Lab 3

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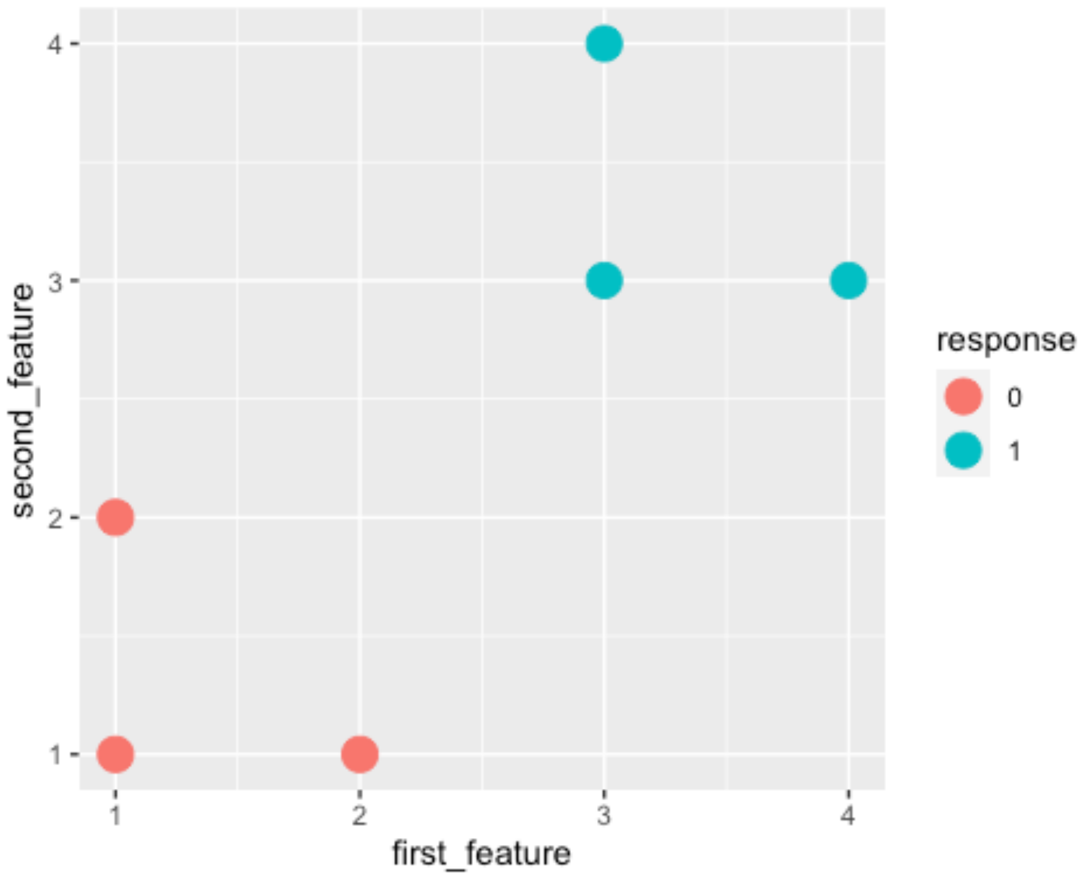
Support Vector Machine vs. Perceptron

We recreate the data from the previous lab and visualize it:

```r
pacman::p_load(ggplot2)
Xy_simple = data.frame(
 response = factor(c(0, 0, 0, 1, 1, 1)), #nominal
 first_feature = c(1, 1, 2, 3, 3, 4),    #continuous
 second_feature = c(1, 2, 1, 3, 4, 3)    #continuous
)
simple_viz_obj = ggplot(Xy_simple, aes(x = first_feature, y = second_feature,
color = response)) +
  geom_point(size = 5)
simple_viz_obj
```

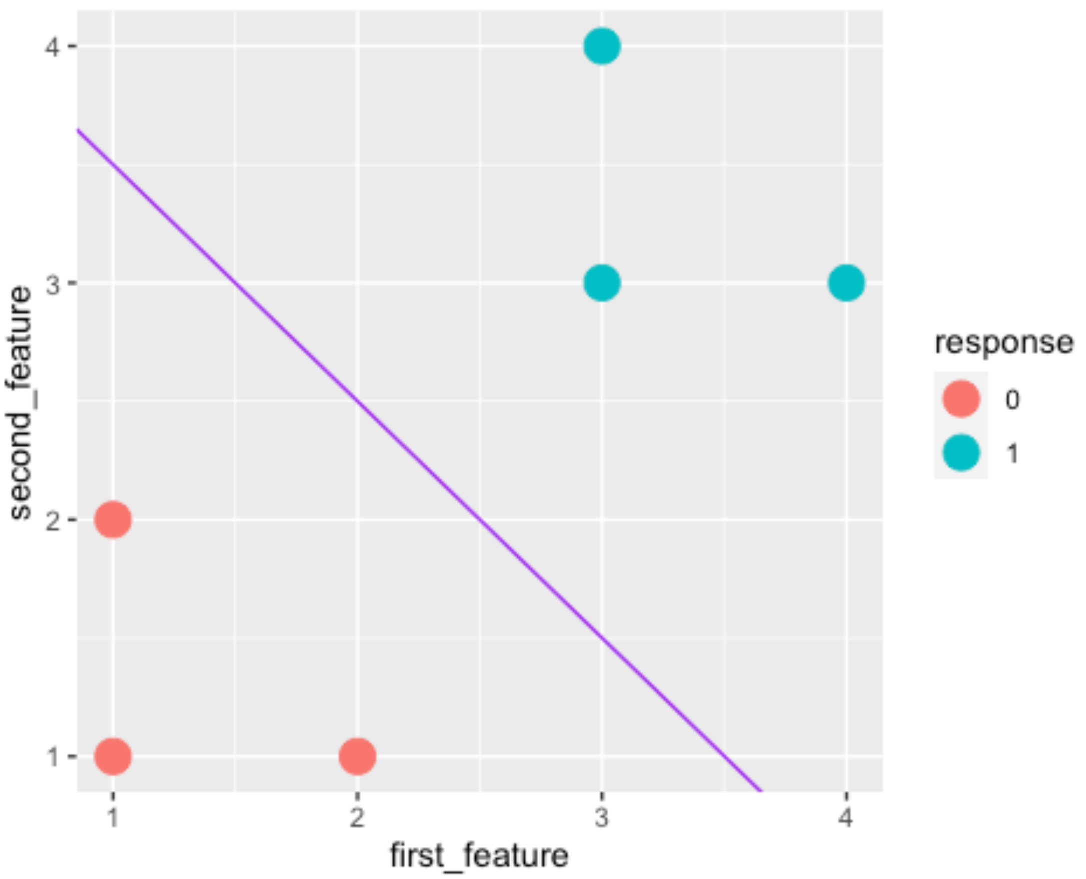


Use the `e1071` package to fit an SVM model to the simple data. Use a formula to create the model, pass in the data frame, set kernel to be `linear` for the linear SVM and don't scale the covariates. Call the model object `svm_model`. Otherwise the remaining code won't work.

```
pacman::p_load(e1071)
svm_model = svm(
  formula = Xy_simple$response ~.,
  data = Xy_simple,
  kernel = "linear",
  scale = FALSE
)
```

and then use the following code to visualize the line in purple:

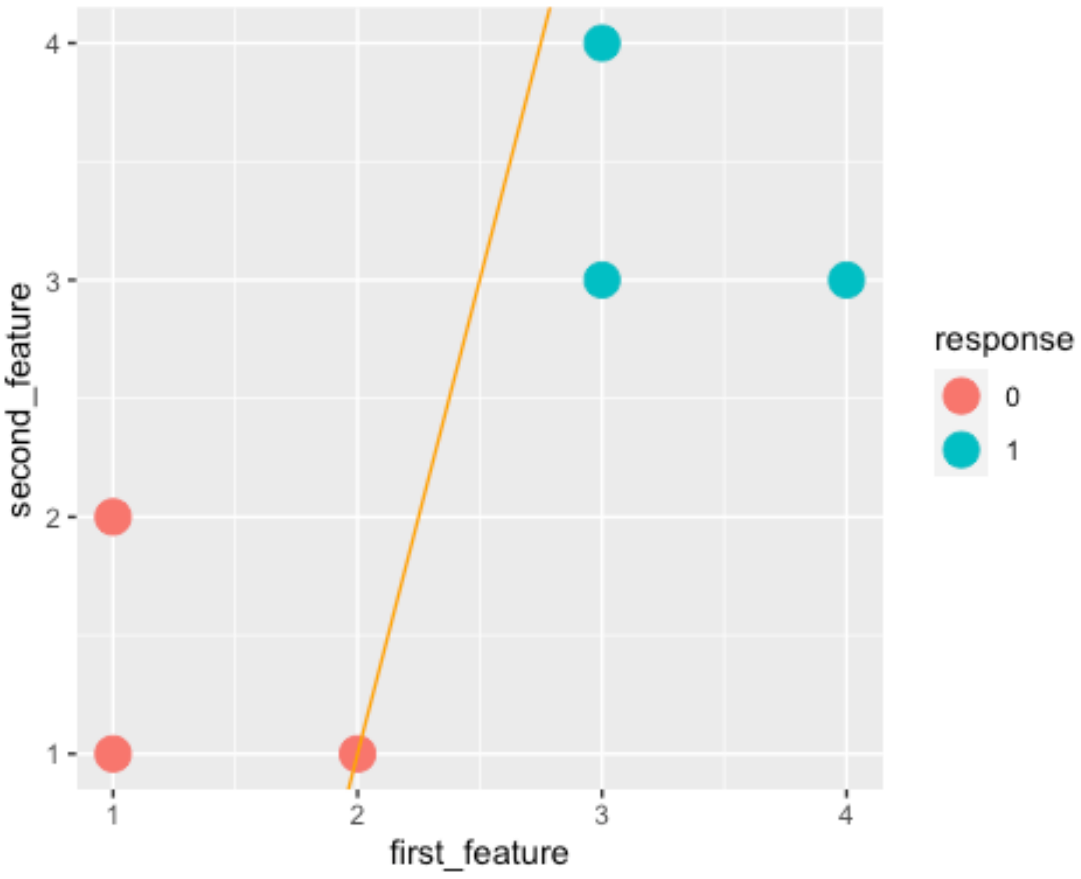
```
w_vec_simple_svm = c(
  svm_model$rho, #the b term
  -t(svm_model$coefs) %*% cbind(Xy_simple$first_feature,
Xy_simple$second_feature)[svm_model$index, ] # the other terms
)
simple_svm_line = geom_abline(
    intercept = -w_vec_simple_svm[1] / w_vec_simple_svm[3],
    slope = -w_vec_simple_svm[2] / w_vec_simple_svm[3],
    color = "purple")
simple_viz_obj + simple_svm_line
```



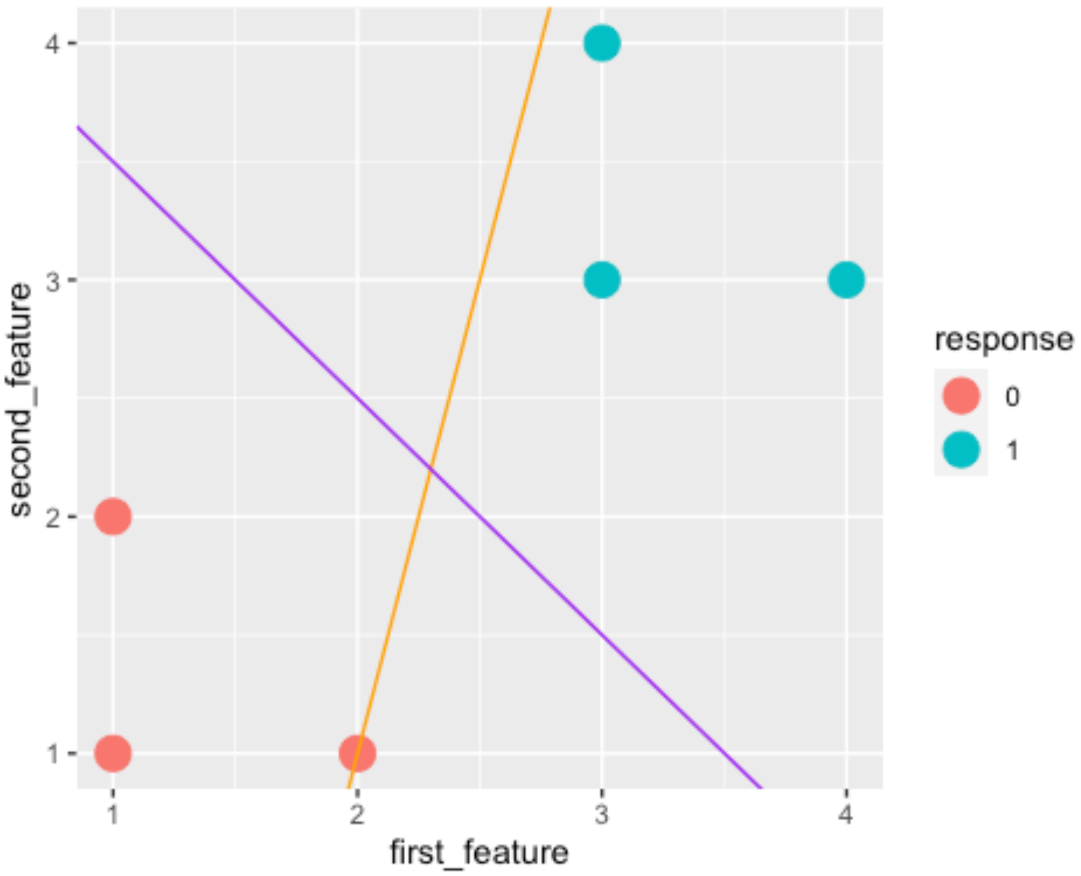
Source the perceptron_learning_algorithm function from lab 2. Then run the following to fit the perceptron and plot its line in orange with the SVM's line:

```
perceptron_learning_algorithm = function(Xinput, y_binary, MAX_ITER = 1000, w
= NULL)
  {
Xinput = as.matrix(cbind(1,Xinput))
p = ncol(Xinput)
w = rep(0, p)

for (iter in 1 : MAX_ITER){
  for (i in 1 : nrow(Xinput)) {
    x_i = Xinput[i, ]
    yhat_i = ifelse(sum(x_i * w) > 0, 1, 0)
    y_i = y_binary[i]
    for(j in 1:p){
      w[j] = w[j] + (y_i - yhat_i) * x_i[j]
    }
  }
}
w
}
w_vec_simple_per = perceptron_learning_algorithm(
  cbind(Xy_simple$first_feature, Xy_simple$second_feature),
  as.numeric(Xy_simple$response == 1)
)
simple_perceptron_line = geom_abline(
    intercept = -w_vec_simple_per[1] / w_vec_simple_per[3],
    slope = -w_vec_simple_per[2] / w_vec_simple_per[3],
    color = "orange")
simple_viz_obj + simple_perceptron_line
```



```
w_vec_simple_perple_perceptron_line = geom_abline(
    intercept = -w_vec_simple_per[1] / w_vec_simple_per[3],
    slope = -w_vec_simple_per[2] / w_vec_simple_per[3],
    color = "orange")
simple_viz_obj + simple_perceptron_line + simple_svm_line
```



Is this SVM line a better fit than the perceptron?

TO-DO: Yes I believe this is a better fit than the perceptron because the line is appears to evenly separate the the maximum margin hyperplane and separte the 0 responses below the line and the 1 responses above the line.

Now write pseudocode for your own implementation of the linear support vector machine algorithm using the Vapnik objective function we discussed.

Note there are differences between this spec and the perceptron learning algorithm spec in question #1. You should figure out a way to respect the `MAX_ITER` argument value.

```
#' Support Vector Machine
#
#' This function implements the hinge-loss + maximum margin linear support
vector machine algorithm of Vladimir Vapnik (1963).
#'
#' @param Xinput      The training data features as an n x p matrix.
#' @param y_binary    The training data responses as a vector of length n
consisting of only 0's and 1's.
#' @param MAX_ITER    The maximum number of iterations the algorithm
performs. Defaults to 5000.
#' @param lambda      A scalar hyperparameter trading off margin of the
```

```
hyperplane versus average hinge loss.
#'                      The default value is 1.
#' @return              The computed final parameter (weight) as a vector of
length p + 1
#SHE = 0
 # initialize a w vector
 # for x in MAX_ITER{
 #   for i in nrow(Xinput){
 #       SHE += max{0, (1/2) - (y_binary[i]-1/2)(w*Xinput[i]-b)}
 #   }
 # }
 # argmin{(SHE/n) + lambda(distance of w)^2}
 # w
  # Set n to be the length of Xinput
  # Set w to be an array of 0's the length of the columns of Xinput
  # Iterate MAX_ITER times
  # Iterate over the number of rows in Xinput
  # Set x_i to be the i-th row in Xinput
  # Set y_i to be the i-th value in y_binary
  # Set sum hinge error to be the sum of the maximum
```

If you are enrolled in 342W the following is extra credit but if you're enrolled in 650, the following is required. Write the actual code. You may want to take a look at the `optimx` package. You can feel free to define another function (a "private" function) in this chunk if you wish. R has a way to create public and private functions, but I believe you need to create a package to do that (beyond the scope of this course).

```
#' This function implements the hinge-loss + maximum margin linear support
vector machine algorithm of Vladimir Vapnik (1963).
#'
#' @param Xinput      The training data features as an n x p matrix.
#' @param y_binary    The training data responses as a vector of length n
consisting of only 0's and 1's.
#' @param MAX_ITER    The maximum number of iterations the algorithm
performs. Defaults to 5000.
#' @param lambda      A scalar hyperparameter trading off margin of the
hyperplane versus average hinge loss.
#'                      The default value is 1.
#' @return              The computed final parameter (weight) as a vector of
length p + 1
linear_svm_learning_algorithm = function(Xinput, y_binary, MAX_ITER = 5000,
lambda = 0.1){
  n = nrow(Xinput)
  Xinput = as.matrix(cbind(1, Xinput))
  w = rep(0, ncol(Xinput))
  for ( iter in 1 : MAX_ITER){
    for (i in 1 : nrow(Xinput)){
      x_i = Xinput[i, ]
      y_i = y_binary[i]
      sum_hinge_error = sum(max(0, 0.5 - (y_i - 0.5)*(x_i * w - w)))
      w = 1 / n * (sum_hinge_error) + lambda * norm(w) ^ 2
    }
  }
  w
}
```

If you wrote code (the extra credit), run your function using the defaults and plot it in brown vis-a-vis the previous model's line:

```
#y_binary = as.matrix(Xy_simple$response)
#X_simple_feature_matrix = as.matrix(Xy_simple)
#X_simple_feature_matrix$response = NULL
#svm_model_weights = linear_svm_learning_algorithm(Xinput, y_binary)
#my_svm_line = geom_abline(
#    intercept = svm_model_weights[1] / svm_model_weights[3],#NOTE: negative
sign removed from intercept argument here
#    slope = -svm_model_weights[2] / svm_model_weights[3],
 #   color = "brown")
#simple_viz_obj  + my_svm_line
```

Is this the same as what the `e1071` implementation returned? Why or why not?

TO-DO: Not sure I had a hard time getting this to work.

We now move on to simple linear modeling using the ordinary least squares algorithm.

Let's quickly recreate the sample data set from practice lecture 7:

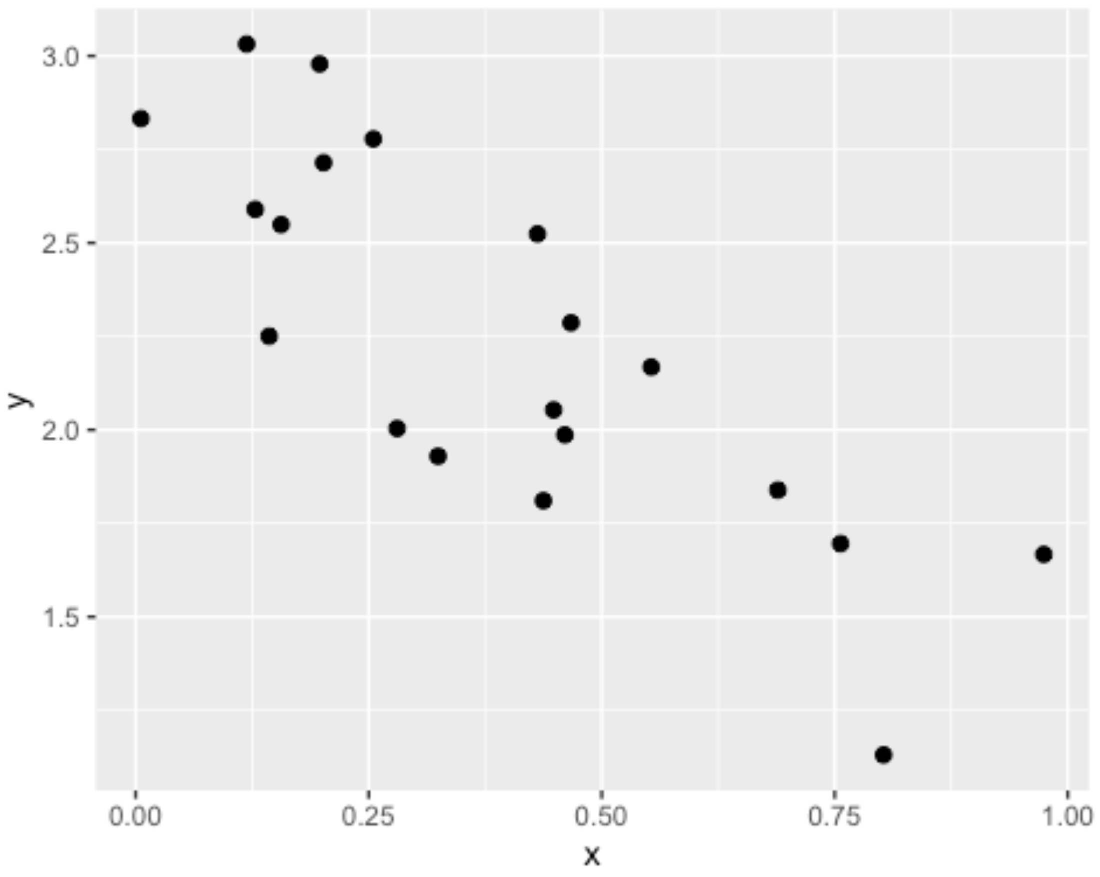
```
n = 20
x = runif(n)
beta_0 = 3
beta_1 = -2
```

Compute $h^*(x)$ as `h_star_x, then draw \epsilon \sim N(0, 0.33^2) as` epsilon`, then compute $\y$.

```
h_star_x = beta_0 + beta_1 * x
epsilon = rnorm(20, mean=0, sd=0.33)
y = h_star_x + epsilon
```

Graph the data by running the following chunk:

```
pacman::p_load(ggplot2)
simple_df = data.frame(x = x, y = y)
simple_viz_obj = ggplot(simple_df, aes(x, y)) +
  geom_point(size = 2)
simple_viz_obj
```



Does this make sense given the values of $beta_0$ and $beta_1$?

This makes sense because beta_0 equals 3 and this corresponds to a estimation of the y-intercept. Beta_1 is the slope which equals -2 and this seems to correspond to a line h_star that would best take in the data.

Write a function `my_simple_ols` that takes in a vector `x` and vector `y` and returns a list that contains the `b_0` (intercept), `b_1` (slope), `yhat` (the predictions), `e` (the residuals), `SSE`, `SST`, `MSE`, `RMSE` and `Rsq` (for the R-squared metric). Internally, you can only use the functions `sum` and `length` and other basic arithmetic operations. You should throw errors if the inputs are non-numeric or not the same length. You should also name the class of the return value `my_simple_ols_obj` by using the `class` function as a setter. No need to create ROxygen documentation here.

```
my_simple_ols = function(x, y){
  n = length(y)
  if (length(x) !=n) {
    stop("x and y need to be saame length.")
  }
  if(class(x) == 'numeric' && class (x) == 'integer') {
    stop("x needs to be numeric")
  }
  if(class(y) == 'numeric' && class (y) == 'integer') {
    stop("y needs to be numeric")
  }
  if (n <= 2) {
    stop("n must be more than 2")
  }
  xbar = sum(x)/n
  ybar = sum(y)/n
  b_1 = (sum(x*y)-n*xbar*ybar)/(sum(x^2) - n*xbar^2)
  b_0 = ybar - b_1*xbar
  yhat = b_0 + b_1*x
  e = y - yhat
  SSE = sum(e^2)
  SST = sum((y-ybar)^2)
  MSE = SSE/(n-2)
  RMSE = sqrt(MSE)
  Rsq = 1 - SSE/SST

  model = list(b_0 = b_0, b_1 = b_1, yhat = yhat, e = e, SSE = SSE, SST =
SST, MSE = MSE, RMSE = RMSE, Rsq = Rsq)

  class(model)= "my_simple_ols_obj"
  model
  }
```

Verify your computations are correct for the vectors x and y from the first chunk using the `lm` function in R:

```
lm_mod = lm(y~x)
my_simple_ols_mod = my_simple_ols(x,y)
#run the tests to ensure the function is up to spec
pacman::p_load(testthat)
expect_equal(my_simple_ols_mod$b_0, as.numeric(coef(lm_mod)[1]), tol = 1e-4)
expect_equal(my_simple_ols_mod$b_1, as.numeric(coef(lm_mod)[2]), tol = 1e-4)
expect_equal(my_simple_ols_mod$RMSE, summary(lm_mod)$sigma, tol = 1e-4)
expect_equal(my_simple_ols_mod$Rsq, summary(lm_mod)$r.squared, tol = 1e-4)
```

Verify that the average of the residuals is 0 using the `expect_equal`. Hint: use the syntax above.

```
mean(my_simple_ols_mod$e)

## [1] 9.992172e-17

expect_equal(mean(my_simple_ols_mod$e), 0) #average function can be close to
0, not 0.
```

Create the X matrix for this data example. Make sure it has the correct dimension.

```
X = cbind(1,x)
```

Use the `model.matrix` function to compute the matrix `X` and verify it is the same as your manual construction.

```
model.matrix(~x)
```

```
##    (Intercept)          x
## 1            1 0.44843867
## 2            1 0.55315575
## 3            1 0.14326148
## 4            1 0.46704281
## 5            1 0.43112114
## 6            1 0.19737658
## 7            1 0.97424881
## 8            1 0.43741391
## 9            1 0.11907041
## 10           1 0.25496015
## 11           1 0.75619439
## 12           1 0.32443350
## 13           1 0.28053023
## 14           1 0.46047326
## 15           1 0.12826948
## 16           1 0.20163307
## 17           1 0.68898295
## 18           1 0.80242589
## 19           1 0.15604481
## 20           1 0.00562785
## attr(,"assign")
## [1] 0 1
```

Create a prediction method g that takes in a vector `x_star` and `my_simple_ols_obj`, an object of type `my_simple_ols_obj` and predicts y values for each entry in `x_star`.

```
g = function(my_simple_ols_obj, x_star) {
  my_simple_ols_obj$b_0 + my_simple_ols_obj$b_1 * x_star
}
```

Use this function to verify that when predicting for the average x, you get the average y.

```
expect_equal(g(my_simple_ols_mod, mean(x)), mean(y))
```

In class we spoke about error due to ignorance, misspecification error and estimation error. Show that as n grows, estimation error shrinks. Let us define an error metric that is the difference between b_0 and b_1 and β_0 and β_1. How about $h = ||b - \beta||^2$ where the quantities are now the vectors of size two. Show as n increases, this shrinks.

```
beta_0 = 3
beta_1 = -2
beta = c(beta_0, beta_1)

ns = 10^(1:8)
errors_in_b = array(NA, length(ns))
```

```
for (i in 1 : length(ns)) {
  n = ns[i]
  x = runif(n)
  h_star_x = beta_0 + beta_1 * x
  epsilon = rnorm(n, mean = 0, sd = 0.33)
  y = h_star_x + epsilon

mod = my_simple_ols(x,y)
b = c(mod$b_0, mod$b_1)

  errors_in_b[i] = sum((beta - b)^2)
}
errors_in_b

## [1] 1.415580e-01 8.163763e-02 1.721436e-03 1.965602e-05 1.498466e-05
## [6] 3.405512e-07 4.174815e-09 1.717293e-08

log(errors_in_b, 10)

## [1] -0.8490656 -1.0881096 -2.7641092 -4.7065045 -4.8243530 -6.4678176 -
8.3793628
## [8] -7.7651555
```

We are now going to repeat one of the first linear model building exercises in history — that of Sir Francis Galton in 1886. First load up package HistData.

```
pacman::p_load(HistData)
```

In it, there is a dataset called Galton. Load it up.

```
data(Galton)
```

You now should have a data frame in your workspace called Galton. Summarize this data frame and write a few sentences about what you see. Make sure you report n, p and a bit about what the columns represent and how the data was measured. See the help file ?Galton. p is 1 and n is 928 the number of observations

```
pacman::p_load(skimr)
skim(Galton)
```

Data summary

Name	Galton
Number of rows	928
Number of columns	2

Column type frequency:

numeric	2

Group variables None

Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100	hist
parent	0	1	68.31	1.79	64.0	67.5	68.5	69.5	73.0	
child	0	1	68.09	2.52	61.7	66.2	68.2	70.2	73.7	

TO-DO ## Find the average height (include both parents and children in this computation).

```
avg_height = mean(c(Galton$parent, Galton$child))
avg_height

## [1] 68.19833
```

If you were predicting child height from parent height and you were using the null model, what would the RMSE be of this model be?

```
n = nrow(Galton)
SST = sum((Galton$child - mean(Galton$child))^2)
sqrt(SST/(n-1))

## [1] 2.517941
```

Note that in Math 241 you learned that the sample average is an estimate of the “mean”, the population expected value of height. We will call the average the “mean” going forward since it is probably correct to the nearest tenth of an inch with this amount of data.

Run a linear model attempting to explain the childrens’ height using the parents’ height. Use `lm` and use the R formula notation. Compute and report b_0, b_1, RMSE and R^2.

```
mod = lm(child~parent, Galton)
b_0 = coef(mod)[1]
b_1 = coef(mod)[2]
summary(mod)$sigma

## [1] 2.238547

summary(mod)$r.squared

## [1] 0.2104629
```

Interpret all four quantities: b_0, b_1, RMSE and R^2. Use the correct units of these metrics in your answer.

b_0 = This line gives the y-intercept that you would need to graph this but it should not be considered as 0 height for the parent because obviously an individual cannot have zero height. b_1 = For every increase 1 inch increase in the parent's height the child's height increases by a value of 0.642906 inches. RMSE = 2.23 times 2 = plus or minus 4.5 inches which would give 9 inch range 95% of the time. R squared: Only 21% variance explained

How good is this model? How well does it predict? Discuss.

This is model is not great for prediction because of the range of 9 inches which I believe is a huge gap. Also this model has only one feature which may not be great for making predictions. However, I think this model is good for giving a general idea of this population to conclude a biological phenomena of height.

TO-DO

It is reasonable to assume that parents and their children have the same height? Explain why this is reasonable using basic biology and common sense.

I would say yes that it is reasonable that parents and their children would have roughly the same height when averaged across a population because height has a hereditary component to it and thus it would be passed from generation to generation.

TO-DO

If they were to have the same height and any differences were just random noise with expectation 0, what would the values of β_0 and β_1 be?

beta 0 = 0 - y intercept beta 1 = 1 - slope

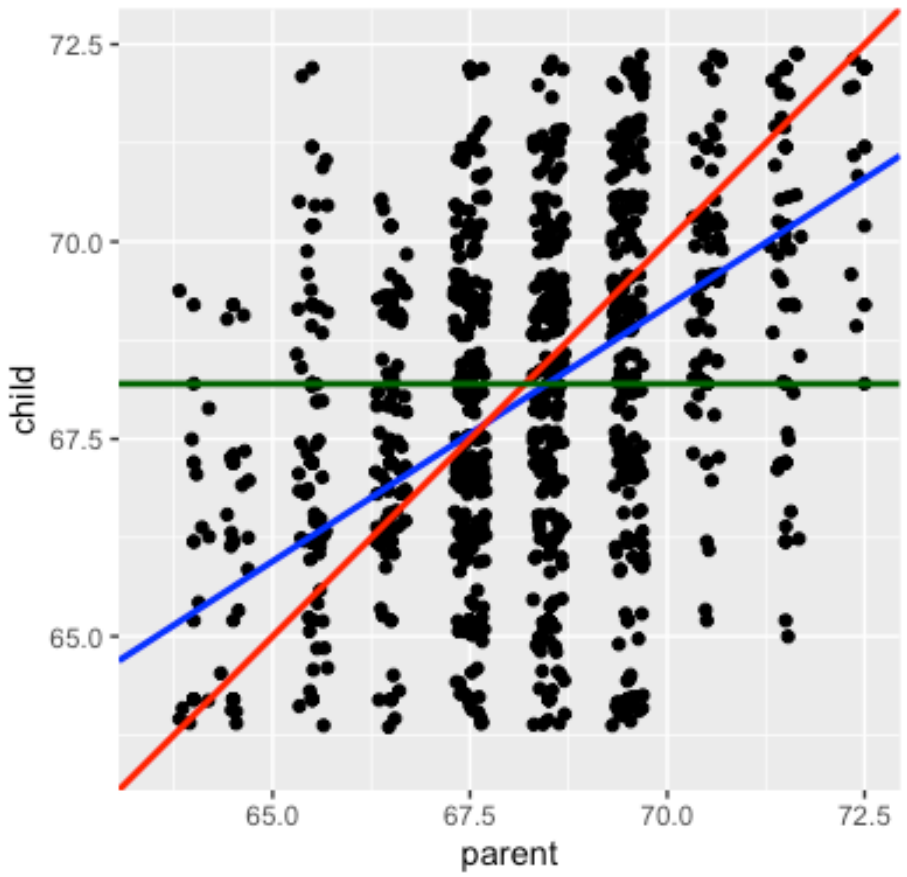
TO-DO

Let's plot (a) the data in $\mathbb{D}$ as black dots, (b) your least squares line defined by b_0 and b_1 in blue, (c) the theoretical line β_0 and β_1 if the parent-child height equality held in red and (d) the mean height in green.

```r
pacman::p_load(ggplot2)
ggplot(Galton, aes(x = parent, y = child)) +
  geom_point() +
  geom_jitter() +
  geom_abline(intercept = b_0, slope = b_1, color = "blue", size = 1) +
  geom_abline(intercept = 0, slope = 1, color = "red", size = 1) +
  geom_abline(intercept = avg_height, slope = 0, color = "darkgreen", size =
1) +
  xlim(63.5, 72.5) +
  ylim(63.5, 72.5) +
  coord_equal(ratio = 1)
```

```
## Warning: Removed 76 rows containing missing values (geom_point).

## Warning: Removed 85 rows containing missing values (geom_point).
```



Fill in the following sentence:

TO-DO: Children of short parents became … on average and children of tall parents became … on average.

Children of short parents became taller on average and children of tall parents became shorter on average.

Why did Galton call it "Regression towards mediocrity in hereditary stature" which was later shortened to "regression to the mean"?

Galton called it "Regression towards mediocrity in hereditary stature" because the children of shorter parents ended up taller and the children of taller parents ended up shorter. Regressing means return to a former state, and thus you see a "regressing" of the entire population towards the former "mean."

This effect should be real because of the nature of human DNA and the recombination of genes where the children do not end up identical to the parents, rather they end up inheriting a recombined set of traits including the possibility of recessive traits. Furthermore there is a limit to human height overall, where you do not observe generation to generation increases in average human height once optimized for nutrition.

You now have unlocked the mystery. Why is it that when modeling with y continuous, everyone calls it "regression"? Write a better, more descriptive and appropriate name for building predictive models with y continuous.

Everyone calls it regression because of the work by Galton and his model of "regression to the mean". A better more descriptive and appropriate name for building predictive models with y continuous would be oridinary least squares, where the model minimizes the error amongst all the data points.

TO-DO

You can now clear the workspace. Create a dataset $\mathbb{D}$ which we call `Xy` such that the linear model as R^2 about 50% and RMSE approximately 1.

```
x = 1:5
y = x^30
Xy = data.frame(x = x, y = y)
model = lm(x ~ y)
summary(model)$r.squared

## [1] 0.5009285

summary(model)$sigma

## [1] 1.289795
```

Create a dataset $\mathbb{D}$ which we call `Xy` such that the linear model as R^2 about 0% but x, y are clearly associated.

```
x = 1:200
y = x^67
Xy = data.frame(x = x, y = y)
model = lm(y ~ x)
summary(model)$r.squared

## [1] 0
```

Extra credit: create a dataset $\mathbb{D}$ and a model that can give you R^2 arbitrarily close to 1 i.e. approximately 1 - epsilon but RMSE arbitrarily high i.e. approximately M.

```
epsilon = 0.01
M = 1000
x = 1:50000
y = x^8
Xy = data.frame(x = x, y = y)

mod = lm(x~y, Xy)
summary(mod)$r.squared

## [1] 0.5100039

summary(mod)$sigma
```

```
## [1] 10103.79
```

Write a function `my_ols` that takes in `X`, a matrix with with p columns representing the feature measurements for each of the n units, a vector of n responses y and returns a list that contains the `b`, the $p+1$-sized column vector of OLS coefficients, `yhat` (the vector of n predictions), `e` (the vector of n residuals), `df` for degrees of freedom of the model, `SSE`, `SST`, `MSE`, `RMSE` and `Rsq` (for the R-squared metric). Internally, you cannot use `lm` or any other package; it must be done manually. You should throw errors if the inputs are non-numeric or not the same length. Or if `X` is not otherwise suitable. You should also name the class of the return value `my_ols` by using the `class` function as a setter. No need to create ROxygen documentation here.

```
my_ols = function(X, y){
  n = length(y)
  if (!is.numeric(X) && !is.integer(X)) {
    stop("X is not numeric")
  }
  X = cbind(rep(1, n), X)
  p = ncol(X)
  df = ncol(X)
  if (n != nrow(X)){
    stop("X rows and length of y need to be the same length.")
  }
  if(class(y) !='numeric' && class(y) !='integer'){
    stop("y needs to be numeric.")
   }
  if(n<=ncol(X)+1){
    stop("n must be more than 2.")
  }

  y_bar = sum(y)/n

  b = solve(t(X) %*% X) %*% t(X) %*% y
  yhat = X %*% b

  e = y - yhat
  SSE = t(e) %*% e
  SST = t(y - y_bar) %*% (y - y_bar)
  MSE = SSE / (n-(p+1))
  RMSE = sqrt(MSE)
  Rsq = 1 - (SSE/SST)

  model = list(
    b=b,
    yhat = yhat,
    df = df,
    e=e,
    SSE = SSE,
    SST = SST,
    MSE = MSE,
    RMSE = RMSE,
    Rsq = Rsq,
    p=p
    )
  class(model) = "my_ols_obj"

  model
}
```

Verify that the OLS coefficients for the `Type` of cars in the cars dataset gives you the same results as we did in class (i.e. the ybar's within group).

```
cars = MASS::Cars93
mod = lm(Price~Type, data=cars)
y = my_ols(as.numeric(data.matrix(data.frame((cars$Type)))), cars$Price)
y

## $b
##         [,1]
##    22.871020
## X -1.001939
##
## $yhat
##            [,1]
##   [1,] 18.86327
##   [2,] 19.86520
##   [3,] 21.86908
##   [4,] 19.86520
##   [5,] 19.86520
##   [6,] 19.86520
##   [7,] 20.86714
##   [8,] 20.86714
##   [9,] 19.86520
##  [10,] 20.86714
##  [11,] 19.86520
##  [12,] 21.86908
##  [13,] 21.86908
##  [14,] 17.86133
##  [15,] 19.86520
##  [16,] 16.85939
##  [17,] 16.85939
##  [18,] 20.86714
##  [19,] 17.86133
##  [20,] 20.86714
##  [21,] 21.86908
##  [22,] 20.86714
##  [23,] 18.86327
##  [24,] 18.86327
##  [25,] 21.86908
## [26,] 16.85939
## [27,] 19.86520
## [28,] 17.86133
## [29,] 18.86327
## [30,] 20.86714
## [31,] 18.86327
## [32,] 18.86327
## [33,] 21.86908
## [34,] 17.86133
## [35,] 17.86133
## [36,] 16.85939
## [37,] 19.86520
## [38,] 20.86714
## [39,] 18.86327
## [40,] 17.86133
## [41,] 17.86133
## [42,] 18.86327
## [43,] 21.86908
## [44,] 18.86327
## [45,] 18.86327
## [46,] 17.86133
## [47,] 19.86520
## [48,] 19.86520
## [49,] 19.86520
## [50,] 19.86520
## [51,] 19.86520
## [52,] 20.86714
## [53,] 18.86327
## [54,] 18.86327
## [55,] 21.86908
## [56,] 16.85939
## [57,] 17.86133
## [58,] 21.86908
## [59,] 19.86520
## [60,] 17.86133
## [61,] 19.86520
## [62,] 18.86327
## [63,] 19.86520
## [64,] 18.86327
## [65,] 21.86908
## [66,] 16.85939
## [67,] 19.86520
## [68,] 21.86908
## [69,] 19.86520
## [70,] 16.85939
## [71,] 20.86714
## [72,] 17.86133
## [73,] 18.86327
## [74,] 21.86908
## [75,] 17.86133
## [76,] 19.86520
## [77,] 20.86714
## [78,] 21.86908
## [79,] 18.86327
## [80,] 18.86327
## [81,] 18.86327
## [82,] 21.86908
## [83,] 18.86327
## [84,] 18.86327
## [85,] 17.86133
## [86,] 19.86520
## [87,] 16.85939
## [88,] 18.86327
## [89,] 16.85939
## [90,] 21.86908
## [91,] 17.86133
## [92,] 21.86908
## [93,] 19.86520
##
## $df
## [1] 2
##
## $e
##              [,1]
##  [1,]  -2.96326531
##  [2,]  14.03479592
##  [3,]   7.23091837
##  [4,]  17.83479592
##  [5,]  10.13479592
##  [6,]  -4.16520408
##  [7,]  -0.06714286
##  [8,]   2.83285714
##  [9,]   6.43479592
## [10,]  13.83285714
## [11,]  20.23479592
## [12,]  -8.46908163
## [13,] -10.46908163
## [14,]  -2.76132653
## [15,]  -3.96520408
## [16,]  -0.55938776
## [17,]  -0.25938776
## [18,]  -2.06714286
## [19,]  20.13867347
## [20,]  -2.46714286
## [21,]  -6.06908163
## [22,]   8.63285714
## [23,]  -9.66326531
## [24,]  -7.56326531
## [25,]  -8.56908163
## [26,]   2.14061224
## [27,]  -4.26520408
## [28,]   7.93867347
## [29,]  -6.66326531
## [30,]  -1.56714286
## [31,] -11.46326531
## [32,]  -8.76326531
## [33,] -10.56908163
## [34,]  -1.96132653
## [35,]  -3.86132653
## [36,]   3.04061224
## [37,]   0.33479592
## [38,]   0.03285714
## [39,] -10.46326531
## [40,]  -5.36132653
## [41,]   1.93867347
## [42,]  -6.76326531
## [43,]  -4.36908163
## [44,] -10.86326531
## [45,]  -8.86326531
## [46,]  -7.86132653
## [47,]  -5.96520408
## [48,]  28.03479592
## [49,]   8.13479592
## [50,]  15.33479592
## [51,]  14.43479592
## [52,]  15.23285714
## [53,] -10.56326531
## [54,]  -7.26326531
## [55,]  -5.36908163
## [56,]   2.24061224
## [57,]  14.63867347
## [58,]  10.03091837
## [59,]  42.03479592
## [60,]  -3.76132653
## [61,]  -4.96520408
## [62,]  -8.56326531
## [63,]   6.23479592
## [64,]  -7.06326531
## [65,]  -6.16908163
## [66,]   2.24061224
## [67,]   1.63479592
## [68,]  -8.36908163
## [69,]  -3.56520408
## [70,]   2.64061224
## [71,]  -0.16714286
## [72,]  -3.46132653
## [73,]  -9.86326531
## [74,] -10.76908163
## [75,]  -0.16132653
## [76,]  -1.36520408
## [77,]   3.53285714
## [78,]   6.83091837
## [79,]  -7.76326531
## [80,] -10.46326531
## [81,]  -7.96326531
## [82,]  -2.36908163
## [83,] -10.26326531
## [84,]  -9.06326531
## [85,]   0.53867347
## [86,]  -1.66520408
## [87,]   5.84061224
## [88,]  -9.76326531
## [89,]   2.84061224
## [90,]  -1.86908163
## [91,]   5.43867347
## [92,]   0.83091837
## [93,]   6.83479592
##
## $SSE
##          [,1]
## [1,] 8361.872
##
## $SST
##          [,1]
## [1,] 8584.021
##
## $MSE
##          [,1]
## [1,] 92.90969
##
## $RMSE
##          [,1]
## [1,] 9.638967
##
## $Rsq
##            [,1]
## [1,] 0.02587939
##
## $p
## [1] 2
##
## attr(,"class")
## [1] "my_ols_obj"
```

Create a prediction method g that takes in a vector `x_star` and the dataset $\mathbb{D}$ i.e. `X` and y and returns the OLS predictions. Let `X` be a matrix with with p columns representing the feature measurements for each of the n units

```
g = function(x_star, X, y){
  b = my_ols(X, y)$b
  x_star = c(1,x_star)
  x_star %*% b
}

X = model.matrix(~Type,cars)[, 2:6]
head(X)

##   TypeLarge TypeMidsize TypeSmall TypeSporty TypeVan
## 1         0           0         1          0       0
## 2         0           1         0          0       0
## 3         0           0         0          0       0
## 4         0           1         0          0       0
## 5         0           1         0          0       0
## 6         0           1         0          0       0

g(X[1,], X, cars$Price)

##          [,1]
## [1,] 10.16667

t(c(1,X[1,])) %*% my_ols(X, cars$Price)$b

##          [,1]
## [1,] 10.16667

X[1,]

##   TypeLarge TypeMidsize   TypeSmall  TypeSporty     TypeVan
##           0           0           1           0           0

predict(mod, cars[1,])

##        1
## 10.16667
```