MAST 90138: MULTIVARIATE STATISTICAL TECHNIQUES

See Hastie and Tibshirani, chapters 2, 4. Clusifier Spiriter

7 LINEAR AND QUADRATIC CLASSIFICATION

7.1 Introduction to classification

- ullet In the classification problem, we know that individuals from the population come from several, K say, different classes/groups
- ightharpoonup Example when K=2: healthy patients, unhealthy patients.
- We have at our disposal a training sample of individuals from the population for which we observe $(\mathbf{X}_1, G_1), \dots, (\mathbf{X}_n, G_n)$, where
 - $G_i = 1, 2, ...$ or K is the class/group label of the ith individual (an individual belong to exactly one group).
 - $\mathbf{X}_i = (X_{i1}, \dots, X_{ip})^T$ is vector of explanatory variables (e.g. age, blood pressure, etc).

trainin

- A new individual from the same population comes in. that I given to sury.
- For that individual we only observe the value $\mathbf{x} = (x_1, \dots, x_p)^T$ of \mathbf{X} but we do not know which group the individual comes from (we don't observe his/her G).
- **◆** Goal: classify the new individual in the correct group, i.e. find the group of that individual. Equivalently, find the class label $G \in \{1, ..., K\}$ of that new individual.
- How can we do that?

Notation: throughout chapter we use the notation (\mathbf{X}, G) for a generic individual from the population. The training data $(\mathbf{X}_1, G_1), \dots, (\mathbf{X}_n, G_n)$ have the same distribution as a generic (\mathbf{X}, G) , and so do observed or unobserved data from new individuals.

7.2 Main ideas of classification techniques

- Main idea: compare the new value x with the X_i 's from the training individuals.
- If x looks more similar to X_i 's from group k than those from the other groups, classify new indiv in group k.
- How to decide if x is more similar to the X_i 's from group k than from other groups?
- For $k=1,\ldots,K$, use training data $(\mathbf{X}_1,G_1),\ldots,(\mathbf{X}_n,G_n)$ to estimate $P(G=k|\mathbf{X}=\mathbf{x})$, and G

the probability that an individual comes from group k given that his/her X is equal to \mathbf{x} , by

$$\hat{P}(G=k|\mathbf{X}=\mathbf{x}).$$

(We will see later how to compute the estimated probabilities).

ightharpoonup Then, classify new individual in group k if

$$\hat{P}(G=k|\mathbf{X}=\mathbf{x})>\max_{j=1,\dots,K,j\neq k}\hat{P}(G=j|\mathbf{X}=\mathbf{x}).$$

Many different methods of classification exist. They essentially correspond to various ways of estimating the above probabilities.

不同分类系统:标学计算代不同。

- Two important classes of methods are based on regression estimation techniques and on so-called Bayes methods.
- We start by introducing methods in the case where we have only K=2 classes. We will see later how to extend them to K>2 classes.

SIMPLE REGRESSION APPROACHES FOR K = 2 CLASSES

 \blacksquare Suppose the individuals come from only K = 2 groups. Then we classify a new individual in group 1 if (始 推動情報)

$$\hat{P}(G=1|\mathbf{X}=\mathbf{x})>\hat{P}(G=2|\mathbf{X}=\mathbf{x})$$
,
 文章 形成
 2 , $\hat{P}(G=k|\mathbf{X}=\mathbf{x})$ is an estimator of $P(G=k|\mathbf{X}=\mathbf{x})$

where, for k = 1, 2, $\hat{P}(G = k | \mathbf{X} = \mathbf{x})$ is an estimator of $P(G = k | \mathbf{X} = \mathbf{x})$ computed from the training sample $(\mathbf{X}_1, G_1), \dots, (\mathbf{X}_n, G_n)$.

- One way to obtain $\hat{P}(G = k | \mathbf{X} = \mathbf{x})$ is through regression. express these the groups into 2 regression curves
- ightharpoonup To see how, for k = 1, 2 define a variable from a generic G by taking

To see flow, for
$$k = 1, 2$$
 define a variable from a generic G by taking G indicator variable.
$$Y_k = I\{G = k\} = \begin{cases} 1 & \text{if } G = k \\ 0 & \text{otherwise.} \end{cases}$$

$$Indicator \text{ which of the wise of the range of the r$$

$$\frac{\text{Gindicator}}{Y_{ik} = I\{G_i = k\}}. \text{ Clahel of ith individual is the }$$

$$\frac{Y_{ik} = I\{G_i = k\}}{Z^{20}}. \text{ Clahel of Kth class}.$$

Aurore Delaigle's lecture notes, MAST 90138, 2023

 \blacksquare Ex: suppose we observe a training sample of size n=7 where the G_i 's are

$$(G_1,\ldots,G_7)=(1,1,1,2,2,2,1).$$
 Then, for $i=1,\ldots,n$ and $k=1,2$, the Y_{ik} 's are given by:

$$(Y_{11}, \dots, Y_{71}) = (1, 1, 1, 0, 0, 0, 1)$$

 $(Y_{12}, \dots, Y_{72}) = (0, 0, 0, 1, 1, 1, 0)$

Note that

$$(Y_{12},\ldots,Y_{72})=(0,0,0,1,1,1,0).$$
 and
$$Y_{1}=\{(x,y)=\{0,0,0,1,1,1,0\}\}.$$
 The proof of the proo

$$P(G = k | \mathbf{X} = \mathbf{x}) = E(I\{G = k\} | \mathbf{X} = \mathbf{x}) = m_k(\mathbf{x}),$$

if we define the regression curve

$$= \mathbf{x}) = E(I\{G = k\} | \mathbf{X} = \mathbf{x}) = m_k(\mathbf{x}),$$

$$= |\mathbf{X} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}) + p \mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}) = m_k(\mathbf{x}),$$
sion curve
$$m_k(\mathbf{x}) = E(Y_k | \mathbf{X} = \mathbf{x}).$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

$$= |\mathbf{x} P G + \mathbf{x}| \mathbf{x} = \mathbf{x}$$

Can use regression estimation techniques to estimate m_k from training data $(\mathbf{X}_1, Y_{1k}), \dots, (\mathbf{X}_n, Y_{nk})$ $(Y_{ik}$'s observed as computed from G_i 's).

1.11

Now every individual must belong to one of the two groups, so that for all $\mathbf{x} \in \mathbb{R}^p$

$$P(G = 1|\mathbf{X} = \mathbf{x}) + P(G = 2|\mathbf{X} = \mathbf{x}) = 1,$$

that is

$$m_2(\mathbf{x}) = 1 - m_1(\mathbf{x}).$$

Thus we only need to estimate m_1 (we can deduce m_2 from it).

Discrimination/classification boundary

• Once we have estimated m_1 and $m_2 = 1 - m_1$ by estimators \hat{m}_1 and $\hat{m}_2 = 1 - \hat{m}_1$, the classification boundary is the boundary between the region where we classify the data in group 1 and the region where we classify the data in group 2. It is obtained by solving the equation

$$\widehat{m}_1(\mathbf{x}) - \widehat{m}_2(\mathbf{x}) = 0$$

which, is equivalent to

$$\widehat{m}_1(\mathbf{x}) = 1/2$$
.

Classify in group 1 if $\widehat{m}_1(\mathbf{x}) > \widehat{m}_2(\mathbf{x}) \iff \widehat{m}_1(\mathbf{x}) > 1/2$, otherwise classify in group 2.

7.3.1 LINEAR REGRESSION CLASSIFIER

When we use a linear regression classifier, we assume

Regression
$$m_1(\mathbf{x}) = E(Y_1|\mathbf{X}=\mathbf{x}) = P(G=1|\mathbf{X}=\mathbf{x}) = \beta_0 + \beta^T\mathbf{x}$$
. The probability to be in a class can be mod elled by the finear regression Estimate m_1 using least squares (LS) estimator of β_0 and β (or PCA).

Estimate m_1 using least squares (LS) estimator of β_0 and β (or PCA or PLS estimators if we need to reduce dimension, see page 260 for how to compute CV in classification) to find

$$\hat{m}_1(\mathbf{x}) = \hat{\beta}_0 + \hat{\beta}^T \mathbf{x} .$$

- Deduce $\hat{m}_2 = 1 \hat{m}_1 = 1 \hat{\beta}_0 \hat{\beta}^T \mathbf{x}$.
- Classify new \mathbf{x} in group 1 if based on the assumption that a reasonable $\hat{m}_1(\mathbf{x}) > \hat{m}_2(\mathbf{x}) \iff \hat{\beta}_0 + \hat{\beta}^T \mathbf{x} > 1 \hat{\beta}_0 \hat{\beta}^T \mathbf{x} \iff \hat{\beta}_0 + \hat{\beta}^T \mathbf{x} > 1/2$;

otherwise classify x in group 2.

NOTE: this method relies on the validity of the linear regression model and is usually only an approximation in real life.

Example: Golub data (ESL, Section 18.4).

Golub TR et al. (1999), Molecular Classification of cancer: class Discovery and Class Prediction by gene expression monitoring, Science 286:531-7.

- Two categories of patients, corresponding to two types of leukemia ("ALL" and "AML").
- $\mathbf{X} = (X_1, X_2)^T$: gene expressions for two genes known to be connected to leukemia type.
- If we fit two linear models $m_1(\mathbf{x}) = \beta_0 + \beta^T \mathbf{x}$ and $m_2(\mathbf{x}) = \beta_{0,2} + \beta_2^T \mathbf{x}$ by LS, we find

$$\widehat{m}_1(\mathbf{x}) = 0.9231 + 0.2454x_1 - 0.4800x_2$$

 $\widehat{m}_2(\mathbf{x}) = 0.07691 - 0.24542x_1 + 0.47999x_2 \approx 1 - \widehat{m}_1(\mathbf{x})$

as expected (the \approx is due to numerical errors). Illustrates we don't need to fit m_2 , just take $\hat{m}_2 = 1 - \hat{m}_1$

For the Golub data, classification boundary obtained by solving

$$\widehat{m}_{1}(\mathbf{x}) = 1/2 \text{ is}$$

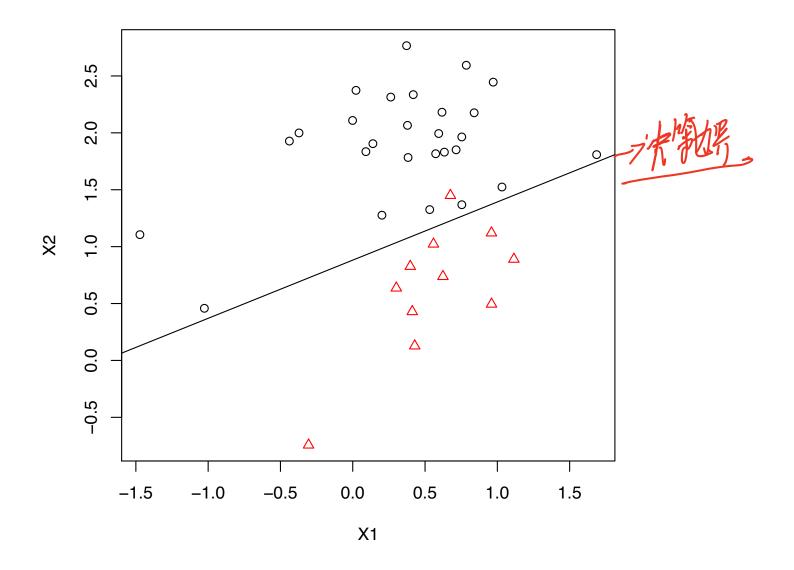
 Decision (0.9231 + 0.2454 x_{1} - 0.4800 x_{2} = 1/2.)

This can be expressed by the line

$$\begin{array}{ll} \text{Plustimel} & x_2 = \frac{0.9231 - 0.5}{0.4800} + \frac{0.2454}{0.4800} x_1 = 0.8815 + 0.5113 x_1 \, . \\ \text{line:} & \text{X2.5} \end{array}$$

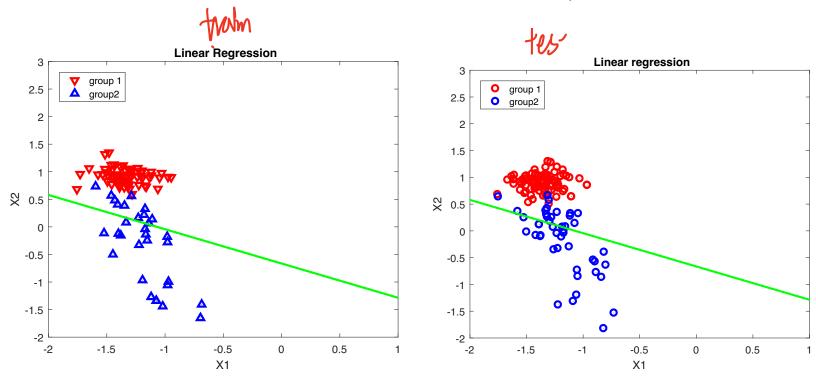
On one side of the line we classify in one class, on the other side we classify in the other class.

Discrimination boundary shown by the line. Training X_i 's from two groups displayed in different colours/symbols. New observations falling below line will be classified in red group; others will be classified in black group.



Other example

- ightharpoonup Left: training X_i 's, different groups shown by blue/red.
- Right: set of new data to be classified
- Green line shows decision boundary $\hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 = 1/2$ constructed from training \mathbf{X}_i 's.
- Data classified in group 2 if below line, in group 1 if above line (classifier makes mistakes: some blues are above line).



Aurore Delaigle's lecture notes, MAST 90138, 2023

A problem with the linear regression classifier is that $\hat{\beta}_0 + \hat{\beta}^T \mathbf{x}$, our estimator of $m_1(\mathbf{x}) = P(G = 1 | \mathbf{X} = \mathbf{x})$, is not guaranteed to be between 0 and 1, whereas it estimates a probability.

一维放松维地的热起, 直到一个一个

 $lue{}$ One way to ensure to be in [0,1] is use logistic regression, i.e. assume

$$(m_1(\mathbf{x}) = P(G = 1 | \mathbf{X} = \mathbf{x}) = E(Y_1 | \mathbf{X} = \mathbf{x}) = \frac{\exp(\beta_0 + \beta^T \mathbf{x})}{1 + \exp(\beta_0 + \beta^T \mathbf{x})}.$$

• Estimate β_0 , β using maximum likelihood (ML) estimators $\hat{\beta}_0$, $\hat{\beta}$ computed from the training data

$$(\mathbf{X}_1, Y_{11}), \ldots, (\mathbf{X}_n, Y_{n1}).$$

(or replace the data by their PCA or PLS components if needed, see page 260 for how to compute CV in classification).

NOTE: here too, the method relies on the logistic model assumption which is usually only an approximation in real life.

 \blacksquare As noted at slide 234, $m_2 = 1 - m_1$, i.e. in this model:

$$m_1(\mathbf{x}) = P(G = 1 | \mathbf{X} = \mathbf{x}) = \frac{\exp(\beta_0 + \beta^T \mathbf{x})}{1 + \exp(\beta_0 + \beta^T \mathbf{x})}$$

$$m_2(\mathbf{x}) = P(G = 2 | \mathbf{X} = \mathbf{x}) = 1 - m_1(\mathbf{x}) = \frac{1}{1 + \exp(\beta_0 + \beta^T \mathbf{x})}.$$

Classify new x in group 1 if

$$\hat{P}(G = 1 | \mathbf{X} = \mathbf{x}) > \hat{P}(G = 2 | \mathbf{X} = \mathbf{x})$$

$$\iff \exp(\hat{\beta}_0 + \hat{\beta}^T \mathbf{x}) > 1 \iff \hat{\beta}_0 + \hat{\beta}^T \mathbf{x} > 0$$
in Grear classification: $\hat{\beta}_0 + \hat{\beta}_0 + \hat{\beta}_$

and otherwise classify x in group 2.

As before, the classification boundary is obtained by solving

$$\widehat{m}_1(\mathbf{x}) = 1/2 \iff \exp(\widehat{\beta}_0 + \widehat{\beta}^T \mathbf{x}) = 1 \iff \widehat{\beta}_0 + \widehat{\beta}^T \mathbf{x} = 0.$$

Classify in group 1 if
$$\widehat{m}_1(\mathbf{x}) > \widehat{m}_2(\mathbf{x}) \iff \widehat{m}_1(\mathbf{x}) > 1/2 \iff \widehat{\beta}_0 + \widehat{\beta}_1^T \mathbf{x} > 0$$
, otherwise classify in group 2.

Example: Golub data

- Two categories of patients, corresponding to two types of leukemia ("ALL" and "AML"); $\mathbf{X} = (X_1, X_2)^T$: expressions of two genes.
- From the estimated logistic model we have

$$\widehat{m}_1(\mathbf{x}) = \frac{\exp(0.9432 + 0.5487x_1 - 10.714x_2)}{1 + \exp(0.9432 + 0.5487x_1 - 10.714x_2)}.$$

In this example the classification boundary is obtained by solving

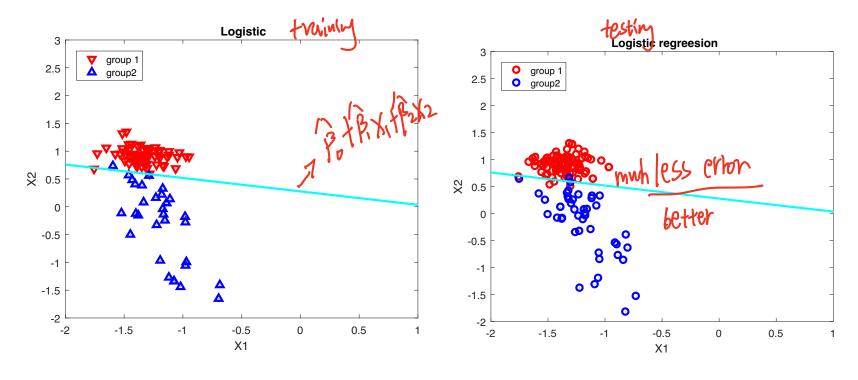
$$0.9432 + 0.5487x_1 - 10.714x_2 = 0,$$

which we can express by the line

$$x_2 = \frac{0.9432}{10.714} + \frac{0.5487}{10.714}x_1 = 0.08803435 + 0.05121337x_1$$

Other example (same as page 239)

- ightharpoonup Left: training X_i 's, different groups shown by blue/red.
- Right: set of new data to be classified
- Cyan line shows decision boundary $\hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 = 0$ constructed from training \mathbf{X}_i 's.
- Data classified in group 2 if below line, in group 1 if above line (classifier makes mistakes: some blues are above line).



Comparison linear and logistic regression

