HW02p

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```
knitr::opts_chunk$set(error = TRUE) #this allows errors to be printed into the PDF
```

Welcome to HW02p where the "p" stands for "practice" meaning you will use R to solve practical problems. This homework is due 11:59 PM Tuesday 3/6/18.

You should have RStudio installed to edit this file. You will write code in places marked "TO-DO" to complete the problems. Some of this will be a pure programming assignment. Sometimes you will have to also write English.

The tools for the solutions to these problems can be found in the class practice lectures. I want you to use the methods I taught you, not for you to google and come up with whatever works. You won't learn that way.

To "hand in" the homework, you should compile or publish this file into a PDF that includes output of your code. To do so, use the knit menu in RStudio. You will need LaTeX installed on your computer. See the email announcement I sent out about this. Once it's done, push the PDF file to your github class repository by the deadline. You can choose to make this respository private.

For this homework, you will need the `testthat` libray.

```
pacman::p_load(testthat)
```

1. Source the simple dataset from lecture 6p:

```
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
)
X_simple_feature_matrix = as.matrix(Xy_simple[, 2 : 3])
y_binary = as.numeric(Xy_simple$response == 1)
```

Try your best to write a general perceptron learning algorithm to the following `Roxygen` spec. For inspiration, see the one I wrote in lecture 6.

```
#' This function implements the "perceptron learning algorithm" of Frank Rosenblatt (1957).
#'
#' @param Xinput      The training data features as an n x (p + 1) matrix where the first column is all
#' @param y_binary    The training data responses as a vector of length n consisting of only 0's and 1'
#' @param MAX_ITER    The maximum number of iterations the perceptron algorithm performs. Defaults to 1
#' @param w           A vector of length p + 1 specifying the parameter (weight) starting point. Defaul
#'                    \code{NULL} which means the function employs random standard uniform values.
#' @return            The computed final parameter (weight) as a vector of length p + 1
perceptron_learning_algorithm = function(Xinput, y_binary, MAX_ITER = 1000, w = NULL){
 if (is.null(w)){
    w = runif(ncol(Xinput)) #intialize a p+1-dim vector with random values
  }
  for (iter in 1 : MAX_ITER){
    for (i in 1 : nrow(Xinput)){
      x_i = Xinput[i, ]
      yhat_i = ifelse(x_i %*% w > 0, 1, 0)
      w = w + as.numeric(y_binary[i] - yhat_i) * x_i
```

```
    }
  }
  w
}
```

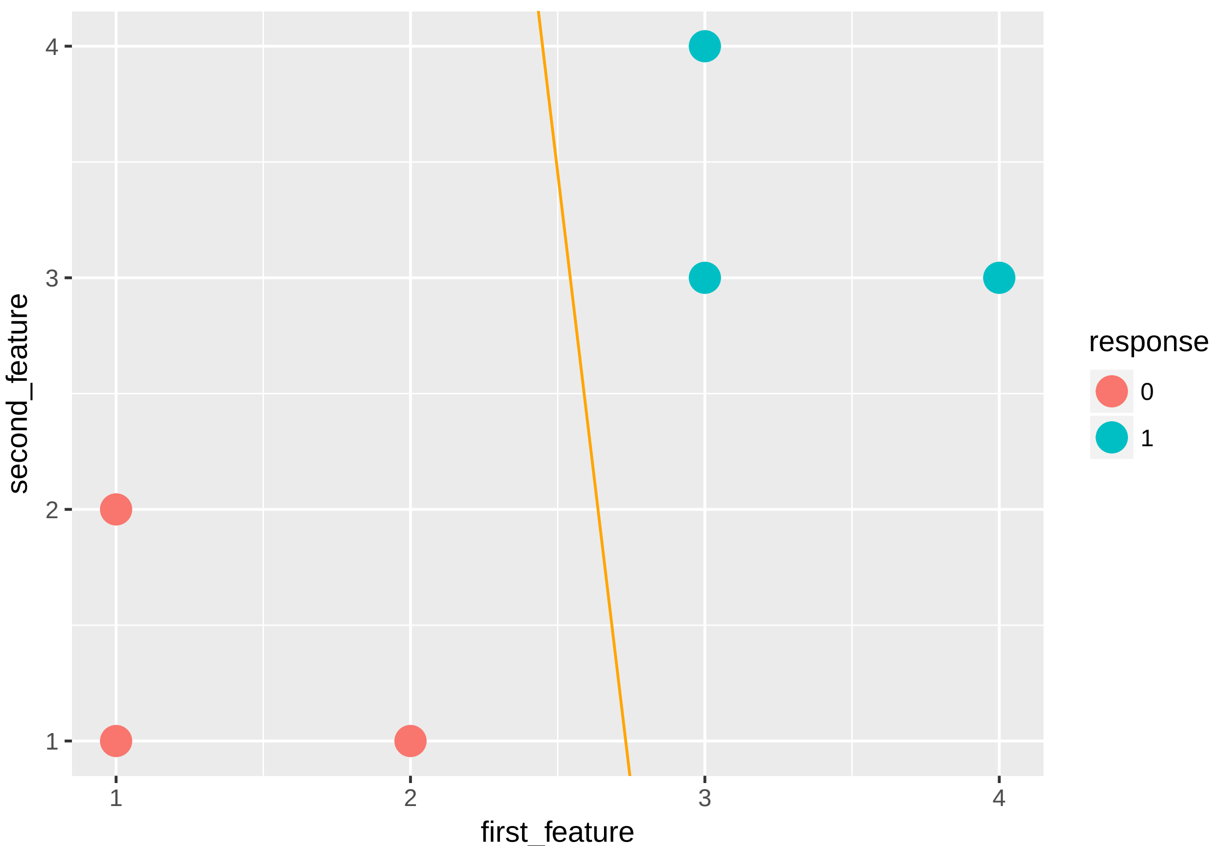
Run the code on the simple dataset above via:

```
w_vec_simple_per = perceptron_learning_algorithm(
  cbind(1, Xy_simple$first_feature, Xy_simple$second_feature),
  as.numeric(Xy_simple$response == 1))
w_vec_simple_per
```

```
## [1] -9.4395798  3.3411723  0.3145835
```

Use the ggplot code to plot the data and the perceptron's g function.

```
pacman::p_load(ggplot2)
simple_viz_obj = ggplot(Xy_simple, aes(x = first_feature, y = second_feature, color = response)) +
  geom_point(size = 5)
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
```



Why is this line of separation not "satisfying" to you?

Because while it is a line that separates the 0s and 1s,it doesn't feel like the "right" line because it doesn't split them evenly; i.e. it's much closer to the 1s.

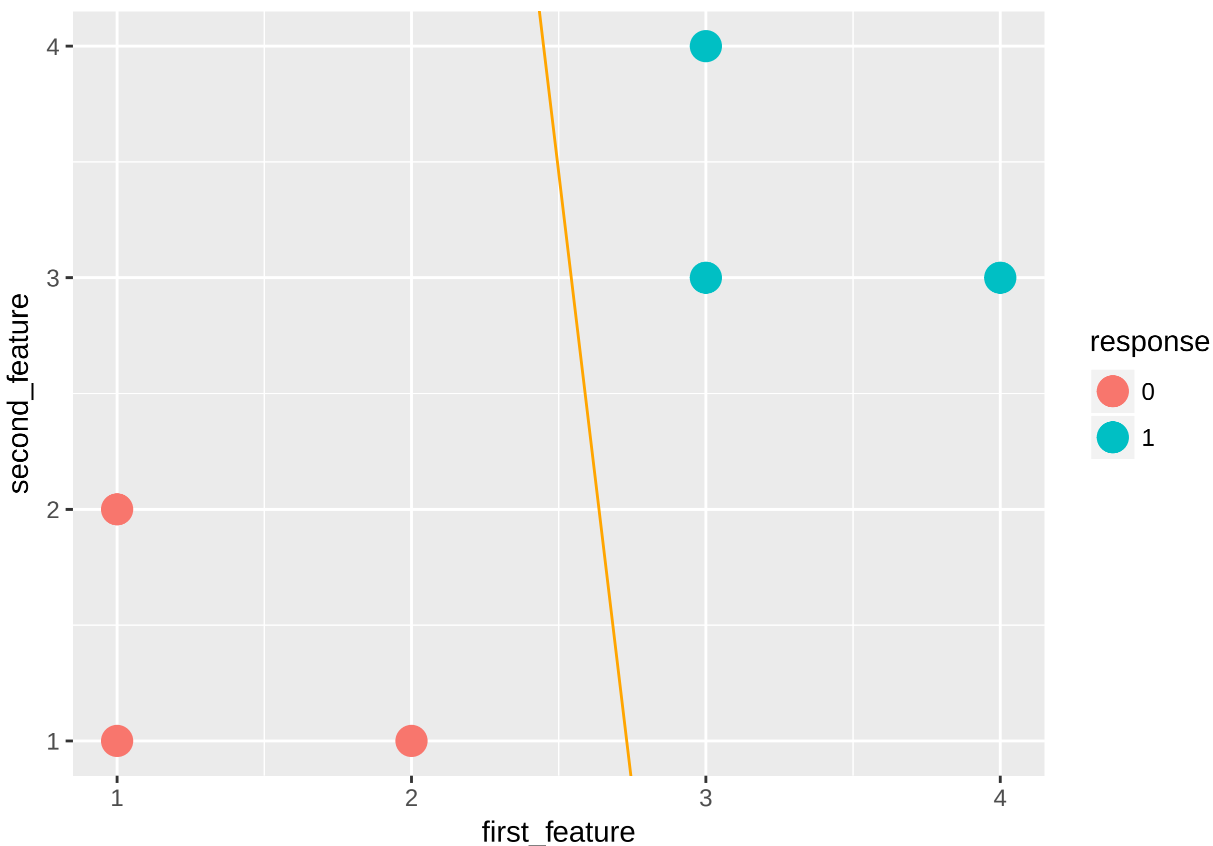
2. Use the `e1071` package to fit an SVM model to `y_binary` using the predictors found in `X_simple_feature_matrix`. Do not specify the λ (i.e. do not specify the `cost` argument).

```
pacman::p_load(e1071)

svm_model = svm(X_simple_feature_matrix, y_binary, kernel = "linear", scale = TRUE)
```

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) %*% X_simple_feature_matrix[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_perceptron_line + simple_svm_line
```



Is this SVM line a better fit than the perceptron?

Yes; it evenly splits the data so that there is an equal amount of space between the line and the 0 responses and the line and the 1 responses.

3. Now write your own implementation of the linear support vector machine algorithm respecting the following spec making use of the nelder mead `optim` function from lecture 5p. It turns out you do not need to load the package `neldermead` to use this function. You can feel free to define a function within this function if you wish.

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.

```
#' This function implements the hinge-loss + maximum margin linear support vector machine algorithm of
#'
#' @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'
#' @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
#'                    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 = 1){
  #
}
```

Run your function using the defaults and plot it in brown vis-a-vis the previous model's line:

```
svm_model_weights = linear_svm_learning_algorithm(X_simple_feature_matrix, y_binary)
my_svm_line = geom_abline(
    intercept = -svm_model_weights[1] / svm_model_weights[3],
    slope = -svm_model_weights[2] / svm_model_weights[3],
    color = "brown")
```

```
## Error in -svm_model_weights[1]: invalid argument to unary operator
```

```
simple_viz_obj + simple_svm_line + my_svm_line
```

```
## Error in eval(expr, envir, enclos): object 'my_svm_line' not found
```

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

4. Write a $k = 1$ nearest neighbor algorithm using the Euclidean distance function. Respect the spec below:

```
#' This function implements the nearest neighbor algorithm.
#'
#' @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'
#' @param Xtest       The test data that the algorithm will predict on as a n* x p matrix.
#' @return            The predictions as a n* length vector.
nn_algorithm_predict = function(Xinput, y_binary, Xtest) {
  best_sqd_distance = Inf
  ij_star = NA
  for (j in 1 : ncol(Xinput)){
    for (i in 1 : nrow(Xinput)) {
      dsqd = (Xinput[i, j] - Xtest[i,j])^2
      if (dsqd < best_sqd_distance) {
      best_sqd_distance = dsqd
      ij_star = Xinput[i,j]
    }
  }
  }
}
```

Write a few tests to ensure it actually works:

```
expect_equal(nn_algorithm_predict(Xinput, y_binary, Xtest), <some value of Xinput)
```

```
## Error: <text>:1:61: unexpected '<'
## 1: expect_equal(nn_algorithm_predict(Xinput, y_binary, Xtest), <
```

```
##
```

For extra credit, add an argument `k` to the `nn_algorithm_predict` function and update the implementation so it performs KNN. In the case of a tie, choose $\hat{y}$ randomly. Set the default `k` to be the square root of the size of $\mathcal{D}$ which is an empirical rule-of-thumb popularized by the "Pattern Classification" book by Duda, Hart and Stork (2007). Also, alter the documentation in the appropriate places.

```
#not required TO-DO --- only for extra credit
```

For extra credit, in addition to the argument `k`, add an argument `d` representing any legal distance function to the `nn_algorithm_predict` function. Update the implementation so it performs KNN using that distance function. Set the default function to be the Euclidean distance in the original function. Also, alter the documentation in the appropriate places.

```
#not required TO-DO --- only for extra credit
```

5. We 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
y = beta_0 + beta_1 * x + rnorm(n, mean = 0, sd = 0.33)
```

Solve for the least squares line by computing b_0 and b_1 *without* using the functions `cor`, `cov`, `var`, `sd` but instead computing it from the x and y quantities manually. See the class notes.

```
least_squares = function(x, y) {
  b_1 = ((sum(x) * sum(y)) - (nrow(x) * mean(x) * mean(y))) / (sum(x^2) - (nrow(x)*mean(x)))
  b_0 = mean(y) - (b_1 * mean(x))
}
```

Verify your computations are correct using the `lm` function in R:

```
lm_mod = lm(y ~ x)
b_vec = coef(lm_mod)
expect_equal(b_0, as.numeric(b_vec[1]), tol = 1e-4) #thanks to Rachel for spotting this bug - the b_vec

## Error in eval_bare(get_expr(quo), get_env(quo)): object 'b_0' not found

expect_equal(b_1, as.numeric(b_vec[2]), tol = 1e-4)

## Error in eval_bare(get_expr(quo), get_env(quo)): object 'b_1' not found
```

6. 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 using the `data` command:

```
data(Galton)

Galton

##     parent child
## 1     70.5  61.7
## 2     68.5  61.7
## 3     65.5  61.7
## 4     64.5  61.7
```

```
## 5      64.0  61.7
## 6      67.5  62.2
## 7      67.5  62.2
## 8      67.5  62.2
## 9      66.5  62.2
## 10     66.5  62.2
## 11     66.5  62.2
## 12     64.5  62.2
## 13     70.5  63.2
## 14     69.5  63.2
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## 41     64.5  63.2
## 42     64.5  63.2
## 43     64.0  63.2
## 44     64.0  63.2
## 45     69.5  64.2
## 46     69.5  64.2
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## 48     69.5  64.2
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## 151   64.0  65.2
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## 402   64.5  67.2
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## 405   64.0  67.2
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## 407   72.5  68.2
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## 476   68.5  68.2
## 477   67.5  68.2
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## 523   65.5  68.2
## 524   65.5  68.2
## 525   65.5  68.2
## 526   64.0  68.2
## 527   72.5  69.2
## 528   72.5  69.2
## 529   71.5  69.2
## 530   71.5  69.2
## 531   71.5  69.2
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## 633   67.5  69.2
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## 667   67.5  69.2
## 668   67.5  69.2
## 669   67.5  69.2
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## 675   66.5  69.2
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## 679   66.5  69.2
## 680   66.5  69.2
## 681   66.5  69.2
## 682   66.5  69.2
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## 686   65.5  69.2
## 687   65.5  69.2
## 688   65.5  69.2
## 689   65.5  69.2
## 690   65.5  69.2
## 691   64.5  69.2
## 692   64.5  69.2
## 693   64.0  69.2
## 694   72.5  70.2
## 695   71.5  70.2
## 696   71.5  70.2
## 697   71.5  70.2
## 698   71.5  70.2
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## 700   71.5  70.2
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## 707   70.5  70.2
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## 727   69.5  70.2
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## 737   69.5  70.2
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## 749   68.5  70.2
## 750   68.5  70.2
## 751   68.5  70.2
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## 755   68.5  70.2
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## 761   68.5  70.2
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## 763   68.5  70.2
## 764   68.5  70.2
## 765   67.5  70.2
## 766   67.5  70.2
## 767   67.5  70.2
## 768   67.5  70.2
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## 776   67.5  70.2
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## 778   67.5  70.2
## 779   67.5  70.2
## 780   67.5  70.2
## 781   67.5  70.2
## 782   67.5  70.2
## 783   67.5  70.2
## 784   66.5  70.2
## 785   66.5  70.2
## 786   66.5  70.2
## 787   66.5  70.2
## 788   65.5  70.2
## 789   65.5  70.2
## 790   65.5  70.2
## 791   65.5  70.2
## 792   65.5  70.2
## 793   72.5  71.2
## 794   72.5  71.2
## 795   71.5  71.2
## 796   71.5  71.2
## 797   71.5  71.2
## 798   71.5  71.2
## 799   70.5  71.2
## 800   70.5  71.2
## 801   70.5  71.2
## 802   70.5  71.2
## 803   70.5  71.2
## 804   70.5  71.2
## 805   70.5  71.2
## 806   69.5  71.2
## 807   69.5  71.2
## 808   69.5  71.2
## 809   69.5  71.2
## 810   69.5  71.2
## 811   69.5  71.2
## 812   69.5  71.2
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## 815   69.5  71.2
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## 819   69.5  71.2
## 820   69.5  71.2
## 821   69.5  71.2
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## 828   68.5  71.2
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## 838   68.5  71.2
## 839   68.5  71.2
## 840   68.5  71.2
## 841   68.5  71.2
## 842   68.5  71.2
## 843   68.5  71.2
## 844   67.5  71.2
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## 846   67.5  71.2
## 847   67.5  71.2
## 848   67.5  71.2
## 849   67.5  71.2
## 850   67.5  71.2
## 851   67.5  71.2
## 852   67.5  71.2
## 853   67.5  71.2
## 854   67.5  71.2
## 855   65.5  71.2
## 856   65.5  71.2
## 857   73.0  72.2
## 858   72.5  72.2
## 859   72.5  72.2
## 860   72.5  72.2
## 861   72.5  72.2
## 862   72.5  72.2
## 863   72.5  72.2
## 864   72.5  72.2
## 865   71.5  72.2
## 866   71.5  72.2
## 867   71.5  72.2
## 868   71.5  72.2
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## 869   71.5  72.2
## 870   71.5  72.2
## 871   71.5  72.2
## 872   71.5  72.2
## 873   71.5  72.2
## 874   70.5  72.2
## 875   70.5  72.2
## 876   70.5  72.2
## 877   70.5  72.2
## 878   69.5  72.2
## 879   69.5  72.2
## 880   69.5  72.2
## 881   69.5  72.2
## 882   69.5  72.2
## 883   69.5  72.2
## 884   69.5  72.2
## 885   69.5  72.2
## 886   69.5  72.2
## 887   69.5  72.2
## 888   69.5  72.2
## 889   68.5  72.2
## 890   68.5  72.2
## 891   68.5  72.2
## 892   68.5  72.2
## 893   67.5  72.2
## 894   67.5  72.2
## 895   67.5  72.2
## 896   67.5  72.2
## 897   65.5  72.2
## 898   73.0  73.2
## 899   73.0  73.2
## 900   73.0  73.2
## 901   72.5  73.2
## 902   72.5  73.2
## 903   71.5  73.2
## 904   71.5  73.2
## 905   70.5  73.2
## 906   70.5  73.2
## 907   70.5  73.2
## 908   69.5  73.2
## 909   69.5  73.2
## 910   69.5  73.2
## 911   69.5  73.2
## 912   68.5  73.2
## 913   68.5  73.2
## 914   68.5  73.2
## 915   72.5  73.7
## 916   72.5  73.7
## 917   72.5  73.7
## 918   72.5  73.7
## 919   71.5  73.7
## 920   71.5  73.7
## 921   70.5  73.7
## 922   70.5  73.7
```

```
## 923   70.5  73.7
## 924   69.5  73.7
## 925   69.5  73.7
## 926   69.5  73.7
## 927   69.5  73.7
## 928   69.5  73.7
```

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`.

```
summary(Galton)
```

```
##      parent          child
##  Min.   :64.00   Min.   :61.70
##  1st Qu.:67.50   1st Qu.:66.20
##  Median :68.50   Median :68.20
##  Mean   :68.31   Mean   :68.09
##  3rd Qu.:69.50   3rd Qu.:70.20
##  Max.   :73.00   Max.   :73.70
```

The Galton dataset is a data frame with n = 928 observations (children born to 205 sets of parents), with p = one feature- the average of the father's and mother's heights, and one response variable- the child's height. The units are in inches, and the heights of females were multiplied by 1.08 to account for the fact that females are generally shorter than males.

The summary shows relatively similar minimum, quartile, mean, and maximum heights between the parent vector and the child vector, suggesting a strong correlation.

Find the average height (include both parents and children in this computation).

```
x = Galton$parent
y = Galton$child
avg_height = (2 * mean(x) + mean (y)) / 3
avg_height
```

```
## [1] 68.23495
```

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. Use the correct units to report these quantities.

```
linear_model = lm(child ~ parent, data = HistData::Galton)
coef(linear_model)
```

```
## (Intercept)      parent
##  23.9415302   0.6462906
```

```
summary(linear_model)$r.squared
```

```
## [1] 0.2104629
```

```
summary(linear_model)$sigma
```

```
## [1] 2.238547
```

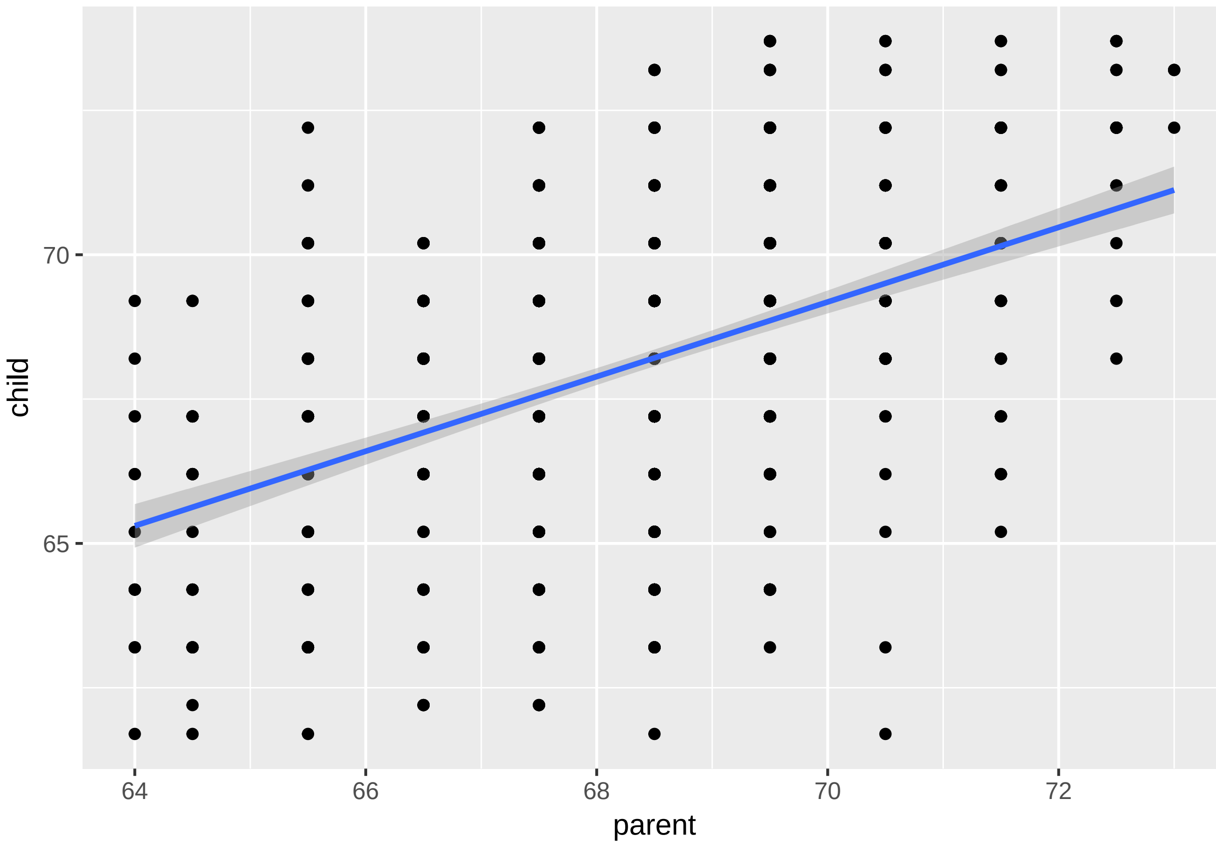
Interpret all four quantities: b_0, b_1, RMSE and R^2.

b_0 is the y-intercept of the line, and b_1 is the slope.

The R^2 value is pretty low, only .21. And the RMSE is 2.24 inches, which means that you can predict the height of a child given the heights of the parents within about 4.5 inches 95% of the time, which is a large margin.

Now use the code from practice lecture 8 to plot the data and a best fit line using package `ggplot2`. Don't forget to load the library.

```
pacman::p_load(ggplot2)
ggplot(HistData::Galton, aes(parent, child)) +
  geom_point() +
  geom_smooth(method = 'lm')
```



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

Because genetics dictate height. A child with two tall parents should get "tall" genes, and a child with short parents should get "short" genes. A child with one tall parent and one short parent should get one "tall" gene and one "short" gene, which is accounted for in the model by taking the average of the parents' heights.

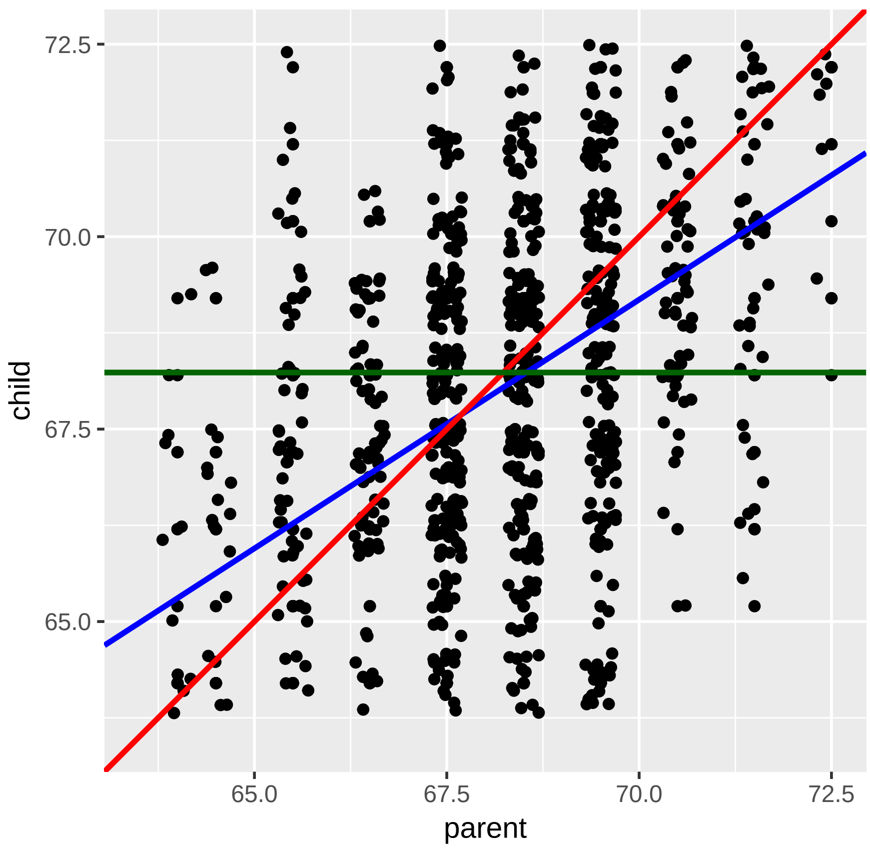
If they were to have the same height and any differences were just random noise with expectation 0, what would the values of β_0 and β_1 be?

The correlation between parent and child would be 1, so beta_0 would be 0, and beta_1 would be 1 (the intercept of the line is at y=0, and it increases by a dactor of 1:1)

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
x = Galton$parent
y = Galton$child

r = cor(x, y)
s_x = sd(x)
s_y = sd(y)
ybar = mean(y)
xbar = mean(x)

b_1 = r * s_y / s_x
b_0 = ybar - b_1 * xbar

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 86 rows containing missing values (geom_point).
```



Fill in the following sentence:

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 defined shortness to be mediocre, and because the slope of the regression line was not equal to 1, it shows that children do not grow to the same height as their parents, but closer to the average height of all people. So over time, genetically speaking, height will continue to "regress" to the mean line.

Why should this effect be real?

Statistically speaking, if heights are normally distributed (which we can assume because n is large), it makes sense for a larger amount of heights to be closer to the mean (67% are within one standard deviation, 95% are within two.)

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.

Linear prediction, linear classification