STAT406- Methods of Statistical Learning Lecture 15

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Classification as prediction

 Most classifiers can be thought of as different ways to estimate or model

$$P(G = \mathbf{c}_j | \mathbf{X} = \mathbf{x})$$

 One way to model these probabilities is via Bayes' Thrm:

$$P(G = \mathbf{c}_{j} | \mathbf{X} = \mathbf{x}) =$$
 $\mathbf{f}(\mathbf{x} | \mathbf{c}_{j}) P(G = \mathbf{c}_{j}) / \mathbf{f}(\mathbf{x})$

LDA vs QDA

LDA classifies an observation into the class c_j for which the estimated (under a normality assumption)

$$P(G=c_i|\mathbf{X}=\mathbf{x})$$

is highest.

If $\mathbf{X}|G=c_{j}\sim\mathcal{N}\left(oldsymbol{\mu}_{j},oldsymbol{\Sigma}
ight)$ it means the class for which

$$\delta_i(\mathbf{x}) = \mathbf{x}' \, \mathbf{a}_i + \mathbf{b}_i$$

is highest, where

$$\mathbf{a}_j = \mathbf{\Sigma}^{-1} \, \mu_j$$
 and $\mathbf{b}_j = -\frac{1}{2} \, \mu_j' \mathbf{\Sigma}^{-1} \, \mu_j + \log(p_j)$

QDA

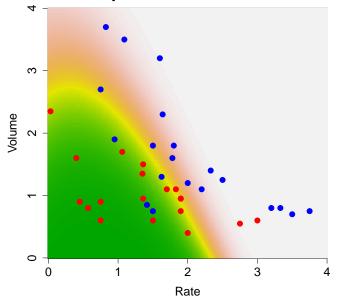
If $\mathbf{X}|G = c_j \sim \mathcal{N}\left(\mu_j, \mathbf{\Sigma}_j\right)$ then, the estimated posterior probabilities look different.

QDA classifies an observation into the class c_i that maximizes

$$\delta_j(\mathbf{x}) = \mathbf{x}' \mathbf{A}_j \mathbf{x} + \mathbf{x}' \mathbf{d}_j + \mathbf{b}_j$$

(see the book for details)

QDA-based probabilities



LDA - QDA - Logistic classifiers

 Multiclass: LDA, QDA and Logistic classifiers extend to the case of more than 2 classes

Examples in R (Zip-code hand-written digits)

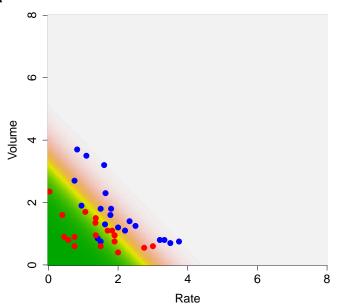
LDA - QDA - Logistic classifiers

 LDA vs QDA: presents the usual "flexibility vs. variability" trade-off

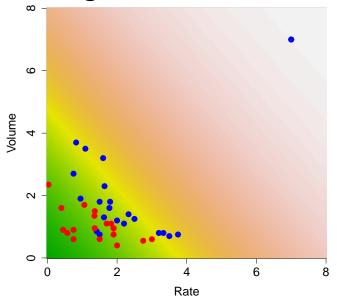
LDA & QDA vs Logistic classifiers:
 Gaussian MLE estimates

 (non-robust, sensitive to the Gaussian assumption) vs. Binomial MLE
 estimates (no distributional assumption of X|G = c_i required).

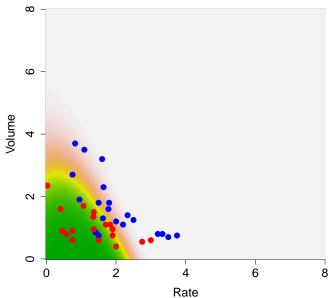
LDA



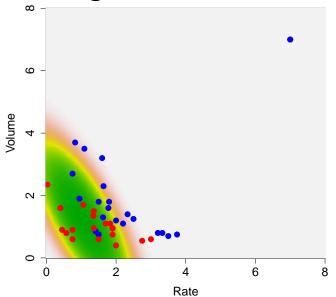
LDA + 2 "good outliers"



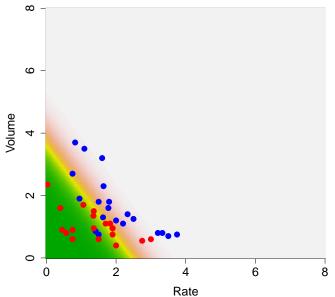
QDA



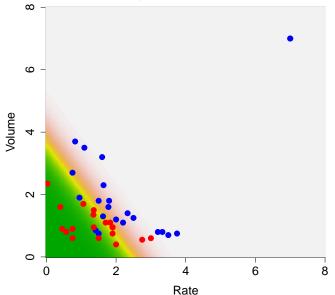
QDA + 2 "good outliers"



Logistic



Logistic + 2 "good outliers"



LDA - QDA - Logistic classifiers

Examples with R

We need to estimate

$$P(G = \mathbf{g} | \mathbf{X} = \mathbf{x})$$

 An intuitive and "model-free" estimator is the nearest-neighbours estimator

- Same spirit as the local-constant (kernel) regression estimator
- The K-NN estimator is

$$\hat{P}(G = \mathbf{g} | \mathbf{X} = \mathbf{x}) = \frac{1}{|N_{\mathbf{x}}^K|} \sum_{j \in N_{\mathbf{x}}^K} \mathbf{I}\left\{Y_j = \mathbf{g}\right\}$$

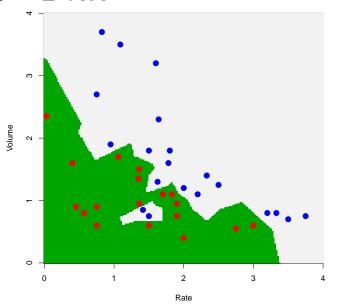
where

$$N_{\mathbf{x}}^{K} = \left\{i : d(\mathbf{X}_{i}, \mathbf{x}) \leq d_{(K)}\right\}$$

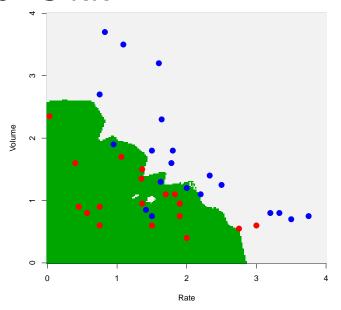
and $d_{(K)}$ is the distance from **x** to the K-th closest point in the sample (**X**_i)

- The K-NN estimator is the proportion of observations from class g among the closest K neighbours
- The K-NN classifier assigns a point to the class most represented among its K neighbours ("peer pressure")

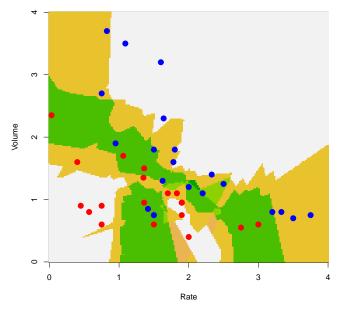
Vaso - 1-NN



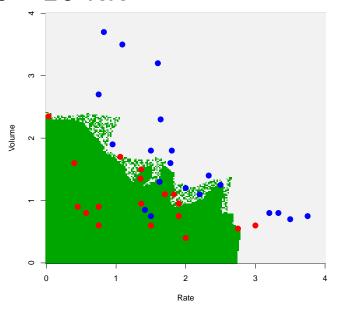
Vaso - 5-NN



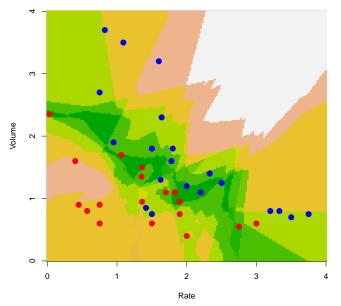
Vaso – 5-NN - votes



Vaso - 10-NN



Vaso - 10-NN - votes



- How can we select the number K of neighbours?
- Zip-code example

 To estimate the probabilities of each class g for a particular value of the feature vector x, nearest neighbours constructs estimates

$$\widehat{P}\left(\mathbf{g} = \mathbf{g} \middle| \mathbf{X} = \mathbf{x}\right)$$
= prop. of objects of class \mathbf{g}
among \mathbf{x} 's neighbours

- Drawback: may not be "local" for moderate number of features (hence, may not represent the distribution of g for X = x
- Yet another incarnation of the "curse of dimensionality"

 If we assume a model for the distribution of the features X for each class

$$f(\mathbf{x}|\mathbf{g}=\mathbf{g}) = f_{\mathbf{g}}(\mathbf{x})$$

then we have a formula for

$$P(\mathbf{g} = \mathbf{g} | \mathbf{X} = \mathbf{x}) = \frac{f_{\mathbf{g}}(\mathbf{x}) P(\mathbf{g} = \mathbf{g})}{\sum_{\mathbf{g}} f_{\mathbf{g}}(\mathbf{x}) P(\mathbf{g} = \mathbf{g})}$$

- We typically have estimates for these probabilities
- Only the numerator is needed
- Drawback: the model may not be correct.
- Model-based inferences are typically more stable than model-free ones
- But they may be biased if the model is a poor approximation to the truth

- Classification trees provide another family of estimates for P(g = g|X = x)
- They do not need a model
- Instead of estimating the local proportion (probability) of each class around a point x, CART's attempt to find regions of the feature space that are "dominated" by one class.

- Classification trees try to identify regions of the domain where one class clearly dominates the others (i.e. where the class proportions are far from being "uniform")
- They search for these regions in a very specific way.

 These regions are searched using a sequential algorithm that at each step partitions the current level ("leaf") into two "leaves" / "children" according to the value of one of the feature variables, for example:

$$X_i \leq \mathbf{a}$$
 versus $X_i > \mathbf{a}$

- At every step, the algorithm searches for the variable X_j and level a that produce the largest increase in "homogeneity" (alternatively: the largest decrease in "heteroscedasticity")
- We need a measure of "homogeneity" (or lack of it)

Some practical considerations in building (spanning) the tree:

- Do not partition nodes / leaves with fewer elements than a fixed threshold (say, 5)
- Do not partition a node if the "gain" in less homogeneity is less than a certain percentage of the current value
- Or both...

Let N denote a "node", that is: a subset of the data.

Let \hat{p}_j , j = 1, ..., K be the proportion of observations of each class in this node

$$\hat{p}_{j} = \frac{\# \text{ of observations of class } j \text{ in node } N}{\text{total } \# \text{ of observations in node } N}$$

Maximum homogeneity when

$$\hat{p}_1 \approx \hat{p}_2 \approx \cdots \approx \hat{p}_K$$

Minimum homogeneity when $\hat{p}_r \approx 1$ for some 1 < r < K

Measures of homogeneity

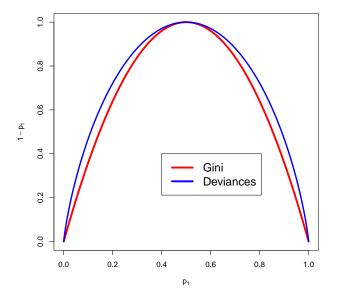
• Gini index:

$$Q_{G}\left(\hat{
ho}_{1},\ldots,\hat{
ho}_{K}
ight) \,=\, \sum_{j
eq i}^{K}\hat{
ho}_{j}\,\hat{
ho}_{i} \,=\, \sum_{j=1}^{K}\,\hat{
ho}_{j}\,\left(1-\hat{
ho}_{j}
ight)$$

• Entropy or deviance:

$$Q_{D}(\hat{p}_{1},\ldots,\hat{p}_{K}) = -2\sum_{i=1}^{K}\hat{p}_{i}\log(\hat{p}_{i})$$

Gini & Deviances - 2 groups



Define the "homogeneity" of a node N as

$$Q(\mathbf{N}) = Q(\hat{p}_1, \dots, \hat{p}_K)$$

where

$$\hat{p}_{j} = \frac{\# \text{ of observations of class } j \text{ in node } N}{\text{total } \# \text{ of observations in node } N}$$

Q could be Q_G or Q_D , for example.

- (a) Start with a node N containing all data points
- (b) Find the variable X_j and value a that minimize

$$\mathbf{n}_L Q \left(\mathbf{X} \in \mathbf{N} : X_j \leq \mathbf{a} \right) + \mathbf{n}_R Q \left(\mathbf{X} \in \mathbf{N} : X_j > \mathbf{a} \right)$$

where $\mathbf{n}_L = \# \{ \mathbf{X} \in \mathbf{N} : X_i \leq \mathbf{a} \}$

- (c) Define the corresponding two "children" of node N
- (d) Apply the same to each "child" / "leaf"

- In practice, we need to weight the homogeneity by the number of observations in each leaf.
- This reflects a probabilistic model for the tree, and represents the probability that a point is observed in this leaf
- In other words: minimize homogeneity more in "larger" (in average) leaves.

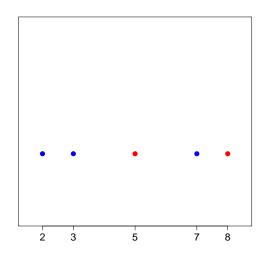
• Let n_c be the size of the node N_c , its homogeneity is

$$n_c Q(\mathbf{N}_c) \propto \frac{n_c}{n} Q(\mathbf{N}_c)$$

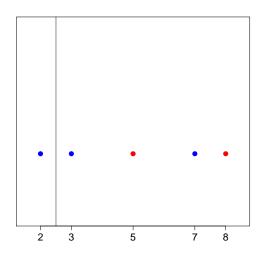
 If we split N_c into N₁ and N₂ the homogeneity is

$$n_1 Q(\mathbf{N}_1) + n_2 Q(\mathbf{N}_2) \propto \frac{n_1}{n} Q(\mathbf{N}_1) + \frac{n_2}{n} Q(\mathbf{N}_2)$$

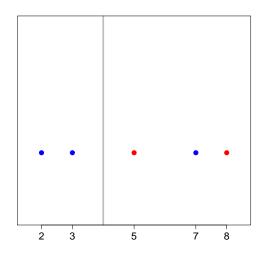
The homogeneity of any split is less than that of the parent node (Breiman, Friedman, Olshen, Stone; 1984).



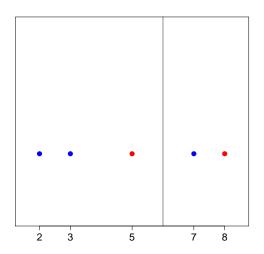
$$(\hat{p}_R = 2/5 \quad \hat{p}_B = 3/5) \quad Q_G = 2.4$$



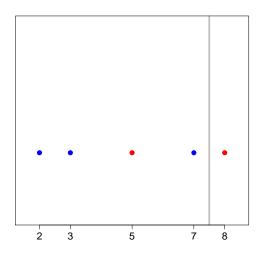
$$(\hat{p}_R = 0 \quad \hat{p}_B = 1) \qquad (\hat{p}_R = 1/2 \quad \hat{p}_B = 1/2) \quad Q_G = 2$$



$$(\hat{p}_R = 0 \quad \hat{p}_B = 1) \qquad (\hat{p}_R = 2/3 \quad \hat{p}_B = 1/3) \quad Q_G = 1.33$$

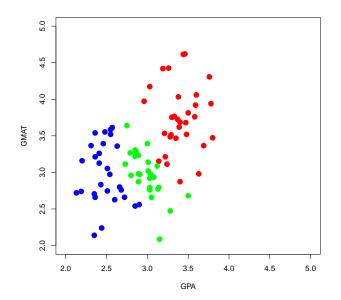


$$(\hat{p}_R = 1/3 \quad \hat{p}_B = 2/3) \quad (\hat{p}_R = 1/2 \quad \hat{p}_B = 1/2) \quad Q_G = 2.33$$

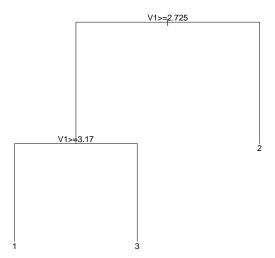


$$(\hat{p}_R = 1/4 \quad \hat{p}_B = 3/4) \qquad (\hat{p}_R = 1 \quad \hat{p}_B = 0) \quad Q_G = 1.5$$

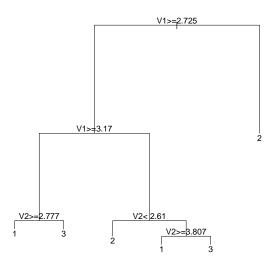
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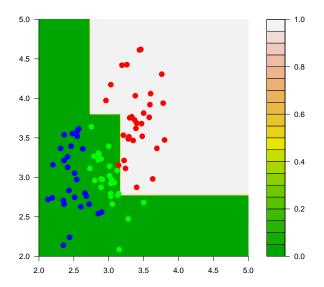


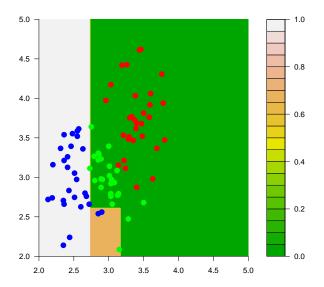
Grad admissions - Gini tree

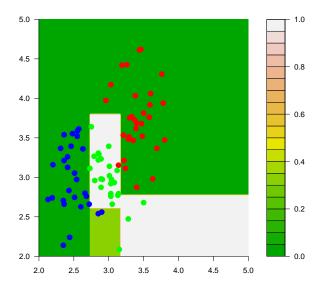


Grad admissions - Deviance tree









- ISOLET data http://archive.ics.uci.edu/ml/datasets/ISOLET
- 150 subjects spoke the name of each letter twice
- 52 samples from each subject, 300 samples for each letter

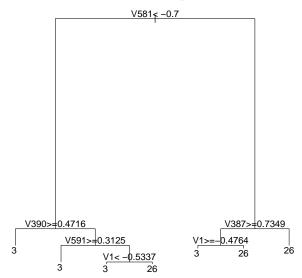
- 617 features (explanatory variables).
 They include: spectral coefficients;
 contour features, sonorant features,
 pre-sonorant features, and
 post-sonorant features.
- Data are split into training (n = 6238) and test (n = 1559)
- Mission: build a classifier to identify future spoken letters

• I separated the letters C and Z

```
> x <- read.table('isolet-train.data', sep=',')
> # 3 and 26 --- "C" and "Z"
>
> xa <- x[ x$V618 == 3, ]
> xb <- x[ x$V618 == 26, ]
>
> xx <- rbind(xa, xb)
> xx$V618 <- as.factor(xx$V618)</pre>
```

Fit a classification tree

```
> myc <- rpart.control(minsplit=7, cp=1e-7,
            xval=10)
>
>
> set.seed(123)
> a.t <- rpart(V618~., data=xx,
      parms = list(split = 'information'),
      control=myc)
> b <- a.t$cptable[</pre>
      which.min(a.t$cptable[,"xerror"]),"CP"]
> d.r <- prune(a.t, cp=b)</pre>
```



Predict on the test data

And we only used 5 explanatory variables!

- The problem is not trivial
- Let's try a 1-NN nearest neighbour classifier

With 5-NN is not much better

```
> u5 <- knn(train=xx[,-618],
          test=dd[,-618], cl=xx[,618],
          k = 5)
>
> table(truth, u5)
          u5
truth  3 26
        3 58 2
        26 5 55
```

With a logistic classifier

```
> xx$V619 \leftarrow as.numeric(xx$V618==3)
> d.glm <- glm(V619 \sim . - V618, data=xx,
      family=binomial)
Warning message:
glm.fit: algorithm did not converge
[...]
> table(truth, pr.qlm)
     pr.qlm
truth 0 1
   3 25 35
   26 33 27
```

• Can we explain the problem?

 How about the approach based on the Gaussian distribution of the features (within each class)?

```
> library(MASS)
>
> d.lda <- lda(V618 ~ ., data=xx)
Warning message:
In lda.default(x, grouping, ...) :
    variables are collinear</pre>
```

Can we explain the problem?