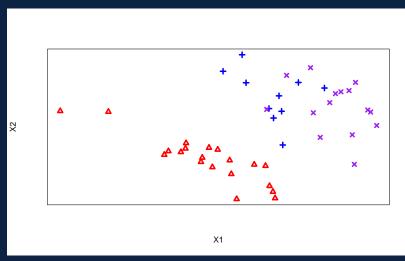


#### Motivation

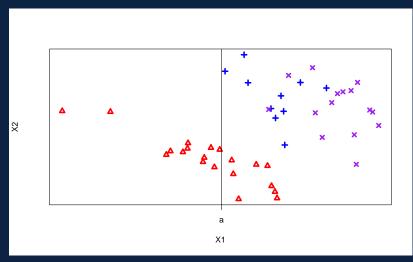


- ▶ Decision trees (or CARTs) partition the predictor space by simple binary splitting rules. Think 'flow chart'.
- ► They have both advantages and disadvantages over other methods…but first, let's motivate their idea.



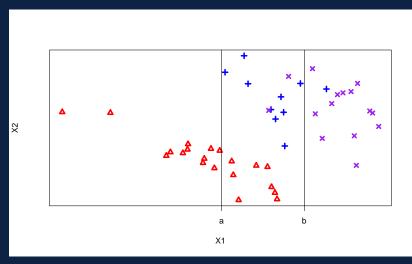




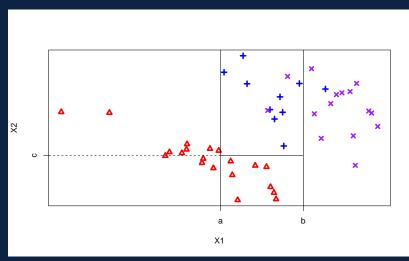


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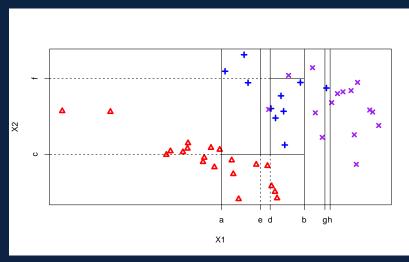




► Are we done with 3 splits?

▶ If no then maybe...



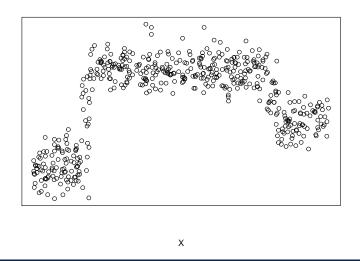


#### Motivation



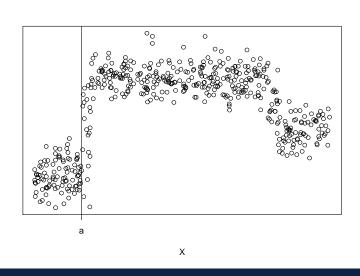
- ▶ So, it appears there are some things we may need to consider going forward in the classification realm.
- ▶ Before diving further into specifics, let's motivate trees for regression through an example.





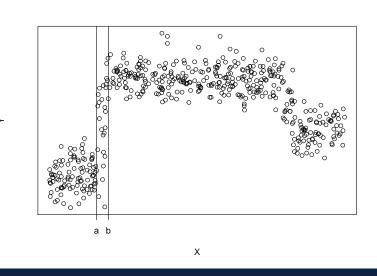
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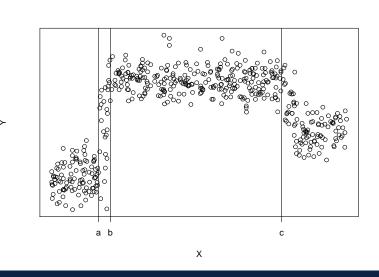
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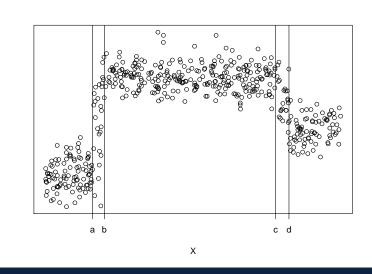
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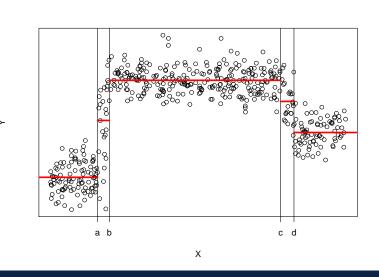
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#### Motivation



- Now that we have regions of relative homogeneity in Y...what would the simplest plan be?
- Average the observations in the region to provide the predicted value...





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### Growing a Tree



#### ► Goals:

- ▶ Divide the predictor space into J non-overlapping regions  $R_1, R_2, \ldots, R_J$ . Using binary splits, these regions are hyper-rectangles.
- ▶ Regression: Predict the mean response for the observations that fall into each region  $R_j$  from the training set.

Classification: Predict the categorical response as the most commonly occurring in each region  $R_j$  from the training set.

### Growing a Tree



- ► How do we 'best' partition the predictor space?
- ► For regression: find binary splits which minimize the RSS

$$\sum_{j=1}^J \sum_{i \in R_j} (y_i - \hat{y}_{R_j})^2$$

► For classification: minimizing the misclassification rate is not usually done at the growth stage. Usually the Gini index, deviance, or cross-entropy is minimized. Most of the time, it won't make a large difference which is chosen. Here's Gini for each node m, where K is the number of response classes...

$$G = \sum_{k=1}^K \hat{p}_{mk} (1-\hat{p}_{mk})$$

## Growing a Tree - Regression



- We run into a common computational hurdle here! We cannot consider all possible hyper-rectangles in our data-set to find the optimal tree...computationally impossible as dimensionality increases.
- ▶ Instead, we can start seek variable *j* and cutpoint *s* such that

$$\sum_{i:x_i \in R_1(j,s)} (y_i - \hat{y}_{R_1})^2 + \sum_{i:x_i \in R_2(j,s)} (y_i - \hat{y}_{R_2})^2$$

▶ Then, via the same process, we subdivide region  $R_1$  into  $R_3$  and  $R_4$ . Then we subdivide  $R_2$  into  $R_5$  and  $R_6$ , etc...until some stopping criteria is met (for example, each region contains a minimum of 3 observations).

#### Problem<sup>1</sup>



- Building a tree through the description just given will tend to heavily overfit the training data.
- ► A common strategy is to grow a large tree, and then prune it back using cross-validation and a cost-complexity tuning parameter.

### Pruning



- ightharpoonup We introduce a non-negative tuning parameter  $\alpha$ .
- ▶ For every value of  $\alpha$  there is a subset (T) of our large tree  $(T_0)$  such that

$$\sum_{m=1}^{|T|} \sum_{i:x_i \in R_m} (y_i - \hat{y}_{R_m})^2 + \alpha |T|$$

is minimized. Where |T| is the number of terminal nodes in the tree.

- ▶ Using k-fold cross validation, we both build trees, and prune them back for possible values of  $\alpha$ . Each tree and subtree built in this fashion will produce an estimate of the MSE.
- Pick the  $\alpha$  that minimizes the predicted MSE using the above cross-validation. Then prune the original tree (built on the full data) with the chosen  $\alpha$ .

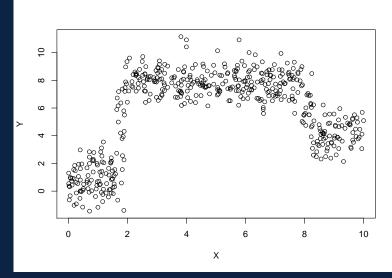
#### Classification Trees



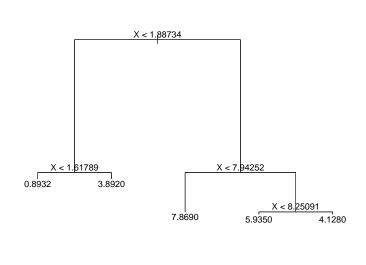
- For classification trees, the process is very much the same.
- ► We use the previously mentioned Gini index for choosing splits (growing the tree), and often use the misclassification rate during the pruning stage (again with cost-complexity tuning parameter).



▶ Back to the motivating example for regression.

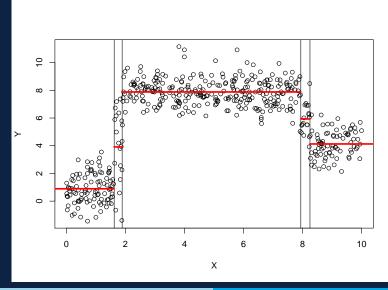


Actual fitting in R gives



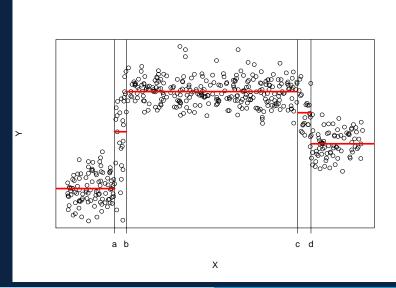
UBC

► Which back to the plot gives



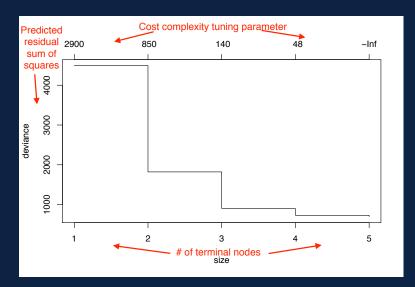


► (Which is very close to what we eyeballed earlier)



UBC

► BUT! We haven't pruned yet

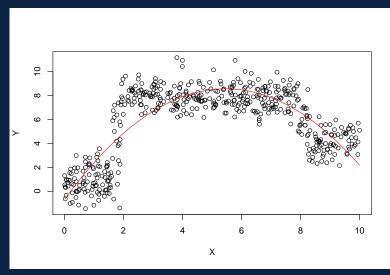




- So it turns out, no pruning needed, according to CV
- Now, how does it compare to (quadratic) linear regression?

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► Training sum squared errors:

► Tree: 590 ► Quad: 1321

CV sum squared errors:

▶ Tree: 699▶ Quad: 1345



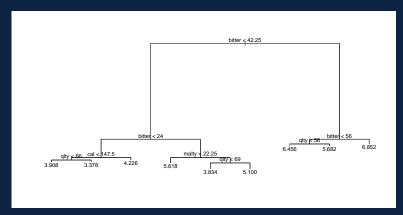
► Let's work with that beer data set again...

```
> head(beer[,-1])
  price qlty cal alc bitter malty
1 6.24 97 159 5.2 52.5 50.5
2 4.79 92 160 5.0 41.5 48.5
3 5.96 90 160 4.9 54.5 48.5
4 4.70 79 162 4.9 37.0 48.0
5 4.11 72 157 5.5 35.5 41.0
6 3.85 66 151 4.9 35.0 24.0
```

▶ Using a standard call, we fit a large tree...



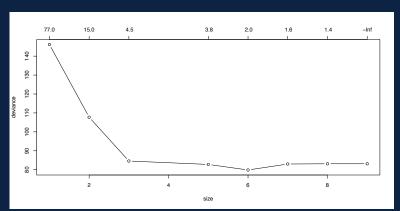
- > library(tree)
- > beert <- tree(price~., data=beerdat)
- > plot(beert)
- > text(beert)





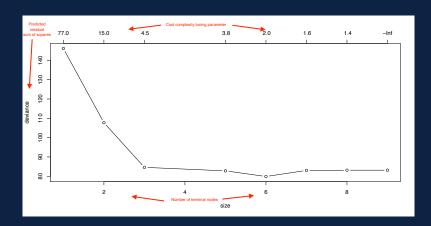
► As previously noted, this is likely heavily overfitting, so...

- > cv.beert <- cv.tree(beert)</pre>
- > plot(cv.beert, type="b")



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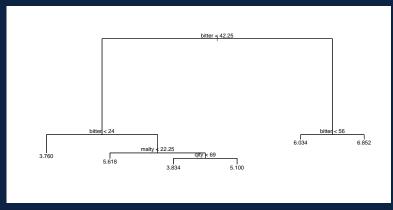




► Time to prune...



- > p.beert <- prune.tree(beert, best=6)</pre>
- > plot(p.beert)
- > text(p.beert)





We can check the RSS, or equivalently (in this case) the deviance, of the model, and compare to the linear model

```
> sum((yhat-beerdat[,1])^2)
[1] 37.22908
> deviance(p.beert)
[1] 37.22908
> beerlm <- lm(price~., data=beerdat)
> sum(residuals(beerlm)^2)
[1] 47.26182
```

► So is the regression tree better?

#### Example: Regression



► Those were training RSS!

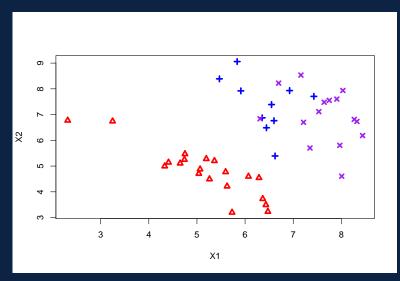
```
> library(DAAG)
> beercv <- cv.lm(data=beerdat, beerlm, m=10)</pre>
> sum((beercv$price-beercv$cvpred)^2) #10CV RSS for lm
[1] 54.6
> min(cv.beert$dev) #10CV RSS for 6 terminal tree
[1] 74.3
```

► So even with relatively simple models we need to be careful!

Lecture 3

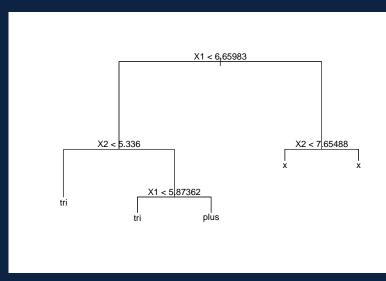


▶ Back to the motivating example for classification.



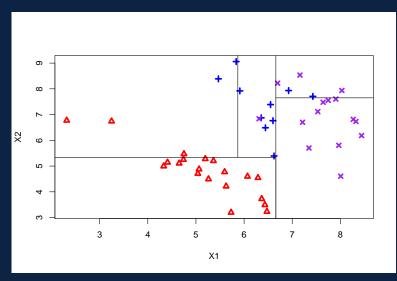


► Under default settings, fitting gives





► Results in the following plot. Concerns?

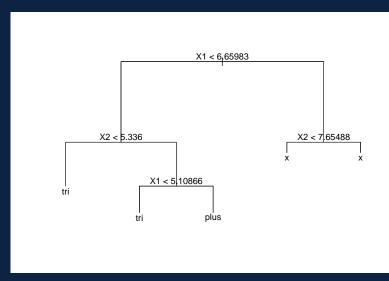




- Default model fitting settings have a minimum of 5 observations in any terminal node.
- ► Change the minimum to 3....and we get

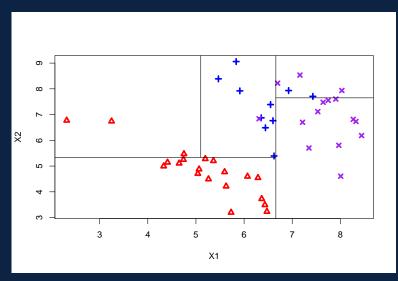


► Under custom settings, fitting gives



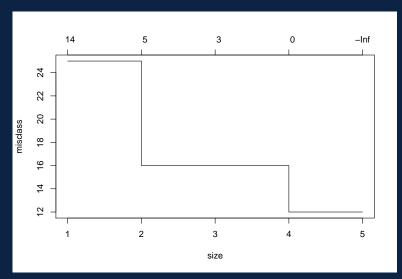


► Results in the following plot.





CV suggests to prune to 4 terminal nodes (for parsimony)



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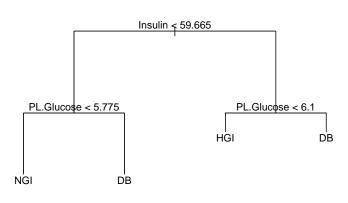
► Misclassification rate: 3/45 = .067

► CV misclassification rate: 12/45 = .267

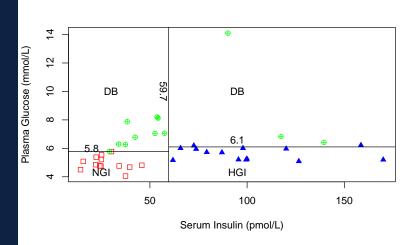


- ► Actual prior consultation I worked on.
- ► Lots of measurements collected on patients with normal glucose levels (NGI), high levels (HGI), and diabetes (DB)
- ▶ I fit a tree to predict the above classifications, and...











- Only 2 misclassifications! Rate 2/39 = 0.0513
- And, I was told, results match fairly closely to current diagnostic procedures.
- Cross validation suggests the full size tree proposed in the previous pictures, though it does predict a higher misclassification rate of 10/39 = 0.256

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#### Discussion



► Pros/cons/discussion on board

