Logistic Regression Models

Justin Post

Logistic Regression Model

Used when you have a **binary** response variable (a Classification task)

- Consider just a binary response
 - $\circ\,$ What is the mean of the response?

Logistic Regression Model

Suppose you have a predictor variable as well, call it \boldsymbol{x}

• Given two values of x we could model separate proportions

$$E(Y|x=x_1) = P(Y=1|x=x_1)$$
 $E(Y|x=x_2) = P(Y=1|x=x_2)$

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• For a continuous *x*, we could consider a SLR model

$$E(Y|x)=P(Y=1|x)=eta_0+eta_1 x$$

• Consider data about heart disease

library(tidyverse)

heart_data <- read_csv("https://www4.stat.ncsu.edu/online/datasets/heart.csv") |>

filter(RestingBP > 0) #remove one value

heart_data |> select(HeartDisease, everything()) #Cholesterol has many values set to 0 so we ignore that

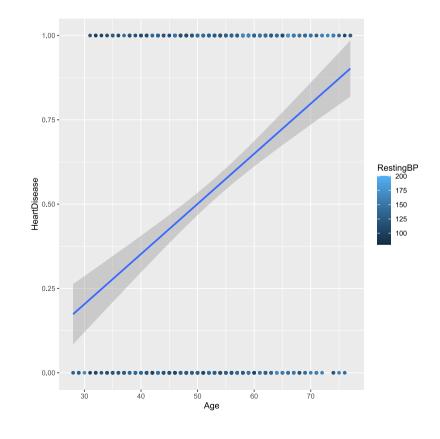
A tibble: 917 x 12 HeartDisease Age Sex ChestPainType RestingBP Cholesterol FastingBS ## <dbl> <dbl> <chr> <chr> ## <dbl><dbl> <dbl>40 M 289 ## 1 ATA 140 0 0 ## 2 49 F NAP 160 180 0 ## 3 37 M ATA 130 283 0 0 ## 4 1 48 F 0 ASY 138 214 ## 5 54 M NAP 150 0 0 195 ## # i 912 more rows ## # i 5 more variables: RestingECG <chr>, MaxHR <dbl>, ExerciseAngina <chr>, Oldpeak <dbl>, ST_Slope <chr> ##

Potability Summary

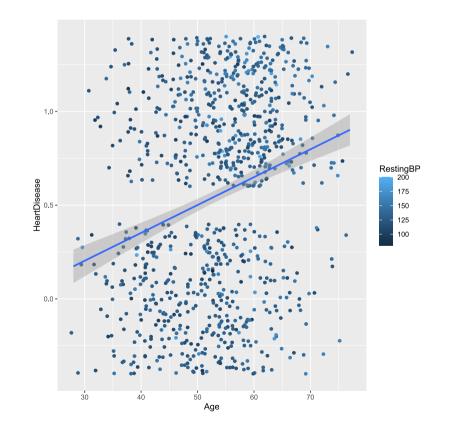
• Summarize heart disease prevalence

```
heart data I>
   group_by(HeartDisease) |>
   summarize(count = n())
## # A tibble: 2 x 2
## HeartDisease count
##
            <dbl> <int>
                   410
## 1
                0
## 2
                    507
                1
 heart_data |>
   group_by(HeartDisease) |>
   summarize(mean_Age = mean(Age),
            mean_RestingBP = mean(RestingBP))
## # A tibble: 2 x 3
##
    HeartDisease mean_Age mean_RestingBP
            <dbl>
                     <dbl>
                                    <dbl>
##
## 1
                     50.6
                                    130.
                0
## 2
                1
                      55.9
                                     134.
```

```
ggplot(heart_data, aes(x = Age, y = HeartDisease, color = RestingBP)) +
    geom_point() +
    geom_smooth(method = "lm")
```



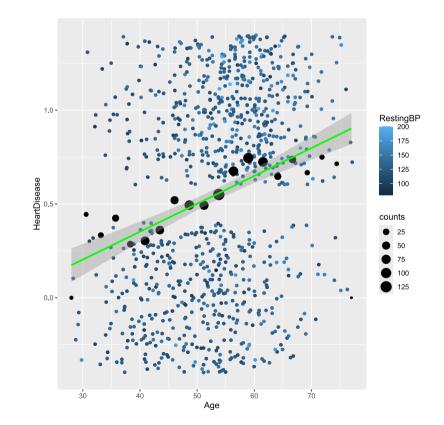
```
ggplot(heart_data, aes(x = Age, y = HeartDisease, color = RestingBP)) +
    geom_jitter() +
    geom_smooth(method = "lm")
```



Obtain proportion with heart disease for different age groups

```
Age_x <- seq(from = min(heart_data$Age), to = max(heart_data$Age), length = 20)</pre>
 heart_data_grouped <- heart_data |>
  mutate(Age_groups = cut(Age, breaks = Age_x)) |>
   group_by(Age_groups) |>
   summarize(HeartDisease_mean = mean(HeartDisease), counts = n())
 heart_data_grouped
## # A tibble: 20 x 3
## Age_groups HeartDisease_mean counts
##
     <fct>
                             <dbl> <int>
## 1 (28,30.6]
                             0
                                       4
## 2 (30.6,33.2]
                            0.444
                                       9
                         0.333
## 3 (33.2,35.7]
                                      18
                         0.424
## 4 (35.7,38.3]
                                      33
                     0.286
## 5 (38.3,40.9]
                                      28
## 6 (40.9,43.5]
                     0.303
                                      66
## 7 (43.5,46.1]
                            0.361
                                      61
## 8 (46.1,48.6]
                            0.52
                                      50
## 9 (48.6,51.2]
                            0.494
                                      81
## 10 (51.2,53.8]
                            0.493
                                      69
## 11 (53.8,56.4]
                            0.550
                                     129
## 12 (56.4,58.9]
                            0.675
                                      80
## 13 (58.9,61.5]
                  0.745
                                      98
## 14 (61.5,64.1]
                            0.724
                                      87
## 15 (64.1,66.7]
                            0.647
                                      34
```

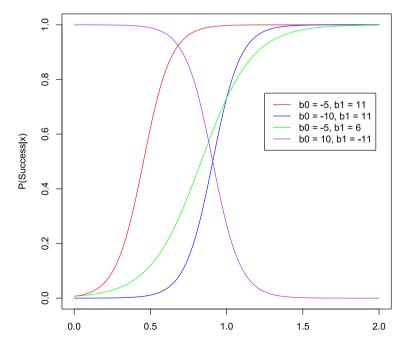
```
ggplot(data = heart_data, aes(x = Age, y = HeartDisease)) +
geom_jitter(aes(color = RestingBP)) +
geom_point(data = heart_data_grouped, aes(x = Age_x, y = HeartDisease_mean, size = counts)) +
geom_smooth(method = "lm", color = "Green")
```



- Response = success/failure, then modeling average number of successes for a given x is a probability!
 - predictions should never go below 0
 - $\circ~$ predictions should never go above 1 $\,$
- Basic Logistic Regression models success probability using the *logistic function*

$$P(Y=1|x)=P(success|x)=rac{e^{eta_0+eta_1x}}{1+e^{eta_0+eta_1x}}$$

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- Back-solving shows the *logit* or *log-odds* of success is linear in the parameters

$$log\left(rac{P(success|x)}{1-P(success|x)}
ight)=eta_0+eta_1 x$$

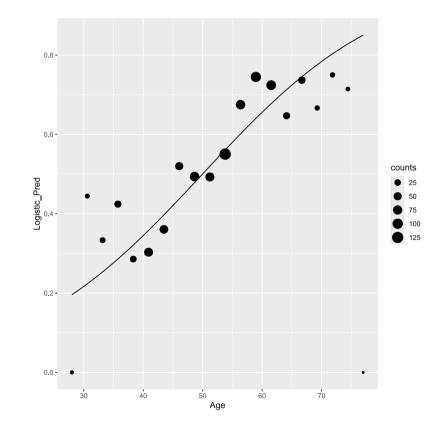
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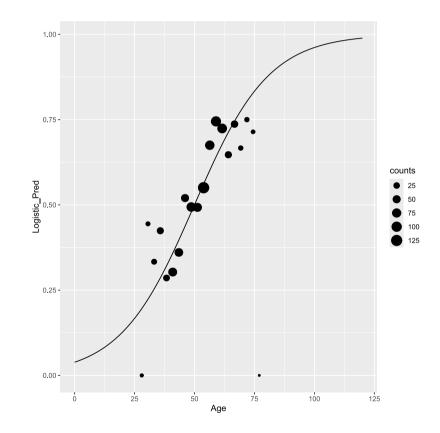
$$log\left(rac{P(success|x)}{1-P(success|x)}
ight)=eta_0+eta_1x$$

- Coefficient interpretation changes greatly from linear regression model!
- β_1 represents a change in the log-odds of success

Using Age to predict HeartDisease via a logistic regression model:

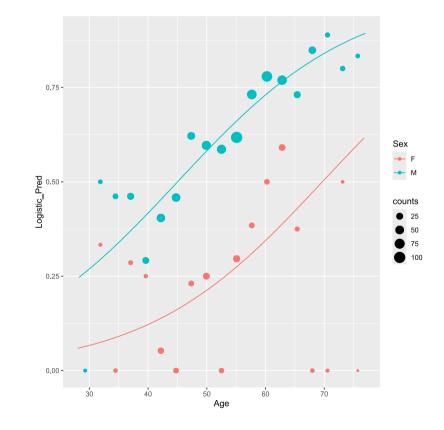


A sigmoid function that looks linear close up!



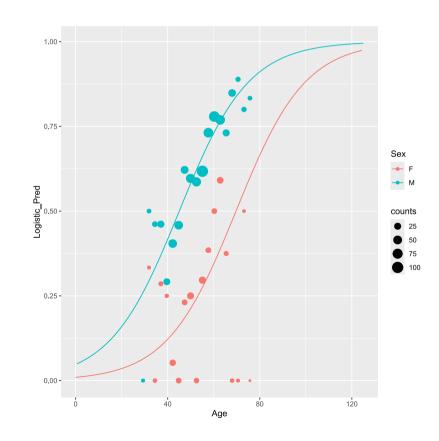
As with linear regression, we can include multiple predictors and interaction terms!

• Adding a dummy variable corresponding to a binary variable just changes the 'intercept'



As with linear regression, we can include multiple predictors and interaction terms!

• Not a constant shift

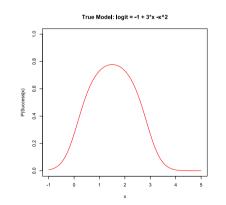


Interaction Terms Can Be Included

- If we fit an interaction term with our dummy variable, we essentially fit two separate logistic regression models
- Can also include more than one numeric predictor

• Difficult to visualize!

• Adding in polynomial terms increases flexibility as well!



Selecting a Model

- Recall we can use k-fold CV as a proxy for **test set** error if we don't want to split the data
- Metric to quantify prediction quality? Basic measures:

• Accuracy:

of correct classifications

Total # of classifications

• Misclassification Rate:

of incorrect classifications

Total # of classifications

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- Recall we can use k-fold CV as a proxy for **test set** error if we don't want to split the data
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 $\# \ {\rm of \ correct \ classifications}$

Total # of classifications

• Misclassification Rate:

 $\# \text{ of incorrect classifications} \\ \text{Total } \# \text{ of classifications} \\ \end{bmatrix}$

 \circ Log-loss: For each observation (y = 0 or 1), $-(ylog(\hat{p})+(1-y)log(1-\hat{p}))$

- First, we'll do a training/test split via initial_split()
- Let's also create our CV splits on the training data

```
library(tidymodels)
set.seed(3557)
heart_data <- heart_data |> mutate(HeartDisease = factor(HeartDisease))
heart_split <- initial_split(heart_data, prop = 0.8)
heart_train <- training(heart_split)
heart_test <- testing(heart_split)
heart_CV_folds <- vfold_cv(heart_train, 10)</pre>
```

• Next, we'll set up our recipes for the data, standardizing these numeric variables

- Model 1: Age and Sex as predictors
- $\circ~Model~2:$ Age, Sex, ChestPainType, RestingBP and RestingECG as predictors
- \circ Model 3: Age, Sex, ChestPainType, RestingBP, RestingECG, MaxHR, and ExerciseAngina

```
LR1_rec <- recipe(HeartDisease ~ Age + Sex,</pre>
                   data = heart train) |>
   step_normalize(Age) |>
   step_dummy(Sex)
 LR2_rec <- recipe(HeartDisease ~ Age + Sex + ChestPainType + RestingBP + RestingECG,
                   data = heart_train) |>
   step_normalize(all_numeric(), -HeartDisease) |>
   step_dummy(Sex, ChestPainType, RestingECG)
 LR3_rec <- recipe(HeartDisease ~ Age + Sex + ChestPainType + RestingBP + RestingECG + MaxHR + ExerciseAngina,
                   data = heart_train) |>
   step_normalize(all_numeric(), -HeartDisease) |>
   step_dummy(Sex, ChestPainType, RestingECG, ExerciseAngina)
 LR3_rec |> prep(heart_train) |> bake(heart_train) |> colnames()
## [1] "Age"
                            "RestingBP"
                                                "MaxHR"
## [4] "HeartDisease"
                            "Sex M"
                                                "ChestPainType_ATA"
## [7] "ChestPainType_NAP" "ChestPainType_TA"
                                                "RestingECG_Normal"
## [10] "RestingECG ST"
                            "ExerciseAngina Y"
```

- Now set up our model type and engine
- LR_spec <- logistic_reg() |>
 set_engine("glm")

• Create our workflows

- LR1_wkf <- workflow() |>
- add_recipe(LR1_rec) |>
- add_model(LR_spec)
- LR2_wkf <- workflow() |>
- add_recipe(LR2_rec) |>
- add_model(LR_spec)
- LR3_wkf <- workflow() |>
- add_recipe(LR3_rec) |>
- add_model(LR_spec)

• Fit to our CV folds!

LR1_fit <- LR1_wkf |>
 fit_resamples(heart_CV_folds, metrics = metric_set(accuracy, mn_log_loss))
LR2_fit <- LR2_wkf |>
 fit_resamples(heart_CV_folds, metrics = metric_set(accuracy, mn_log_loss))
LR3_fit <- LR3_wkf |>
 fit_resamples(heart_CV_folds, metrics = metric_set(accuracy, mn_log_loss))

• Collect our metrics and see which model did the best!

```
rbind(LR1_fit |> collect_metrics(),
      LR2_fit |> collect_metrics(),
      LR3_fit |> collect_metrics()) |>
   mutate(Model = c("Model1", "Model1", "Model2", "Model2", "Model3", "Model3")) |>
   select(Model. everything())
## # A tibble: 6 x 7
   Model .metric
                       .estimator mean
                                           n std_err .config
##
## <chr> <chr>
                       <chr>
                                  <dbl> <int> <dbl> <chr>
## 1 Model1 accuracy
                       binarv
                                  0.689
                                          10 0.0235 Preprocessor1 Model1
## 2 Model1 mn_log_loss binary
                                  0.606
                                         10 0.0246 Preprocessor1_Model1
## 3 Model2 accuracy
                       binarv
                                  0.768
                                         10 0.0178 Preprocessor1_Model1
## 4 Model2 mn_log_loss binary
                                  0.499
                                         10 0.0268 Preprocessor1 Model1
## 5 Model3 accuracy
                       binary
                                  0.783
                                         10 0.0144 Preprocessor1_Model1
## 6 Model3 mn_log_loss binary
                                  0.456
                                          10 0.0204 Preprocessor1 Model1
```

```
#compare to proportion of 1's in training data
mean(heart_train$HeartDisease == "1")
```

[1] 0.5607094

• Find the confusion matrix for our best model on the training set

```
LR_train_fit <- LR3_wkf |>
  fit(heart_train)
conf_mat(heart_train |> mutate(estimate = LR_train_fit |> predict(heart_train) |> pull()), #data
        HeartDisease, #truth
        estimate) #estimate from model
```

Truth
Prediction 0 1
0 242 69
1 80 342

• Grab our 'best' model and test it on the test set

conf_mat(heart_test |> mutate(estimate = LR_train_fit |> predict(heart_test) |> pull()), HeartDisease, estimate)

Truth ## Prediction 0 1 ## 0 63 10 ## 1 25 86

• Suppose we like this model the best *overall*, we'd fit it to the entire data set

```
fit(heart_data)
 tidv(final model)
## # A tibble: 11 x 5
                        estimate std.error statistic p.value
##
      term
##
                           <dbl>
      <chr>
                                     <dbl>
                                               <dbl>
                                                        < dbl >
##
   1 (Intercept)
                         -0.468
                                    0.281
                                              -1.67 9.56e-2
##
   2 Age
                          0.324
                                    0.103
                                               3.13 1.74e- 3
    3 RestingBP
                          0.0877
                                    0.0931
                                               0.942 3.46e- 1
##
                                    0.105
                                              -3.48
                                                     5.09e- 4
##
   4 MaxHR
                         -0.363
   5 Sex M
                                    0.230
                                               5.84 5.27e-9
##
                          1.34
    6 ChestPainType_ATA
                         -2.31
                                    0.274
                                              -8.43 3.33e-17
##
   7 ChestPainType_NAP
                         -1.51
                                    0.215
                                              -7.02 2.17e-12
##
    8 ChestPainType_TA
                         -0.937
                                    0.360
                                              -2.60 9.24e- 3
##
    9 RestingECG_Normal
                         -0.113
                                    0.233
                                              -0.486 6.27e- 1
##
## 10 RestingECG_ST
                                    0.294
                                              -0.250 8.02e- 1
                         -0.0737
## 11 ExerciseAngina_Y
                                    0.201
                                               7.50 6.37e-14
                          1.51
```

final_model <- LR3_wkf |>

Recap

- Logistic regression often a reasonable model for a binary response
- Uses a sigmoid function to ensure valid predictions
- Can predict success or failure using estimated probabilities
 - \circ Usually predict success if probability > 0.5
 - $\circ~$ Common metrics for classification are accuracy and log-loss