Bayesian and Predictive Analysis

DATA 606 - Statistics & Probability for Data Analytics

Jason Bryer, Ph.D.

April 30, 2025

One Minute Paper Results

What was the most important thing you learned during this class?

What important question remains unanswered for you?

Bayesian Analysis

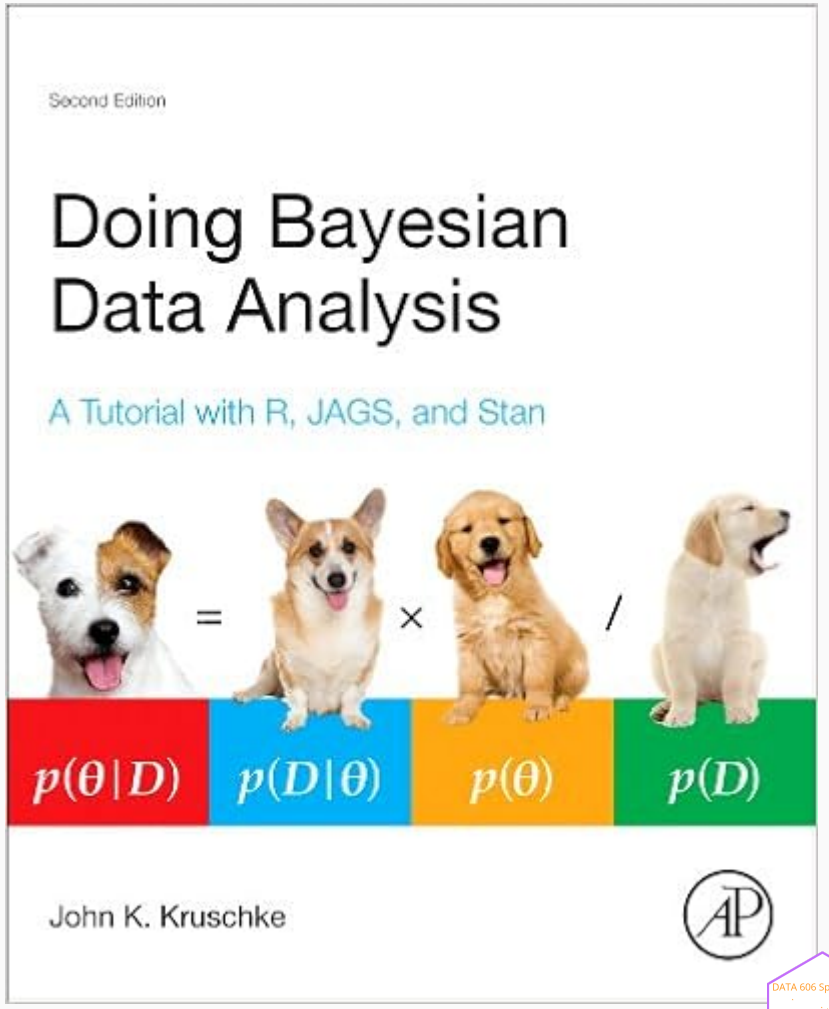
Kruschke's videos are an excelent introduction to Bayesian Analysis https://www.youtube.com/watch?v=YyohWpjl6KU!

Doing Bayesian Data Analysis, Second Edition: A Tutorial with R, JAGS, and Stan

The Theory That Would Not Die: How Bayes' Rule Cracked the Enigma Code, Hunted Down Russian Submarines, and Emerged Triumphant from Two Centuries of Controversy by Sharon Bertsch McGrayne

Video series by Rasmus Baath Part 1, Part 2, Part 3

Billiards with Fred the Frequentist and Bayer the Bayesian



Bayes Theorem

$$P(A|B) = \frac{P(B|A)P(A)}{P(B|A)P(A) + P(B|A^{'})P(A^{'})}$$

Consider the following data from a cancer test:

- 1% of women have breast cancer (and therefore 99% do not).
- 80% of mammograms detect breast cancer when it is there (and therefore 20% miss it).
- 9.6% of mammograms detect breast cancer when it's not there (and therefore 90.4% correctly return a negative result).

	Cancer (1%)	**No Cancer (99%)**
Test postive	80%	9.6%
Test negative	20%	90.4%

How accurate is the test?

Now suppose you get a positive test result. What are the chances you have cancer?
80%? 99%? 1%?

- Ok, we got a positive result. It means we're somewhere in the top row of our table. Let's not assume anything - it could be a true positive or a false positive.
- The chances of a true positive = chance you have cancer *chance test caught it* = *1%* 80% = .008
- The chances of a false positive = chance you don't have cancer *chance test caught it anyway* = *99%* 9.6% = 0.09504

	Cancer (1%)	**No Cancer (99%)**	
Test postive	True +: 1% * 80%	False +: 99% * 9.6%	**10.304%**
Test negative	False -: 1% * 20%	True -: 99% * 90.4%	**89.696%**

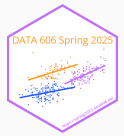
How accurate is the test?

$$Probability = \frac{desired \quad event}{all \quad possibilities}$$

The chance of getting a real, positive result is .008. The chance of getting any type of positive result is the chance of a true positive plus the chance of a false positive (.008 + 0.09504 = .10304).

$$P(C|P) = \frac{P(P|C)P(C)}{P(P)} = \frac{.8 * .01}{.008 + 0.095} \approx .078$$

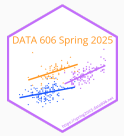
So, our chance of cancer is .008/.10304 = 0.0776, or about 7.8%.

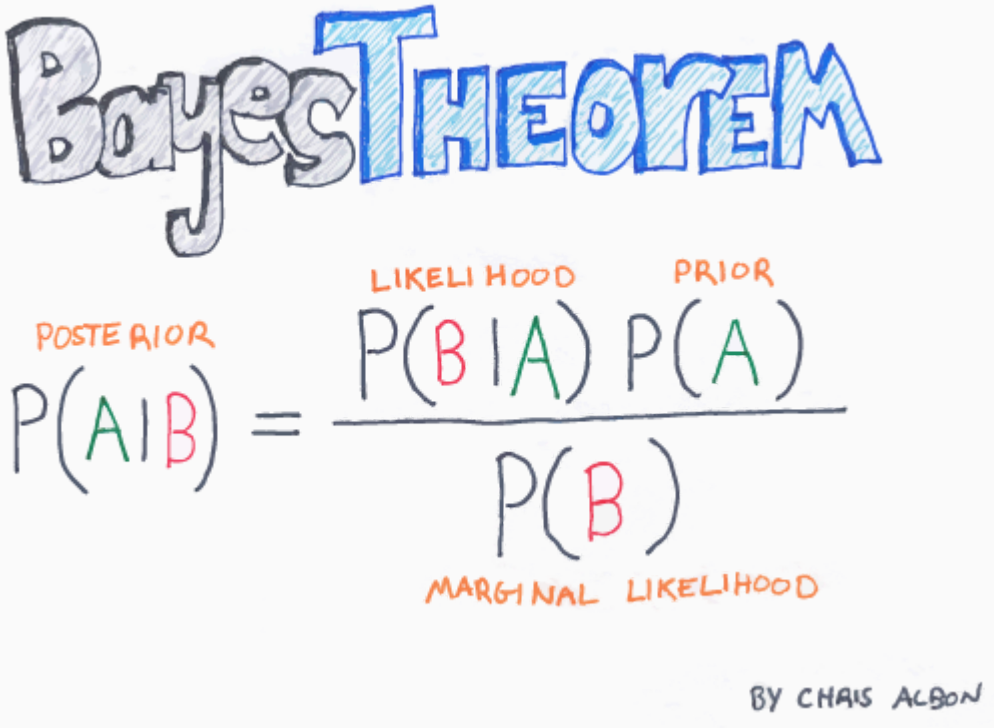


Bayes Formula

It all comes down to the chance of a true positive result divided by the chance of any positive result. We can simplify the equation to:

$$P(A|B) = \frac{P(B|A)\,P(A)}{P(B)}$$




Bayes Theorem
POSTERIOR
LIKELIHOOD
PRIOR
P(A|B) = P(B|A) P(A) / P(B)
MARGINAL LIKELIHOOD
BY CHRIS ALBON

How many fish are in the lake?

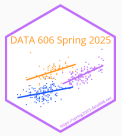
- Catch them all, count them. Not practical (or even possible)!
- We can sample some fish.

Our strategy:

1. Catch some fish.
2. Mark them.
3. Return the fish to the pond. Let them get mixed up (i.e. wait a while).
4. Catch some more fish.
5. Count how many are marked.

For example, we initially caught 20 fish, marked them, returned them to the pond. We then caught another 20 fish and 5 of them were marked (i.e they were caught the first time).

Adopted from Rasmath Bääth useR! 2015 workshop: http://www.sumsar.net/files/academia/user_2015_tutorial_bayesian_data_analysis_short_version.pdf



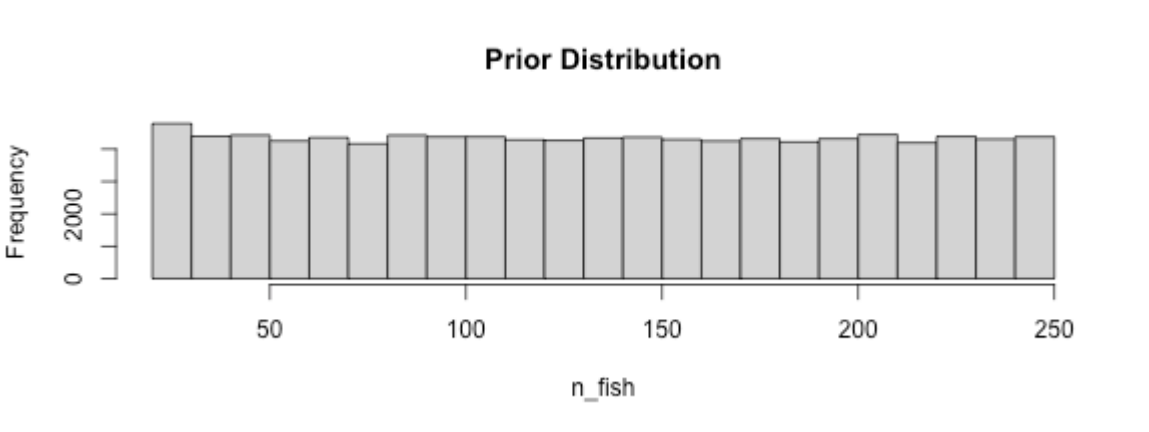
Strategy for fitting a model

Step 1: Define Prior Distribution. Draw a lot of random samples from the "prior" probability distribution on the parameters.

```
n_draw <- 100000
n_fish <- sample(20:250, n_draw, replace = TRUE)
head(n_fish, n=10)
```

```
##  [1] 233  94 234 138 250  25 222 165 218 156
```

```
hist(n_fish, main="Prior Distribution")
```

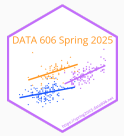


Strategy for fitting a model

Step 2: Plug in each draw into the generative model which generates "fake" data.

```
pick_fish <- function(n_fish) { # The generative model
    fish <- rep(0:1, c(n_fish - 20, 20))
    sum(sample(fish, 20))
}
n_marked <- rep(NA, n_draw)
for(i in 1:n_draw) {
    n_marked[i] <- pick_fish(n_fish[i])
}
head(n_marked, n=10)
```

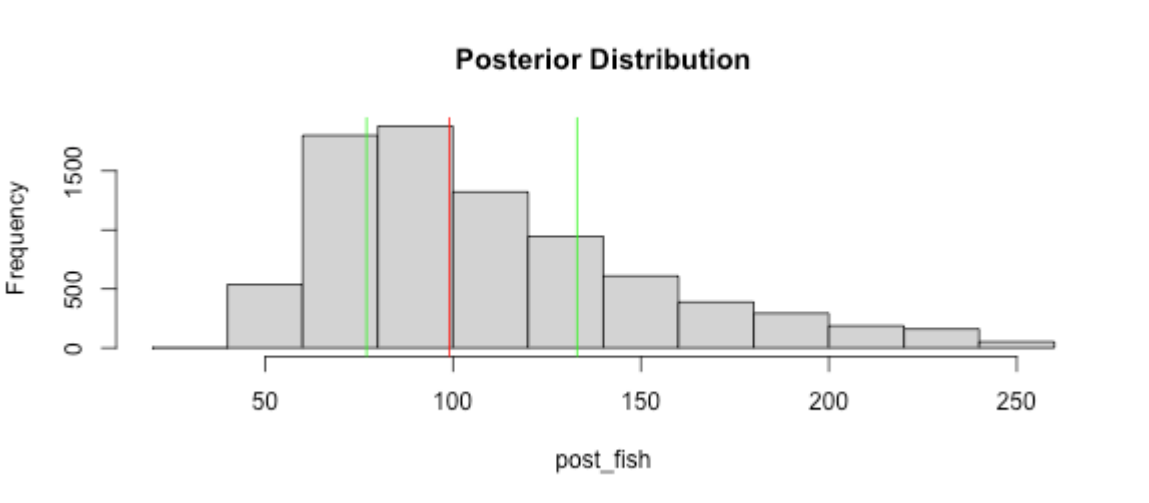
```
##  [1]  1  5  1  3  0 15  1  2  1  5
```



Strategy for fitting a model

Step 3: Keep only those parameter values that generated the data that was actually observed (in this case, 5).

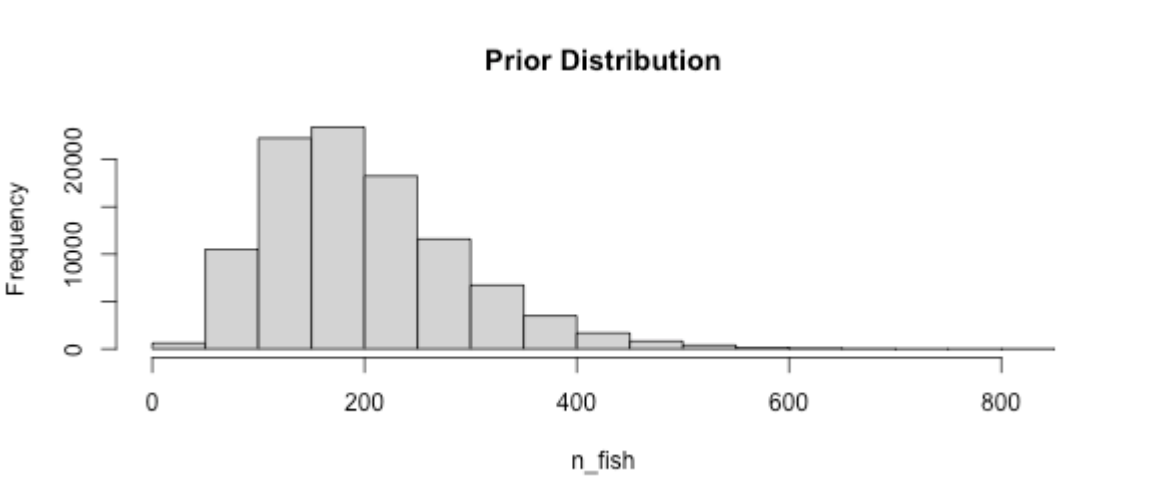
```
post_fish <- n_fish[n_marked == 5]
hist(post_fish, main='Posterior Distribution')
abline(v=median(post_fish), col='red')
abline(v=quantile(post_fish, probs=c(.25, .75)), col='green')
```



What if we have better prior information?

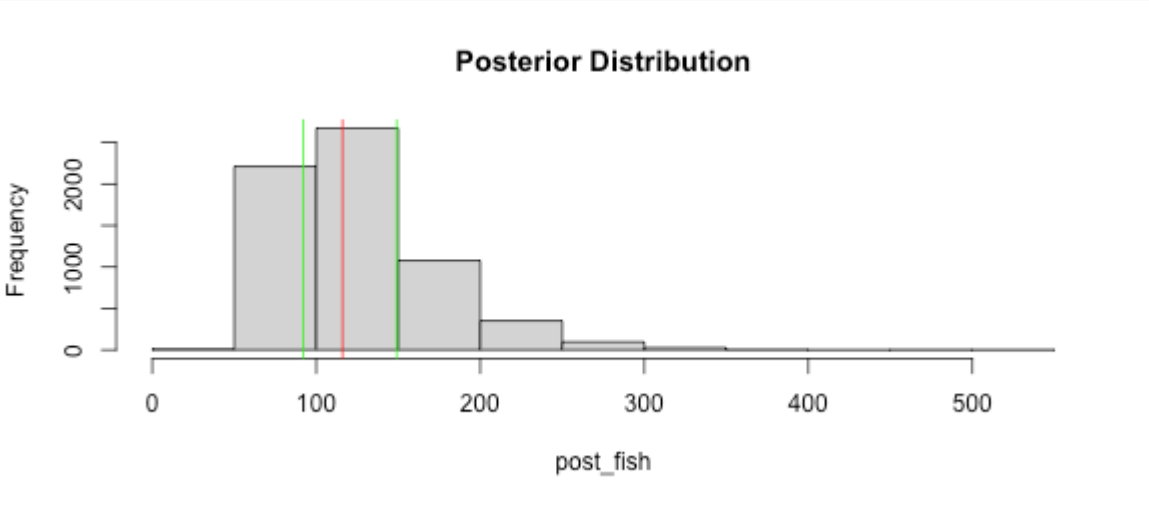
An "expert" believes there are around 200 fish in the pond. Insteand of a uniform distribution, we can use a binomial distribution to define our "prior" distribution.

```
n_fish <- rnbinom(n_draw, mu = 200 - 20, size = 4) + 20
hist(n_fish, main='Prior Distribution')
```



What if we have better prior information?

```
n_marked <- rep(NA, n_draw)
for(i in 1:n_draw) {
    n_marked[i] <- pick_fish(n_fish[i])
}
post_fish <- n_fish[n_marked == 5]
hist(post_fish, main='Posterior Distribution')
abline(v=median(post_fish), col='red')
abline(v=quantile(post_fish, probs=c(.25, .75)), col='green')
```

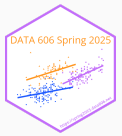


Bayes Billiards Balls

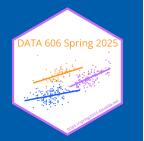
Consider a pool table of length one. An 8-ball is thrown such that the likelihood of its stopping point is uniform across the entire table (i.e. the table is perfectly level). The location of the 8-ball is recorded, but not known to the observer. Subsequent balls are thrown one at a time and all that is reported is whether the ball stopped to the left or right of the 8-ball. Given only this information, what is the position of the 8-ball? How does the estimate change as more balls are thrown and recorded?

```
DATA606::shiny_demo('BayesBilliards', package='DATA606')
```

See also: http://www.bryer.org/post/2016-02-21-bayes_billiards_shiny/



Predictive Modeling

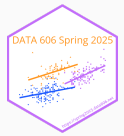


Example: Hours Studying Predicting Passing

```
study <- data.frame(
    Hours=c(0.50,0.75,1.00,1.25,1.50,1.75,1.75,2.00,2.25,2.50,2.75,3.00,
            3.25,3.50,4.00,4.25,4.50,4.75,5.00,5.50),
    Pass=c(0,0,0,0,0,0,1,0,1,0,1,0,1,0,1,1,1,1,1,1)
)
study[sample(nrow(study), 5),]
```

```
##    Hours Pass
## 12  3.00    0
## 5   1.50    0
## 11  2.75    1
## 18  4.75    1
## 10  2.50    0
```

```
tab <- describeBy(study$Hours, group = study$Pass, mat = TRUE, skew = FALSE)
tab$group1 <- as.integer(as.character(tab$group1))
```



Prediction

Odds (or probability) of passing if studied **zero** hours?

$$log(\frac{p}{1-p}) = -4.078 + 1.505 \times 0$$

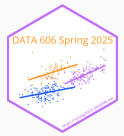
$$\frac{p}{1-p} = exp(-4.078) = 0.0169$$

$$p = \frac{0.0169}{1.169} = .016$$

Odds (or probability) of passing if studied **4** hours?

$$log(\frac{p}{1-p}) = -4.078 + 1.505 \times 4$$

$$\frac{p}{1-p} = exp(1.942) = 6.97$$



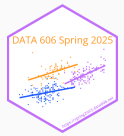
Fitted Values

```
study[1,]
```

```
##   Hours Pass
## 1   0.5    0
```

```
logistic <- function(x, b0, b1) {
    return(1 / (1 + exp(-1 * (b0 + b1 * x)) ))
}
logistic(.5, b0=-4.078, b1=1.505)
```

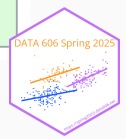
```
## [1] 0.03470667
```



Model Performance

The use of statistical models to predict outcomes, typically on new data, is called predictive modeling. Logistic regression is a common statistical procedure used for prediction. We will utilize a **confusion matrix** to evaluate accuracy of the predictions.

		True condition				
	Total population	Condition positive	Condition negative	Prevalence = $\frac{\Sigma \text{ Condition positive}}{\Sigma \text{ Total population}}$	Accuracy (ACC) = $\frac{\Sigma \text{ True positive} + \Sigma \text{ True negative}}{\Sigma \text{ Total population}}$	
Predicted condition	Predicted condition positive	**True positive**	**False positive**, Type I error	Positive predictive value (PPV), Precision = $\frac{\Sigma \text{ True positive}}{\Sigma \text{ Predicted condition positive}}$	False discovery rate (FDR) = $\frac{\Sigma \text{ False positive}}{\Sigma \text{ Predicted condition positive}}$	
	Predicted condition negative	**False negative**, Type II error	**True negative**	False omission rate (FOR) = $\frac{\Sigma \text{ False negative}}{\Sigma \text{ Predicted condition negative}}$	Negative predictive value (NPV) = $\frac{\Sigma \text{ True negative}}{\Sigma \text{ Predicted condition negative}}$	
		True positive rate (TPR), Recall, Sensitivity, probability of detection, Power = $\frac{\Sigma \text{ True positive}}{\Sigma \text{ Condition positive}}$	False positive rate (FPR), Fall-out, probability of false alarm = $\frac{\Sigma \text{ False positive}}{\Sigma \text{ Condition negative}}$	Positive likelihood ratio (LR+) = $\frac{\text{TPR}}{\text{FPR}}$	Diagnostic odds ratio (DOR) = $\frac{\text{LR+}}{\text{LR−}}$	F_1 score = $2 \cdot \frac{\text{Precision} \cdot \text{Recall}}{\text{Precision} + \text{Recall}}$
		False negative rate (FNR), Miss rate = $\frac{\Sigma \text{ False negative}}{\Sigma \text{ Condition positive}}$	Specificity (SPC), Selectivity, True negative rate (TNR) = $\frac{\Sigma \text{ True negative}}{\Sigma \text{ Condition negative}}$	Negative likelihood ratio (LR−) = $\frac{\text{FNR}}{\text{TNR}}$		



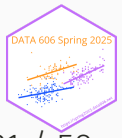
Predicting Heart Attacks

Source: https://www.kaggle.com/datasets/imnikhilanand/heart-attack-prediction?select=data.csv

```
heart <- read.csv('../course_data/heart_attack_predictions.csv')
heart <- heart |>
    mutate_if(is.character, as.numeric) |>
    select(!c(slope, ca, thal))
str(heart)
```

```
## 'data.frame':    294 obs. of  11 variables:
##  $ age     : int  28 29 29 30 31 32 32 32 33 34 ...
##  $ sex     : int  1 1 1 0 0 0 1 1 1 0 ...
##  $ cp      : int  2 2 2 1 2 2 2 2 3 2 ...
##  $ trestbps: num  130 120 140 170 100 105 110 125 120 130 ...
##  $ chol    : num  132 243 NA 237 219 198 225 254 298 161 ...
##  $ fbs     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ restecg : num  2 0 0 1 1 0 0 0 0 0 ...
##  $ thalach : num  185 160 170 170 150 165 184 155 185 190 ...
##  $ exang   : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ oldpeak : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ num     : int  0 0 0 0 0 0 0 0 0 0 ...
```

Note: `num` is the diagnosis of heart disease (angiographic disease status) (i.e. Value 0: < 50% diameter narrowing -- Value 1: > 50% diameter narrowing)



Missing Data

We will save this for another day...

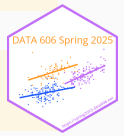
```
complete.cases(heart) |> table()
```

```
##
## FALSE  TRUE
##    33   261
```

```
mice_out <- mice::mice(heart, m = 1)
```

```
##
##  iter imp variable
##   1   1  trestbps  chol  fbs  restecg  thalach  exang
##   2   1  trestbps  chol  fbs  restecg  thalach  exang
##   3   1  trestbps  chol  fbs  restecg  thalach  exang
##   4   1  trestbps  chol  fbs  restecg  thalach  exang
##   5   1  trestbps  chol  fbs  restecg  thalach  exang
```

```
heart <- mice::complete(mice_out)
```



Data Setup

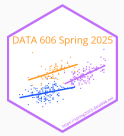
We will split the data into a training set (70% of observations) and validation set (30%).

```
train.rows <- sample(nrow(heart), nrow(heart) * .7)
heart_train <- heart[train.rows,]
heart_test <- heart[-train.rows,]
```

This is the proportions of survivors and defines what our "guessing" rate is. That is, if we guessed no one had a heart attack, we would be correct 62% of the time.

```
(heart_attack <- table(heart_train$num) %>% prop.table)
```

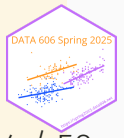
```
##
##         0         1
## 0.6341463 0.3658537
```



Model Training

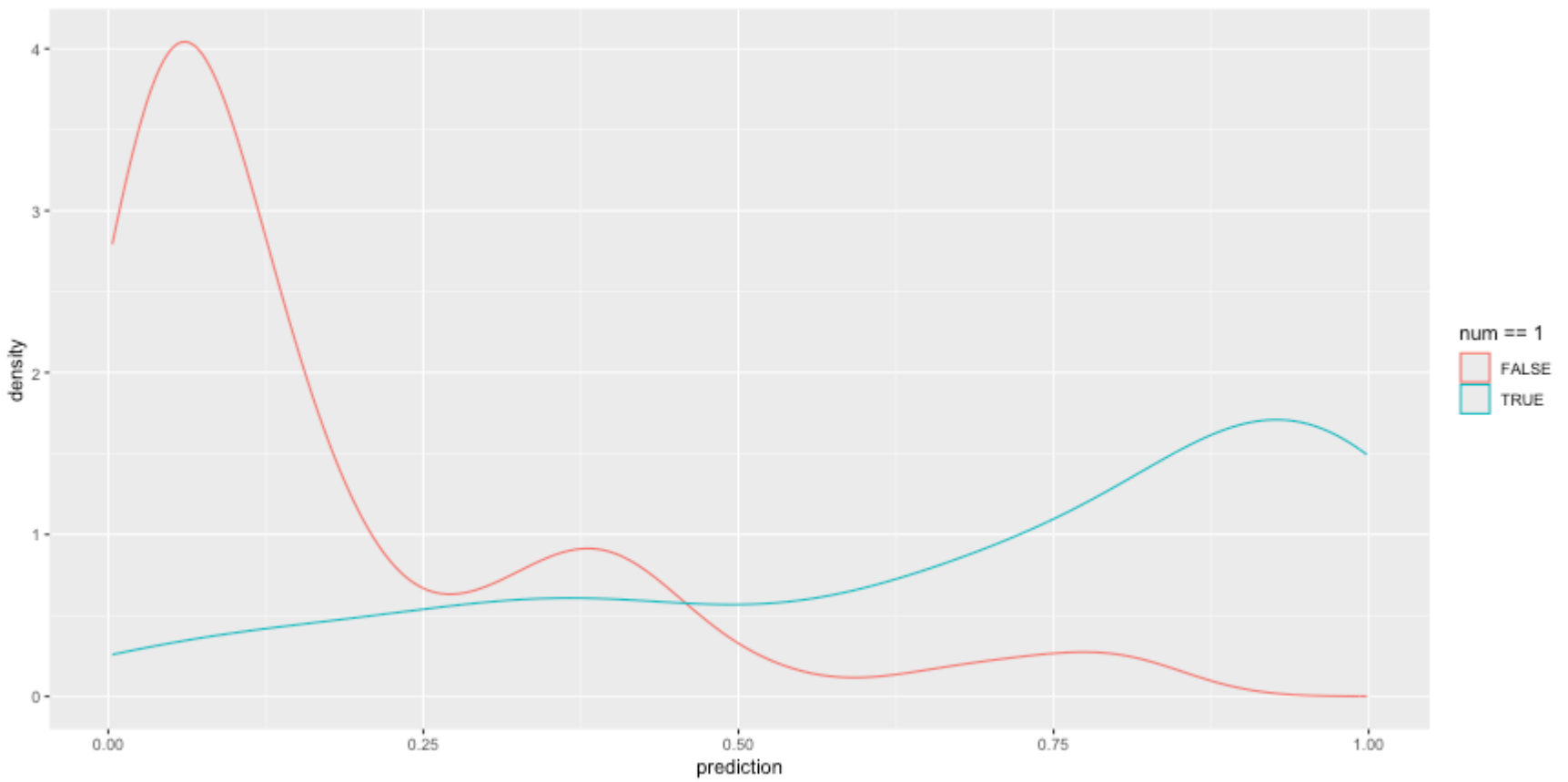
```
lr.out <- glm(num ~ ., data=heart_train, family=binomial(link = 'logit'))
summary(lr.out)
```

```
##
## Call:
## glm(formula = num ~ ., family = binomial(link = "logit"), data = heart_train)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -7.411222   3.354052  -2.210 0.027131 *
## age          0.006097   0.031515   0.193 0.846584
## sex          1.487602   0.547228   2.718 0.006559 **
## cp           0.997312   0.256496   3.888 0.000101 ***
## trestbps    -0.000568   0.013147  -0.043 0.965539
## chol         0.005927   0.003501   1.693 0.090438 .
## fbs          1.835570   0.824286   2.227 0.025957 *
## restecg     -0.093726   0.489456  -0.191 0.848141
## thalach     -0.001827   0.010879  -0.168 0.866596
## exang        1.359498   0.550205   2.471 0.013478 *
## oldpeak      1.167187   0.320889   3.637 0.000275 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 269.25  on 204  degrees of freedom
## Residual deviance: 147.33  on 194  degrees of freedom
## AIC: 169.33
##
```



Predicted Values

```
heart_train$prediction <- predict(lr.out, type = 'response', newdata = heart_train)
ggplot(heart_train, aes(x = prediction, color = num == 1)) + geom_density()
```

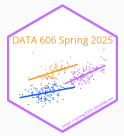


Results

```
heart_train$prediction_class <- heart_train$prediction > 0.5
tab <- table(heart_train$prediction_class,
             heart_train$num) %>% prop.table() %>% print()
```

```
##
##                   0          1
##   FALSE 0.58536585 0.09756098
##   TRUE  0.04878049 0.26829268
```

For the training set, the overall accuracy is 85.37%. Recall that 63.41% people did not have a heart attach. Therefore, the simplest model would be to predict that no one had a heart attack, which would mean we would be correct 63.41% of the time. Therefore, our prediction model is 21.95% better than guessing.



Checking with the validation dataset

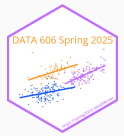
```
(survived_test <- table(heart_test$num) %>% prop.table())
```

```
##
##         0         1
## 0.6516854 0.3483146
```

```
heart_test$prediction <- predict(lr.out, newdata = heart_test, type = 'response')
heart_test$prediciton_class <- heart_test$prediction > 0.5
tab_test <- table(heart_test$prediciton_class, heart_test$num) %>%
    prop.table() %>% print()
```

```
##
##                   0          1
##    FALSE 0.53932584 0.04494382
##    TRUE  0.11235955 0.30337079
```

The overall accuracy is 84.27%, or 19.1% better than guessing.

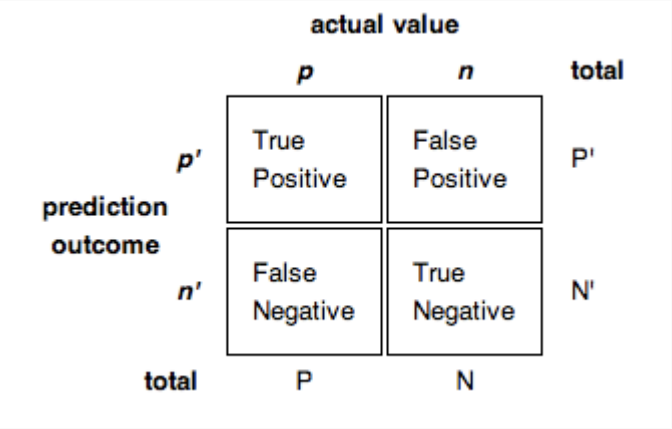


Receiver Operating Characteristic (ROC) Curve

The ROC curve is created by plotting the true positive rate (TPR; AKA sensitivity) against the false positive rate (FPR; AKA probability of false alarm) at various threshold settings.

In a classification model, outcomes are either as positive (*p*) or negative (*n*). There are then four possible outcomes:

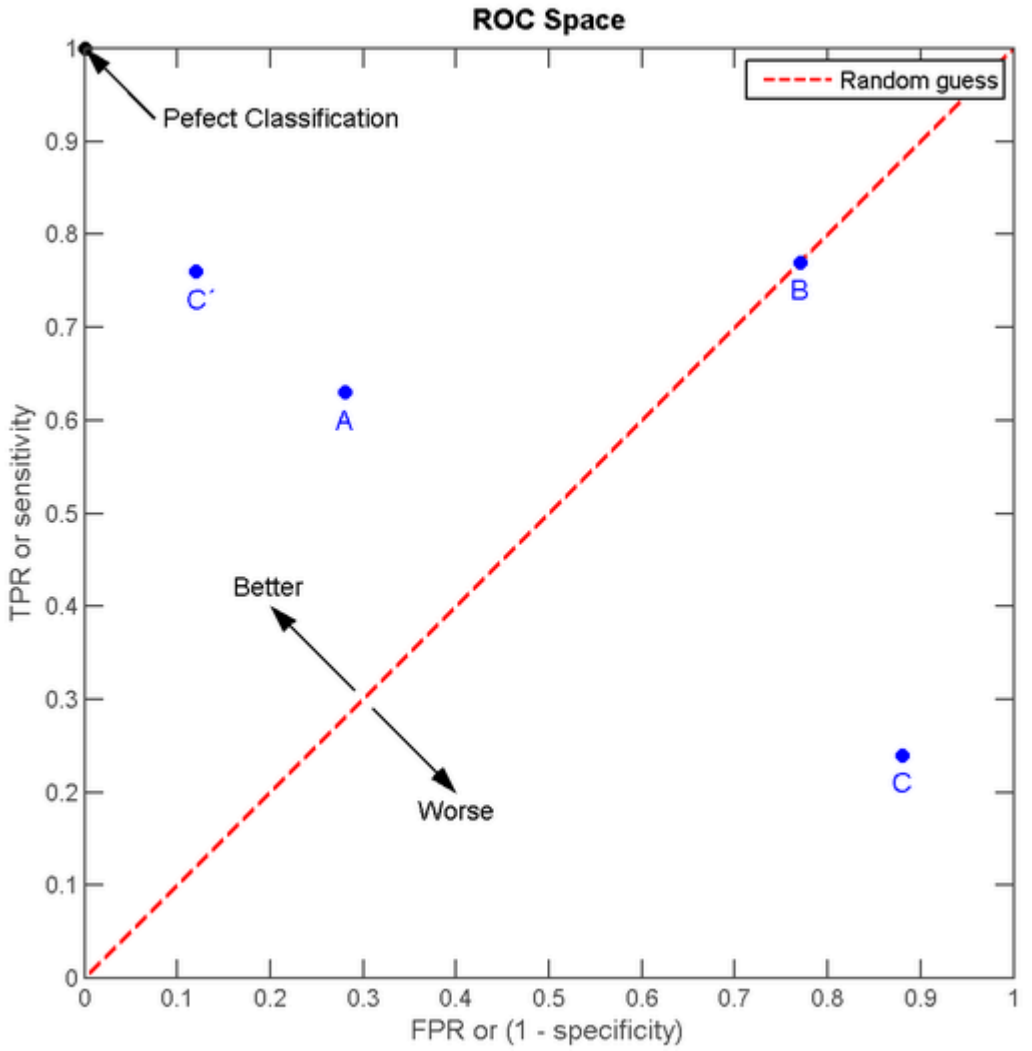
- **true positive** (TP) The outcome from a prediction is *p* and the actual value is also *p*.
- **false positive** (FP) The actual value is *n*.
- **true negative** (TN) Both the prediction outcome and the actual value are *n*.
- **false negative** (FN) The prediction outcome is *n* while the actual value is *p*.




```
roc <- calculate_roc(heart_train$prediction,
                     heart_train$num == 1)
summary(roc)
```

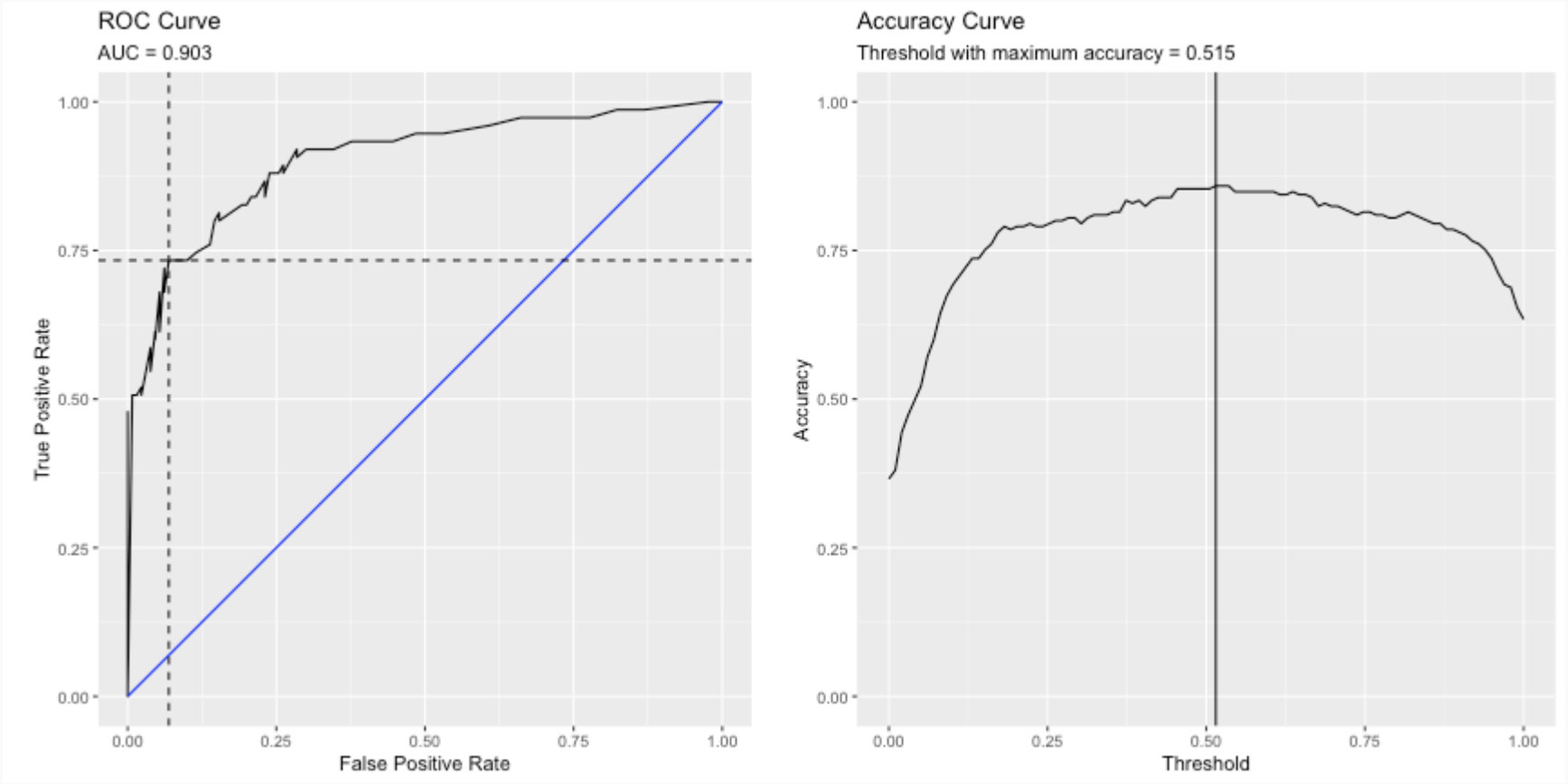
```
## AUC = 0.903
## Cost of false-positive = 1
## Cost of false-negative = 1
## Threshold with minimum cost = 0.515
```

ROC Curve


ROC Space
Random guess
Pefect Classification
C´
B
A
Better
Worse
C
TPR or sensitivity
FPR or (1 - specificity)
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1

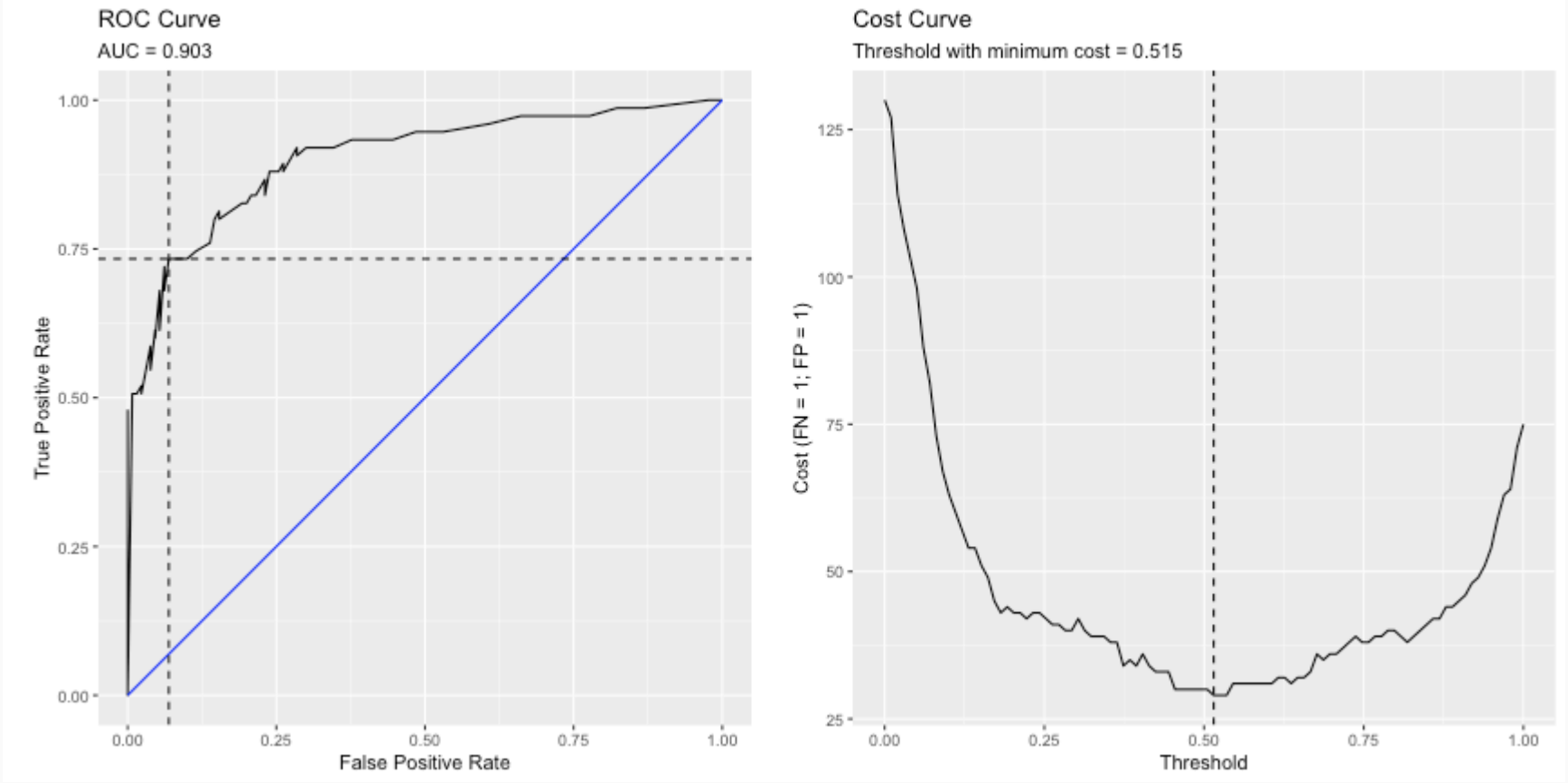
ROC Curve

```
plot(roc, curve = 'accuracy')
```



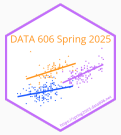
ROC Curve

```
plot(roc)
```



Caution on Interpreting Accuracy

- Loh, Sooo, and Zing (2016) predicted sexual orientation based on Facebook Status.
- They reported model accuracies of approximately 90% using SVM, logistic regression and/or random forest methods.
- Gallup (2018) poll estimates that 4.5% of the Americal population identifies as LGBT.
- *My proposed model:* I predict all Americans are heterosexual.
- The accuracy of my model is 95.5%, or *5.5% better than Facebook's model!*
- Predicting "rare" events (i.e. when the proportion of one of the two outcomes large) is difficult and requires independent (predictor) variables that strongly associated with the dependent (outcome) variable.



Fitted Values Revisited

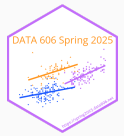
What happens when the ratio of true-to-false increases (i.e. want to predict "rare" events)?

Let's simulate a dataset where the ratio of true-to-false is 10-to-1. We can also define the distribution of the dependent variable. Here, there is moderate separation in the distributions.

```
test.df2 <- getSimulatedData(
    treat.mean=.6, control.mean=.4)
```

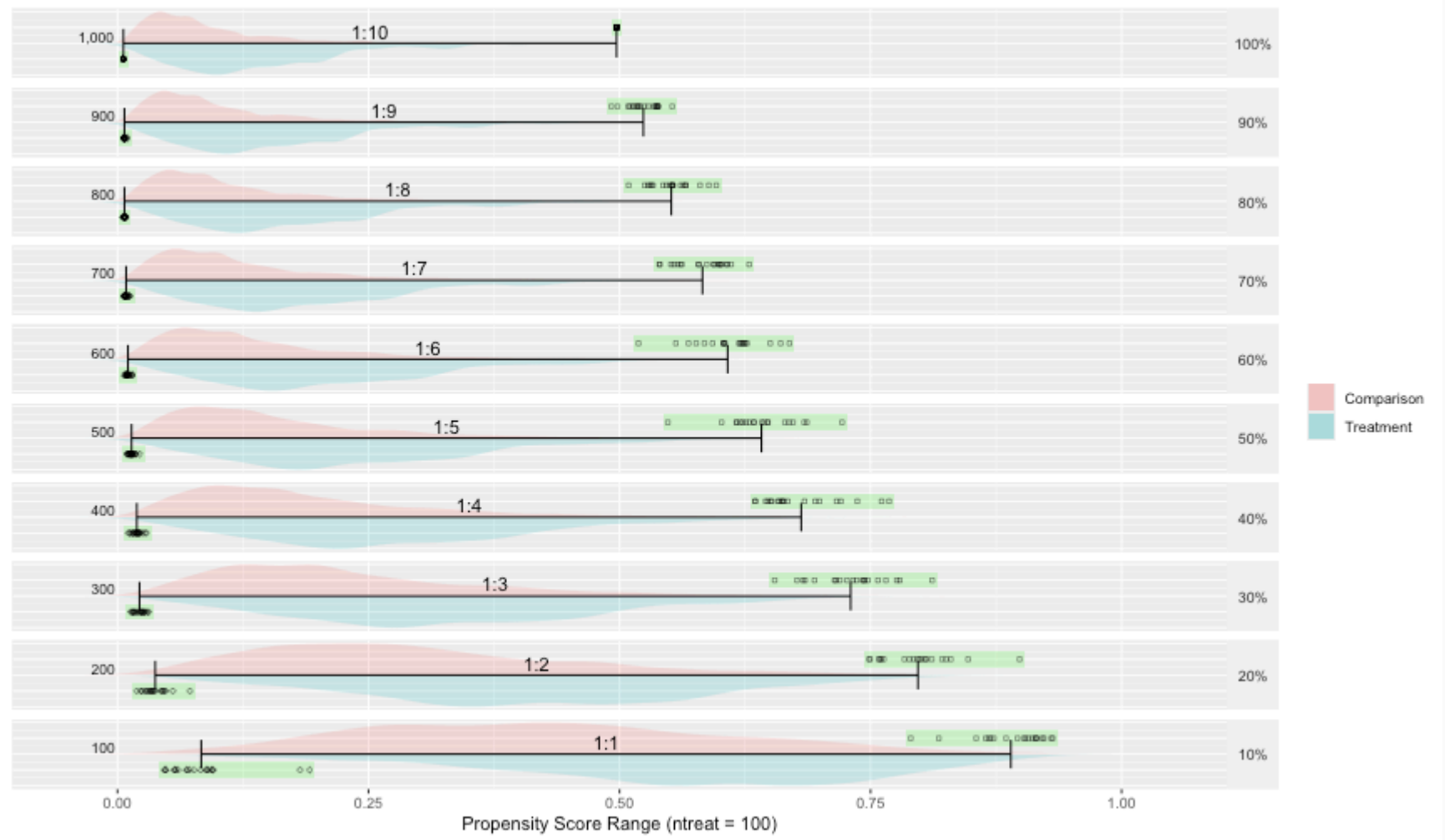
The `multilevelPSA::psrange` function will sample with varying ratios from 1:10 to 1:1. It takes multiple samples and averages the ranges and distributions of the fitted values from logistic regression.

```
psranges2 <- psrange(test.df2, test.df2$treat, treat ~ .,
                     samples=seq(100,1000,by=100), nboot=20)
```



Fitted Values Revisited (cont.)

```
plot(psranges2)
```

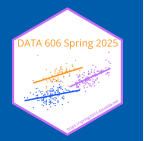


One Minute Paper

1. What was the most important thing you learned during this class?
2. What important question remains unanswered for you?

https://forms.gle/ETg8tW9YRHQJHjE28

BONUS: Classification and Regression Trees



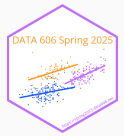
Classification and Regression Trees

The goal of CART methods is to find best predictor in X of some outcome, y. CART methods do this recursively using the following procedures:

- Find the best predictor in X for y.
- Split the data into two based upon that predictor.
- Repeat 1 and 2 with the split data sets until a stopping criteria has been reached.

There are a number of possible stopping criteria including: Only one data point remains.

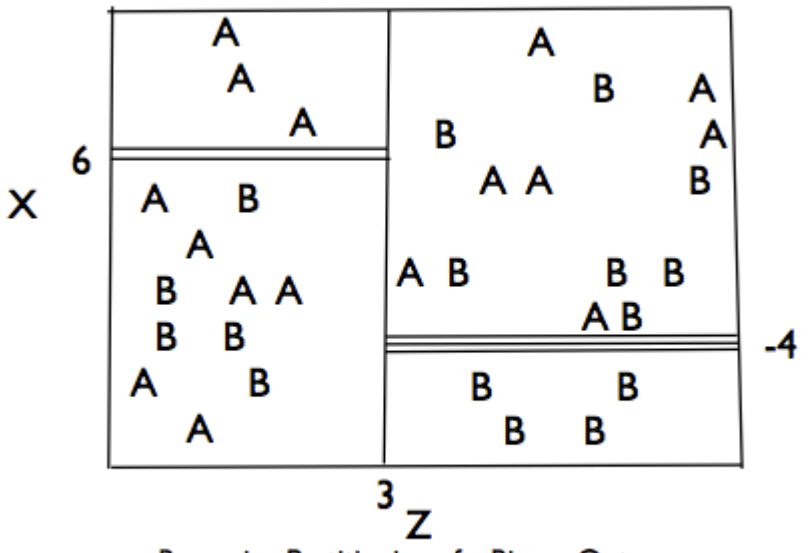
- All data points have the same outcome value.
- No predictor can be found that sufficiently splits the data.



Recursive Partitioning Logic of CART

Consider the scatter plot to the right with the following characteristics:

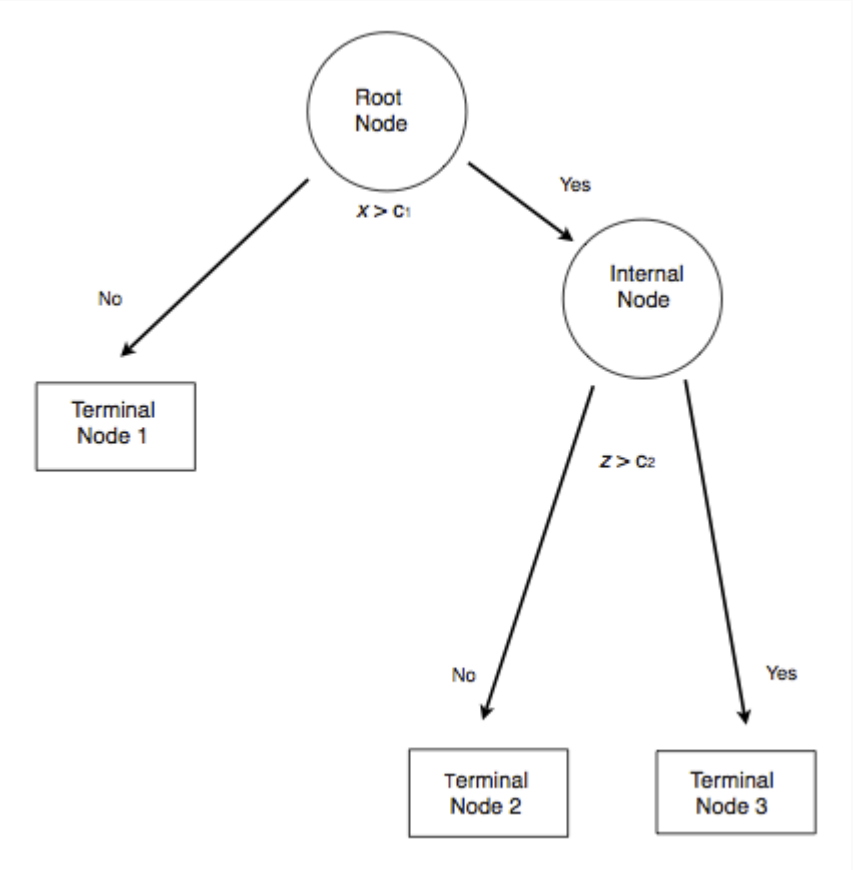
- Binary outcome, G, coded “A” or “B”.
- Two predictors, x and z
- The vertical line at z = 3 creates the first partition.
- The double horizontal line at x = -4 creates the second partition.
- The triple horizontal line at x = 6 creates the third partition.



Recursive Partitioning of a Binary Outcome
(where G = A or B and predictors are Z and X)

Tree Structure

- The root node contains the full data set.
- The data are split into two mutually exclusive pieces. Cases where x > ci go to the right, cases where x <= ci go to the left.
- Those that go to the left reach a terminal node.
- Those on the right are split into two mutually exclusive pieces. Cases where z > c2 go to the right and terminal node 3; cases where z <= c2 go to the left and terminal node 2.



Sum of Squared Errors

The sum of squared errors for a tree *T* is:

$$S = \sum_{c \in leaves(T)} \sum_{i \in c} (y - m_c)^2$$

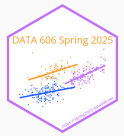
Where, $m_c = \frac{1}{n} \sum_{i \in c} y_i$, the prediction for leaf \textit{c}.

Or, alternatively written as:

$$S = \sum_{c \in leaves(T)} n_c V_c$$

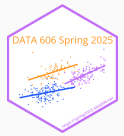
Where V_c is the within-leave variance of leaf \textit{c}.

Our goal then is to find splits that minimize S.



Advantages of CART Methods

- Making predictions is fast.
- It is easy to understand what variables are important in making predictions.
- Trees can be grown with data containing missingness. For rows where we cannot reach a leaf node, we can still make a prediction by averaging the leaves in the sub-tree we do reach.
- The resulting model will inherently include interaction effects. There are many reliable algorithms available.

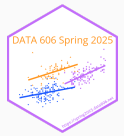


Regression Trees

In this example we will predict the median California house price from the house's longitude and latitude.

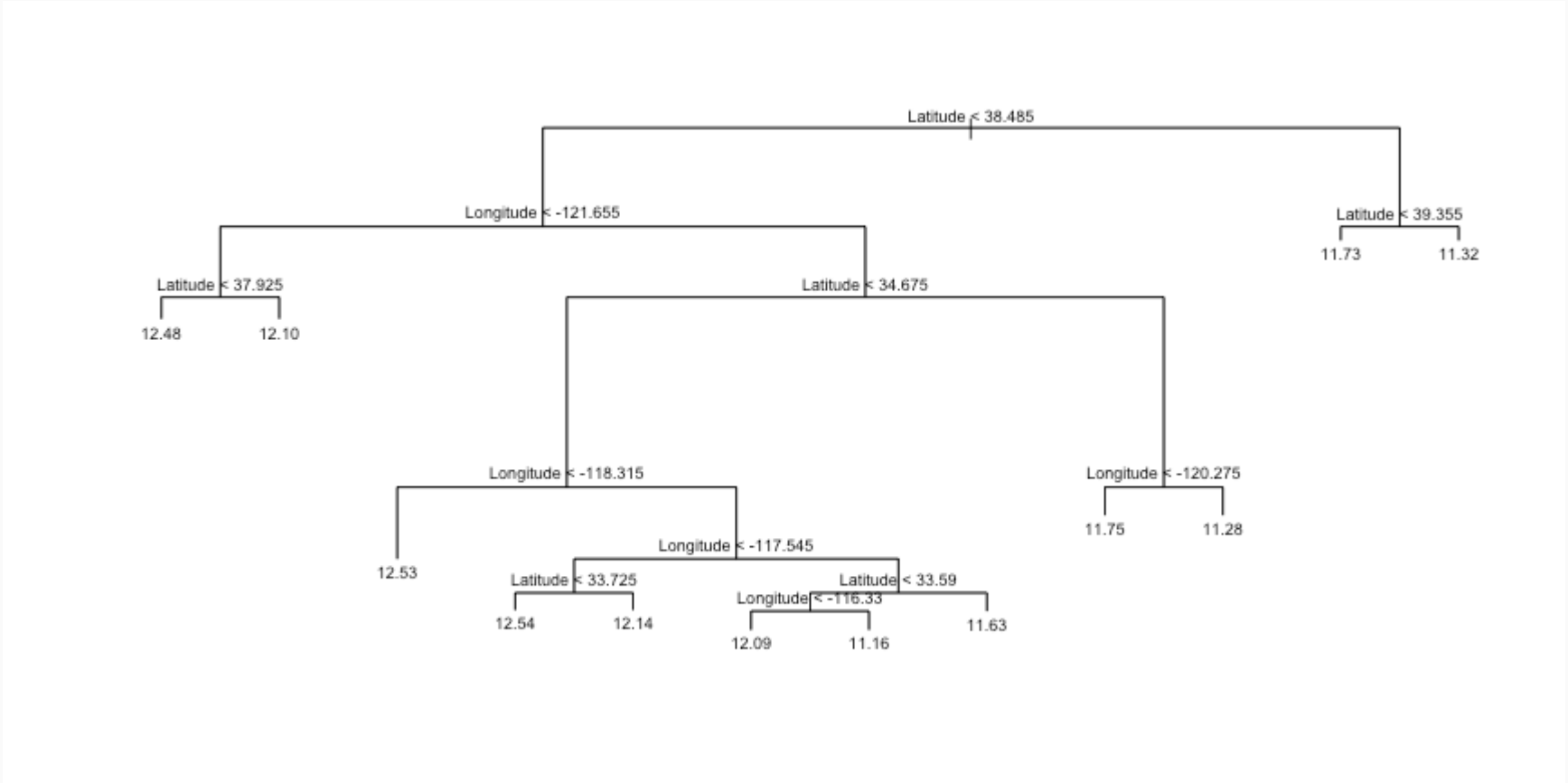
```
str(calif)
```

```
## 'data.frame':    20640 obs. of  10 variables:
##  $ MedianHouseValue: num  452600 358500 352100 341300 342200 ...
##  $ MedianIncome    : num  8.33 8.3 7.26 5.64 3.85 ...
##  $ MedianHouseAge  : num  41 21 52 52 52 52 52 52 42 52 ...
##  $ TotalRooms      : num  880 7099 1467 1274 1627 ...
##  $ TotalBedrooms   : num  129 1106 190 235 280 ...
##  $ Population      : num  322 2401 496 558 565 ...
##  $ Households      : num  126 1138 177 219 259 ...
##  $ Latitude        : num  37.9 37.9 37.9 37.9 37.9 ...
##  $ Longitude       : num  -122 -122 -122 -122 -122 ...
##  $ cut.prices      : Factor w/ 4 levels "[1.5e+04,1.2e+05]",..: 4 4 4 4 4 4 4 3 3 3 ...
```

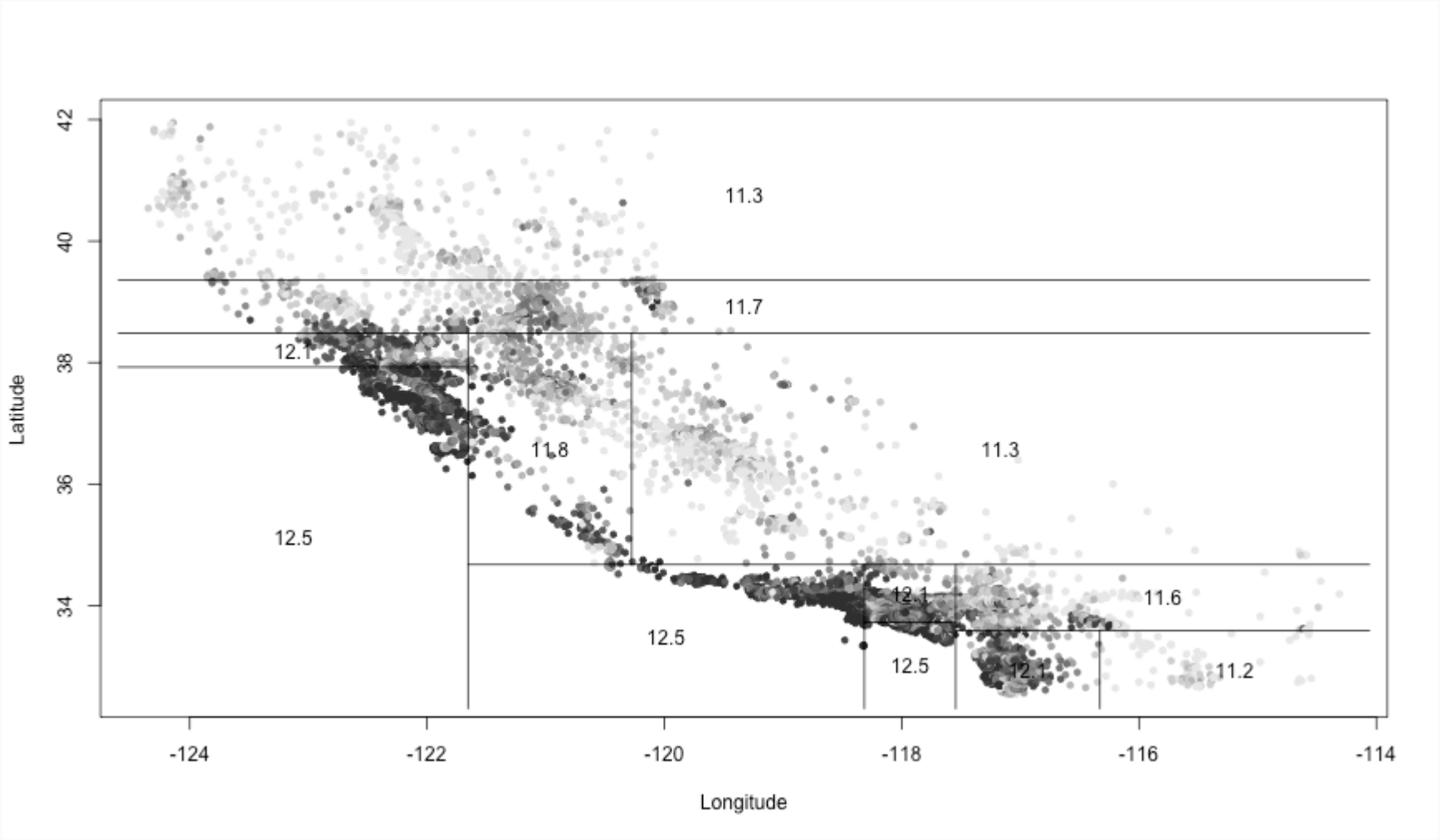


Tree 1

```
treefit <- tree(log(MedianHouseValue) ~ Longitude + Latitude, data=calif)
plot(treefit); text(treefit, cex=0.75)
```



Tree 1

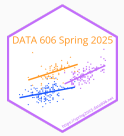

Latitude
42
40
38
36
34
11.3
11.7
12.1
11.8
11.3
12.5
12.1
11.6
12.5
12.5
12.1
11.2
-124
-122
-120
-118
-116
-114
Longitude

Tree 1

```
summary(treefit)
```

```
##
## Regression tree:
## tree(formula = log(MedianHouseValue) ~ Longitude + Latitude,
##     data = calif)
## Number of terminal nodes:  12
## Residual mean deviance:  0.1662 = 3429 / 20630
## Distribution of residuals:
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -2.75900 -0.26080 -0.01359  0.00000  0.26310  1.84100
```

Here “deviance” is the mean squared error, or root-mean-square error of $\sqrt{.166} = 0.41$.



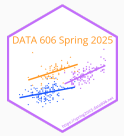
Tree 2, Reduce Minimum Deviance

We can increase the fit but changing the stopping criteria with the mindev parameter.

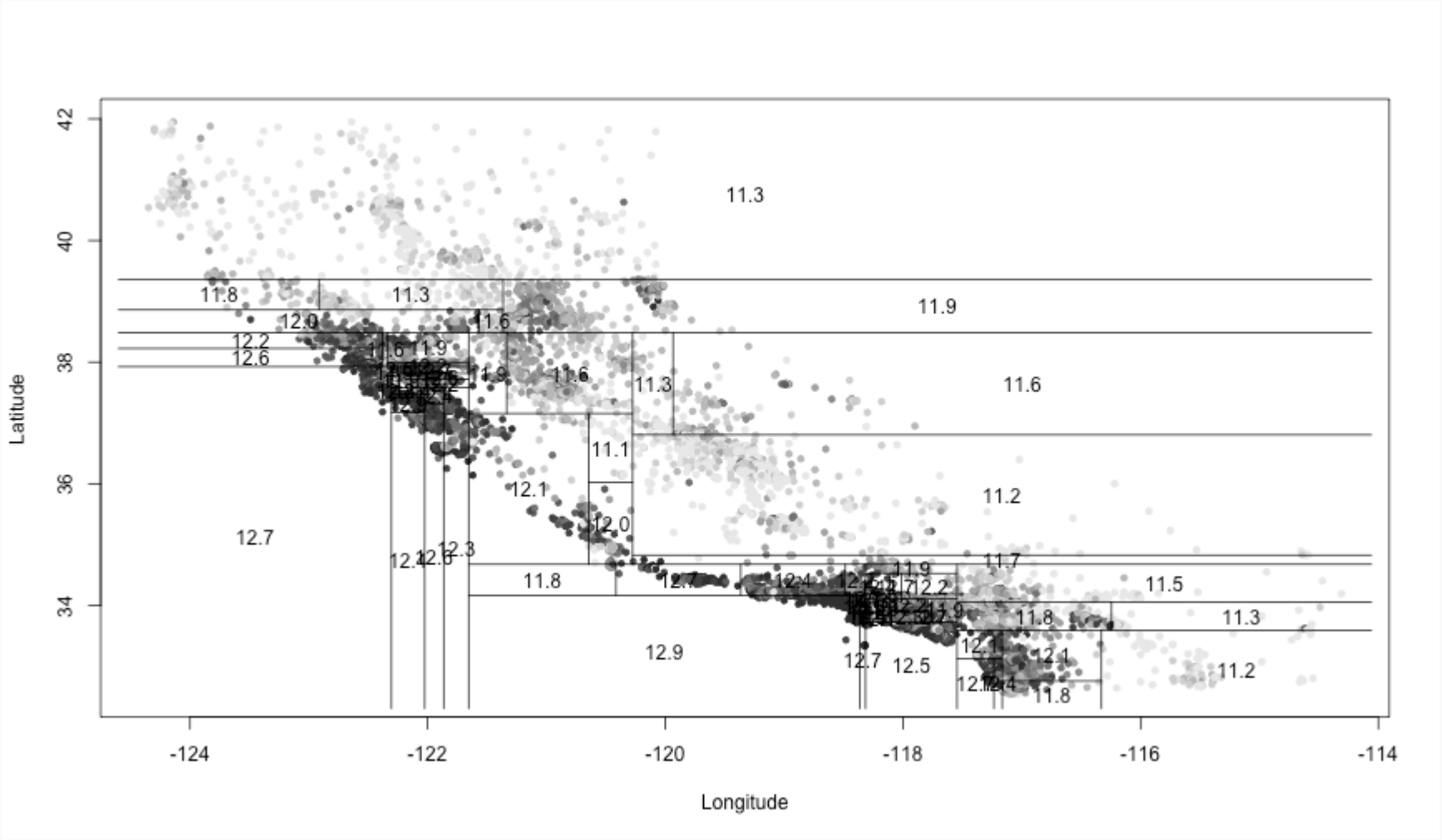
```
treefit2 <- tree(log(MedianHouseValue) ~ Longitude + Latitude, data=calif, mindev=.001)
summary(treefit2)
```

```
##
## Regression tree:
## tree(formula = log(MedianHouseValue) ~ Longitude + Latitude,
##     data = calif, mindev = 0.001)
## Number of terminal nodes:  68
## Residual mean deviance:  0.1052 = 2164 / 20570
## Distribution of residuals:
##     Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
## -2.94700 -0.19790 -0.01872  0.00000  0.19970  1.60600
```

With the larger tree we now have a root-mean-square error of 0.32.



Tree 2, Reduce Minimum Deviance



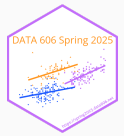
Tree 3, Include All Variables

However, we can get a better fitting model by including the other variables.

```
treefit3 <- tree(log(MedianHouseValue) ~ ., data=calif)
summary(treefit3)
```

```
##
## Regression tree:
## tree(formula = log(MedianHouseValue) ~ ., data = calif)
## Variables actually used in tree construction:
## [1] "cut.prices"
## Number of terminal nodes:  4
## Residual mean deviance:  0.03608 = 744.5 / 20640
## Distribution of residuals:
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
## -1.718000 -0.127300  0.009245  0.000000  0.130000  0.358600
```

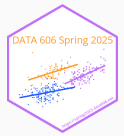
With all the available variables, the root-mean-square error is 0.11.



Classification Trees

Predicting who survived the Titanic.

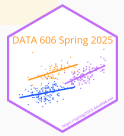
- `pclass`: Passenger class (1 = 1st; 2 = 2nd; 3 = 3rd)
- `survival`: A Boolean indicating whether the passenger survived or not (0 = No; 1 = Yes); this is our target
- `name`: A field rich in information as it contains title and family names
- `sex`: male/female
- `age`: Age, a significant portion of values are missing
- `sibsp`: Number of siblings/spouses aboard
- `parch`: Number of parents/children aboard
- `ticket`: Ticket number.
- `fare`: Passenger fare (British Pound).
- `cabin`: Does the location of the cabin influence chances of survival?
- `embarked`: Port of embarkation (C = Cherbourg; Q = Queenstown; S = Southampton)
- `boat`: Lifeboat, many missing values
- `body`: Body Identification Number
- `home.dest`: Home/destination



Classification using `rpart`

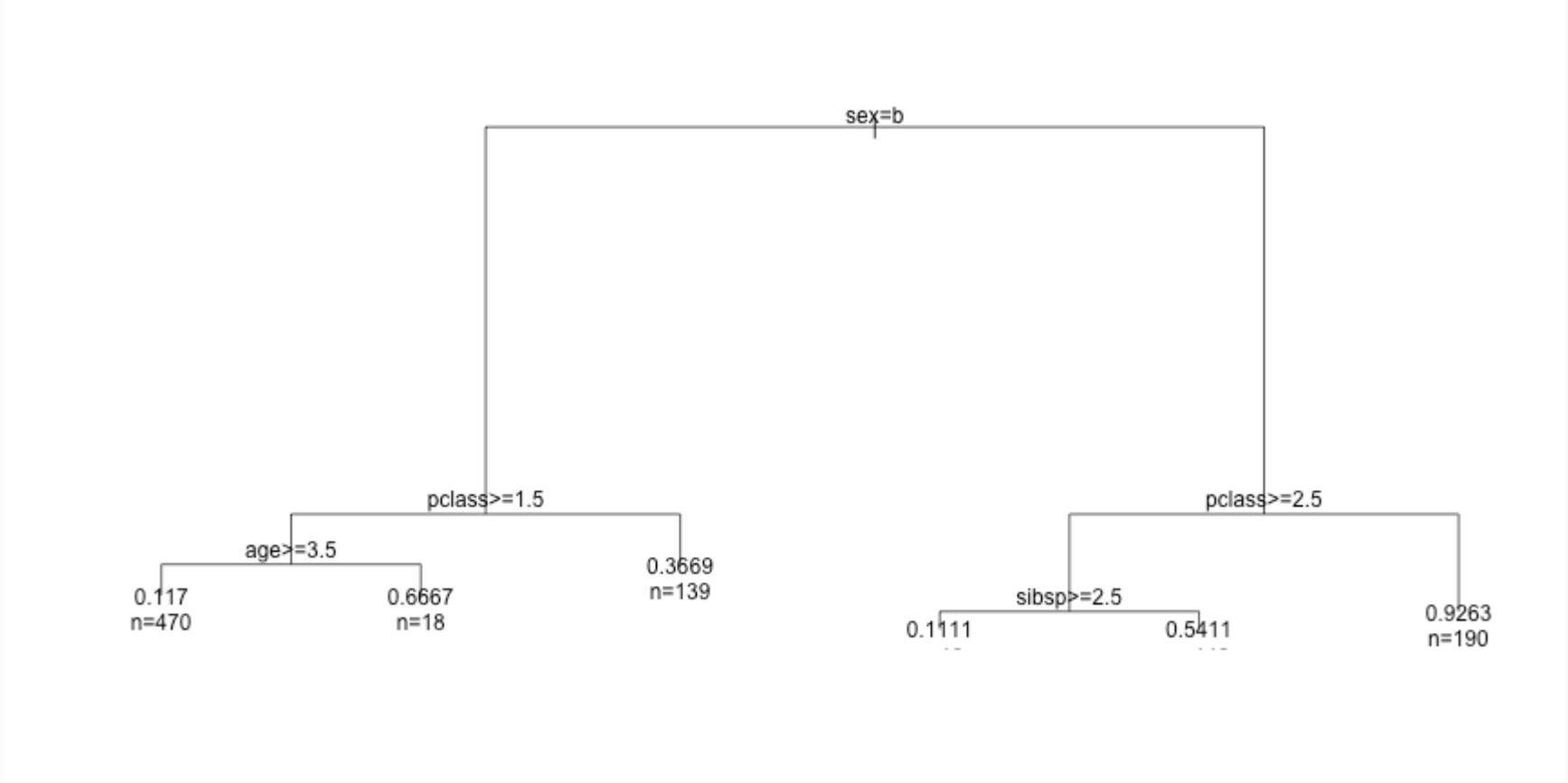
```
(titanic.rpart <- rpart(survived ~ pclass + sex + age + sibsp,
   data=titanic.train))
```

```
## n= 981
##
## node), split, n, deviance, yval
##       * denotes terminal node
##
##  1) root 981 231.651400 0.3822630
##    2) sex=male 627  95.792660 0.1881978
##      4) pclass>=1.5 488  57.801230 0.1372951
##        8) age>=3.5 470  48.563830 0.1170213 *
##        9) age< 3.5 18   4.000000 0.6666667 *
##      5) pclass< 1.5 139  32.287770 0.3669065 *
##    3) sex=female 354  70.420900 0.7259887
##      6) pclass>=2.5 164  40.993900 0.4939024
##       12) sibsp>=2.5 18   1.777778 0.1111111 *
##       13) sibsp< 2.5 146  36.253420 0.5410959 *
##      7) pclass< 2.5 190  12.968420 0.9263158 *
```



Classification using `rpart`

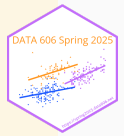
```
plot(titanic.rpart); text(titanic.rpart, use.n=TRUE, cex=1)
```



Classification using `ctree`

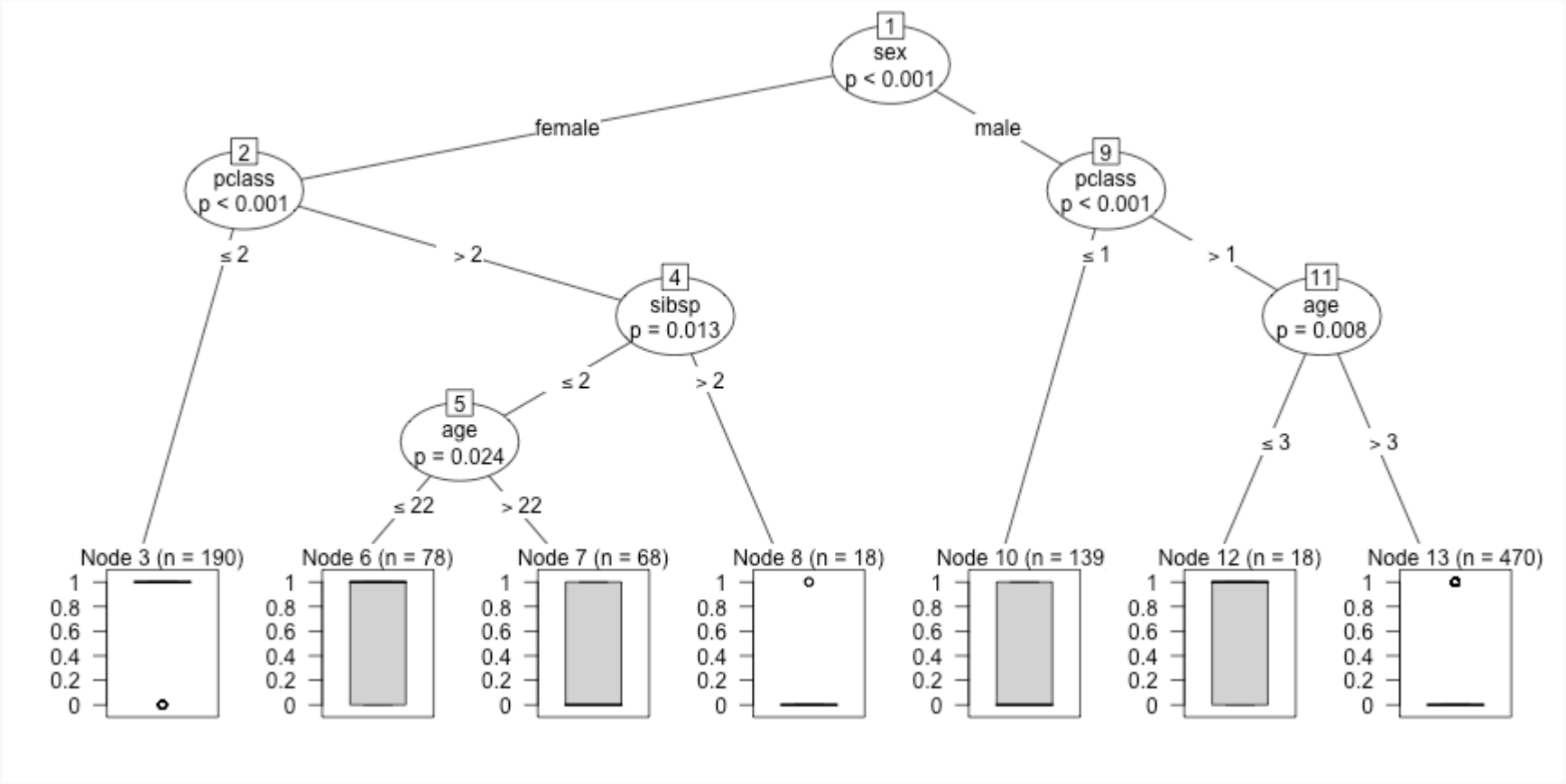
```
(titanic.ctree <- ctree(survived ~ pclass + sex + age + sibsp, data=titanic.train))
```

```
##
##      Conditional inference tree with 7 terminal nodes
##
## Response:  survived
## Inputs:  pclass, sex, age, sibsp
## Number of observations:  981
##
## 1) sex == {female}; criterion = 1, statistic = 276.834
##   2) pclass <= 2; criterion = 1, statistic = 77.749
##     3)*  weights = 190
##   2) pclass > 2
##     4) sibsp <= 2; criterion = 0.987, statistic = 8.716
##       5) age <= 22; criterion = 0.976, statistic = 7.505
##         6)*  weights = 78
##       5) age > 22
##         7)*  weights = 68
##     4) sibsp > 2
##       8)*  weights = 18
## 1) sex == {male}
##   9) pclass <= 1; criterion = 1, statistic = 34.187
##     10)*  weights = 139
```



Classification using `ctree`

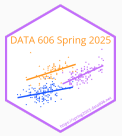
```
plot(titanic.ctree)
```



Ensemble Methods

Ensemble methods use multiple models that are combined by weighting, or averaging, each individual model to provide an overall estimate. Each model is a random sample of the sample. Common ensemble methods include:

- *Boosting* - Each successive trees give extra weight to points incorrectly predicted by earlier trees. After all trees have been estimated, the prediction is determined by a weighted “vote” of all predictions (i.e. results of each individual tree model).
- *Bagging* - Each tree is estimated independent of other trees. A simple “majority vote” is take for the prediction.
- *Random Forests* - In addition to randomly sampling the data for each model, each split is selected from a random subset of all predictors.
- *Super Learner* - An ensemble of ensembles. See https://cran.r-project.org/web/packages/SuperLearner/vignettes/Guide-to-SuperLearner.html



Random Forests

The random forest algorithm works as follows:

1. Draw n_{tree} bootstrap samples from the original data.

2. For each bootstrap sample, grow an unpruned tree. At each node, randomly sample m_{try} predictors and choose the best split among those predictors selectedBagging is a special case of random forests where $m_{try} = p$ where p is the number of predictors.

3. Predict new data by aggregating the predictions of the ntree trees (majority votes for classification, average for regression).

Error rates are obtained as follows:

1. At each bootstrap iteration predict data not in the bootstrap sample (what Breiman calls “out-of-bag”, or OOB, data) using the tree grown with the bootstrap sample.

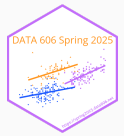
2. Aggregate the OOB predictions. On average, each data point would be out-of-bag 36% of the times, so aggregate these predictions. The calculated error rate is called the OOB estimate of the error rate.

Random Forests: Titanic

```
titanic.rf <- randomForest(factor(survived) ~ pclass + sex + age + sibsp,
                           data = titanic.train,
                           ntree = 5000,
                           importance = TRUE)
```

```
importance(titanic.rf)
```

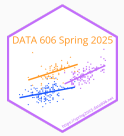
```
##                0         1 MeanDecreaseAccuracy MeanDecreaseGini
## pclass  87.70927 115.46598             127.50822          50.56644
## sex    212.69670 306.52265             289.46247         125.67778
## age     89.83804  56.48383             115.48253          56.14144
## sibsp   73.43383 -10.36146              56.90253          16.85598
```



Random Forests: Titanic (cont.)

```
importance(titanic.rf)
```

```
##                0         1 MeanDecreaseAccuracy MeanDecreaseGini
## pclass  87.70927 115.46598             127.50822         50.56644
## sex    212.69670 306.52265             289.46247        125.67778
## age     89.83804  56.48383             115.48253         56.14144
## sibsp   73.43383 -10.36146              56.90253         16.85598
```



Random Forests: Titanic

```
min_depth_frame <- min_depth_distribution(titanic.rf)
```

```
plot_min_depth_distribution(min_depth_frame)
```