## 2 (Q2)

```
sample_size <- 100</pre>
mu_0 <- 1
sigma_0 <- 4
df \leftarrow data.frame(trial = seq(0.01, 0.20, 0.01)) \%
  mutate(samples = map(.x = trial, .f = ~rnorm(n = sample_size, mean = mu_0, sd = sigma_0))) %>%
  mutate(p_val = map_dbl(.x = samples, ~chi_square_test_one_sample_var(.x, sigma_0)))
alpha_list \leftarrow seq(0.01, 0.20, 0.01)
compute_test_size <- function(alpha) {</pre>
  reject_null <- df$p_val[df$p_val < alpha]</pre>
 return (mean(reject_null))
multiple_alpha_test_size_simulation_df <- data.frame(significance_level = alpha_list) %>%
  mutate(test_size = map_dbl(significance_level, compute_test_size))
multiple_alpha_test_size_simulation_df %>%
  ggplot(aes(x = significance_level, y = test_size)) +
  geom_point() +
 theme_bw()
```



### 2 (Q4)

```
sample_size <- 100
mu_0 <- 1
sigma <- 6
sigma_0 <- 4

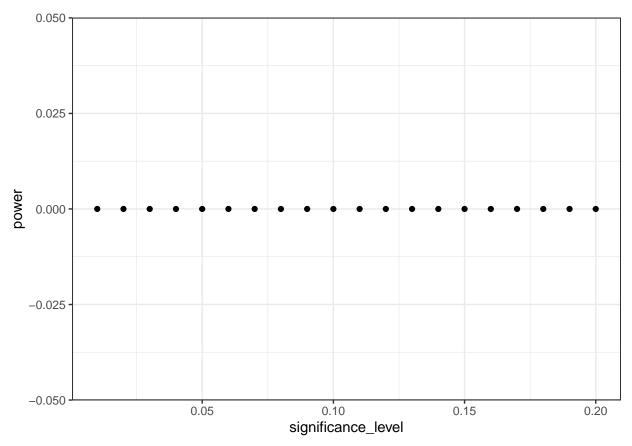
df <- data.frame(trial = seq(0.01, 0.20, 0.01)) %>%
    mutate(samples = map(.x = trial, .f = ~rnorm(n = sample_size, mean = mu_0, sd = sigma))) %>%
    mutate(p_val = map_dbl(.x = samples, ~chi_square_test_one_sample_var(.x, sigma_0)))

compute_power <- function(alpha) {
    reject_null <- df$p_val[df$p_val < alpha]
    return (mean(reject_null))
}

multiple_alpha_power_df <- data.frame(significance_level = seq(0.01, 0.20, 0.01)) %>%
    mutate(power = map_dbl(significance_level, compute_power))

multiple_alpha_power_df %>%
    ggplot(aes(x = significance_level, y = power)) +
```

```
geom_point() +
theme_bw()
```



## 5

```
bill_adelie <- penguins %>%
  filter(species == "Adelie") %>%
  pull(bill_length_mm)

bill_adelie <- bill_adelie[!is.na(bill_adelie)]
bill_adelie</pre>
```

```
## [1] 39.1 39.5 40.3 36.7 39.3 38.9 39.2 34.1 42.0 37.8 37.8 41.1 38.6 34.6 36.6 ## [16] 38.7 42.5 34.4 46.0 37.8 37.7 35.9 38.2 38.8 35.3 40.6 40.5 37.9 40.5 39.5 ## [31] 37.2 39.5 40.9 36.4 39.2 38.8 42.2 37.6 39.8 36.5 40.8 36.0 44.1 37.0 39.6 ## [46] 41.1 37.5 36.0 42.3 39.6 40.1 35.0 42.0 34.5 41.4 39.0 40.6 36.5 37.6 35.7 ## [61] 41.3 37.6 41.1 36.4 41.6 35.5 41.1 35.9 41.8 33.5 39.7 39.6 45.8 35.5 42.8 ## [76] 40.9 37.2 36.2 42.1 34.6 42.9 36.7 35.1 37.3 41.3 36.3 36.9 38.3 38.9 35.7 ## [91] 41.1 34.0 39.6 36.2 40.8 38.1 40.3 33.1 43.2 35.0 41.0 37.7 37.8 37.9 39.7 ## [106] 38.6 38.2 38.1 43.2 38.1 45.6 39.7 42.2 39.6 42.7 38.6 37.3 35.7 41.1 36.2 ## [136] 35.6 40.2 37.0 39.7 40.2 40.6 32.1 40.7 37.3 39.0 39.2 36.6 36.0 37.8 36.0 ## [151] 41.5
```