



# Welcome to the Machine Learning Toolbox!



## Supervised learning

- caret R package
- Automates supervised learning (a.k.a. predictive modeling)
- Target variable





## Supervised learning

- Two types of predictive models
  - Classification —— Qualitative
  - Regression —— Quantitative
- Use *metrics* to evaluate models
  - Quantifiable
  - Objective
- Root Mean Squared Error (RMSE) for regression (e.g. lm())



### Evaluating model performance

- Common to calculate in-sample RMSE
  - Too optimistic
  - Leads to overfitting
- Better to calculate out-of-sample error (a la caret)
  - Simulates real-world usage
  - Helps avoid overfitting



#### In-sample error

```
> # Fit a model to the mtcars data
> data(mtcars)
> model <- lm(mpg ~ hp, mtcars[1:20, ])

> # Predict in-sample
> predicted <- predict(model, mtcars[1:20, ], type = "response")

> # Calculate RMSE
> actual <- mtcars[1:20, "mpg"]
> sqrt(mean((predicted - actual)^2))
[1] 3.172132
```





The Machine Learning Toolbox

# Let's practice!





# Out-of-sample error measures



### Out-of-sample error

- Want models that don't overfit and generalize well
- Do the models perform well on <u>new</u> data?
- Test models on new data, or a test set
  - Key insight of machine learning
  - In-sample validation almost guarantees overfitting
- Primary goal of caret and this course: don't overfit



### Example: out-of-sample RMSE

```
> # Fit a model to the mtcars data
> data(mtcars)
> model <- lm(mpg ~ hp, mtcars[1:20, ])

> # Predict out-of-sample
> predicted <- predict(model, mtcars[21:32, ], type = "response")

> # Evaluate error
> actual <- mtcars[21:32, "mpg"]
> sqrt(mean((predicted - actual)^2))
[1] 5.507236
```



### Compare to in-sample RMSE





# Let's practice!





#### Cross-validation



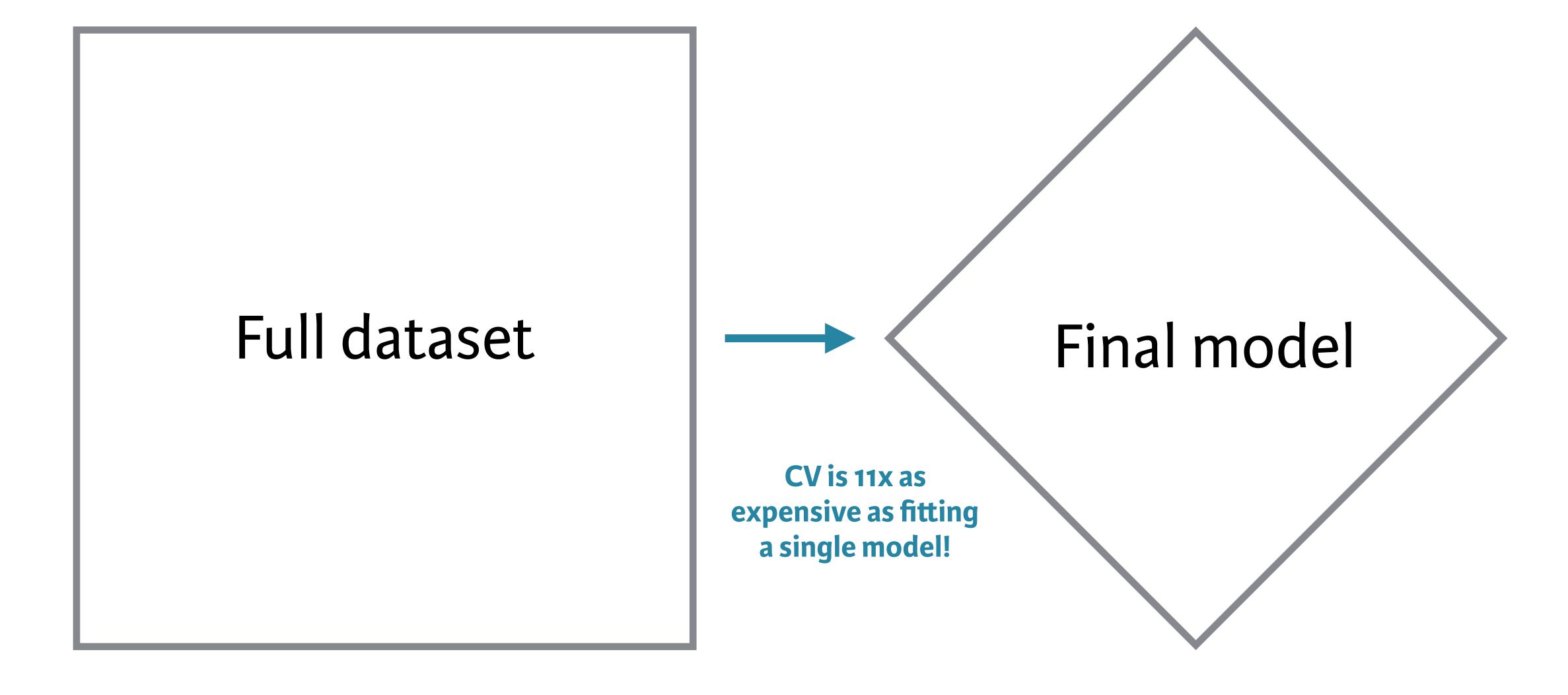
#### Cross-validation

Full dataset

Rows are randomly assigned

Fold 1
Fold 2
Fold 3
Fold 4
Fold 5
Fold 6
Fold 7
Fold 8
Fold 9
Fold 10

#### Fit final model on full dataset





#### Cross-validation

```
> # Set seed for reproducibility
> library(caret)
> data(mtcars)
> set.seed(42)
> # Fit linear regression model
> model <- train(mpg ~ hp, mtcars,</pre>
                 method = "lm",
                 trControl = trainControl(
                   method = "cv", number = 10,
                   verboseIter = TRUE
+ Fold01: parameter=none
+ Fold02: parameter=none
Fold10: parameter=none
Aggregating results
Fitting final model on full training set
```





# Let's practice!





# Logistic regression on Sonar



#### Classification models

- Categorical (i.e. qualitative) target variable
- Example: will a loan default?
- Still a form of supervised learning
- Use a train/test split to evaluate performance
- Use the Sonar dataset
- Goal: distinguish rocks from mines



#### Example: Sonar data

```
Load the Sonar dataset
> library(mlbench)
> data(Sonar)
> # Look at the data
> Sonar[1:6, c(1:5, 61)]
                                 V5 Class
                    V3
                         V4
      V1
1 0.0200 0.0371 0.0428 0.0207 0.0954
2 0.0453 0.0523 0.0843 0.0689 0.1183
3 0.0262 0.0582 0.1099 0.1083 0.0974
4 0.0100 0.0171 0.0623 0.0205 0.0205
5 0.0762 0.0666 0.0481 0.0394 0.0590
6 0.0286 0.0453 0.0277 0.0174 0.0384
```



# Splitting the data

- Randomly split data into training and test sets
- Use a 60/40 split, instead of 80/20
- Sonar dataset is small, so 60/40 gives a larger, more reliable test set



# Splitting the data

```
# Randomly order the dataset
> rows <- sample(nrow(Sonar))
> Sonar <- Sonar[rows, ]

# Find row to split on
> split <- round(nrow(Sonar) * .60)
> train <- Sonar[1:split, ]
> test <- Sonar[(split + 1):nrow(Sonar), ]

# Confirm test set size
> nrow(train) / nrow(Sonar)
[1] 0.6009615
```





# Let's practice!







#### Reference

Prediction

	Yes	No
Yes	True positive	False positive
No	False negative	True negative



```
# Fit a model
> model <- glm(Class ~ ., family = binomial(link = "logit"),</pre>
train)
> p <- predict(model, test, type = "response")</pre>
> summary(p)
   Min. 1st Qu. Median Mean 3rd Qu. Max.
0.0000 0.0000 0.9885 0.5296 1.0000 1.0000
# Turn probabilities into classes and look at their frequencies
> p_class <- ifelse(p > .50, "M", "R")
> table(p_class)
p_class
44 39
```



- Make a 2-way frequency table
- Compare predicted vs. actual classes

```
# Make simple 2-way frequency table
> table(p_class, test[["Class"]])
p_class M R
M 13 31
R 30 9
```



```
# Use caret's helper function to calculate additional statistics
> confusionMatrix(p_class, test[["Class"]])
         Reference
Prediction M R
        M 13 31
        R 30 9
              Accuracy : 0.2651
                95% CI: (0.1742, 0.3734)
    No Information Rate: 0.5181
    P-Value [Acc > NIR] : 1
                  Kappa: -0.4731
 Mcnemar's Test P-Value: 1
           Sensitivity: 0.3023
           Specificity: 0.2250
         Pos Pred Value: 0.2955
         Neg Pred Value: 0.2308
```





# Let's practice!





# Class probabilities and class predictions



#### Different thresholds

- Not limited to 50% threshold
  - 10% would catch more mines with less certainty
  - 90% would catch fewer mines with more certainty
- Balance true positive and false positive rates
- Cost-benefit analysis





#### Confusion matrix with caret

```
# Use caret to produce confusion matrix
> confusionMatrix(p_class, test[["Class"]])
          Reference
Prediction M R
        M 13 28
        R 30 12
              Accuracy : 0.3012
                 95% CI: (0.2053, 0.4118)
   No Information Rate: 0.5181
    P-Value [Acc > NIR] : 1.0000
                  Kappa: -0.397
 Mcnemar's Test P-Value: 0.8955
           Sensitivity: 0.3023
            Specificity: 0.3000
         Pos Pred Value: 0.3171
         Neg Pred Value: 0.2857
```





# Let's practice!





# Introducing the ROC curve



### The challenge

- Many possible classification thresholds
- Requires manual work to choose
- Easy to overlook a particular threshold
- Need a more systematic approach



#### ROC curves

- Plot true/false positive rate at every possible threshold
- Visualize tradeoffs between two extremes o% false positive rate vs.
- Result is an ROC curve
- Developed as a method for analyzing radar signals

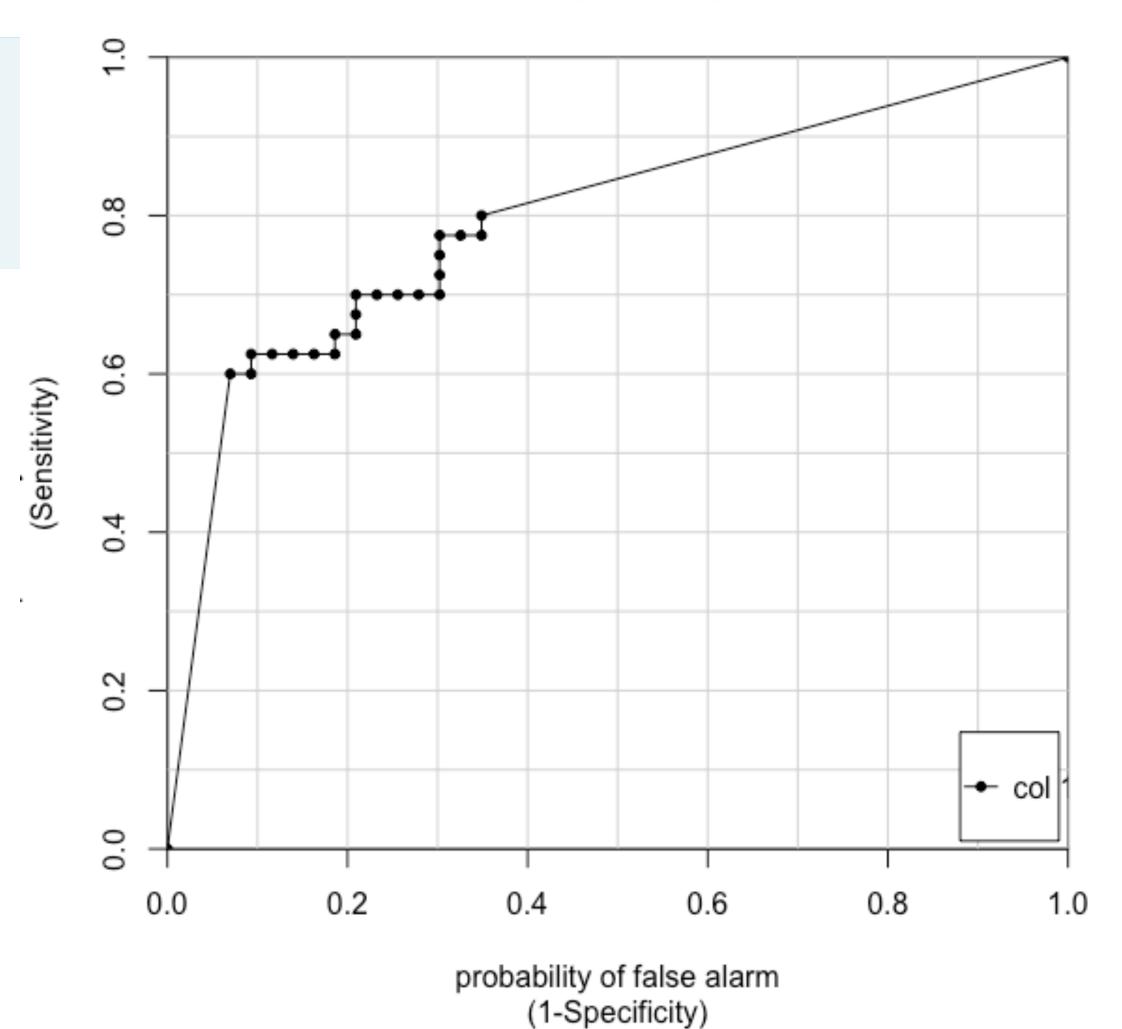


## An example ROC curve

```
# Create ROC curve
> library(caTools)
> colAUC(p, test[["Class"]], plotROC = TRUE)
```

- X-axis: false positive rate
- Y-axis: true positive rate
- Each point along the curve represents a different threshold

#### **ROC Curves**







## Let's practice!





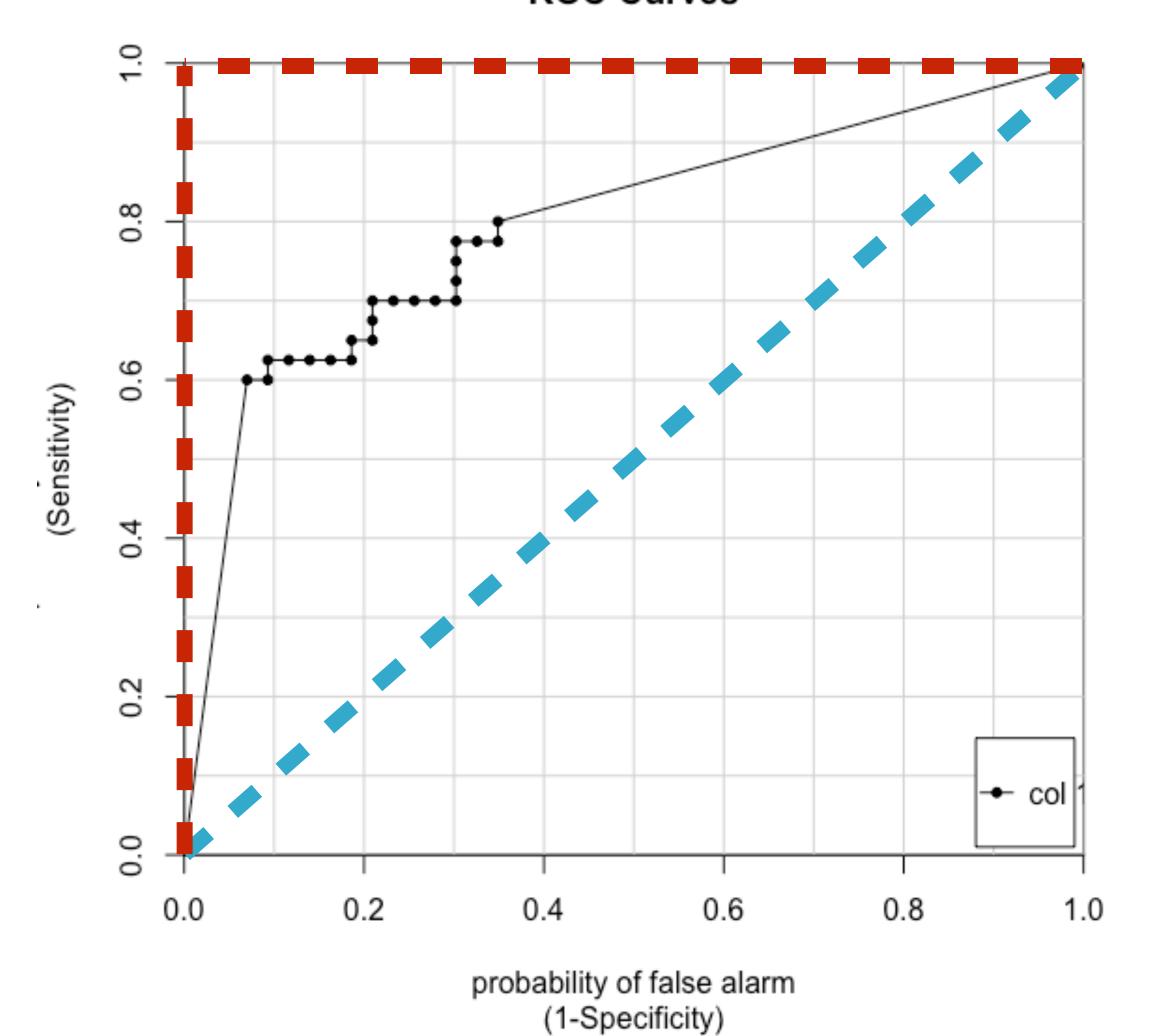
## Area under the curve (AUC)





### From ROC to AUC







## Defining AUC

- Single-number summary of model accuracy
- Summarizes performance across all thresholds
- Rank different models within the same dataset



## Defining AUC

- Ranges from 0 to 1
  - 0.5 = random guessing
  - 1 = model always right
  - o = model always wrong
- Rule of thumb: AUC as a letter grade
  - 0.9 = "A"
  - o.8 = "B"
  - • •





## Let's practice!





## Random forests and wine



- Popular type of machine learning model
- Good for beginners
- Robust to overfitting
- Yield very accurate, non-linear models

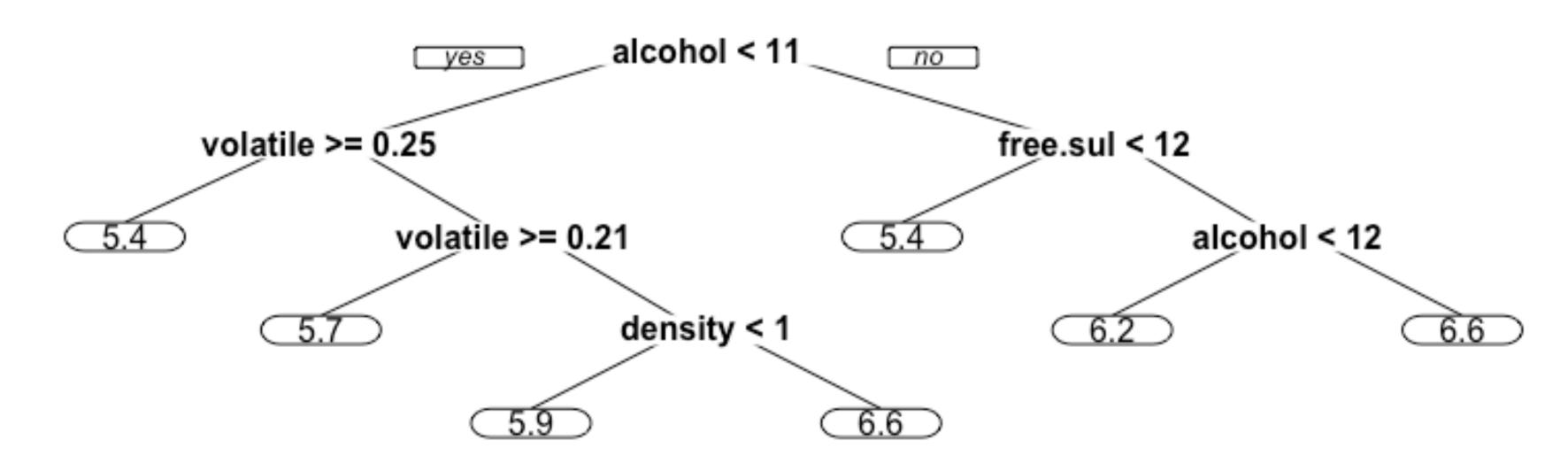


- Unlike linear models, they have hyperparameters
- Hyperparameters require manual specification
- Can impact model fit and vary from dataset-to-dataset
- Default values often OK, but occasionally need adjustment



- Start with a simple decision tree
- Decision trees are fast, but not very accurate

#### Wine Quality Decision Tree





- Improve accuracy by fitting many trees
- Fit each one to a bootstrap sample of your data
- Called bootstrap aggregation or bagging
- Randomly sample columns at each split



```
# Load some data
> library(caret)
> library(mlbench)
> data(Sonar)
                                                0.795
# Set seed
> set.seed(42)
# Fit a model
> model <- train(Class~.,</pre>
                                                0.780
                    data = Sonar,
                    method = "ranger"
                                                0.775
  Plot the results
                                                                    #Randomly Selected Predictors
> plot(model)
```





## Let's practice!





# Explore a wider model space



## Random forests require tuning

- Hyperparameters control how the model is fit
- Selected "by hand" before the model is fit
- Most important is mtry
  - Number of randomly selected variables used at each split
  - Lower value = more random
  - Higher value = less random
- Hard to know the best value in advance



#### caret to the rescue!

- Not only does caret do cross-validation...
- It also does grid search
- Select hyperparameters based on out-of-sample error

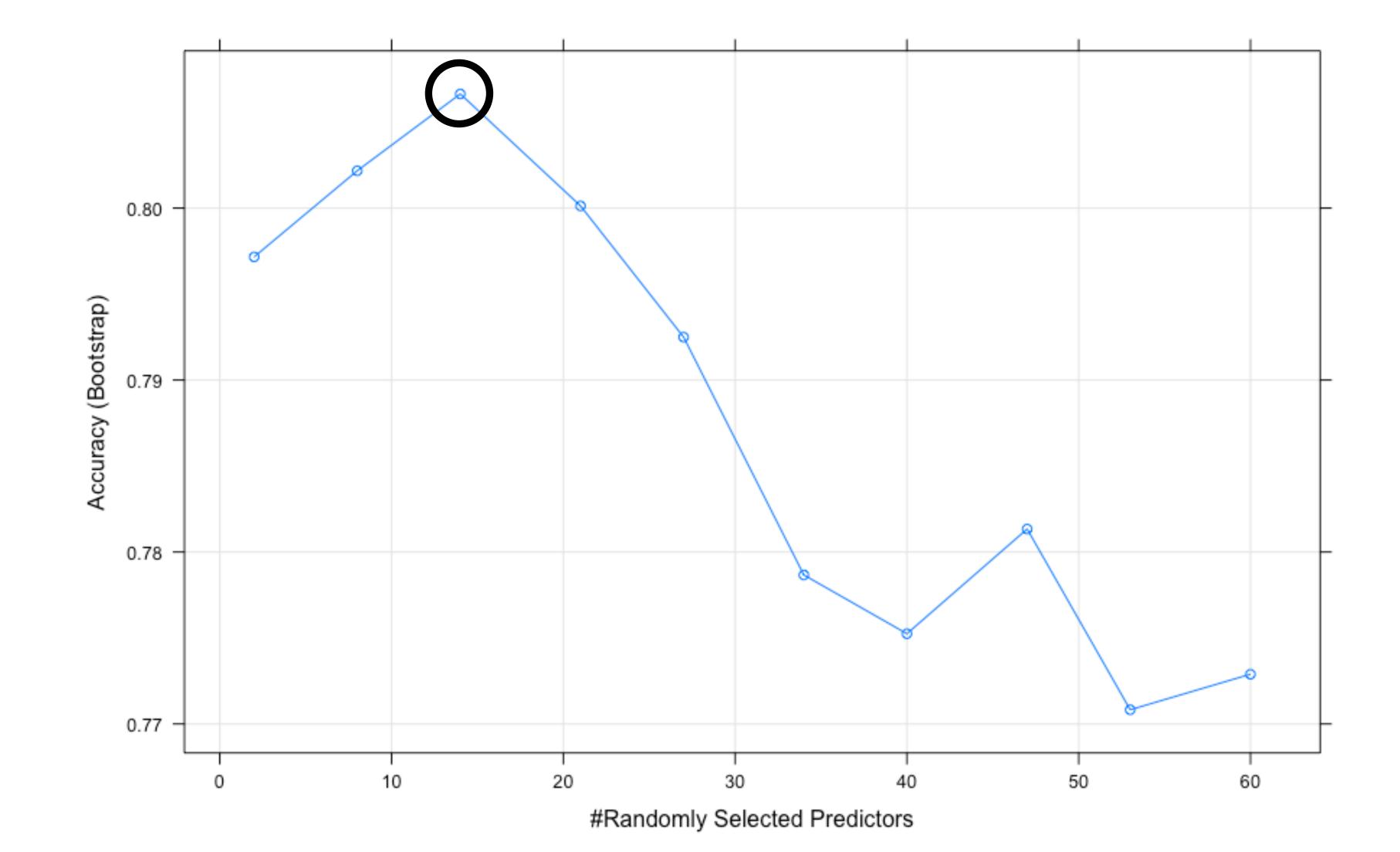


### Example: sonar data

- tuneLength argument to caret::train()
- Tells caret how many different variations to try



#### Plot the results







## Let's practice!





## Custom tuning grids



## Pros and cons of custom tuning

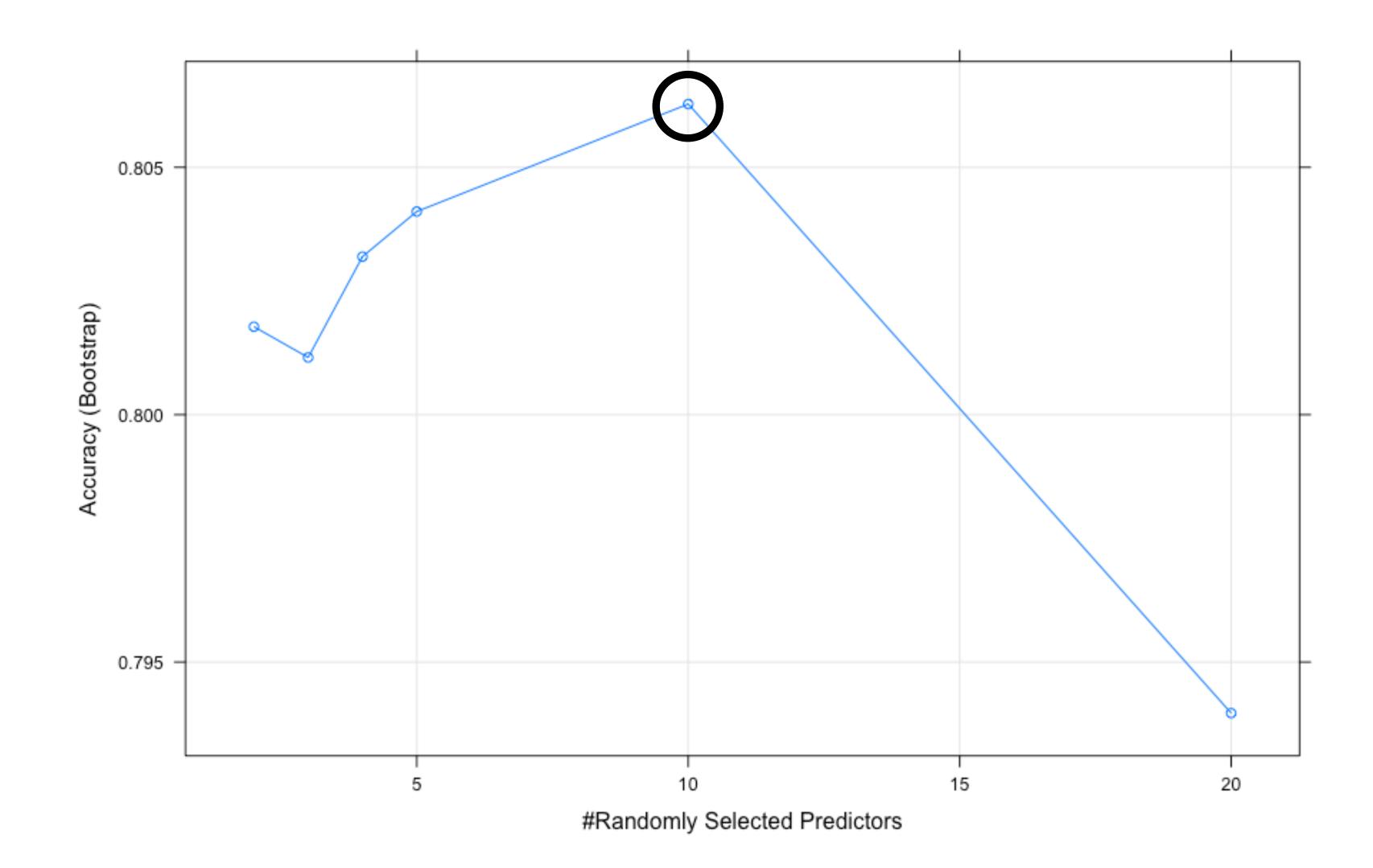
- Pass custom tuning grids to tuneGrid argument
- Advantages
  - Most flexible method for fitting caret models
  - Complete control over how the model is fit
- Disadvantages
  - Requires some knowledge of the model
  - Can dramatically increase run time



## Custom tuning example



## Custom tuning







## Let's practice!





## Introducing glmnet



## Introducing glmnet

- Extension of glm models with built-in variable selection
- Helps deal with collinearity and small samples sizes
- Two primary forms
  - Lasso regression Penalizes number of non-zero coefficients
  - Ridge regression Penalizes absolute magnitude of coefficients
- Attempts to find a parsimonious (i.e. simple) model
- Pairs well with random forest models



### Tuning glmnet models

- Combination of lasso and ridge regression
- Can fit a mix of the two models
- alpha [0, 1]: pure lasso to pure ridge
- lambda (o, infinity): size of the penalty



## Example: "don't overfit"

```
# Load data
> overfit <- read.csv("http://s3.amazonaws.com/assets.datacamp.com/
production/course_1048/datasets/overfit.csv")

# Make a custom trainControl
> myControl <- trainControl(
    method = "cv", number = 10,
    summaryFunction = twoClassSummary,
    classProbs = TRUE, # Super important!
    verboseIter = TRUE
)</pre>
```

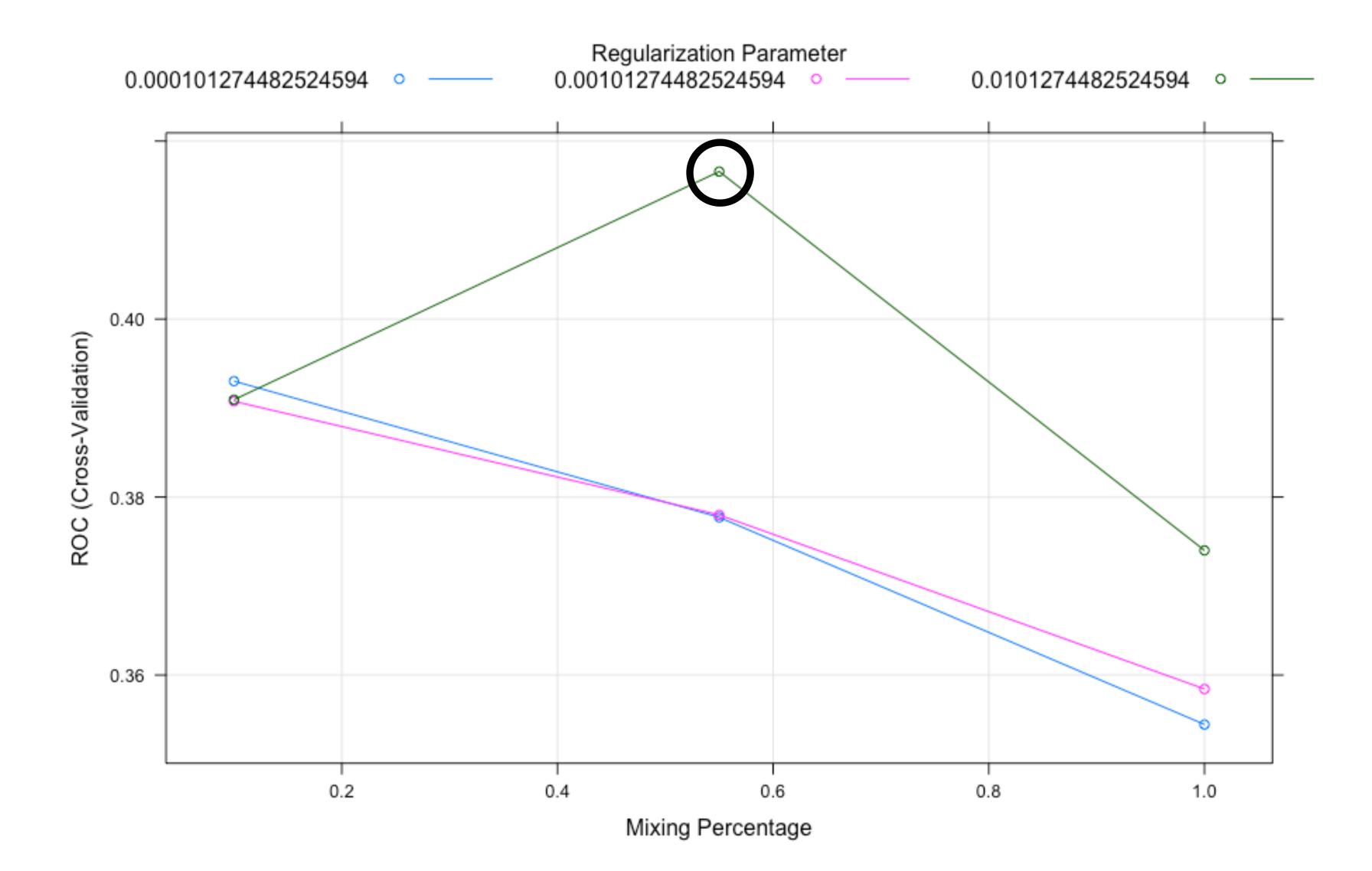


## Try the defaults

- 3 values of alpha
- 3 values of lambda



### Plot the results







## Let's practice!





# glmnet with custom tuning grid



## Custom tuning glmnet models

- 2 tuning parameters: alpha and lambda
- For single alpha, all values of lambda fit simultaneously
- Many models for the "price" of one

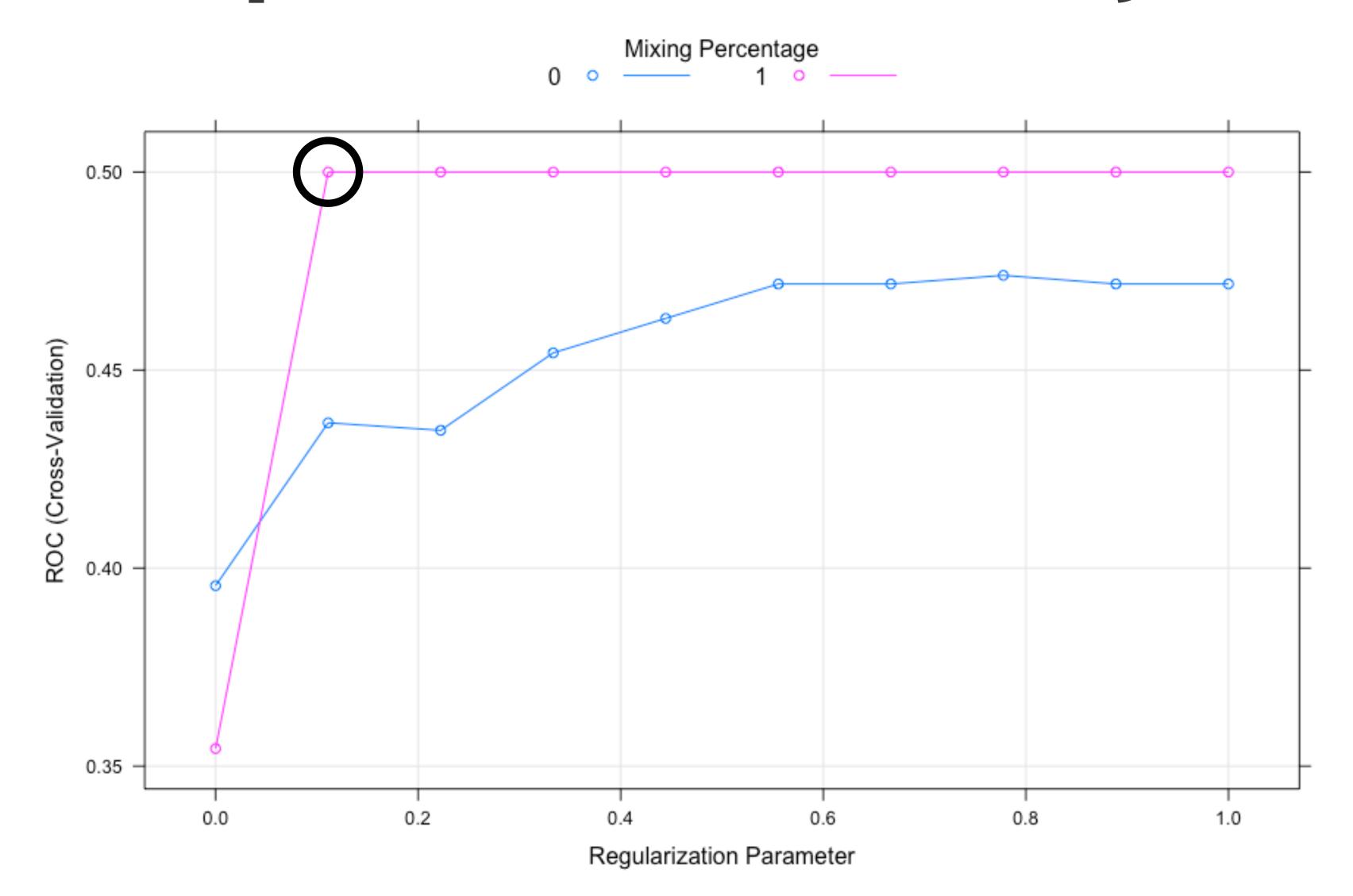


## Example: glmnet tuning

```
# Make a custom tuning grid
> myGrid <- expand.grid(</pre>
    alpha = 0:1,
    lambda = seq(0.0001, 0.1, length = 10)
# Fit a model
> set.seed(42)
> model <- train(y ~ ., overfit, method = "glmnet",
                 tuneGrid = myGrid, trControl = myControl)
# Plot results
> plot(model)
```



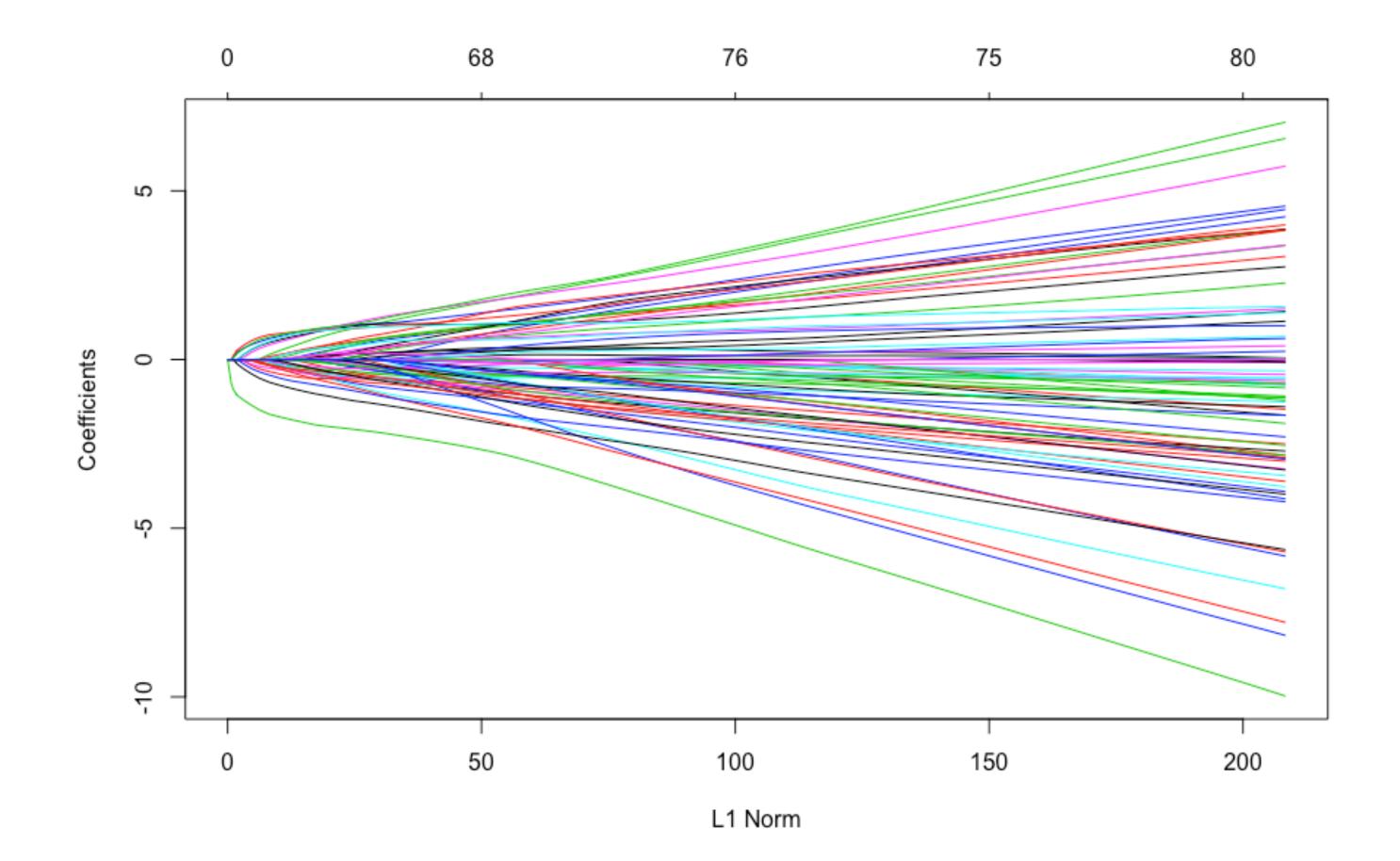
## Compare models visually





# Full regularization path

> plot(model\$finalModel)







# Let's practice!





# Median imputation



# Dealing with missing values

- Most models require numbers, can't handle missing data
- Common approach: remove rows with missing data
  - Can lead to biases in data
  - Generate over-confident models
- Better strategy: median imputation!
  - Replace missing values with medians
  - Works well if data missing at random (MAR)



### Example: mtcars

```
# Generate some data with missing values
> data(mtcars)
> set.seed(42)
> mtcars[sample(1:nrow(mtcars), 10), "hp"] <- NA</pre>
# Split target from predictors
> Y <- mtcars$mpg</pre>
> X <- mtcars[, 2:4]
# Try to fit a caret model
> library(caret)
> model <- train(x = X, y = Y)
Error in train.default(x = X, y = Y): Stopping
```



# A simple solution

```
# Now fit with median imputation
> model <- train(x = X, y = Y, preProcess = "medianImpute")</pre>
> print(model)
Random Forest
32 samples
 3 predictor
Pre-processing: median imputation (3)
Resampling: Bootstrapped (25 reps)
Summary of sample sizes: 32, 32, 32, 32, 32, ...
Resampling results across tuning parameters:
                  Rsquared
       RMSE
  mtry
        2.617096
                  0.8234652
        2.670550
                  0.8164535
RMSE was used to select the optimal model using the smallest value.
The final value used for the model was mtry = 2.
```





# Let's practice!





# KNN imputation



# Dealing with missing values

- Median imputation is fast, but...
- Can produce incorrect results if data missing not at random
- k-nearest neighbors (KNN) imputation
- Imputes based on "similar" non-missing rows



# Example: missing not at random

- Pretend smaller cars don't report horsepower
- Median imputation incorrect in this case
   Assumes small cars have medium-large horsepower



# Example: missing not at random

- KNN imputation is better
- Uses cars with similar disp/cyl to impute
- Yields a more accurate (but slower) model





# Let's practice!





# Multiple preprocessing methods



### The wide world of preProcess

- You can do a lot more than median or knn imputation!
- Can chain together multiple preprocessing steps
- Common "recipe" for linear models (order matters!)
   Median imputation -> center -> scale -> fit glm
- See?preProcess for more detail



### Example: preprocessing mtcars

```
# Generate some data with missing values
> data(mtcars)
> set.seed(42)
> mtcars[sample(1:nrow(mtcars), 10), "hp"] <- NA</pre>
> Y <- mtcars$mpg
                        Missing at random
> X <- mtcars[,2:4]
# Use linear model "recipe"
> set.seed(42)
> model <- train(</pre>
    x = X, y = Y, method = "glm",
    preProcess = c("medianImpute", "center", "scale")
> print(min(model$results$RMSE))
[1] 3.612713
```



### Example: preprocessing mtcars

```
# PCA before modeling
> set.seed(42)
> model <- train(
    x = X, y = Y, method = "glm",
    preProcess = c("medianImpute", "center", "scale", "pca")
)
> min(model$results$RMSE)
[1] 3.402557
```



### Example: preprocessing mtcars

```
# Spatial sign transform
> set.seed(42)
> model <- train(
    x = X, y = Y, method = "glm",
    preProcess = c("medianImpute", "center", "scale", "spatialSign"))
> min(model$results$RMSE)
[1] 4.284904
```



# Preprocessing cheat sheet

- Start with median imputation Try KNN imputation if data missing not at random
- For linear models...
  - Center and scale
  - Try PCA and spatial sign
- Tree-based models don't need much preprocessing





# Let's practice!





# Handling low-information predictors



## No (or low) variance variables

- Some variables don't contain much information
  - Constant (i.e. no variance)
  - Nearly constant (i.e. low variance)
- Easy for one fold of CV to end up with constant column
- Can cause problems for your models
- Usually remove extremely low variance variables



### Example: constant column in mtcars

```
# Reproduce dataset from last video
> data(mtcars)
> set.seed(42)
> mtcars[sample(1:nrow(mtcars), 10), "hp"] <- NA
> Y <- mtcars$mpg
> X <- mtcars[, 2:4]

# Add constant-valued column to mtcars
> X$bad <- 1</pre>
```



#### Example: constant column in mtcars

```
# Try to fit a model with PCA + glm
> model <- train(</pre>
   x = X, y = Y, method = "glm",
    preProcess = c("medianImpute", "center", "scale", "pca")
Warning in preProcess.default(thresh = 0.95, k = 5, method =
c("medianImpute", :
 These variables have zero variances: bad
Something is wrong; all the RMSE metric values are missing:
                 Rsquared
      RMSE
Min. : NA Min. : NA
1st Qu.: NA 1st Qu.: NA
Median : NA Median : NA
 Mean :NaN
                     :NaN
              Mean
 3rd Qu.: NA
              3rd Qu.: NA
        : NA
                      : NA
              Max.
 Max.
 NA's
               NA's
        :1
                      :1
```



### caret to the rescue (again)

- "zv" removes constant columns
- "nzv" removes nearly constant columns

```
# Have caret remove those columns during modeling
> set.seed(42)
> model <- train(
    x = X, y = Y, method = "glm",
    preProcess = c("zv", "medianImpute", "center", "scale", "pca")
)
> min(model$results$RMSE)
[1] 3.402557
```





# Let's practice!





# Principle components analysis (PCA)



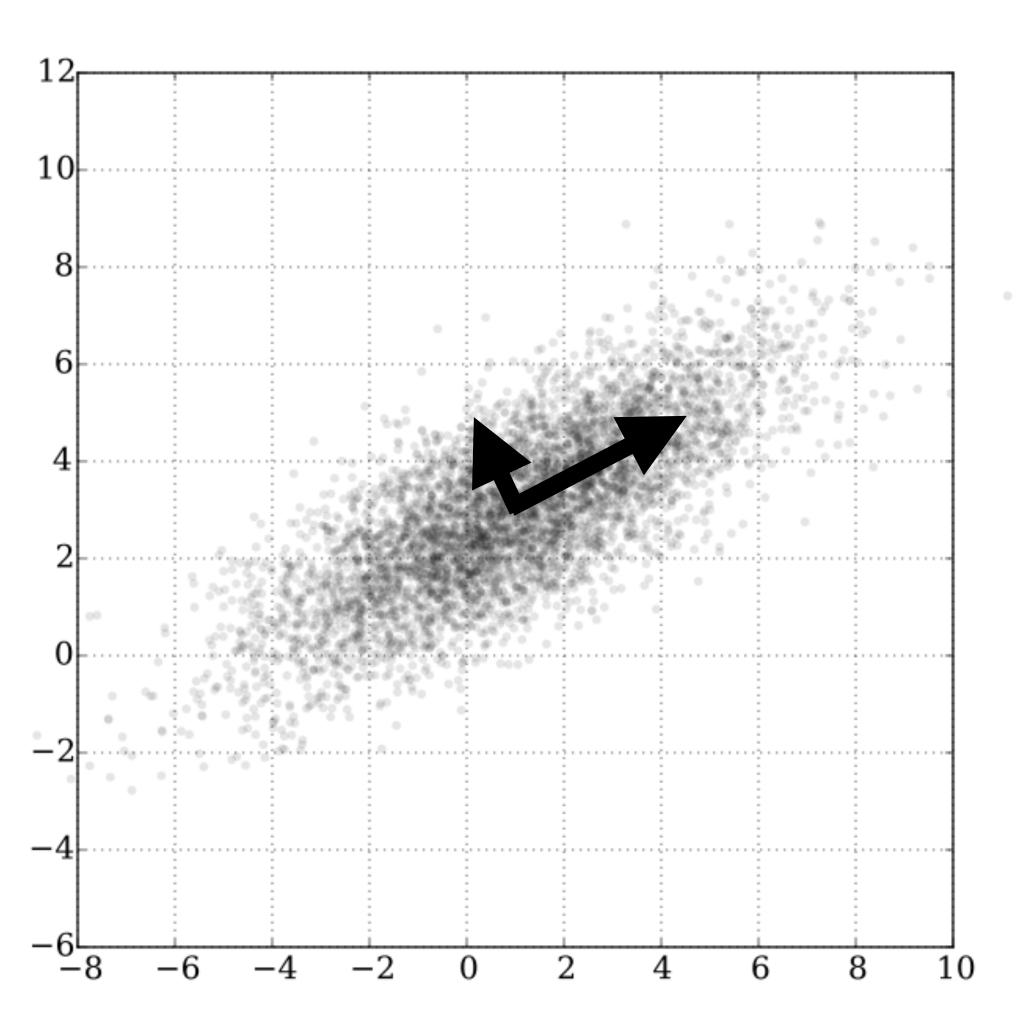
# Principle components analysis

- Combines low-variance and correlated variables
- Single set of high-variance, perpendicular predictors
- Prevents collinearity (i.e. correlation among predictors)



# PCA: a visual representation

- First component has highest variance
- Second component has second highest variance
- And so on...





- Lots of predictors
- Many of them low-variance

```
# Load the blood brain dataset
> data(BloodBrain)
> names(bbbDescr)[nearZeroVar(bbbDescr)]
[1] "negative" "peoe_vsa.2.1" "peoe_vsa.3.1" "a_acid"
[5] "vsa_acid" "frac.anion7." "alert"
```



```
# Basic model
> set.seed(42)
> data(BloodBrain)
> model <- train(
    x = bbbDescr, y = logBBB, method = "glm",
    trControl = trainControl(method = "cv", number = 10, verbose = TRUE),
    preProcess = c("zv", "center", "scale")
)
> min(model$results$RMSE)
[1] 1.107702
```



DataCamp



```
# Remove low-variance predictors
> set.seed(42)
> data(BloodBrain)
> model <- train(
    x = bbbDescr, y = logBBB, method = "glm",
    trControl = trainControl(method = "cv", number = 10, verbose = TRUE),
    preProcess = c("nzv", "center", "scale")
)
> min(model$results$RMSE)
[1] 0.9796199
```



```
# Add PCA
> set.seed(42)
> data(BloodBrain)
> model <- train(
    x = bbbDescr, y = logBBB, method = "glm",
    trControl = trainControl(method = "cv", number = 10, verbose = TRUE),
    preProcess = c("zv", "center", "scale", "pca")
)
> min(model$results$RMSE)
[1] 0.9796199
```





# Let's practice!





# Reusing a trainControl



## A real-world example

- The data: customer churn at telecom company
- Fit different models and choose the best
- Models must use the same training/test splits
- Create a shared trainControl object



# Example: customer churn data

```
# Summarize the target variables
> library(caret)
> library(C50)
> data(churn)
> table(churnTrain$churn) / nrow(churnTrain)
      yes
                 no
0.1449145 0.8550855
# Create train/test indexes
> set.seed(42)
> myFolds <- createFolds(churnTrain$churn, k = 5)</pre>
# Compare class distribution
> i <- myFolds$Fold1</pre>
> table(churnTrain$churn[i]) / length(i)
      yes
                  no
0.1441441 0.8558559
```



### Example: customer churn data

```
> myControl <- trainControl(
    summaryFunction = twoClassSummary,
    classProbs = TRUE,
    verboseIter = TRUE,
    savePredictions = TRUE,
    index = myFolds
)</pre>
```

- Use folds to create a trainControl object
- Exact same cross-validation folds for each model





# Let's practice!





# Reintroduce glmnet



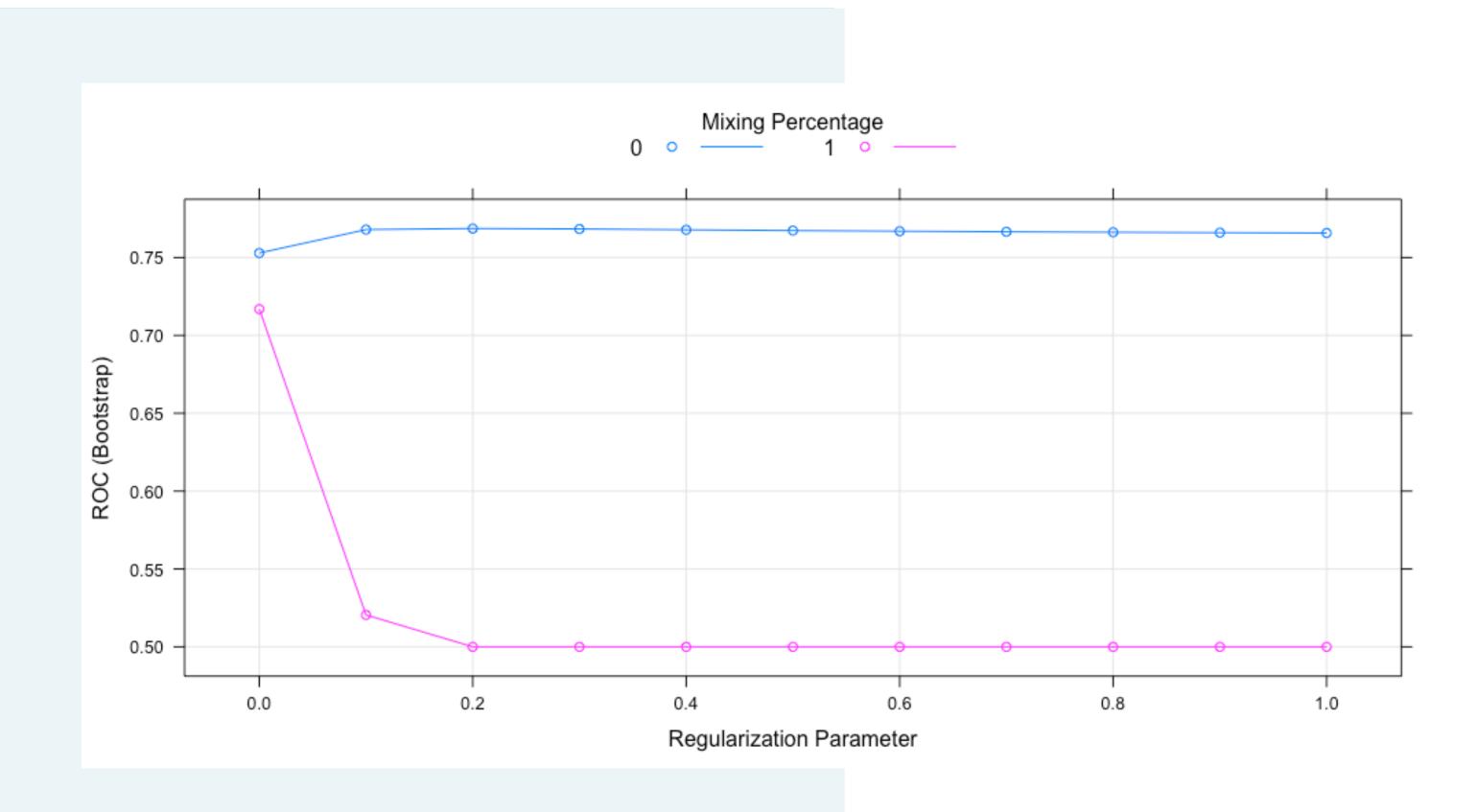
### glmnet review

- Linear model with built-in variable selection
- Great baseline model
- Advantages
  - Fits quickly
  - Ignores noisy variables
  - Provides interpretable coefficients



### Example: glmnet on churn data

```
> # Fit the model
> set.seed(42)
> model_glmnet <- train(</pre>
    churn ~ ., churnTrain,
    metric = "ROC",
    method = "glmnet",
    tuneGrid = expand.grid(
      alpha = 0:1,
      lambda = 0:10/10
    trControl = myControl
   Plot the results
> plot(model_glmnet)
```

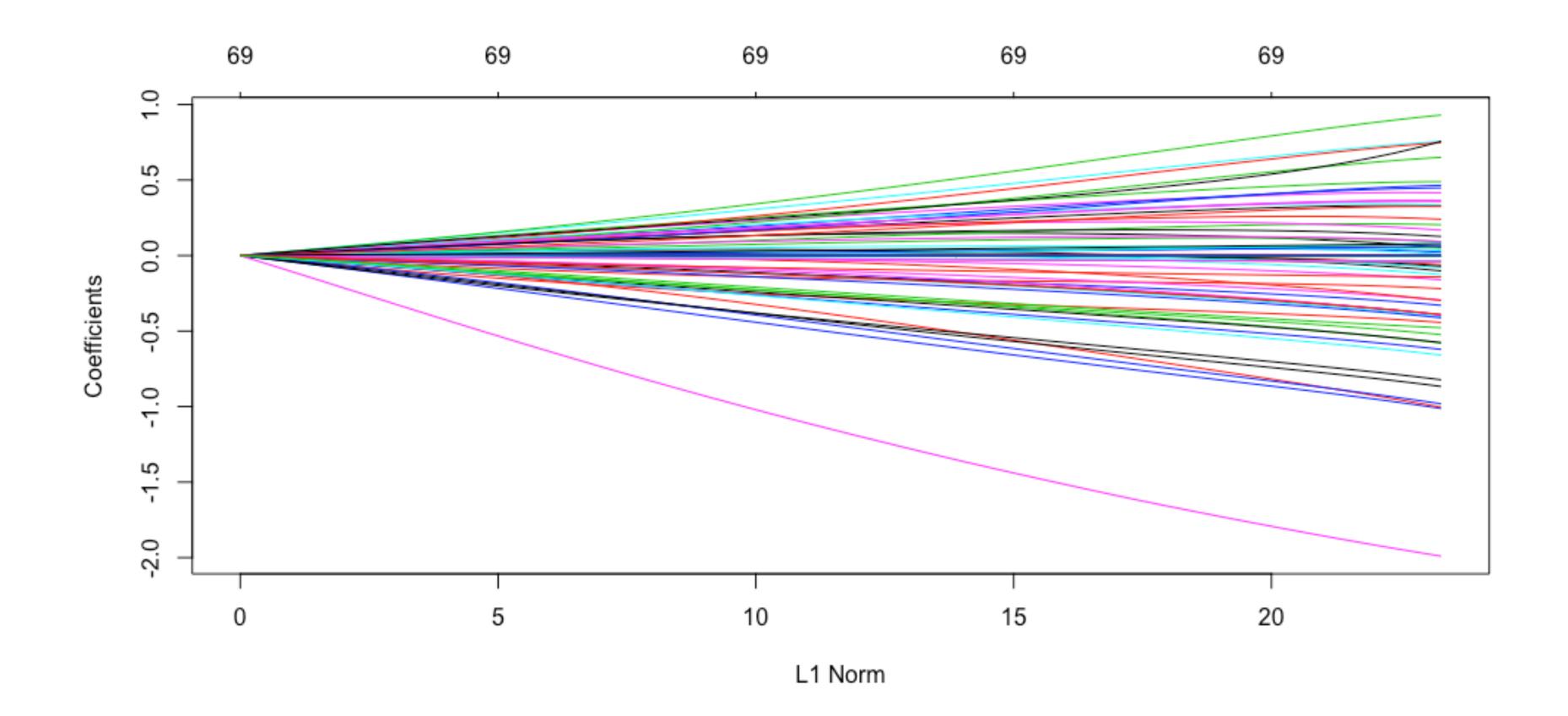






### Plot the coefficients

> plot(model\_glmnet\$finalModel)







# Let's practice!





# Reintroduce random forest



#### Random forest review

- Slower to fit than glmnet
- Less interpretable
- Often (but not always) more accurate than glmnet
- Easier to tune
- Require little preprocessing
- Capture threshold effects and variable interactions



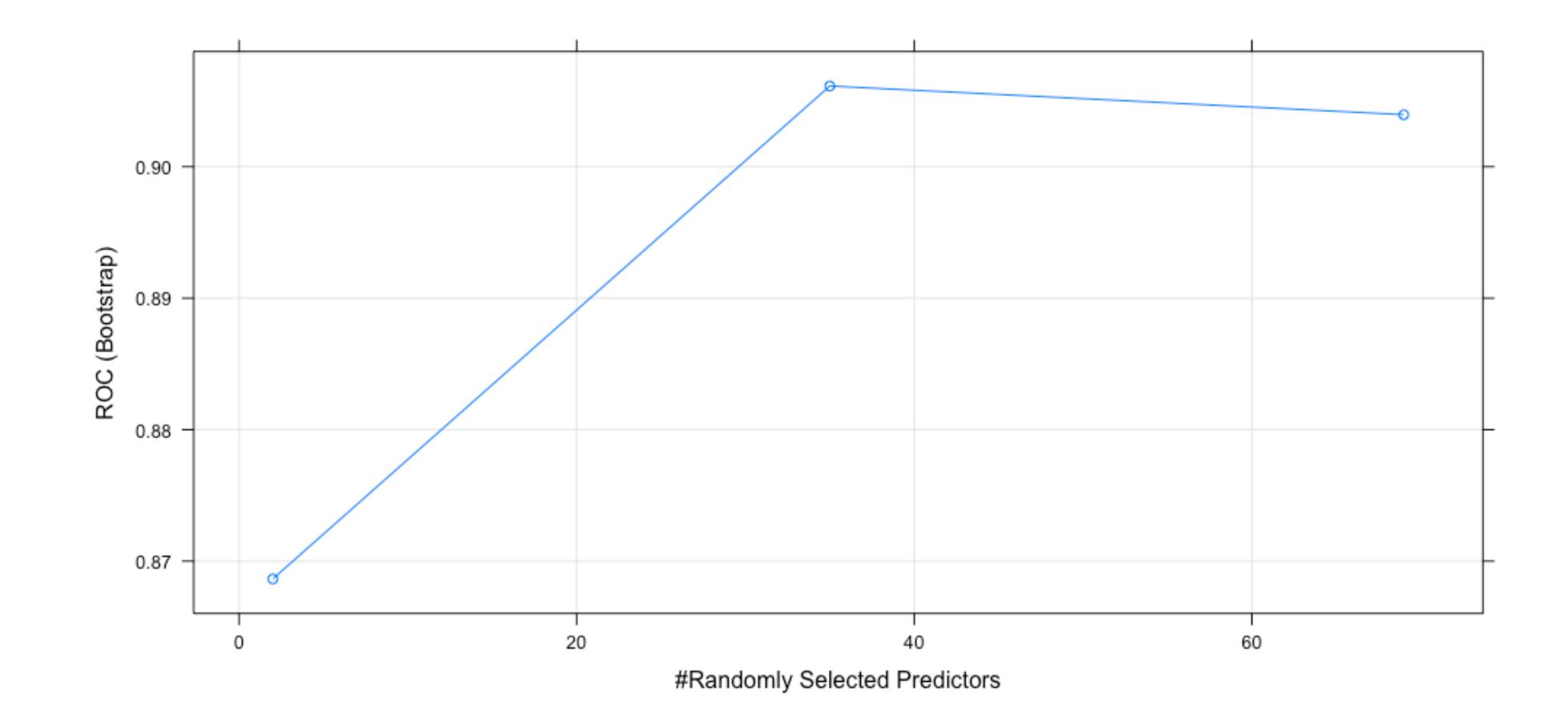
#### Random forest on churn data

```
> set.seed(42)
> churnTrain$churn <- factor(churnTrain$churn, levels = c("no", "yes"))
> model_rf <- train(
    churn ~ ., churnTrain,
    metric = "ROC",
    method = "ranger",
    trControl = myControl
)</pre>
```



#### Random forest on churn data

> plot(model\_rf)







# Let's practice!





# Comparing models



### Comparing models

- Make sure they were fit on the same data!
- Selection criteria
  - Highest average AUC
  - Lowest standard deviation in AUC
- The resamples () function is your friend



#### Example: resamples() on churn data

```
# Make a list
> model_list <- list(</pre>
    glmnet = model_glmnet,
    rf = model_rf
# Collect resamples from the CV folds
> resamps <- resamples(model_list)</pre>
> resamps
Call:
resamples.default(x = model_list)
Models: glmnet, rf
Number of resamples: 5
Performance metrics: ROC, Sens, Spec
Time estimates for: everything, final model fit
```



#### Summarize the results





# Let's practice!





### Moreonresamples



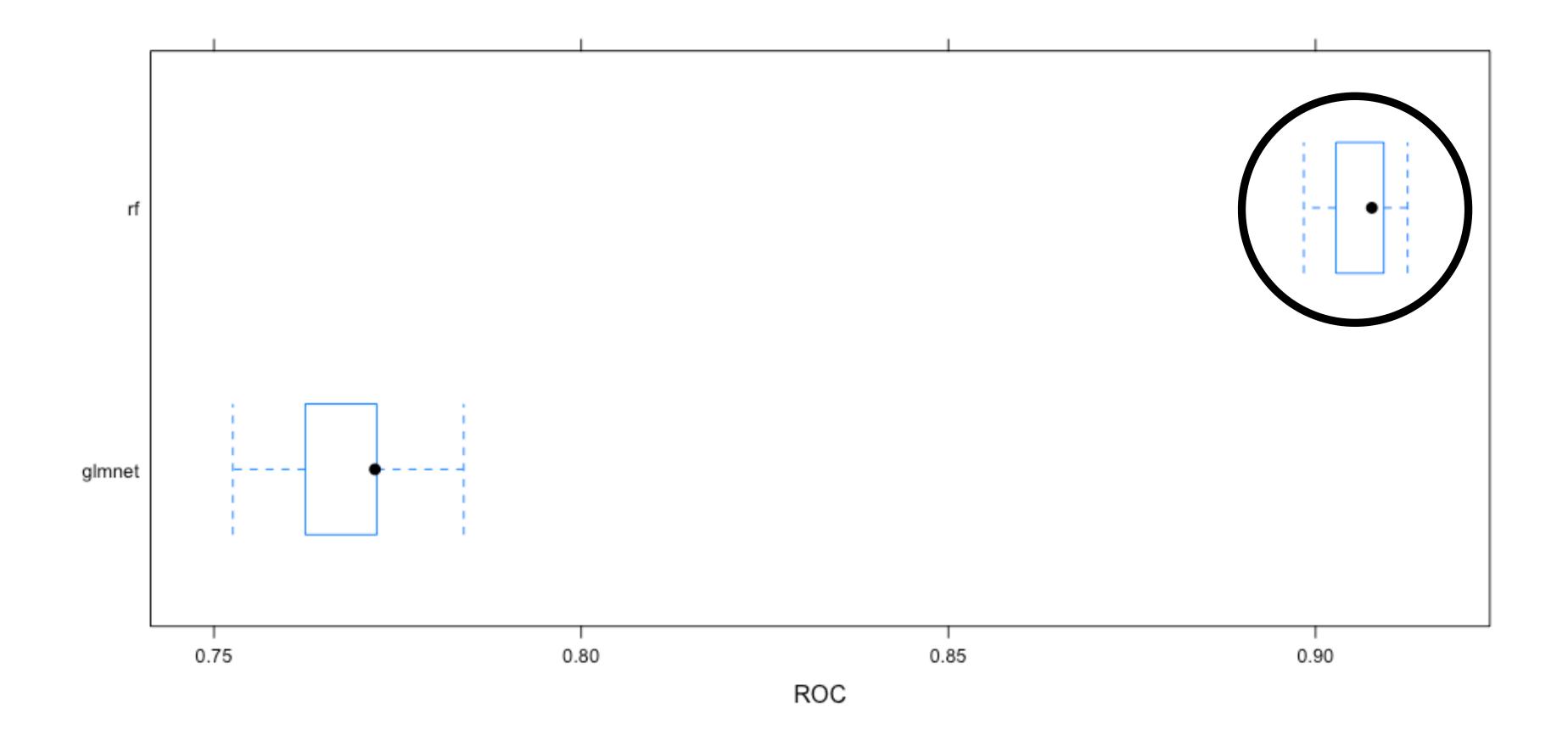
### Comparing models

- Resamples has tons of cool methods
- One of my favorite functions (thanks Max!)
- Inspired the caretEnsemble package



#### Box-and-whisker

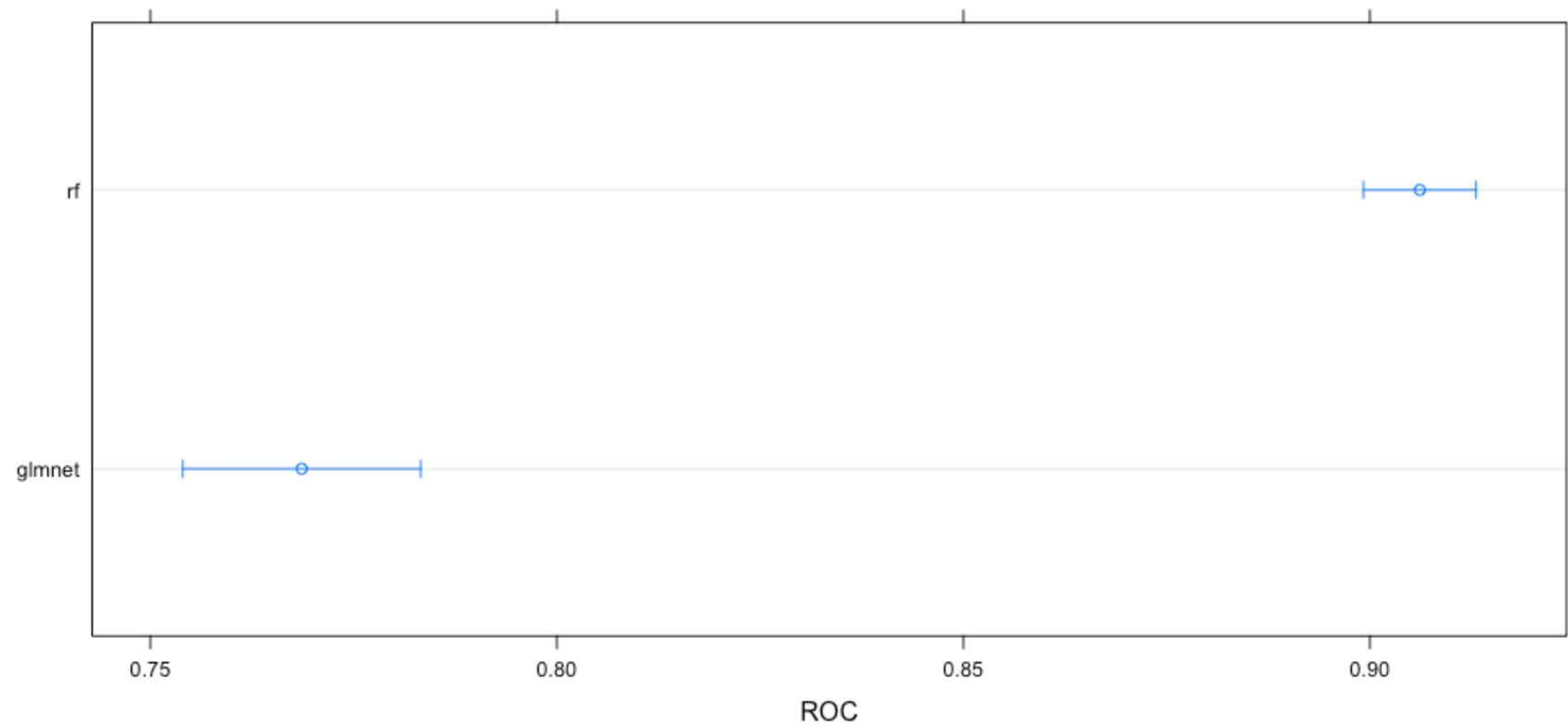
> bwplot(resamps, metric = "ROC")





### Dotplot

```
> dotplot(resamps, metric = "ROC")
```

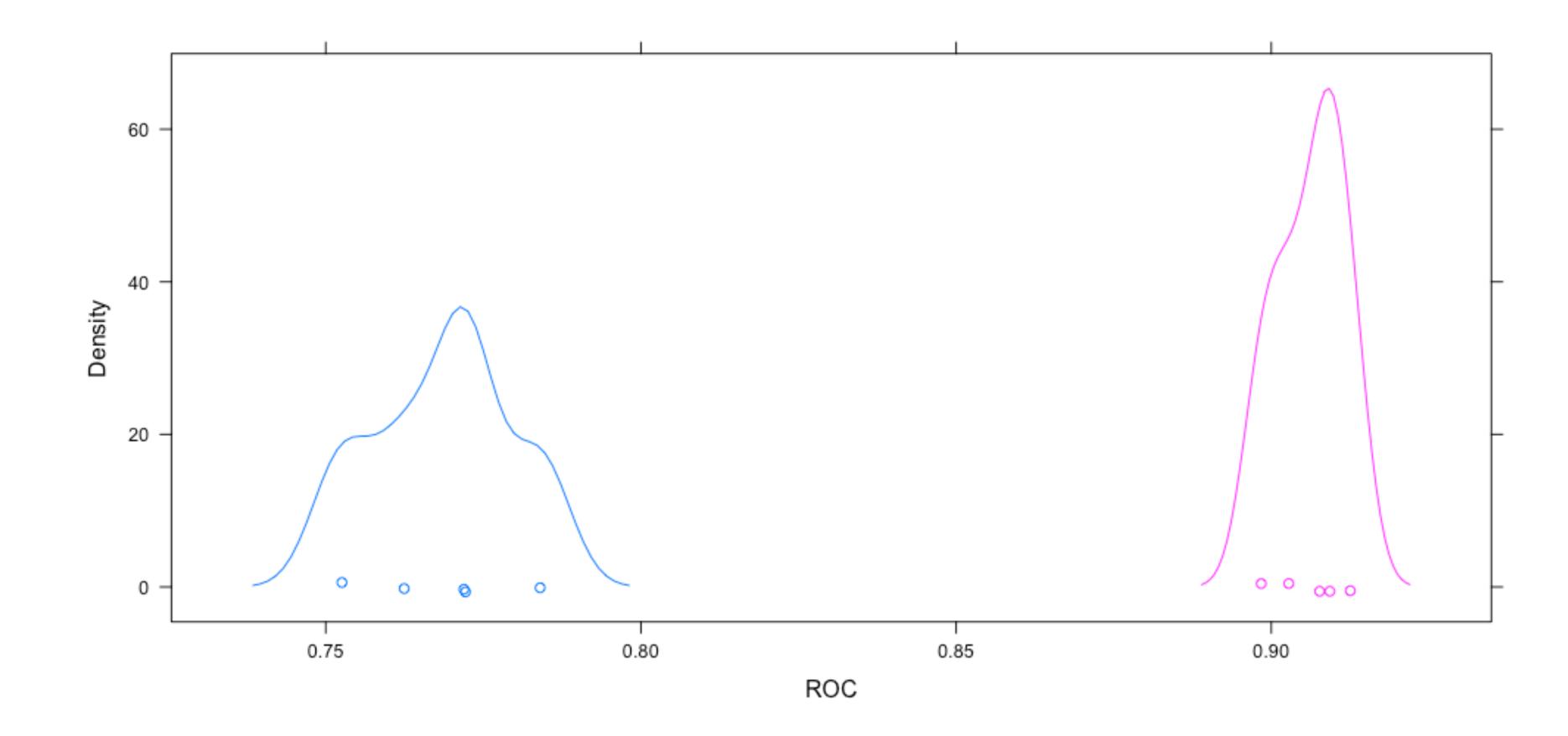


Confidence Level: 0.95



### Density plot

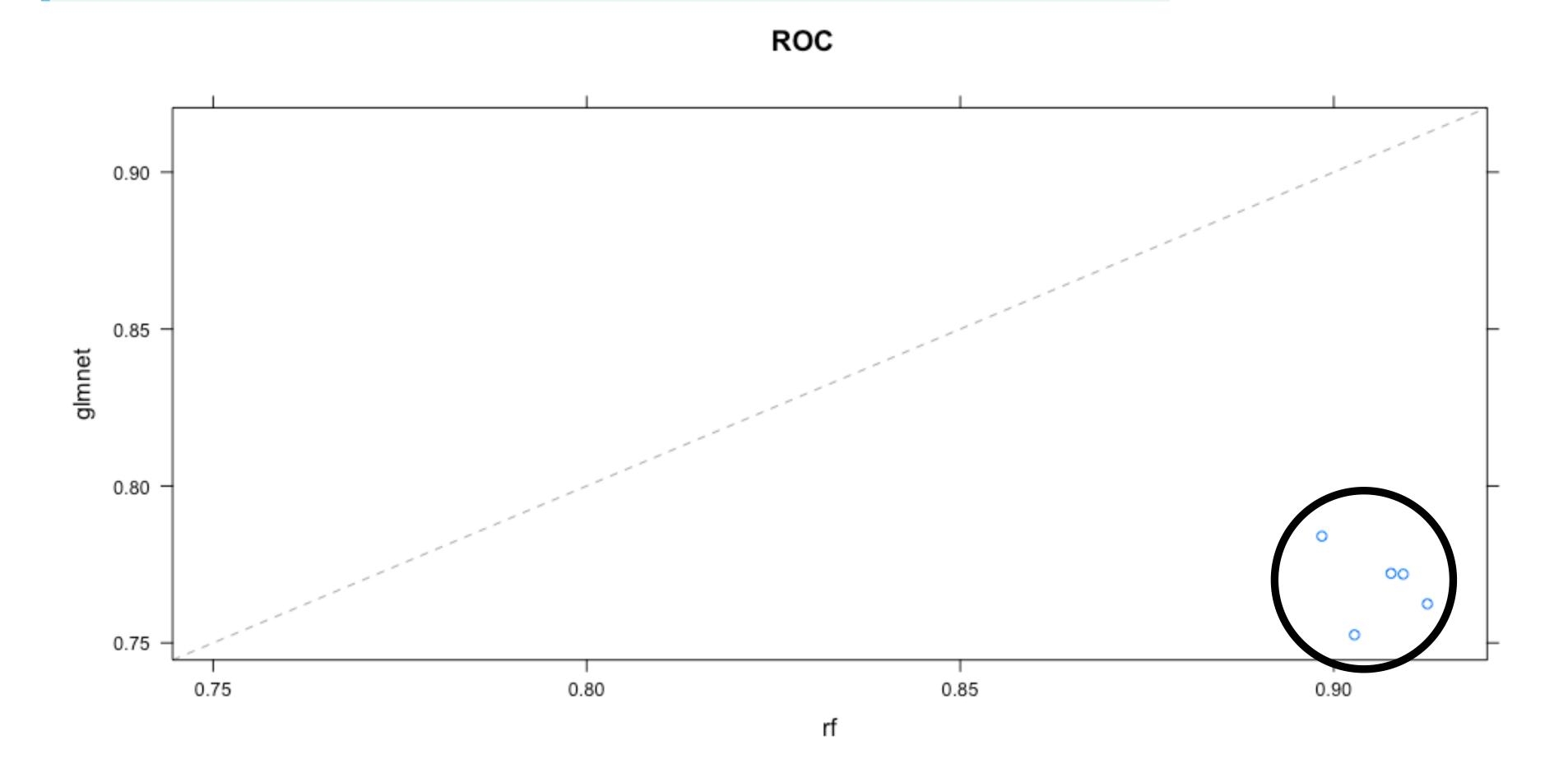
```
> densityplot(resamps, metric = "ROC")
```





### Scatter plot

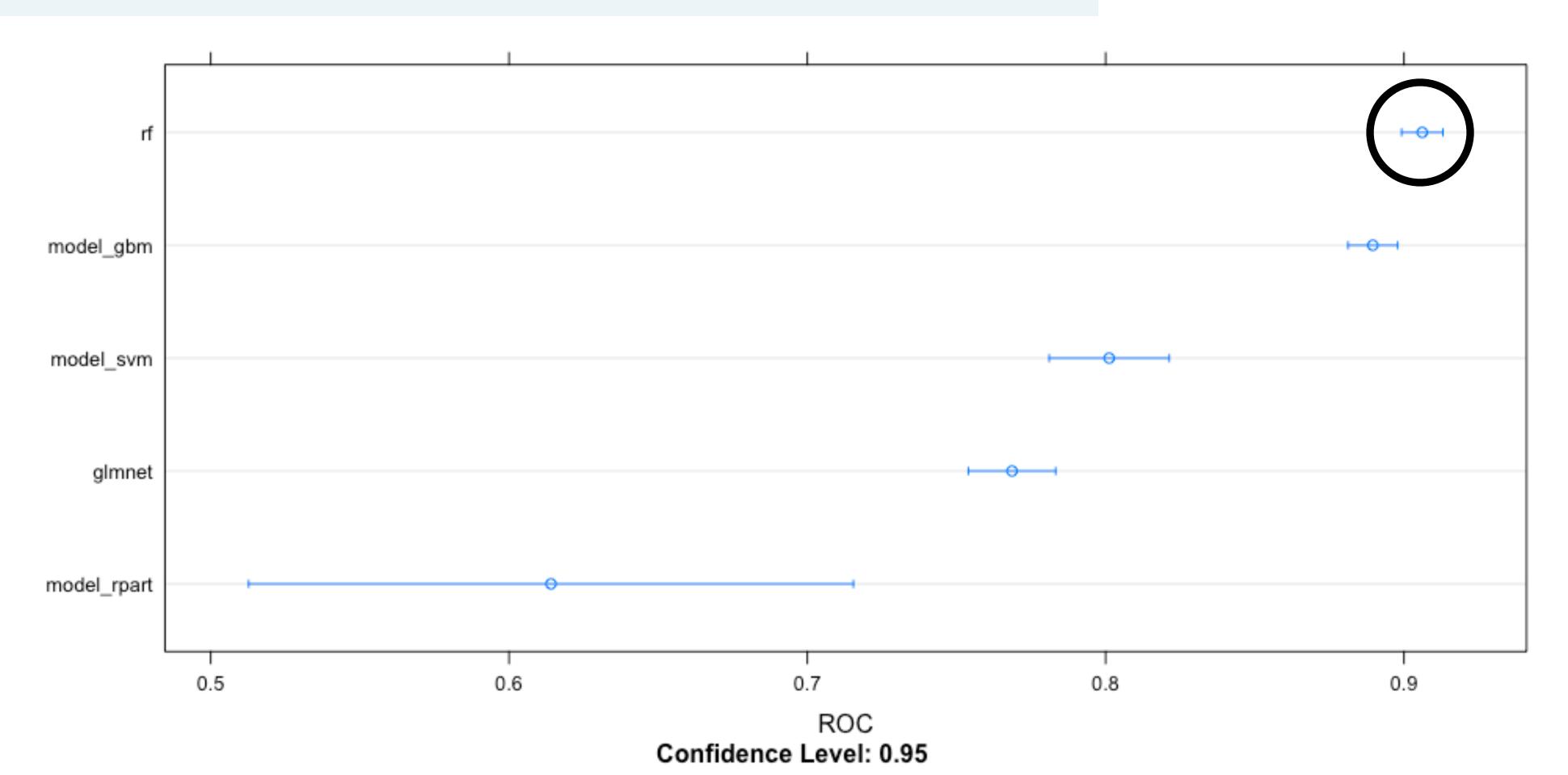
```
> xyplot(resamps, metric = "ROC")
```





### Another dot plot

> dotplot(lots\_of\_models, metric = "ROC")







# Let's practice!





# Summary



### What you've learned

- How to use the caret package
- Model fitting and evaluation
- Parameter tuning for better results
- Data preprocessing



### Goals of the caret package

- Simplify the predictive modeling process
- Make it easy to try many models and techniques
- Provide common interface to many useful packages





#### Go build some models!