

# 106-1 生物統計學二 實習課

**R : ROC curve**

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# 大綱

- ROC curve
  - Fit logistic model & calculate  $\hat{p}_X$
  - Scatter plot & classification boundary
  - Calculate sensitivities & specificities
  - Plot ROC curve
    - Calculate AUC
    - Find optimal cut point
  - Calculate misclassification rate
  - Histogram

# ROC curve

Fit logistic model & calculate  $\hat{p}_X$

Scatter plot & classification boundary

Calculate sensitivities & specificities

Plot ROC curve

Calculate misclassification rate

Histogram

# Logistic model & $\hat{p}_X$

- Fit logistic model & calculate  $\hat{p}_X = \frac{e^{\hat{\beta}_0 + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2}}{1 + e^{\hat{\beta}_0 + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2}}$

- ✓ `model <- glm( Y ~ X1 + X2 , family = binomial , data = 資料檔名稱 )`
- ✓ 利用 `predict` 指令: `predict(model, type="response")`

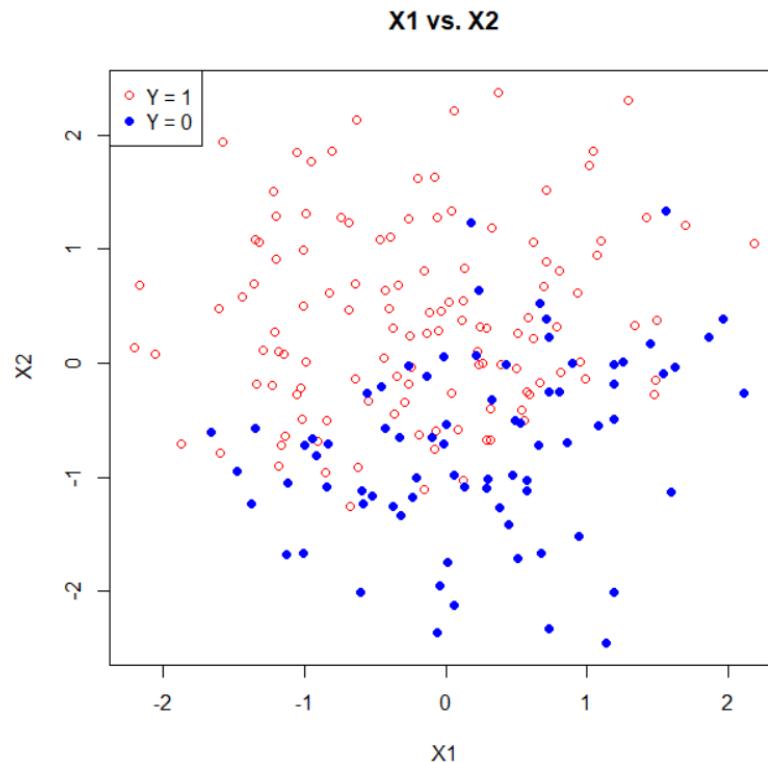
```
> model.1 <- glm(Y~ X1+X2, family = binomial, data = data_hw6 )
> pred.value <- predict(model.1, type="response")
```

也可以利用公式計算  $\hat{p}_X$ :  $\exp(\dots)/(1+\exp(\dots))$

# Scatter plot

- Plot the data points  $(X_1, X_2)$  with different symbols for  $Y = 0$  and  $Y = 1$ .

```
> plot(X1, X2, pch = 1, main="X1 vs. X2")
> points(X1[Y==1],X2[Y==1], col="red", pch=1)
> points(X1[Y==0],X2[Y==0], col="blue", pch=16)
> legend("topleft", c("Y = 1", "Y = 0"), col=c("red", "blue"), pch=c(1, 16))
```

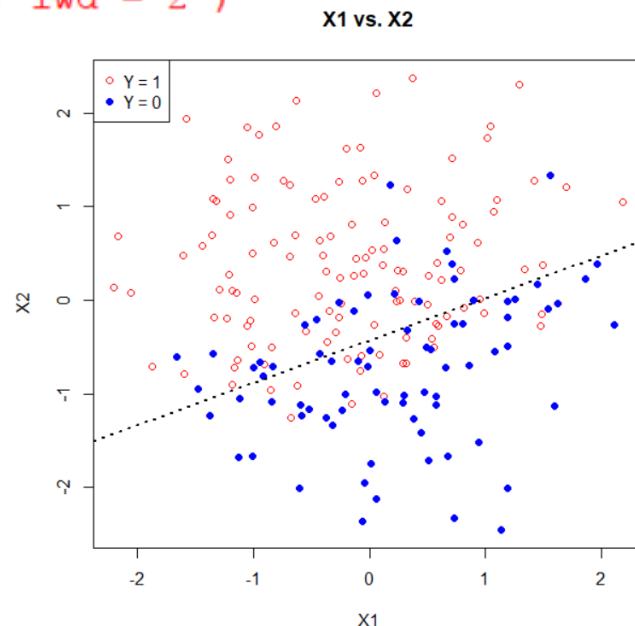


# Classification boundary

- Add classification boundary on scatter plot with prediction rule  $\{\hat{p}_X > 0.5\}$

$$\ln \left\{ \frac{\hat{p}_X}{1-\hat{p}_X} \right\} = \ln \left\{ \frac{0.5}{1-0.5} \right\} = 0 = \hat{\beta}_0 + \hat{\beta}_1 X_1 + \hat{\beta}_2 X_2 \implies X_2 = -\frac{\hat{\beta}_0}{\hat{\beta}_2} - \frac{\hat{\beta}_1}{\hat{\beta}_2} X_1$$

```
> b.coef <- model.1$coefficients  
> intercept.cb <- -b.coef[1]/b.coef[3]  
> slope.cb <- -b.coef[2]/b.coef[3]  
>  
> abline(intercept.cb, slope.cb, lty = 3, lwd = 2 )
```



# Sensitivities & Specificities

- Calculate sensitivity & specificity
- Prediction rule  $\{\hat{p}_X > c\}$ :

分子:  $Y = 1$ 的那一類中， $\hat{p}_X$ 大於  $c$  的個數  
分母:  $Y = 1$  的個數

$$se(c) = P(\hat{p}_X > c | Y = 1) = \frac{\text{number of } (\hat{p}_X > c \text{ and } Y=1)}{\text{number of } (Y=1)}$$

$$sp(c) = P(\hat{p}_X < c | Y = 0) = \frac{\text{number of } (\hat{p}_X < c \text{ and } Y=0)}{\text{number of } (Y=0)}$$

→ 紿定一個  $c$ ，就得到一個  $se(c)$  和一個  $sp(c)$

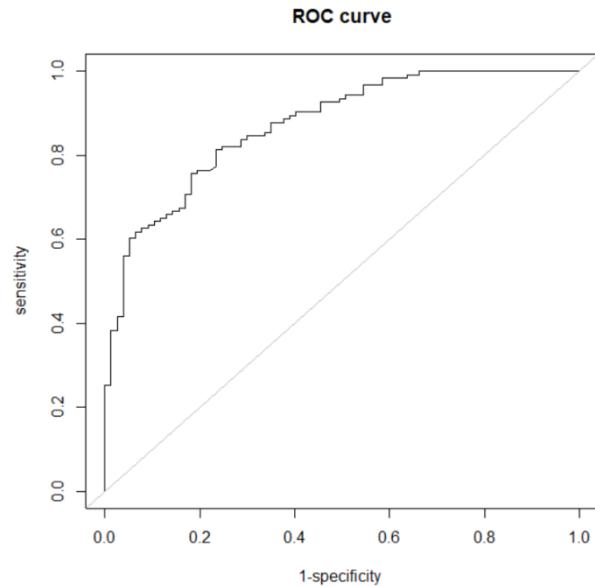
```
> se.1 <- c() ] 定義物件空間
> sp.1 <- c()
> c.seq <- seq(0, 1, 0.0001)
>
> for(ii in 1:length(c.seq)){
+
+ se.1[ii] <- sum( pred.value[Y==1] > c.seq[ii] ) / sum(Y==1)
+ sp.1[ii] <- sum( pred.value[Y==0] < c.seq[ii] ) / sum(Y==0)
+
+ }
```

# ROC curve

- Plot ROC curve

```
> plot(1-sp.1, se.1, xlim = c(0,1), ylim = c(0,1), type="l",
+       main = "ROC curve", xlab = "1-specificity ", ylab = "sensitivity" )
>
> abline(0,1, col = "grey")
```

加上最沒有預測能力的ROC curve (45度線)  
✓ `abline`(截距, 斜率)

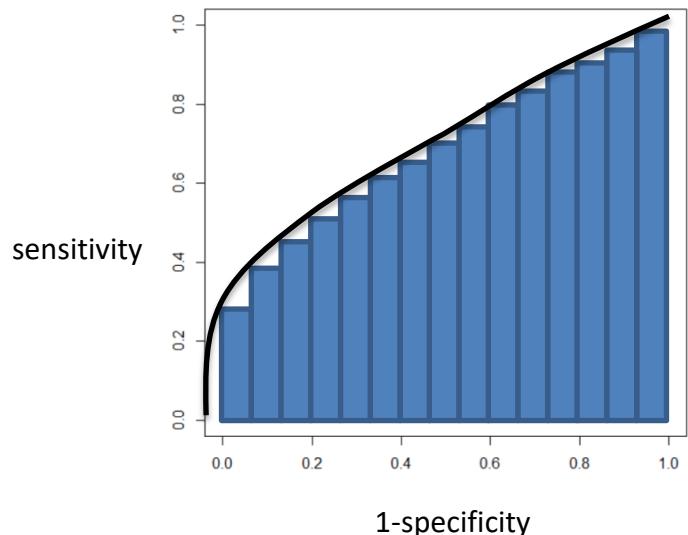


# AUC

- Calculate AUC

→ 計算曲線下面積

概念：計算每個長方形的面積後加總



```
> auc.value <- c()  
> for(ii in 1:length(c.seq)-1){  
+  
+ height.auc <- se.1[ii+1]  
+ width.auc <- abs((1-sp.1[ii]) - (1-sp.1[ii+1]))  
+  
+ auc.value[ii] <- height.auc*width.auc  
+  
+}  
>  
> sum(auc.value)
```

計算每個長方形的面積

將每個長方形的面積加總

# Optimal cut point

- Find the optimal cut point  $c^*$

Youden index :  $\max\{se(c) + sp(c)\}$

optimal ←

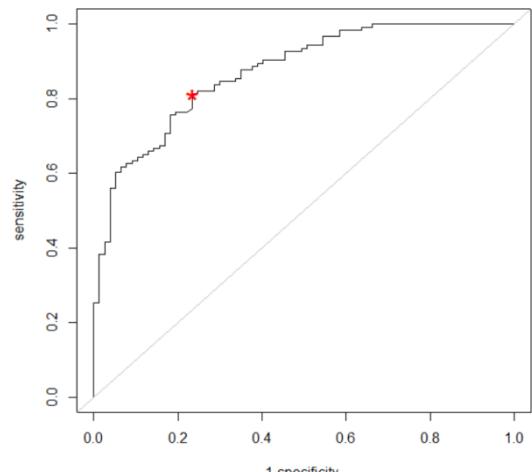
$c$	specificity	sensitivity
$c_1$	$sp(c_1)$	$se(c_1)$
:	:	:
$c^*$	$sp(c^*)$	$se(c^*)$
:	:	:
$c_k$	$sp(c_k)$	$se(c_k)$

```
> youden.index <- max(se.1 + sp.1)
> optimal.cutpoint <- which.max(se.1 + sp.1)
> c.seq[optimal.cutpoint]
```

找出  $c^*$

找出  $c^*$  的位置

ROC curve



- Add  $(1 - sp(c^*), se(c^*))$  on ROC curve

```
> se.opt <- se.1[optimal.cutpoint]
> sp.opt <- sp.1[optimal.cutpoint]
>
> points(1-sp.opt, se.opt, pch = "*", cex = 2.5, col = "red")
```

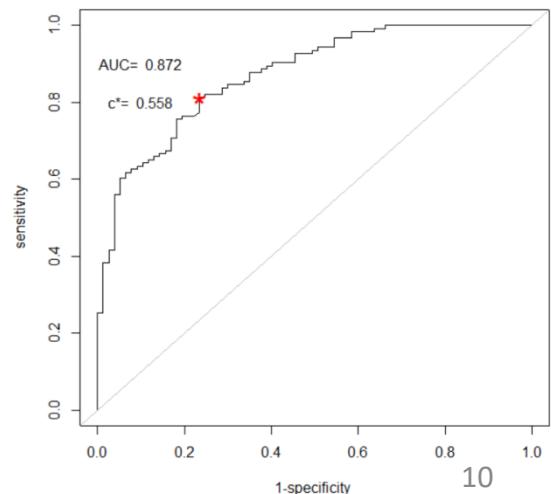
- Add text on ROC curve

```
> text(0.1, 0.9, paste("AUC= ", round(sum(auc.value), 3) ))
> text(0.1, 0.8, paste("c*= ", c.seq[optimal.cutpoint] ))
```

在圖上加AUC和 $c^*$ 的數值

- ✓ `paste(...)`: 串聯字串和計算數值
- ✓ `round(..., 3)`: 計算到小數第三位

ROC curve



# Misclassification rate

- Calculate misclassification rate

$$MR_{(c)} = \frac{\text{number of } (Y_i \neq \hat{Y}_i)}{n}$$

```
> se.05 <- sum( pred.value[Y==1] > 0.5 ) / sum(Y==1)
> sp.05 <- sum( pred.value[Y==0] < 0.5 ) / sum(Y==0)
> mis.rate.05 <- ( (1-se.05)*sum(Y==1) + (1-sp.05)*sum(Y==0) ) / length(Y)
> 計算  $MR_{(0.5)}$ 
>
> mis.rate.youden <- ( (1-se.opt)*sum(Y==1) + (1-sp.opt)*sum(Y==0) ) / length(Y)
> 計算  $MR_{(c^*)}$ 
```

# Histogram

- Prediction rule  $\{f(X_1) > c\}$  with  $f(X_1) = \frac{e^{X_1}}{1+e^{X_1}}$ :

利用 plogis 計算  $\frac{e^{X_1}}{1+e^{X_1}}$

```
> pred.value8 <- plogis( X1 )
```

在長方形中以密度為 15，  
畫 45 度的斜線

```
> hist(pred.value8[Y==1], xlim=c(0,1), main="histogram of f(X1)",  
+        xlab="f(X1)", ylab="frequency", col="red", density= 15, angle= 45)  
> hist(pred.value8[Y==0], add=T, col="blue", density= 15, angle= 135)  
> abline(v=0.5, col="black", lwd=2)  
> legend( "topright", c("Y = 1", "Y = 0"), col=c("red", "blue"), lty=1 )
```

