

Prediction Trees

CART, Bagging, and Random Forest

SYS 6018 | Spring 2024

trees.pdf

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Some of the figures in this presentation are taken from "An Introduction to Statistical Learning, with applications in R" (Springer, 2013) with permission from the authors: G. James, D. Witten, T. Hastie and R. Tibshirani.

1 Classification and Regression Tree Intro

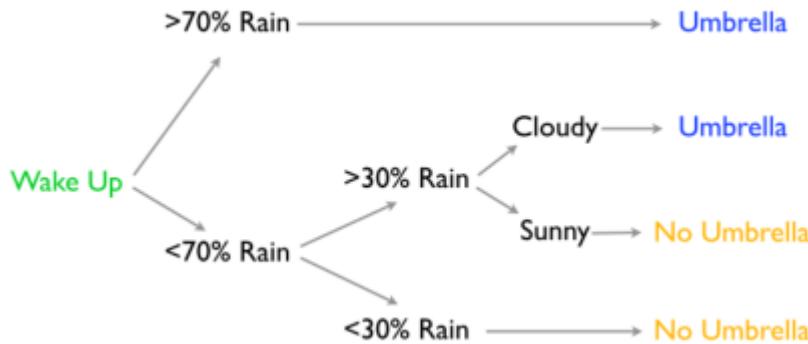
Tree-based methods:

1. Partition the feature space into a set of (hyper) rectangles.
2. Fit a simple model (e.g., constant) in each region.

They are conceptually simple yet powerful.

- Main Characteristics:
 - flexibility, intuitive, non-model based
 - natural graphical display, easy to interpret
 - building blocks of Random Forest and (Tree-based) Boosting
 - naturally includes feature interactions
 - reduces need for monotonic feature transformations
- Main Implementations:
 - CART (Classification and Regression Trees) by Breiman, Friedman, Olshen, Stone (1984)
 - C4.5 Quinlan (1993)
 - Conditional Inference Trees (`party` R package)

1.1 Decision Trees



1.2 Building Prediction Trees

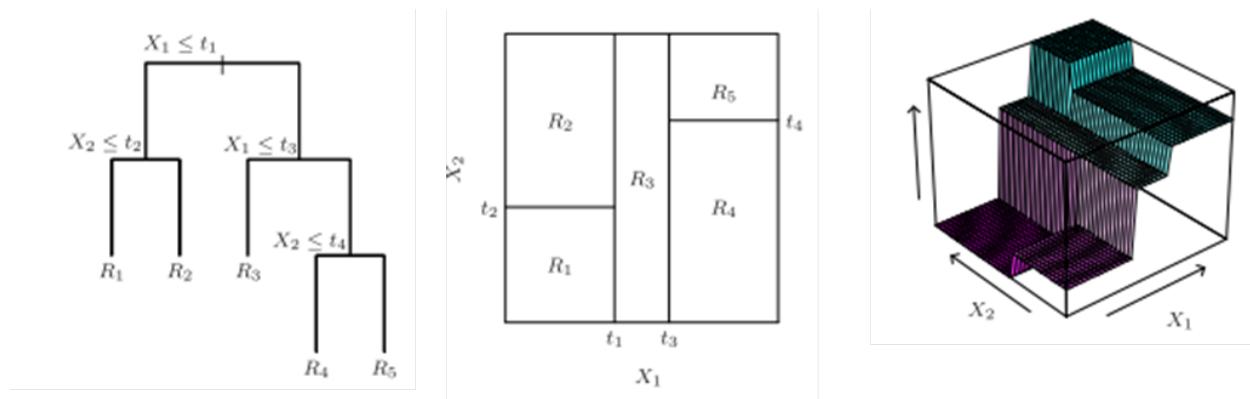
As usual, we want find the trees that make predictions which minimizes some loss function.

- **Classification trees** have class probabilities at the leaves (e.g., the probability I'll be in heavy rain is 0.9).
 - E.g., Loss = Negative Binomial likelihood.
- **Regression trees** have a mean response at the leaves. (e.g., the expected amount of rain is 2in).
 - E.g., Loss = Mean squared error.

1.3 Recursive Binary Partition (CART)

Because the number of possible trees is too large to exhaustively search, we usually restrict attention to **recursive binary partition trees** (CART).

- These are also easy to interpret



Think of the *reverse* of agglomerative hierarchical clustering

- In hierarchical clustering, we started with all observations in clusters of size 1 and then sequentially grouped them together, according to some measure of *homogeneity/similarity/distance/dissimilarity/loss*, until there was one big cluster.
 - The optimal clustering is usually somewhere between the two extremes
- In CART, all observations start in one big group and are split into two subgroups. Each subgroup is then split into two additional subgroups. This is repeated until some stopping criteria is met (e.g., not enough observations in to split further). The terminal subgroup (leaf nodes) are used to make predictions.
 - The splitting is also based on some measure of homogeneity/similarity/loss.
 - Since we are in a supervised setting, the splitting criterion should be based on how well the new groups estimate the outcome variable.
 - There is another important difference: in CART **only a single feature** is used to determine the split into subgroups.

1.3.1 Model and Model Parameters

Trees model the outcome as a *constant* in each region

$$\hat{f}(\mathbf{x}) = \sum_{m=1}^M \hat{c}_m \mathbb{1}(\mathbf{x} \in \hat{R}_m)$$

- The *model parameters* of a tree, T , with M leaf nodes, are:
 - The regions (*leaf nodes*) R_1, \dots, R_M
 - The coefficients/scores for the regions c_1, \dots, c_M
- The coefficients are based on the loss
 - Under Squared Error (regression):

$$\begin{aligned} \hat{c}_m &= \text{Ave}(\{y_i : \mathbf{x}_i \in R_m\}) \\ &= \frac{1}{N_m} \sum_{i:\mathbf{x}_i \in R_m} y_i \end{aligned}$$

- Under log-loss (soft classification), the coefficients are probability *vectors* (one element for each class; sums to one).

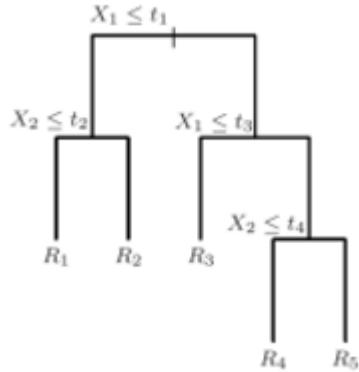
$$\begin{aligned} \hat{c}_{mk} &= \text{Proportion of class } k \text{ in region } R_m \\ &= \frac{1}{N_m} \sum_{i:\mathbf{x}_i \in R_m} \mathbb{1}(y_i = k) \end{aligned}$$

- Under 0-1 loss (hard classification), the coefficients are one-hot vectors.

$$\begin{aligned}\hat{c}_{mk} &= \text{One hot for majority class} \\ &= \mathbb{1}(k \text{ is majority class in region } R_m)\end{aligned}$$

- Other options possible; choose the coefficients to optimize your particular objective function.
Note: check the loss (implicitly) used in growing the tree!

1.3.2 Basis Expansion Interpretation



$$f(x) = \sum_{m=1}^M \theta_m b_m(x)$$

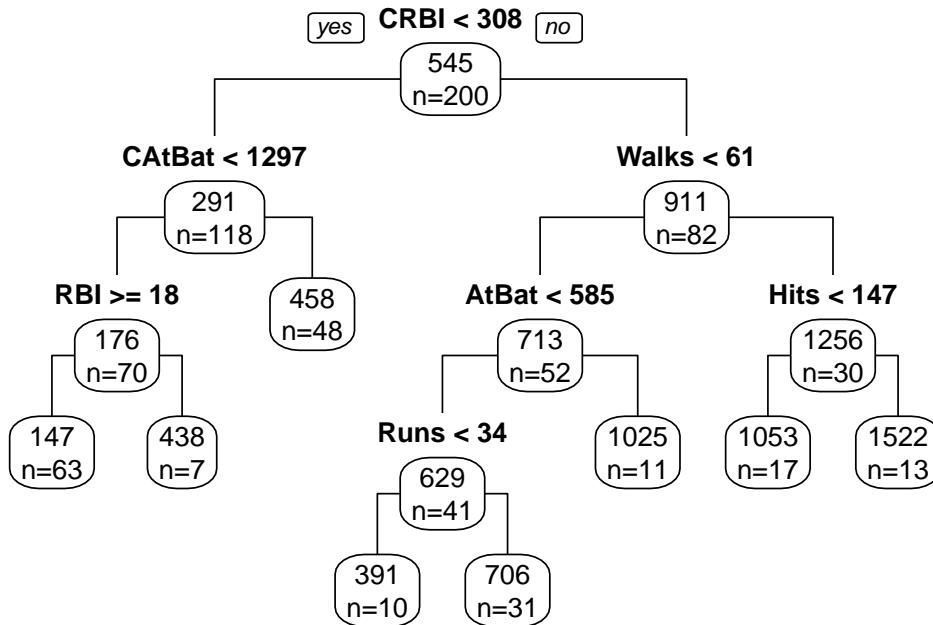
$$\begin{aligned}R_1 : b_1(x_1, x_2) &= \mathbb{1}(x_1 \leq t_1) \mathbb{1}(x_2 \leq t_2) \\R_2 : b_2(x_1, x_2) &= \mathbb{1}(x_1 \leq t_1) \mathbb{1}(x_2 > t_2) \\R_3 : b_3(x_1, x_2) &= \mathbb{1}(x_1 > t_1) \mathbb{1}(x_1 \leq t_3) \\R_4 : b_4(x_1, x_2) &= \mathbb{1}(x_1 > t_1) \mathbb{1}(x_1 > t_3) \mathbb{1}(x_2 \leq t_4) \\R_5 : b_5(x_1, x_2) &= \mathbb{1}(x_1 > t_1) \mathbb{1}(x_1 > t_3) \mathbb{1}(x_2 > t_4)\end{aligned}$$

1.3.3 Example: Baseball Salaries

The `ISLR` R package (corresponding to the [ISLR textbook](#)), contains data (`Hitters`) on Major League Baseball players for the 1986-1987 season.

```
data(Hitters, package='ISLR')
```

Here is a CART tree for predicting the salary (in thousands dollars):



Your Turn #1 : Tree Interpretation

1. How many leaves are on the tree?
2. What do the numbers in the boxes mean?
3. How could you evaluate the prediction in a leaf node?

1.4 Growing a Tree

CART uses a greedy algorithm to grow a tree.

- Split the feature space into two pieces and predict the outcome in each region
 - Find the predictor j (out of $1, 2, \dots, p$) and split point t (from unique ordered values of X_j or categories) to minimize the [loss function](#)
 - Produces two regions:

$$R_1(j, t) = \{x : x_j \leq t\} \text{ and } R_2(j, t) = \{x : x_j > t\} \quad \text{Numeric/Ordered Feature}$$

or

$$R_1(j, t) = \{x : x_j \in A_j\} \text{ and } R_2(j, t) = \{x : x_j \notin A_j\} \quad \text{Nominal/Categorical Feature}$$

- Repeat this step for each [child](#) region
- Continue until stopping criteria met, e.g.
 - Minimum number of observations in region
 - Loss function has minimal improvement

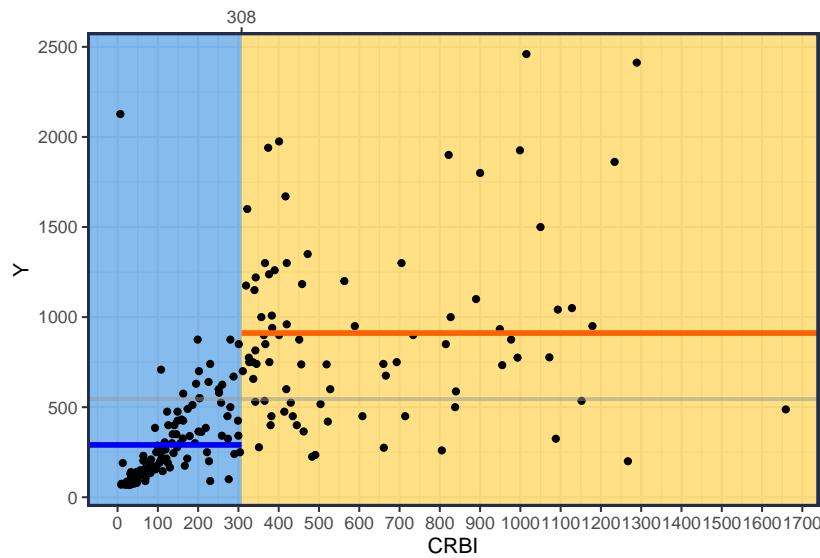
- Maximum depth (number of interactions)
- The final regions are called **leaf** nodes

1.5 Splitting Details

1.5.1 Regression Trees and Numeric Features

Notice in the fitted tree for the baseball data that the first split was based on a player's *Career RBIs* (CRBI). Specifically, if a player has less than 308 Career RBIs they go down the left side, otherwise they go down the right side.

Let's examine this first split:



- This is basically a univariate *change point model*
 - The split point ($\text{CRBI} < 308$) is the best change point (change in mean) using a Gaussian model
 - An alternative perspective is to see that the reduction in MSE/SSE is maximized by splitting at ($\text{CRBI} < 308$) and fitting the data on each side of the split with a constant.

Splitting Details: Squared Error Loss

Notation

- $y \in \mathbb{R}$
- $\mathbf{x} = [x_1, \dots, x_p]^T$
- n observations (in current node/region)

Consider a split on feature j :

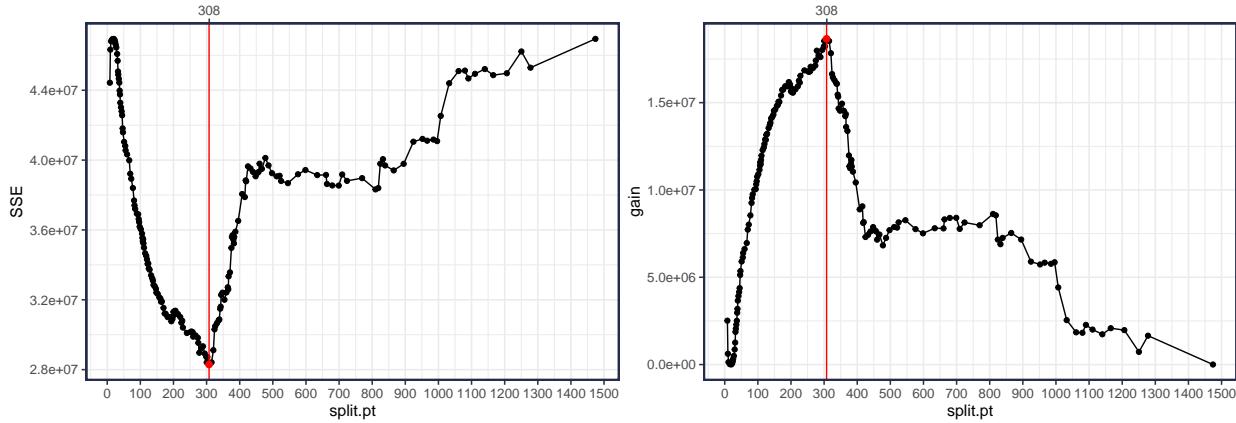
- Before split, the quality of the model, based on SSE is:

$$Q_0 = \sum_{i=1}^n (y_i - \bar{y})^2 \quad \text{where } \bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$$

- Consider a split at s (on feature j)

<u>Left Region</u>	<u>Right Region</u>
$R_1(s) = \{x : x_j < s\}$	$R_2(s) = \{x : x_j \geq s\}$
$\bar{y}_1(s) = \frac{1}{n_1} \sum_{\{i:x_i \in R_1(s)\}} y_i$	$\bar{y}_2(s) = \frac{1}{n_2} \sum_{\{i:x_i \in R_2(s)\}} y_i$
$Q_1(s) = \sum_{\{i:x_i \in R_1(s)\}} (y_i - \bar{y}_1(s))^2$	$Q_2(s) = \sum_{\{i:x_i \in R_2(s)\}} (y_i - \bar{y}_2(s))^2$
<ul style="list-style-type: none"> • Updated SSE: $Q(s) = Q_1(s) + Q_2(s)$ • Gain(s) = $Q_0 - Q(s)$ 	

We can examine the SSE (or Gain) for all possible split points:

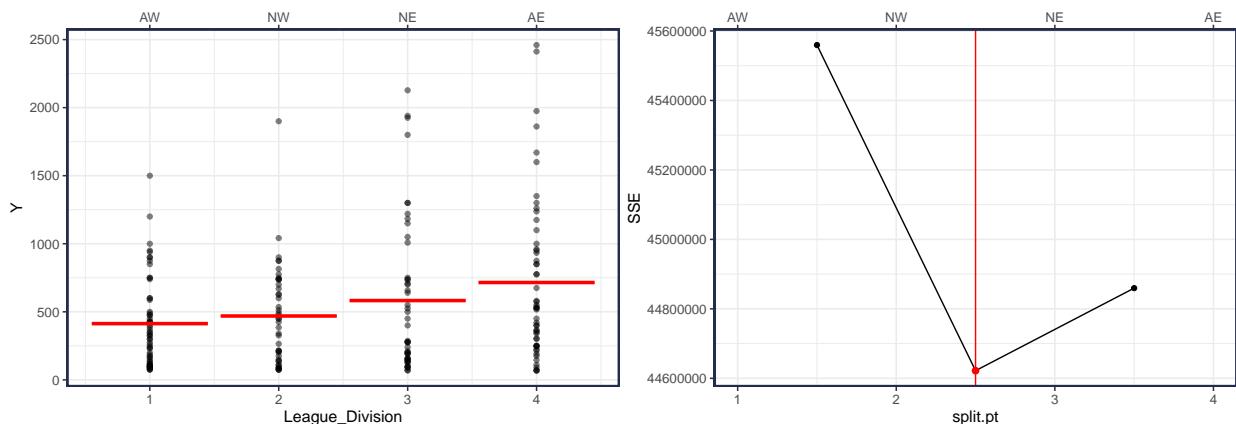


1.5.2 Regression Trees and Categorical (Nominal) Features

A categorical feature (with k levels) can be split into two groups $2^{k-1} - 1$ different ways.

- $k = 3$: 3 possible partitions
- $k = 4$: 7 possible partitions
- $k = 10$: 511 possible partitions

The CART approach sorts the categories by the mean response (recodes to numeric) and then splits like its a numeric feature.



Note

- Note: features with many levels will be split too often. Consider the quote from ESL (pg. 310)
The partitioning algorithm tends to favor categorical predictors with many levels k ; the number of partitions grows exponentially in k , and the more choices we have, the more likely we can find a good one for the data at hand. This can lead to severe overfitting if k is large, and such variables should be avoided.
- An alternative is to use one-hot-encoding to split a categorical feature into k new features.
 - As done by [XGBoost](#)
- There are other ways to *encode* categorical data so they can be treated like numeric (i.e., ordered data)
 - See e.g., [CatBoost](#)

1.5.3 Classification Trees

A [classification tree](#) is used when the outcome is categorical $y \in \mathcal{G} = (1, 2, \dots, K)$.

- In region R_m , the probability of class k can be estimated:

$$\begin{aligned}\bar{p}_m(k) &= \widehat{\Pr}(y = k \mid \mathbf{x} \in R_m) \\ &= \frac{1}{n_m} \sum_{\{i: \mathbf{x} \in R_m\}} \mathbb{1}(y_i = k) \\ &= \frac{n_{m,k}}{n_m}\end{aligned}$$

- Each region has K -vector of probability estimates: $\bar{p}_m = [\bar{p}_m(1), \dots, \bar{p}_m(K)]$
 - $\sum_{k=1}^K \bar{p}_m(k) = 1$

There are three common measures of *node impurity* in this setting:

1. **Misclassification Error:**

$$Q_m = 1 - \max_k \bar{p}_m(k)$$

2. **Gini Index:**

$$\begin{aligned}Q_m &= \sum_{k=1}^K \bar{p}_m(k)(1 - \bar{p}_m(k)) \\ &= 1 - \sum_{k=1}^K \bar{p}_m^2(k)\end{aligned}$$

3. **Cross-entropy/Deviance:**

$$\begin{aligned}Q_m &= - \sum_{k=1}^K \bar{p}_m(k) \log \bar{p}_m(k) \\ &= \sum_{k=1}^K \bar{p}_m(k) \log \frac{1}{\bar{p}_m(k)}\end{aligned}$$

1.5.4 Splitting Summary

For each iteration, we calculate the Gain/Loss for *all* features $j = 1, 2, \dots, p$ and *all* possible split points and choose the pair that minimizes the loss (or maximizes the gain):

$$(j^*, s^*) = \arg \min_{j,s} \text{Loss}(j, s) = \arg \max_{j,s} \text{Gain}(j, s)$$

- where $\text{Loss}(j, s)$ is the loss of splitting the current node on the j predictor at split point s .

1.6 Stopping and Pruning

- Tree Size
 - A large tree (many leaf nodes with few observations) can overfit
 - A small tree can not capture important structure
 - Tree size is a tuning parameter governing the model's complexity, and the optimal tree size should be adaptively chosen from the data
- Early Stopping
 - Stop splitting when loss function has insignificant improvement (like forward stepwise)
 - However, a seemingly worthless initial split can lead to a good split further down the tree (short-sighted)
- Pruning
 - Grow a full tree (minimum node size) and prune back (like backwards stepwise)

1.6.1 Cost Complexity Pruning

- Let N_m be the number of observations in node R_m and $Q_m(T)$ be the loss in region m for a given tree T . E.g. using sum of squared error loss,

$$Q_m(T) = \sum_{\{i:x_i \in R_m\}} (y_i - \hat{c}_m)^2$$

- Weakest link pruning:** Successively collapse the internal node that produces the smallest per-node increase in $\sum_{m=1}^{|T|} Q_m(T)$ until you reach the single node (root) tree. This produces a finite sequence of sub-trees.
- For each sub-tree T , define its **cost complexity**

$$\begin{aligned} C_\lambda(T) &= \frac{1}{n} \sum_{m=1}^{|T|} Q_m(T) + \lambda |T| \\ &= \text{Loss}(T) + \lambda \text{Penalty}(T) \end{aligned}$$

where the m cover all terminal nodes in T and λ is a penalty on tree size $|T|$.

- Note: The *complexity* of a tree in this setting is measured by the *number of leaf nodes*, $|T|$

1.6.2 Penalty Tuning

- For each λ , there is a unique smallest sub-tree T_λ that minimizes $C_\lambda(T)$.
- The sequence of sub-trees from weakest link pruning contains every T_λ
- The tuning parameter, λ can be chosen by: cross-validation, AIC/BIC, Out-of-Bag (OOB), etc.

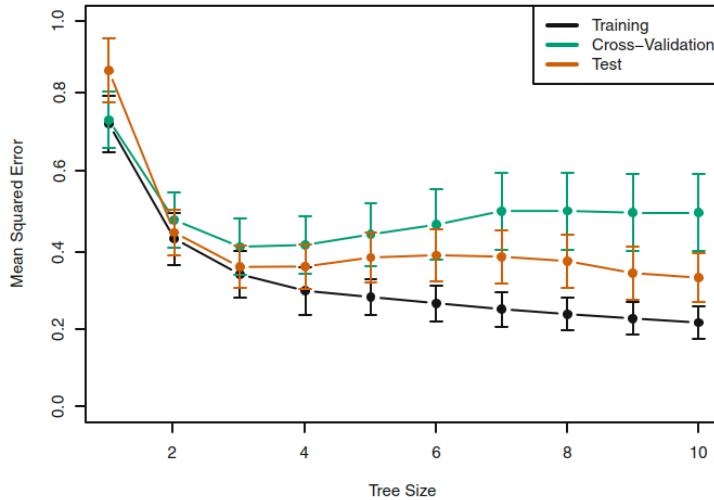


FIGURE 8.5. Regression tree analysis for the `Hitters` data. The training, cross-validation, and test MSE are shown as a function of the number of terminal nodes in the pruned tree. Standard error bands are displayed. The minimum cross-validation error occurs at a tree size of three.

1.7 Special Considerations

1.7.1 Missing Predictor Values

- Omit observations with missing values
- For categorical predictors, create an additional level “missing”
 - This can reveal important patterns if *missing* is not at random.
- Surrogate splits
 - At every split, create a list of *surrogate splits* that mimics the original splits
 - * For prediction, if an observation has a missing value use the surrogate splits to determine which child group it should go into
- Alternatively, before splitting we could impute (replace missing values with an estimate)
 - The surrogate approach is similar to imputation, but is based on the “nearest neighbors”; the observations in the same branch of the tree.

1.7.2 Binary Splitting

- Multiway splits are possible, but could partition the data too quickly (overfit)
- Multiway splits can be achieved from a combination of binary splits
 - I.e., split on X_1 at s_1 and then split again on X_1 at s_2
 - This will/should happen when the true response is not a constant.

1.7.3 Variable/Feature Importance

There are several ways to measure the *importance* of a feature in a tree. Here are only a few:

1. The number of times the feature was used to make a split

$$\mathcal{I}_j(T) = \sum_t \mathbb{1}(\text{split } t \text{ uses feature } j)$$

The sum is over all splits t in tree T .

2. The total reduction in loss (or increase in gain) for all the splits made by the feature

- This is a weighted version of number of times feature used to make a split
- In CART, the features used to make the surrogate splits are also included

The importance of predictor j in a single tree T :

$$\mathcal{I}_j(T) = \sum_t \text{gain}(t) \cdot \mathbb{1}(\text{split } t \text{ uses feature } j)$$

That is, the importance of feature j in tree T is the total *gain* from all splits involving feature j . In the equation, the sum is over all splits t in tree T .

3. Permutation based importance (prediction version): First, calculate the tree's performance on hold-out data. Then *permute/shuffle/resample* one of the features' values and reassess predictive performance. Any decrease in performance indicates the feature was important.

$$\mathcal{I}_j(T) = \text{Loss}(\text{using permuted column } j) - \text{Loss}(\text{original})$$

Note

This is only one type of permutation importance. We will explore other ways to assess variable importance later in the course.

1.8 Tree Advantages

- Handles categorical and continuous data in consistent manner
- Automatic variable selection (any predictor not split)
- Automatically discover interactions between multiple predictors
 - The tree depth determines the possible number of interactions
- Because the partitions are made from the data, trees give a *locally adaptive* estimate
- Invariant to monotone transformations (some caveats)
- Can be robust to outliers in the feature space. This is because trees split on sample quantiles rather than raw values.
- Easy to interpret

1.9 Tree Limitations

- Instability (high variance) due to greedy hierarchical structure; one change at top split can change remaining tree.
- Difficulty capturing additive structure

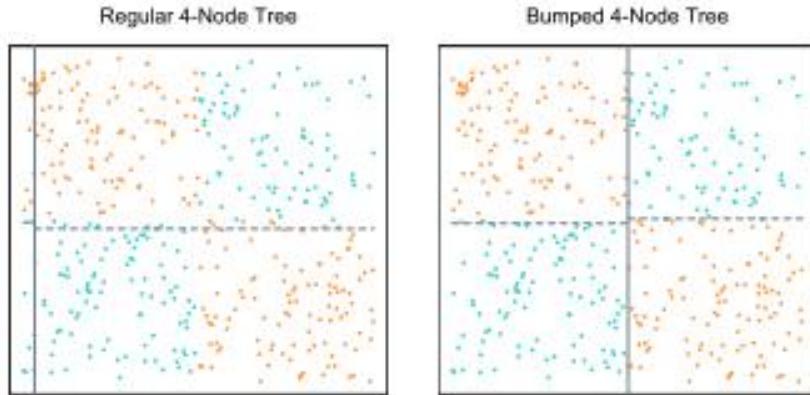


FIGURE 8.13. Data with two features and two classes (blue and orange), displaying a pure interaction. The left panel shows the partition found by three splits of a standard, greedy, tree-growing algorithm. The vertical grey line near the left edge is the first split, and the broken lines are the two subsequent splits. The algorithm has no idea where to make a good initial split, and makes a poor choice. The right panel shows the near-optimal splits found by bumping the tree-growing algorithm 20 times.

1.10 Trees in R

Main R packages: `tree` and `rpart` and `party`

2 Trees Demo

2.1 Required R Packages

```
library(ISLR)           # Hitters baseball data
library(rpart)          # classification and regression trees (CART)
library(rpart.plot)     # for `prp()` which allows more plotting control for trees
library(randomForest)   # for `randomForest()` function
library(tidyverse)       # data manipulation and visualization
```

2.2 Baseball Salary Data

The goal is to build models to predict the salary of baseball players

```
##-- Make Baseball Data
# Goal is to predict the log Salary

library(ISLR)
Hitters = ISLR::Hitters %>%
  filter(!is.na(Salary)) %>%           # remove missing Salary
  rename(Y = Salary)

set.seed(2019) # choose 200 samples for training (leaving only 63 for testing)
train.ind = sample(nrow(Hitters), size=200)
bball = Hitters[train.ind, ]

#- test data
X.test = Hitters[-train.ind, ] %>% select(-Y)
Y.test = Hitters[-train.ind, ] %>% pull(Y)

bball %>% arrange(-Y) %>% head() %>% as_tibble(rownames = "name")
#> # A tibble: 6 x 21
#>   name      AtBat  Hits HmRun  Runs   RBI Walks Years CAtBat CHits CHmRun CRuns
#>   <chr>    <int> <int>
#> 1 -Eddie Mu~  495   151    17    61    84    78    10    5624   1679    275    884
#> 2 -Jim Rice   618   200    20    98   110    62    13    7127   2163    351   1104
#> 3 -Mike Sch~   20     1     0     0     0     0     2     41     9     2     6
#> 4 -Don Matt~  677   238    31   117   113    53     5    2223    737    93    349
#> 5 -Ozzie Sm~  514   144     0    67    54    79     9    4739   1169    13    583
#> 6 -Gary Car~  490   125    24    81   105    62    13    6063   1646    271    847
#> # i 9 more variables: CRBI <int>, CWalks <int>, League <fct>, Division <fct>,
#> # PutOuts <int>, Assists <int>, Errors <int>, Y <dbl>, NewLeague <fct>
```

2.3 Regression Tree

```
#####
##-- Regression Trees in R
# trees are in many packages: rpart, tree, party, ...
# there are also many packages to display tree results
#
# Formulas: you don't need to specify interactions as the tree does this
# naturally.
#####
##-- Build Tree
library(rpart)
```

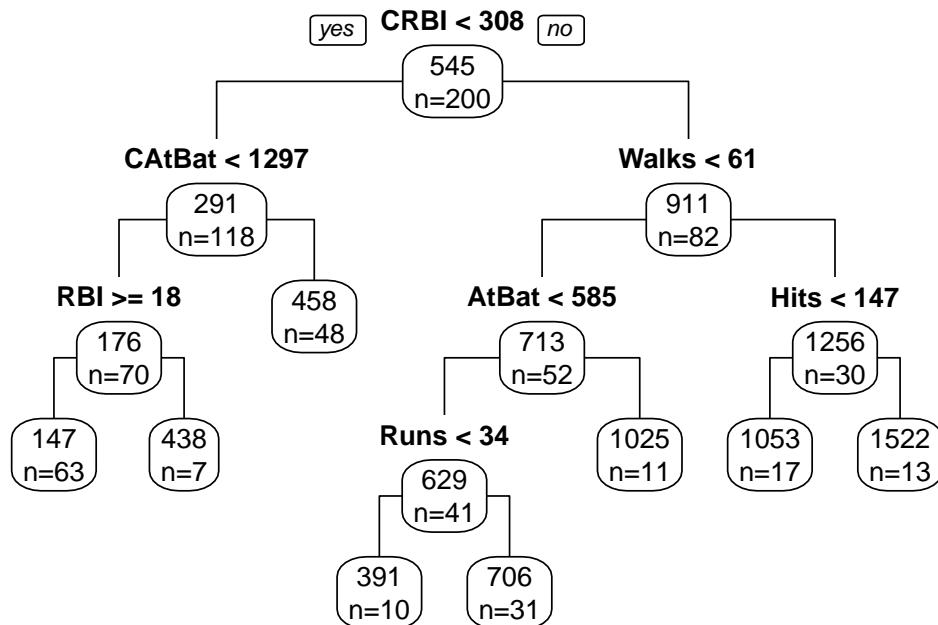
```

tree = rpart(Y~., data=bball)
summary(tree, cp=1)
#> Call:
#> rpart(formula = Y ~ ., data = bball)
#> n= 200
#>
#>      CP nsplit rel error xerror   xstd
#> 1 0.39734      0     1.0000 1.0071 0.1517
#> 2 0.11976      1     0.6027 0.6265 0.1140
#> 3 0.04832      2     0.4829 0.5959 0.1127
#> 4 0.03453      3     0.4346 0.5672 0.1154
#> 5 0.02898      4     0.4001 0.6263 0.1211
#> 6 0.01593      5     0.3711 0.6296 0.1208
#> 7 0.01143      6     0.3551 0.6272 0.1207
#> 8 0.01000      7     0.3437 0.6294 0.1204
#>
#> Variable importance
#> CRBI    CRuns   CHits   CATBat   CWalks   CHmRun   Walks    Runs    Hits    AtBat    RBI
#>      16       15      14       14       14       12        5       4       2       2       1
#> HmRun
#>      1
#>
#> Node number 1: 200 observations
#> mean=545.1, MSE=2.347e+05
length(unique(tree$where))           # number of leaf nodes
#> [1] 8

-- Plot Tree
library(rpart.plot)    # for prp() which allows more plotting control
prp(tree, type=1, extra=1, branch=1)

# rpart() functions can also plot (just not as good):
# plot(tree, uniform=TRUE)
# text(tree, use.n=TRUE, xpd=TRUE)

```



2.3.2 Evaluate Tree

```
#- mean squared error function
mse <- function(yhat, y){
  yhat = as.matrix(yhat)
  apply(yhat, 2, \((f) mean((y-f)^2)))
}

mse(predict(tree), bball$Y)           # training error
#> [1] 80680
mse(predict(tree, X.test), Y.test)    # testing error
#> [1] 59872
```

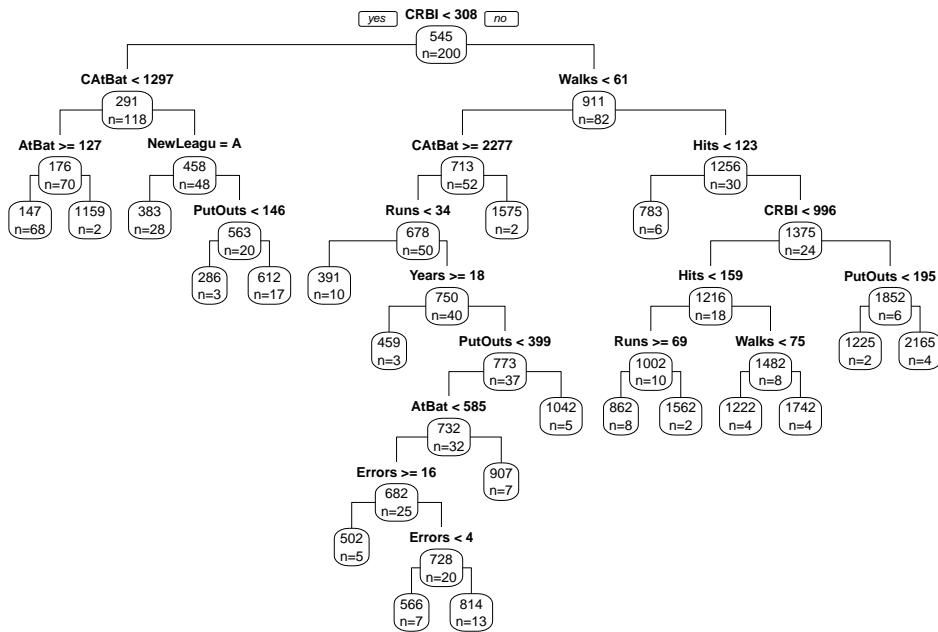
Build a more complex tree

```
-- More complex tree
# see ?rpart.control() for details
# xval: number of cross-validations
# minsplit: min obs to still allow a split
# cp: complexity parameter

tree2 = rpart(Y ~ ., data=bball, xval=0, minsplit=5, cp=0.005)
summary(tree2, cp=1)
#> Call:
#> rpart(formula = Y ~ ., data = bball, xval = 0, minsplit = 5,
#>       cp = 0.005)
#>     n= 200
#>
#>          CP nsplit rel error
#> 1  0.397337      0   1.0000
#> 2  0.119759      1   0.6027
#> 3  0.048320      2   0.4829
#> 4  0.042372      3   0.4346
#> 5  0.037284      4   0.3922
#> 6  0.032953      6   0.3176
#> 7  0.025089      7   0.2847
#> 8  0.021944      8   0.2596
#> 9  0.021814      9   0.2377
#> 10 0.016670     10   0.2158
#> 11 0.011547     11   0.1992
#> 12 0.008095     12   0.1876
#> 13 0.007354     13   0.1795
#> 14 0.005854     15   0.1648
#> 15 0.005786     16   0.1590
#> 16 0.005148     17   0.1532
#> 17 0.005000     19   0.1429
#>
#> Variable importance
#>   CRuns    CRBI   CATBat    CHits   CWalks   CHmRun   Walks   Runs   Hits   AtBat
#>     14      14      13      12      11      10       6       5      5      4
#>   PutOuts      RBI   Years Assists   HmRun   Errors
#>     1        1      1       1       1       1
#>
#> Node number 1: 200 observations
#>   mean=545.1, MSE=2.347e+05
length(unique(tree2$where))
#> [1] 20
```

```
prp(tree2, type=1, extra=1, branch=1)

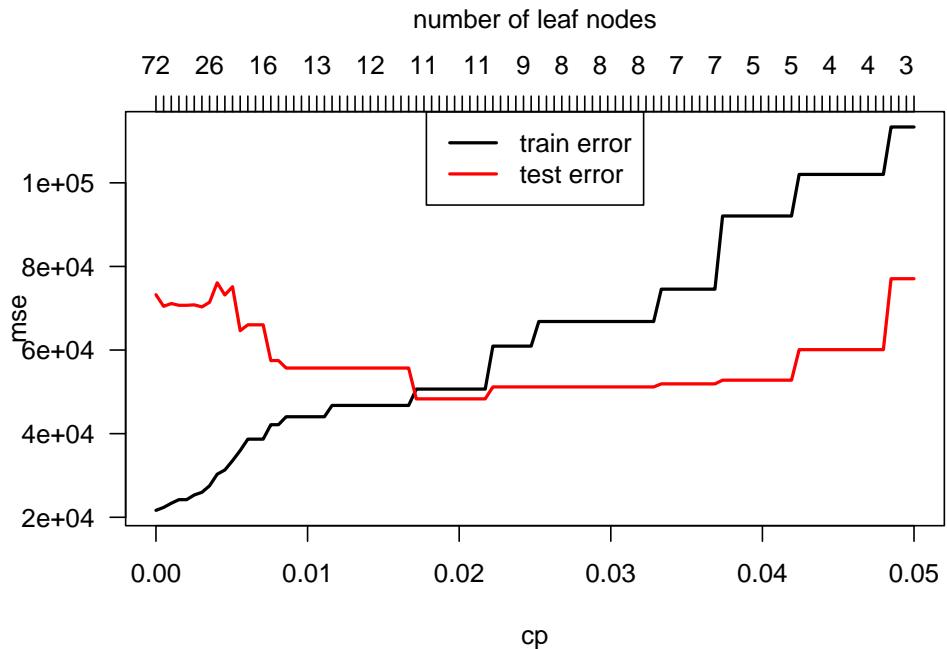
mse(predict(tree2), bball$Y)                      # training error
#> [1] 33541
mse(predict(tree2, X.test), Y.test)               # testing error
#> [1] 75146
```



Now, fit a set of trees for sequence of cp values.

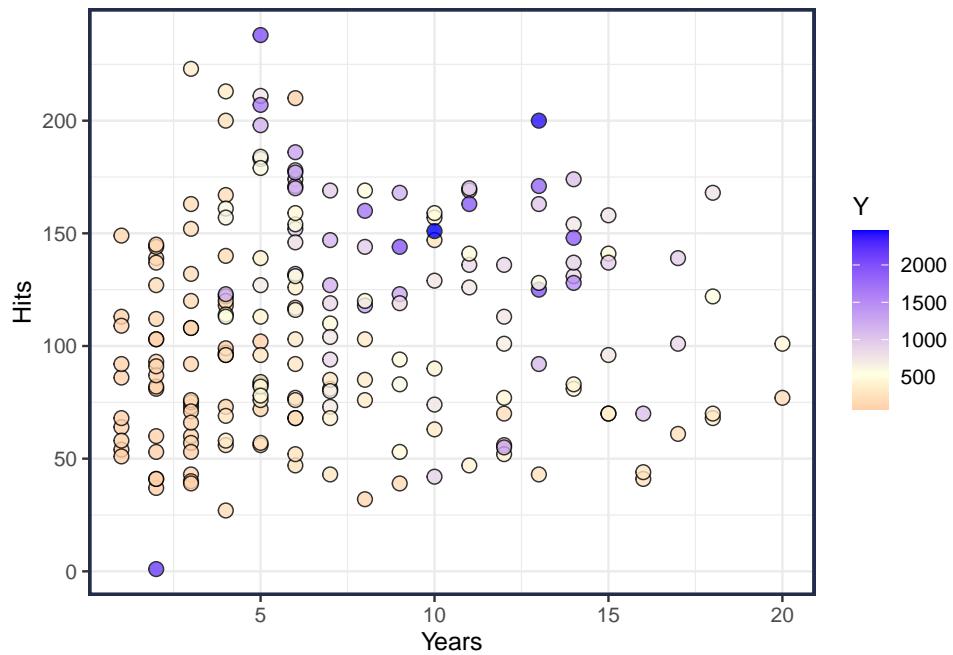
```
cp = seq(.05,0,length=100)  # cp is like a penalty on the tree size
for(i in 1:length(cp)){
  if(i == 1){train.error = test.error = nleafs = numeric(length(cp)) }
  tree.fit = rpart(Y~,data=bball, xval=0, minsplit=5, cp=cp[i])
  train.error[i] = mse(predict(tree.fit),bball$Y)                  # training error
  test.error[i] = mse(predict(tree.fit,X.test),Y.test)             # testing error
  nleafs[i] = length(unique(tree.fit$where))
}

plot(range(cp),range(train.error,test.error),typ='n',xlab="cp",ylab="mse",las=1)
lines(cp,train.error,col="black",lwd=2)
lines(cp,test.error,col="red",lwd=2)
legend("top",c('train error','test error'),col=c("black","red"),lwd=2)
axis(3,at=cp,labels=nleafs)
mtext("number of leaf nodes",3,line=2.5)
```

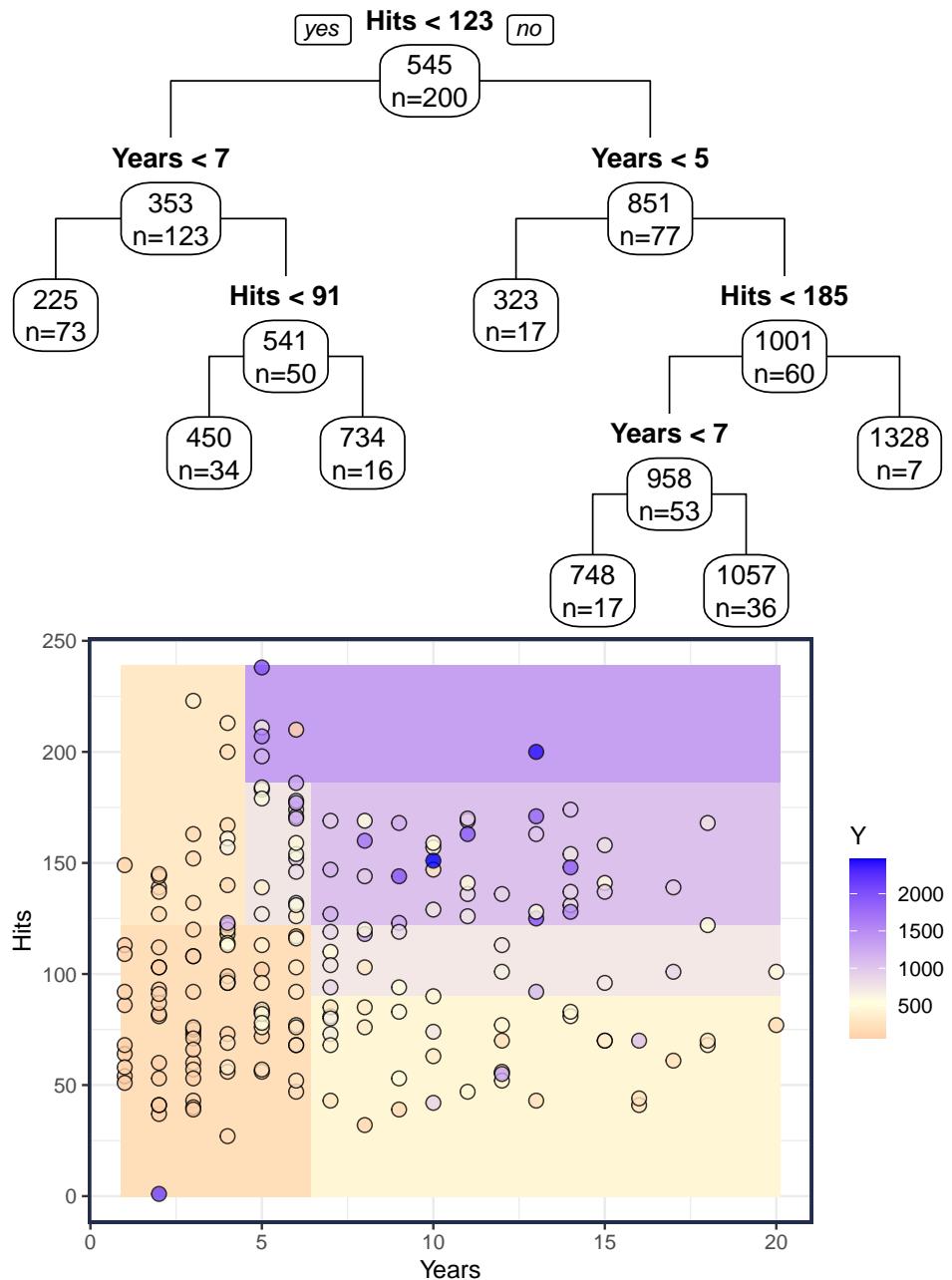


2.3.3 Regression Tree example with 2 dimensions only

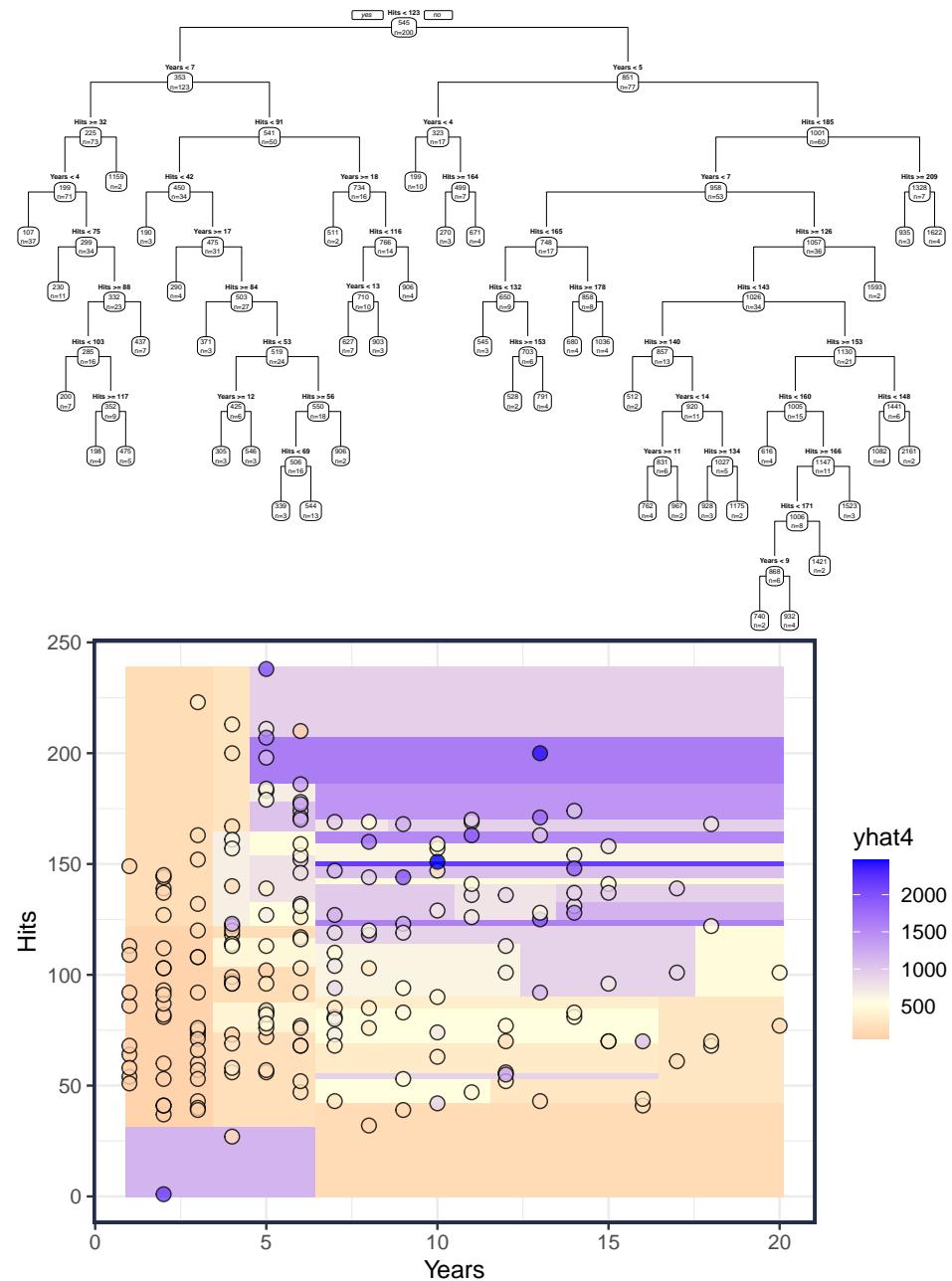
Consider the two variables Years and Hits and their relationship to Y.



Let's fit a tree with the two predictors

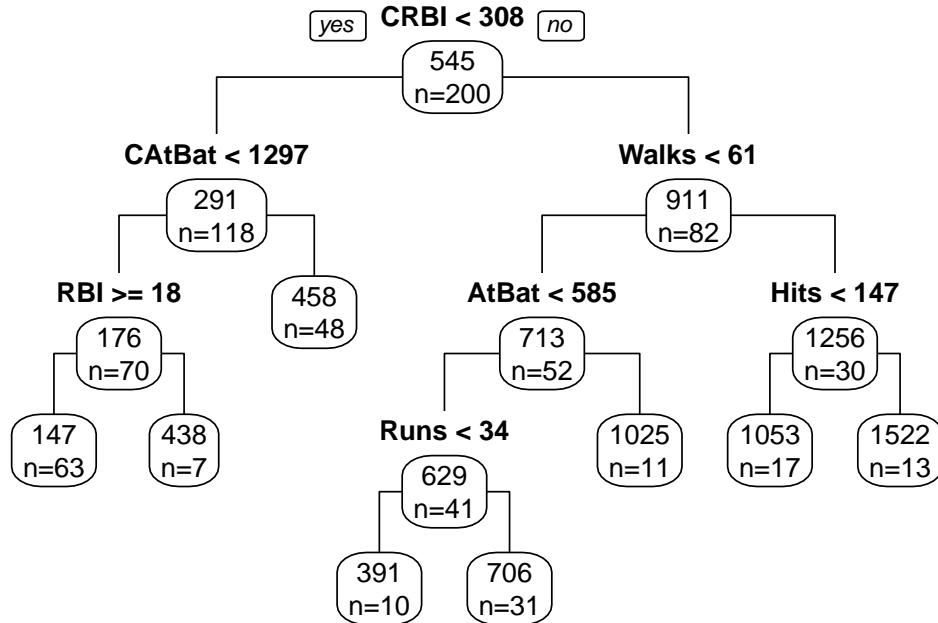


And we can also use more complex trees:



2.4 Details of Splitting (for Regression Trees)

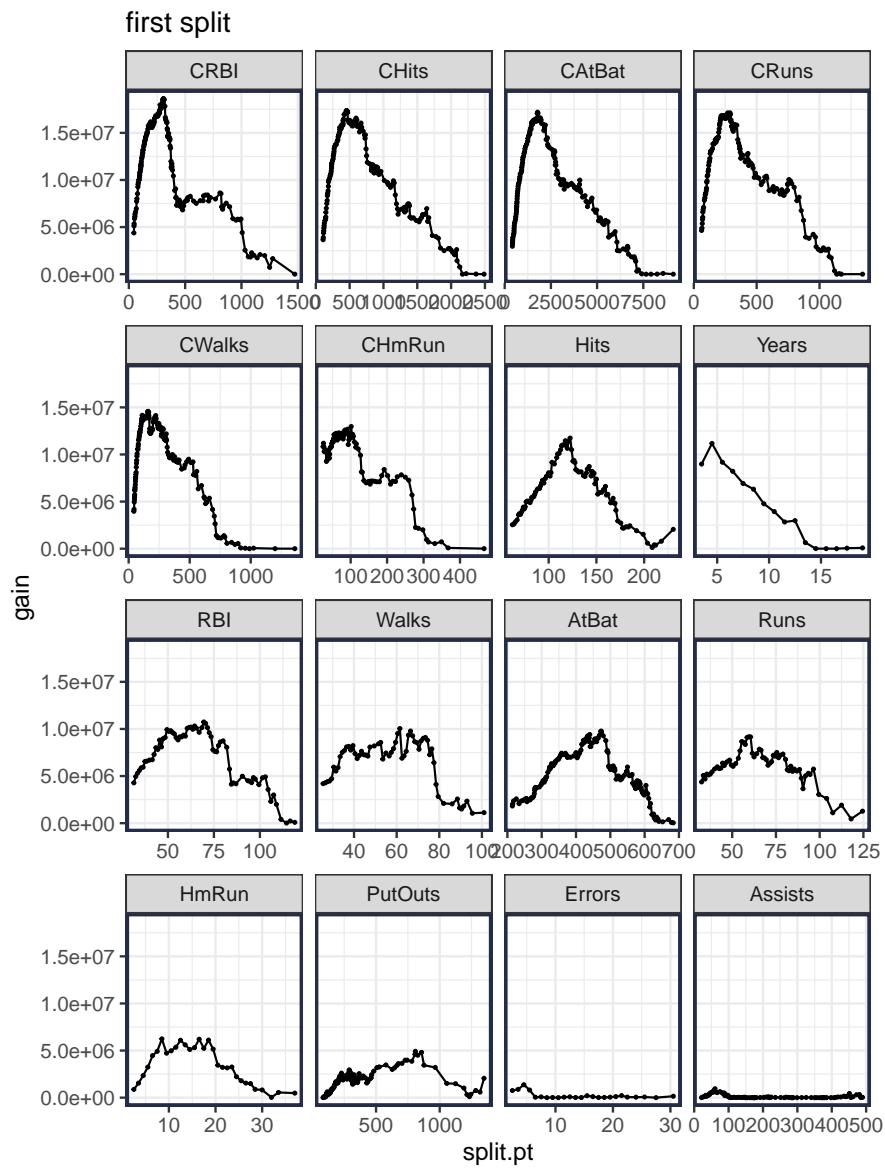
Going back to building a tree with all predictor variables. Recall that CRBI is split at 307.5.



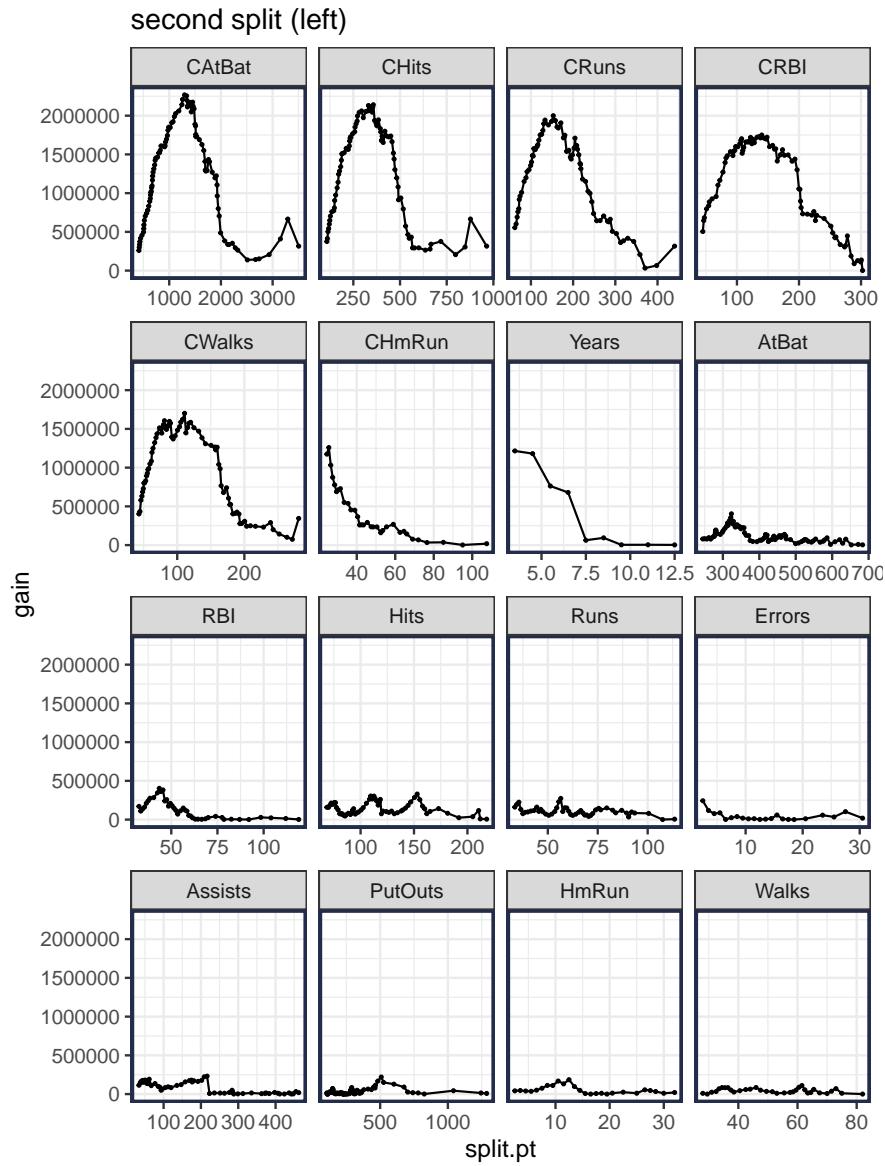
2.4.1 First Split

Under the hood, trees will search all possibly split points for all predictor variables. It will use the variable and associated split point that has the maximum gain (or improvement in evaluation metric).

var	split.pt	n.L	n.R	est.L	est.R	SSE.L	SSE.R	SSE	gain
CRBI	307.5	118	82	290.5	911.5	8010622	20282448	28293070	18653665
CHits	457.5	93	107	229.0	819.9	5299313	24273274	29572587	17374148
CAtBat	1779.5	95	105	236.8	824.0	5574003	24175441	29749444	17197291
CRuns	288.0	109	91	277.7	865.4	7452616	22368698	29821314	17125421
CWalks	157.5	90	110	246.6	789.3	6768757	25600645	32369403	14577333
CHmRun	101.5	156	44	409.9	1024.6	21520628	12459474	33980101	12966634
Hits	122.5	123	77	353.4	851.4	11979104	23225406	35204510	11742225
Years	4.5	69	131	219.5	716.6	5807172	29967467	35774639	11172096
RBI	69.5	147	53	406.0	931.1	18079731	18126052	36205783	10740952
Walks	61.5	155	45	424.4	961.0	19360871	17541643	36902514	10044222
AtBat	473.5	124	76	372.1	827.4	13829528	23351912	37181440	9765295
Runs	59.5	115	85	361.0	794.2	11945002	25829983	37774985	9171750
HmRun	8.5	94	106	357.6	711.4	12526389	28182028	40708417	6238318
PutOuts	809.0	186	14	502.1	1116.7	35199872	6828501	42028373	4918362
Errors	4.5	71	129	433.5	606.5	7733767	37842076	45575843	1370892
Assists	60.5	111	89	483.4	622.1	20984841	25011176	45996017	950719

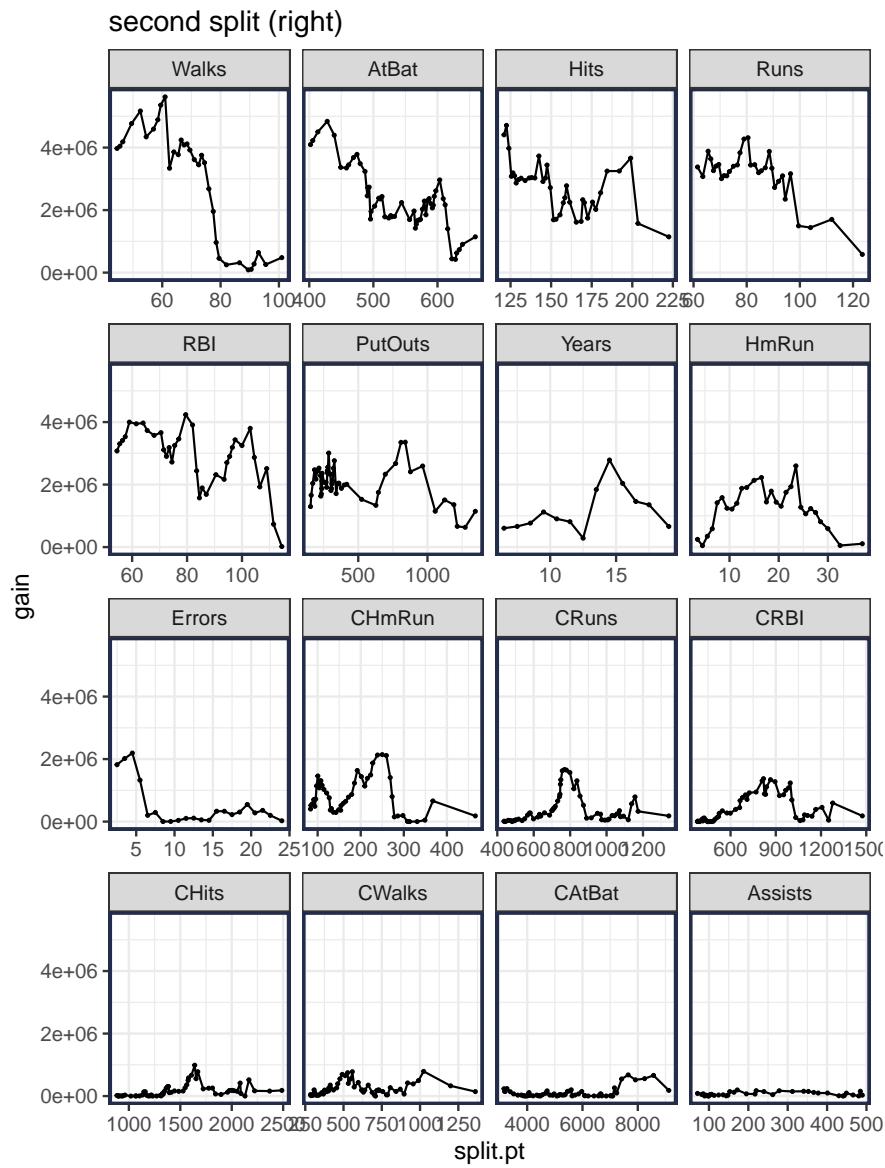


2.4.2 Second Split (left): CATBat < 1296.5



var	split.pt	n.L	n.R	est.L	est.R	SSE.L	SSE.R	SSE	gain
CAtBat	1296.5	70	48	175.7	458.0	4142792	1599385	5742177	2268445
CHits	357.0	77	41	192.2	475.1	4385523	1484232	5869754	2140868
CRuns	153.0	68	50	178.9	442.3	4202620	1808176	6010797	1999825
CRBI	140.0	73	45	194.9	445.6	4612088	1648340	6260429	1750193
CWalks	111.0	74	44	197.9	446.2	4682658	1626914	6309572	1701050
CHmRun	25.5	73	45	209.4	422.1	4950482	1800792	6751274	1259349
Years	3.5	48	70	168.0	374.6	4065840	2729314	6795153	1215469
AtBat	323.5	50	68	222.3	340.7	4391102	3215583	7606685	403937
RBI	43.5	64	54	236.8	354.2	5514802	2092255	7607057	403565
Hits	153.0	105	13	271.9	440.8	7158659	522192	7680851	329771
Runs	56.5	77	41	255.4	356.5	5887826	1849136	7736962	273661
Errors	2.5	17	101	179.9	309.2	172699	7594684	7767383	243239
Assists	216.5	90	28	265.8	369.9	3189715	4589431	7779145	231477
PutOuts	508.0	107	11	276.7	425.3	7138760	651614	7790374	220248
HmRun	12.5	84	34	265.3	352.8	6395242	1429943	7825185	185437
Walks	61.5	103	15	278.9	370.7	7018267	881993	7900261	110361

2.4.3 Second Split (right): Walks < 61



var	split.pt	n.L	n.R	est.L	est.R	SSE.L	SSE.R	SSE	gain
Walks	61.0	52	30	712.6	1256.2	5842326	8817840	14660166	5622282
AtBat	428.0	26	56	554.9	1077.0	2032940	13410065	15443005	4839443
Hits	122.5	30	52	595.9	1093.5	2674697	12898042	15572738	4709710
Runs	80.5	58	24	763.9	1268.1	9627677	6339423	15967100	4315348
RBI	79.5	57	25	760.9	1254.7	8028152	8016141	16044292	4238156
PutOuts	839.5	73	9	840.4	1487.7	14312345	2613789	16926134	3356314
Years	14.5	64	18	1009.2	563.9	16198744	1298244	17496988	2785460
HmRun	23.5	65	17	820.4	1259.5	14245529	3438753	17684283	2598166
Errors	4.5	29	53	690.4	1032.4	3230563	14859766	18090329	2192119
CHmRun	250.0	69	13	841.3	1283.9	11497937	6641903	18139840	2142609
CRuns	769.0	56	26	814.3	1120.7	8769462	9847003	18616465	1665983
CRBI	818.5	59	23	830.7	1118.7	9605277	9304706	18909983	1372466
CHits	1640.0	62	20	849.2	1104.6	10823636	8472147	19295784	986665
CWalks	1023.5	79	3	930.6	407.5	19425851	65712	19491563	790885
CAtBat	7653.5	77	5	934.6	554.8	19376696	228517	19605214	677234
Assists	172.0	60	22	941.0	830.9	16318132	3769004	20087137	195311

3 Bagging Trees

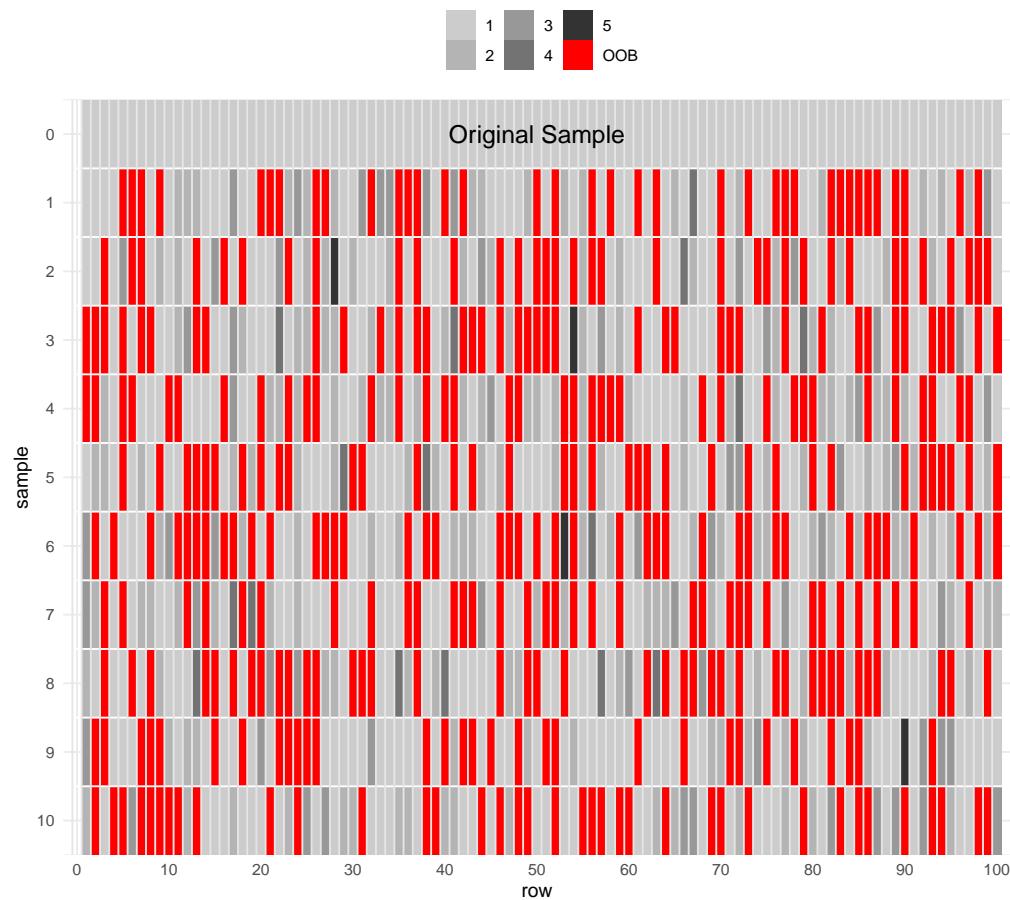
3.1 Better Trees

- Because of the instability of trees, they are great candidates for methods like bagging that will reduce the variance.
- Grow a set of B trees from a bootstrap samples and average their predictions:

$$\hat{f}(x) = \frac{1}{B} \sum_{b=1}^B T(x; \hat{\theta}_b)$$

where $\hat{\theta}_b = \hat{\theta}(\mathcal{D}_b)$ are all the estimated parameters for fitting the tree (split variables, cutpoints, and terminal (leaf) node values) from the bootstrap sample \mathcal{D}_b .

- Details and discussion can be found in Breiman's article "Bagging Predictors" (1996, *Machine Learning*).
 - Bagging = Bootstrap Aggregating
 - Lots of advice on when Bagging will help and when it won't
 - Bagging will help with variance reduction, but not bias
- Bagging produces an *ensemble model*
- Aggregation of Bagged Predictors:
 - For regression: use the average predictions
 - For classification: use the average of the predicted class probabilities (majority vote is possible too, but be careful about class imbalance or unequal misclassification costs)



3.1.1 Variance Reduction with Bagging

Note

A helpful probability cheatsheet can be found here: https://github.com/wzchen/probability_cheatsheet/blob/master/probability_cheatsheet.pdf

Properties of Variance/Covariance

$$\begin{aligned} V(X) &= E(X^2) - (E(X))^2 \\ &= \text{Cov}(X, X) \\ \text{Cov}(X_1, X_2) &= E(X_1 X_2) - E(X_1) E(X_2) \\ \text{Cor}(X_i, X_j) &= \frac{\text{Cov}(X_i, X_j)}{\sqrt{V(X_i) V(X_j)}} \\ V(X_1 + X_2) &= V(X_1) + V(X_2) + 2 \text{Cov}(X_1, X_2) \\ V\left(a \sum_{i=1}^p X_i\right) &= a^2 \sum_{i=1}^p V(X_i) + 2a^2 \sum_{i < j} \text{Cov}(X_i, X_j) \end{aligned}$$

Variance Reduction

- Let θ be something we want to estimate (e.g., $\theta = f(x)$) and $\hat{\theta}$ an estimate.
- Suppose we have M models to estimate θ which produces the estimates $\{\hat{\theta}_1, \hat{\theta}_2, \dots, \hat{\theta}_M\}$
- One way to make an *ensemble prediction* is from the average

$$\bar{\theta} = \frac{1}{M} \sum_{i=1}^M \hat{\theta}_i$$

- The **expected value** of the ensemble is:

$$E(\bar{\theta}) = \frac{1}{M} \sum_{i=1}^M E(\hat{\theta}_i)$$

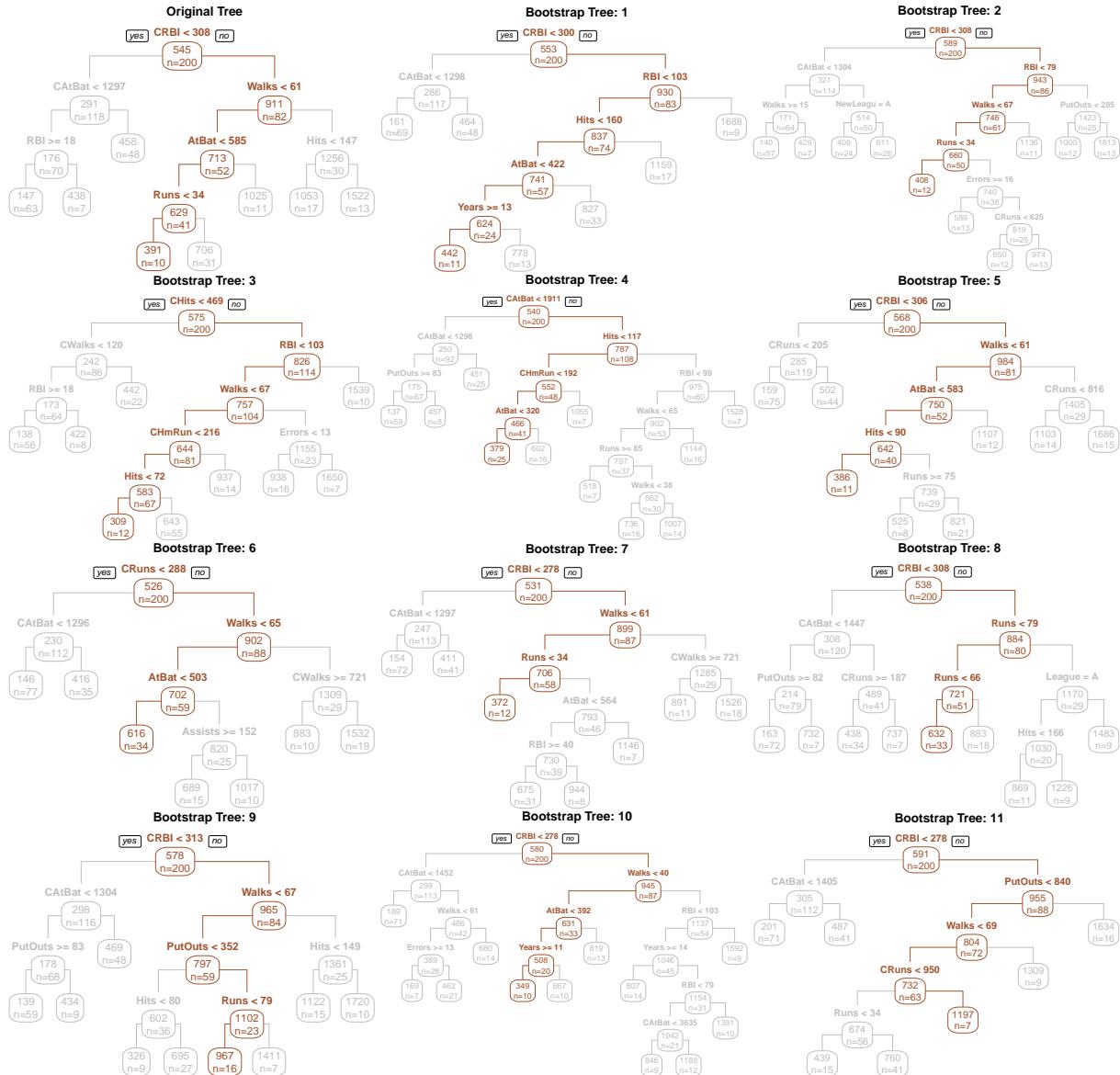
- The **variance** of the ensemble is:

$$\begin{aligned} V(\bar{\theta}) &= \frac{1}{M^2} \sum_{i=1}^M V(\hat{\theta}_i) + \frac{2}{M^2} \sum_{i < j} \text{Cov}(\hat{\theta}_i, \hat{\theta}_j) \\ &= \frac{1}{M^2} \sum_{i=1}^M V(\hat{\theta}_i) + \frac{2}{M^2} \sum_{i < j} \sqrt{V(\hat{\theta}_i) V(\hat{\theta}_j)} \text{Cor}(\hat{\theta}_i, \hat{\theta}_j) \end{aligned}$$

- Thus to reduce the variance, we want to **use models that have low correlation**.
 - If $\text{Cor}(\hat{\theta}_i, \hat{\theta}_j) = 0 \quad \forall i, j$, then variance is minimized (for example, when the models are *independent*)
 - If $\text{Cor}(\hat{\theta}_i, \hat{\theta}_j) = 1 \quad \forall i, j$, then there is no (variance reduction) benefit of using an ensemble.
 - In Bagging, each *model* is a tree fit with a bootstrap sample.
 - For unstable models, like trees, the bagged models will have low correlation, but for more stable models, like linear regression, the bagged models will maintain high correlation.

3.2 Bagging Trees

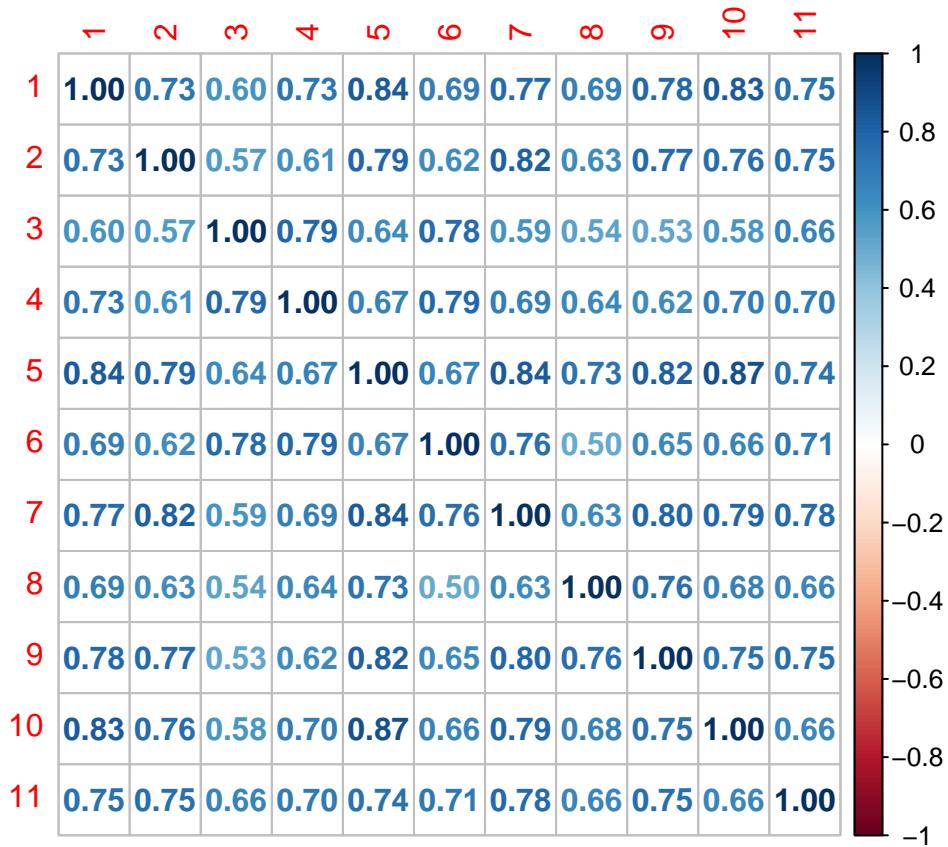
Highlight node is for Pete Rose.



(ESL pg 587) “The essential idea in bagging is to average many noisy but approximately unbiased models, and hence reduce the variance.”

- Thus when Bagging trees, grow **deep trees to reduce bias** and use **many bootstrap samples to reduce variance**

3.2.1 Correlation



3.2.2 Bagging can smooth visual

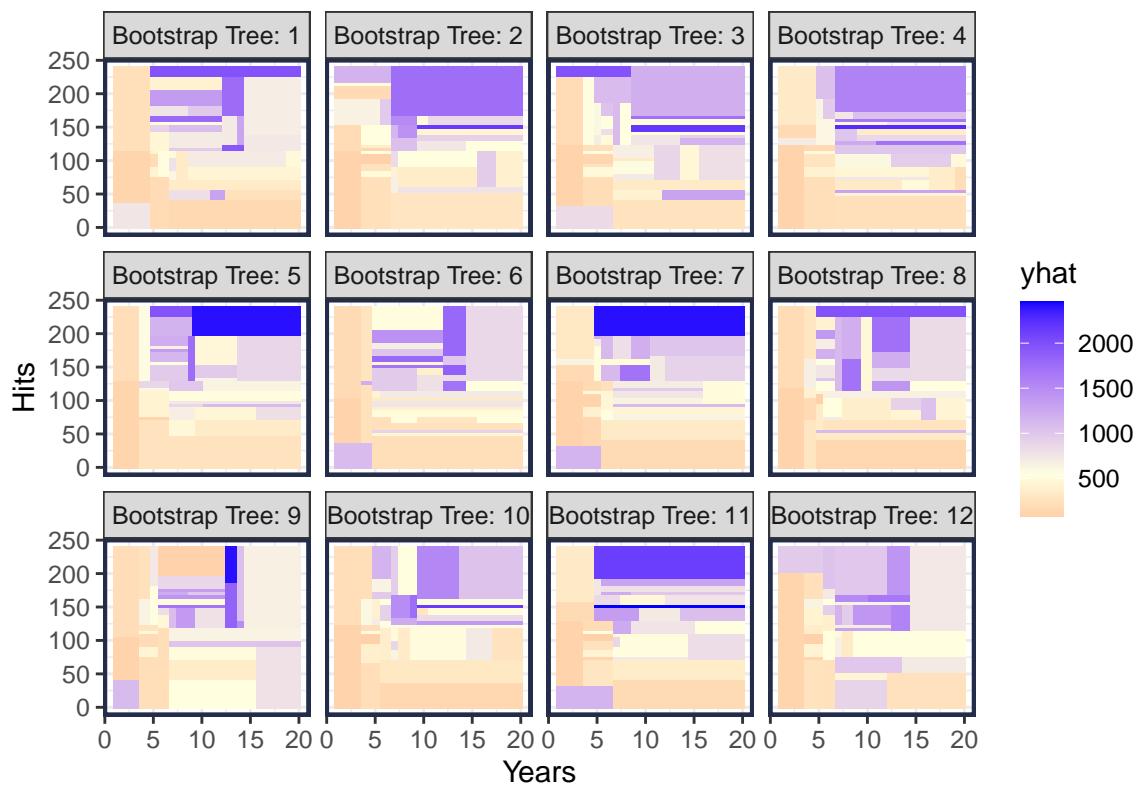


Figure 1: Bagging in 2 dimensions (Years and Hits)

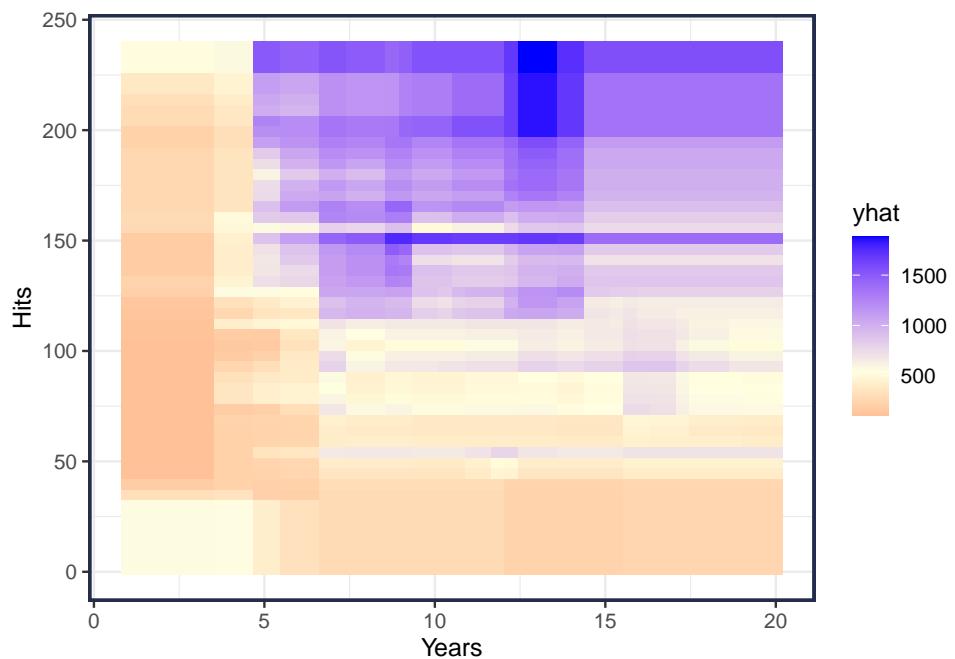


Figure 2: Average of bootstrap predictions

4 Random Forest

4.1 Random Forest

Random Forest is a modification of bagging that attempts to build *de-correlated trees* by considering a restricted set of features for splitting.

Algorithm 15.1 Random Forest for Regression or Classification.

1. For $b = 1$ to B :
 - (a) Draw a bootstrap sample \mathbf{Z}^* of size N from the training data.
 - (b) Grow a random-forest tree T_b to the bootstrapped data, by recursively repeating the following steps for each terminal node of the tree, until the minimum node size n_{min} is reached.
 - i. Select m variables at random from the p variables.
 - ii. Pick the best variable/split-point among the m .
 - iii. Split the node into two daughter nodes.
2. Output the ensemble of trees $\{T_b\}_1^B$.

To make a prediction at a new point x :

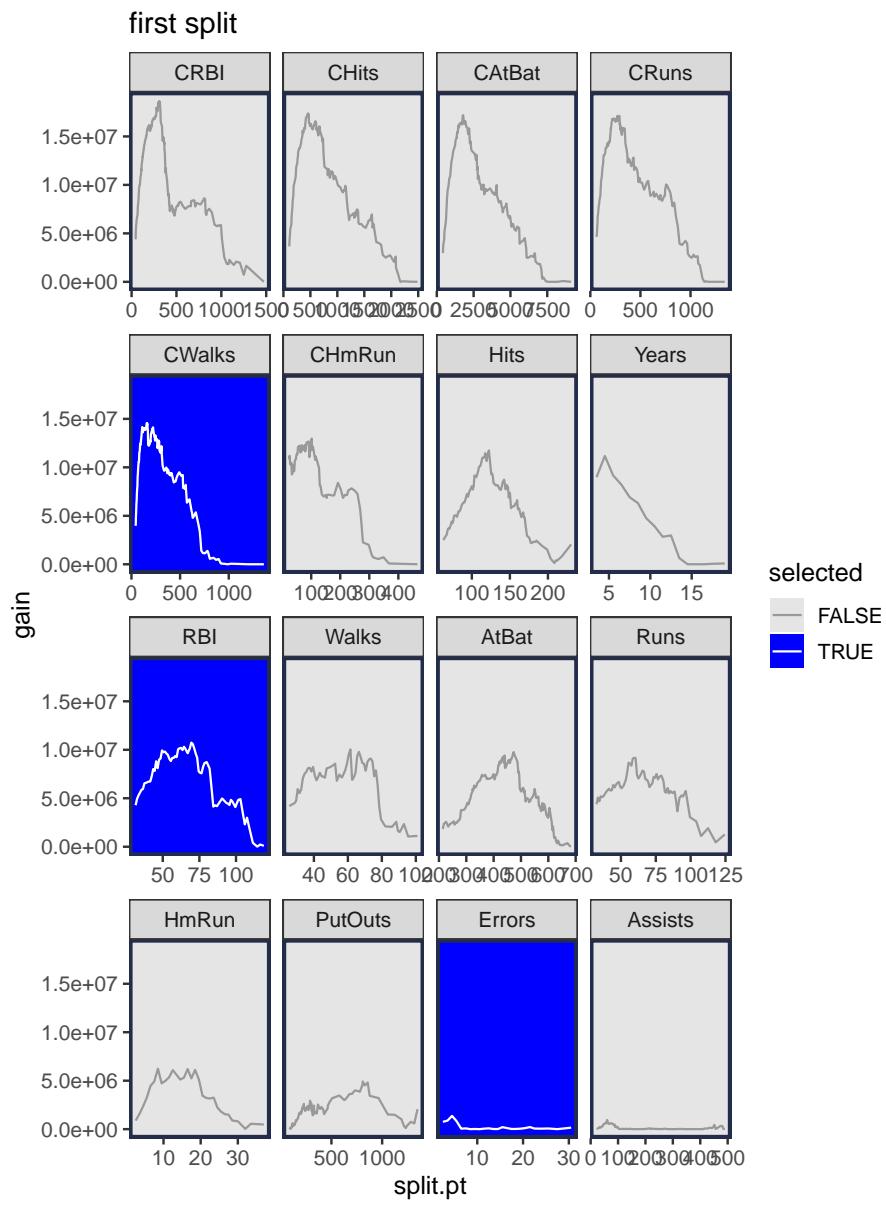
Regression: $\hat{f}_{rf}^B(x) = \frac{1}{B} \sum_{b=1}^B T_b(x)$.

Classification: Let $\hat{C}_b(x)$ be the class prediction of the b th random-forest tree. Then $\hat{C}_{rf}^B(x) = \text{majority vote } \{\hat{C}_b(x)\}_1^B$.

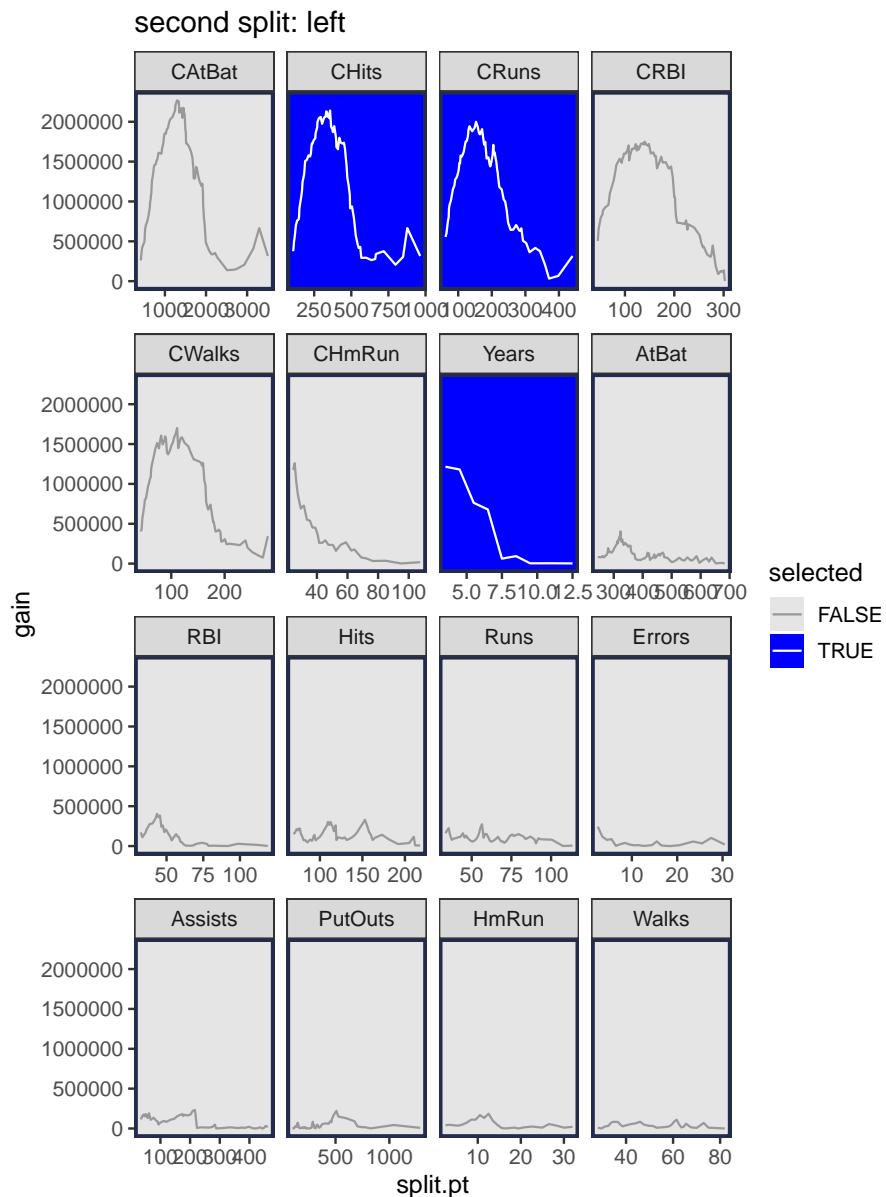
- Note: I recommend aggregating the probabilities for classification trees instead of majority vote.

4.1.1 Illustration of Restricted Set of Features for Splitting

var	split.pt	n.L	n.R	est.L	est.R	SSE.L	SSE.R	SSE	gain
CRBI	307.5	118	82	290.5	911.5	8010622	20282448	28293070	18653665
CHits	457.5	93	107	229.0	819.9	5299313	24273274	29572587	17374148
CAtBat	1779.5	95	105	236.8	824.0	5574003	24175441	29749444	17197291
CRuns	288.0	109	91	277.7	865.4	7452616	22368698	29821314	17125421
CWalks	157.5	90	110	246.6	789.3	6768757	25600645	32369403	14577333
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Hits	122.5	123	77	353.4	851.4	11979104	23225406	35204510	11742225
Years	4.5	69	131	219.5	716.6	5807172	29967467	35774639	11172096
RBI	69.5	147	53	406.0	931.1	18079731	18126052	36205783	10740952
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AtBat	473.5	124	76	372.1	827.4	13829528	23351912	37181440	9765295
Runs	59.5	115	85	361.0	794.2	11945002	25829983	37774985	9171750
HmRun	8.5	94	106	357.6	711.4	12526389	28182028	40708417	6238318
PutOuts	809.0	186	14	502.1	1116.7	35199872	6828501	42028373	4918362
Errors	4.5	71	129	433.5	606.5	7733767	37842076	45575843	1370892
Assists	60.5	111	89	483.4	622.1	20984841	25011176	45996017	950719



var	split.pt	n.L	n.R	est.L	est.R	SSE.L	SSE.R	SSE	gain
CAtBat	1296.5	70	48	175.7	458.0	4142792	1599385	5742177	2268445
CHits	357.0	77	41	192.2	475.1	4385523	1484232	5869754	2140868
CRuns	153.0	68	50	178.9	442.3	4202620	1808176	6010797	1999825
CRBI	140.0	73	45	194.9	445.6	4612088	1648340	6260429	1750193
CWalks	111.0	74	44	197.9	446.2	4682658	1626914	6309572	1701050
CHmRun	25.5	73	45	209.4	422.1	4950482	1800792	6751274	1259349
Years	3.5	48	70	168.0	374.6	4065840	2729314	6795153	1215469
AtBat	323.5	50	68	222.3	340.7	4391102	3215583	7606685	403937
RBI	43.5	64	54	236.8	354.2	5514802	2092255	7607057	403565
Hits	153.0	105	13	271.9	440.8	7158659	522192	7680851	329771
Runs	56.5	77	41	255.4	356.5	5887826	1849136	7736962	273661
Errors	2.5	17	101	179.9	309.2	172699	7594684	7767383	243239
Assists	216.5	90	28	265.8	369.9	3189715	4589431	7779145	231477
PutOuts	508.0	107	11	276.7	425.3	7138760	651614	7790374	220248
HmRun	12.5	84	34	265.3	352.8	6395242	1429943	7825185	185437
Walks	61.5	103	15	278.9	370.7	7018267	881993	7900261	110361



4.2 Random Forest Tuning

There are two primary tuning parameters for Random Forest:

1. Variety: m controls the number of predictors that are evaluated for each split (this is named `mtry` argument in `randomForest` package)
2. Complexity: The depth/size of the trees are controlled by setting the *minimum number of observations in the leaf nodes* (`min.obs`) or the *depth* of the tree or the number of leaf nodes

Your Turn #2

How do these tuning parameters relate to the bias/variance trade-off?

- The tuning parameters can be determined from cross-validation or OOB error
- In `randomForest` package:
 - For classification, the default value is $mtry = \lfloor \sqrt{p} \rfloor$ and $min.obs = 1$.
 - For regression, the default value is $mtry = \lfloor p/3 \rfloor$ and $min.obs = 5$.
- The *number of trees* is another tuning parameter, but want this to be as large as possible (subject to computational and memory constraints)
 - See [This stats.stackexchange answer](#) for further explanation.

4.3 OOB error

For each observation (x_i, y_i) , construct its OOB prediction by averaging only those trees corresponding to bootstrap samples in which observation i did not appear.

$$\hat{f}(x_i) = \frac{1}{N_B(i)} \sum_{b=1}^B \mathbb{1}(x_i \in \text{OOB}(b)) \cdot T(x_i; \hat{\theta}_b)$$

where $N_B(i)$ is the number of trees with observation i out-of-bag.

- Recall that there is a 37% chance that any observation is out-of-bag in any bootstrap sample.
- Thus, $N_B(i) \approx 0.37B$ (the number of trees used to estimate the OOB error is about 37% of the total number of trees in the forest).
 - More encouragement to use *many* trees in the forest

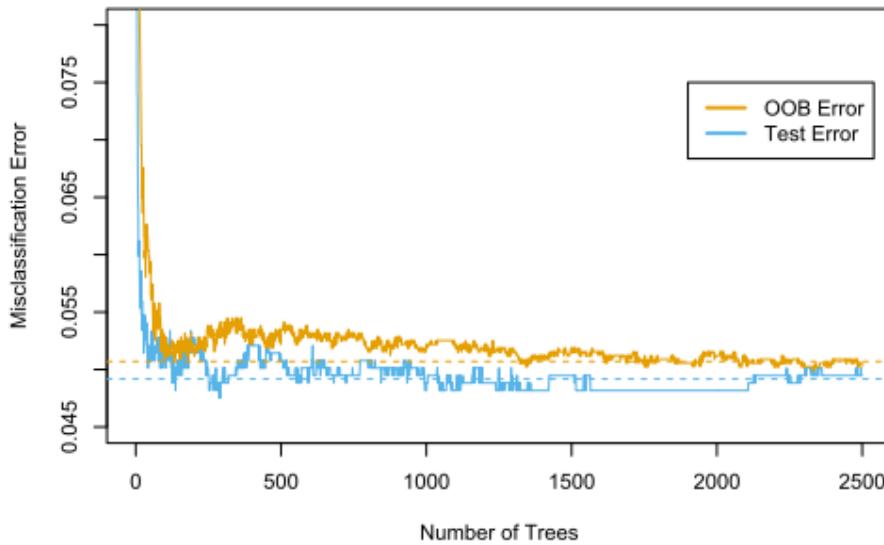


Figure 15.4 in ESL

4.4 Variable Importance

At each split in each tree, the improvement in the split-criterion is the importance measure attributed to the splitting variable, and is accumulated over all the trees in the forest separately for each variable.

The importance of predictor j in a single tree T :

$$\mathcal{I}_j(T) = \sum_t \text{gain}(t) \cdot \mathbb{1}(\text{split } t \text{ uses feature } j)$$

That is, the importance of feature j in tree T is the total *gain* from all splits involving feature j . In the equation, the sum is over all splits t in tree T .

The importance of predictor j in a forest is the average importance from all trees in the forest:

$$\mathcal{I}_j = \frac{1}{B} \sum_{b=1}^B \mathcal{I}_j(T_b)$$

- Note: a final normalizing step may transform importance scores to sum to 1
- There are other ways to measure feature importance, like permutation.

4.5 Random Forest and k-NN

Random Forests (especially with almost fully grown trees) are similar to k -NN methods, but they adaptively determines the neighbors instead of needing to pre-specify a distance metric.

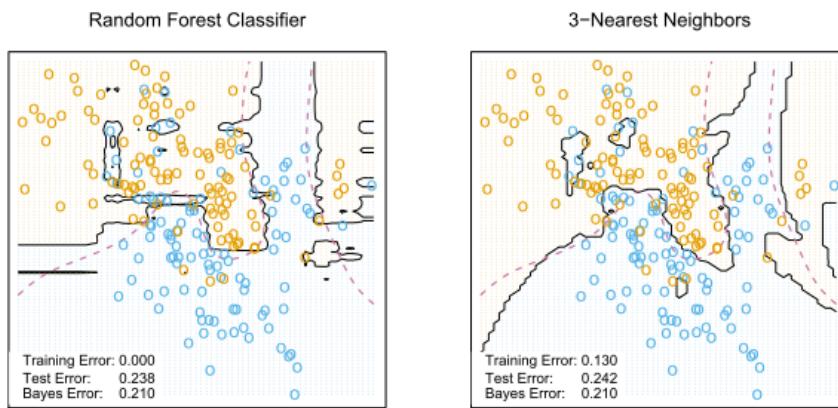


FIGURE 15.11. Random forests versus 3-NN on the mixture data. The axis-oriented nature of the individual trees in a random forest lead to decision regions with an axis-oriented flavor.

4.6 Random Forests in R

- `randomForest`
- `ranger`
- `randomForestSRC`
- `Rborist`
- `party`
- `tidymodels` https://parsnip.tidymodels.org/reference/rand_forest.html