

An example of R for ROC curve

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Source: Documentation for package of R `ROCR`

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安裝程式 R

選擇 <http://cran.r-project.org/> → R Binaries → Windows → bases

→ R-2.2.0-win32.exe (約 25.9 MB),

安裝至選擇元件時 記得 PDF Reference Manual 打勾

安裝 ROCR 套件

安裝完成後 執行 R: 程式集 → R → R 2.2.2

因 ROC curve 之功能包含於 ROCR 套件中,所以準備下載套件:

程式套件 → 安裝程式套件... → CRAN mirror 選單

Taiwan (Taipeh) → 確定 → 選擇 ROCR → 確定

此時 C:\Program Files\R\R-2.2.0\library 會新增 ROCR 資料夾

查詢 ROCR 功能

輔助 → Html 輔助

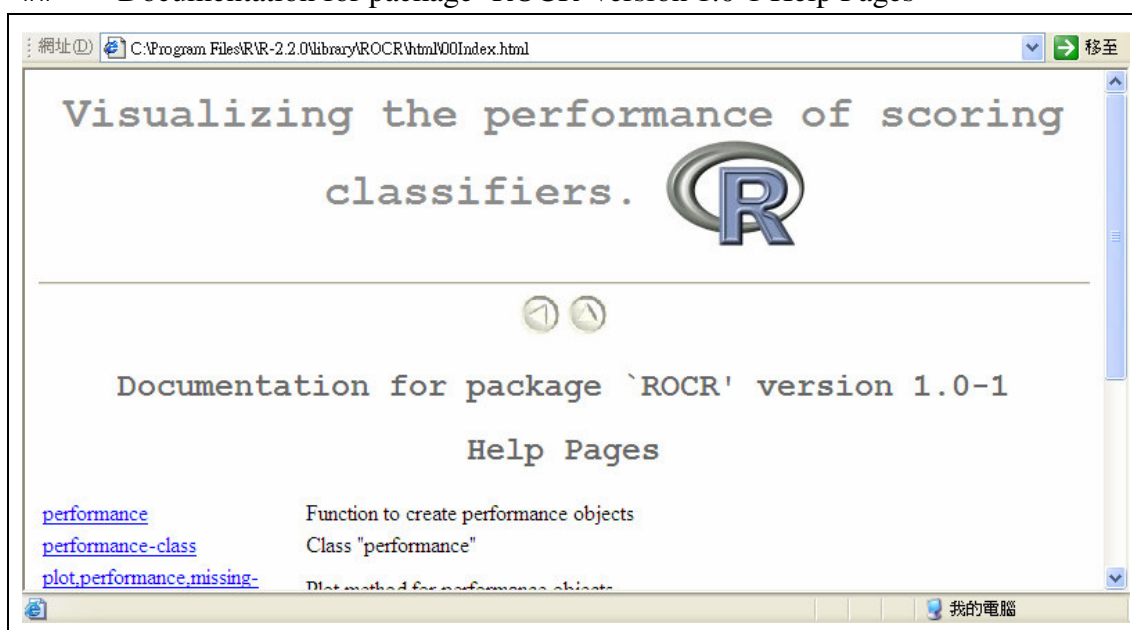
→ 按 packages

→ Package Index 畫面(此畫面表示已下## 載的套件

→ 按 ROCR

→ 顯示 Visualizing the performance of scoring classifiers

Documentation for package `ROCR' version 1.0-1 Help Pages



檢視所有資料集

```
data # 顯示載入套件的資料集
```

```
data(package = .packages(all.available = TRUE)) #顯示所有資料集(含未載入套件)
```

載入套件 ROCR

```
## 程式套件 → 載入程式套件... → ROCR → 確定
```

```
## 或直接採用以下指令 > library(ROCR), ">" 表示 R 的提示符號
```

```
## ? svm → 會顯示 svm 的輔助說明
```

```
## 如果沒有載入套件 直接輸入 ? svm → 會有錯誤訊息
```

```
library(ROCR)
```

載入資料集 ROCR.simple

```
## 資料集 200 個觀測值, class 0: 107 筆資料, class 1: 93 筆資料
```

```
## ROCR.simple$predictions, is a vector of numerical predictions.
```

```
## ROCR.simple$labels, is a vector of corresponding class labels.
```

```
data(ROCR.simple)
```

觀察 ROCR.simple 資料內容

```
## 直接輸入資料集名稱即可顯示其內容,資料總共有 200 個
```

```
ROCR.simple
```

```
# summary 可計算 5 大統計值: Min, 1st Qu., Median, Mean, 3rd Qu., Max.
```

```
summary(ROCR.simple$predictions)
```

繪製 ROC curve (x-axis: FPR, y-axis: TPR)

```
pred <- prediction(ROCR.simple$predictions, ROCR.simple$labels)
```

```
perf <- performance(pred, "tpr", "fpr")
```

```
plot(perf)
```

繪製 precision/recall curve (x-axis: recall, y-axis: precision)

```
perf1 <- performance(pred, "prec", "rec")
```

```
plot(perf1)
```

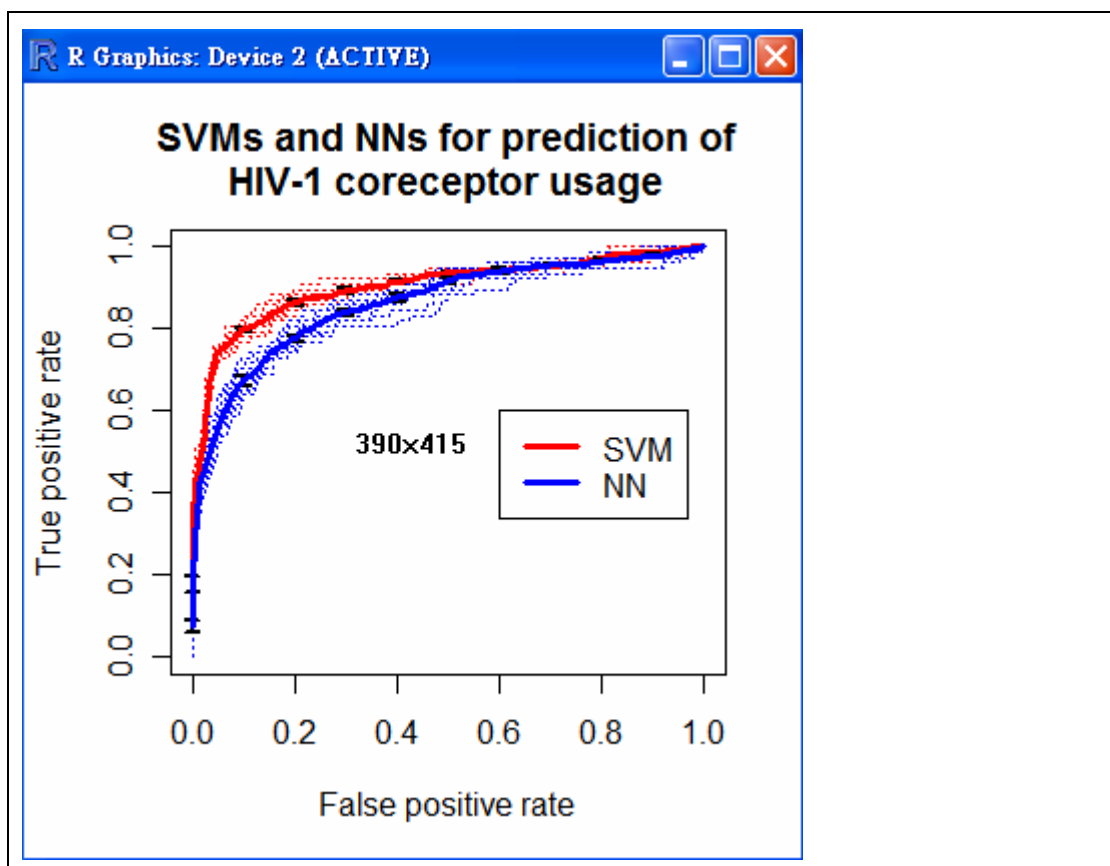
繪製 sensitivity/specificity curve (x-axis: specificity, y-axis: sensitivity)

```
perf2 <- performance(pred, "sens", "spec")
```

```
plot(perf2)
```

比較 SVM and Feed-forward Neural Networks

```
data(ROCR.hiv)
attach(ROCR.hiv)
pred.svm <- prediction(hiv.svm$predictions, hiv.svm$labels)
perf.svm <- performance(pred.svm, 'tpr', 'fpr')
pred.nn <- prediction(hiv.nn$predictions, hiv.svm$labels)
perf.nn <- performance(pred.nn, 'tpr', 'fpr')
plot(perf.svm, lty=3, col="red", main="SVMs and NNs for prediction of
HIV-1 coreceptor usage")
plot(perf.nn, lty=3, col="blue", add=TRUE)
plot(perf.svm, avg="vertical", lwd=3, col="red",
spread.estimate="stderror", plotCI.lwd=2, add=TRUE)
plot(perf.nn, avg="vertical", lwd=3, col="blue",
spread.estimate="stderror", plotCI.lwd=2, add=TRUE)
legend(0.6, 0.6, c('SVM', 'NN'), col=c('red', 'blue'), lwd=3)
```



--- END ---