

Bayes

Capture the Confusion Matrix assuming ALL is the positive class

Construct the Confusion Matrix assuming AML is the positive class

Calculate the class-dependent TP and FP rates. Show your work and compare to Weka.

Compare with results from HW 2

Correctly Classified Instances 68 94.4444 %

TP Rate	FP Rate	Class
1.000	0.143	ALL
0.857	0.000	AML

True Class	Predicted class	
	Yes	No
Yes	TP: True Positive	FN: False Negative
No	FP: False Positive	TN: True Negative

$$TP\ rate = \frac{TP}{TP + FN}$$

$$FP\ rate = \frac{FP}{FP + TN}$$

=== Confusion Matrix ===

ALL as the positive class (Weka):

```

a  b  <-- classified as
44  0 |  a = ALL
 4 24 |  b = AML

```

$$TP\ rate = \frac{44}{44 + 0} = 1.000$$

$$FP\ rate = \frac{4}{4 + 24} = 0.143$$

AML as the positive class (Derived):

```

b  a  <-- classified as
24  4 |  b = AML
 0 44 |  a = ALL

```

$$TP\ rate = \frac{24}{24 + 4} = 0.857$$

$$FP\ rate = \frac{0}{0 + 44} = 0.000$$

My calculated values match the Weka results.

The Bayes confusion matrix is equal to the KNN confusion matrix from HW2.

<u>KNN</u>				<u>Bayes</u>			
	ROC Area	PRC Area	Class		ROC Area	PRC Area	Class
	0.976	0.978	ALL		0.942	0.933	ALL
	0.976	0.967	AML		0.978	0.976	AML
Weighted Avg.	0.976	0.973		Weighted Avg.	0.956	0.949	

Bayes

=== Run information ===

Scheme: weka.classifiers.bayes.NaiveBayes
Relation: leukemia gene expression data names changed
Instances: 72
Attributes: 151
[list of attributes omitted]
Test mode: 5-fold cross-validation

=== Classifier model (full training set) ===

Naive Bayes Classifier

Class
Attribute
ALL AML
(0.61) (0.39)

...

Time taken to build model: 0.01 seconds

=== Stratified cross-validation ===

=== Summary ===

Correctly Classified Instances	68	94.4444 %
Incorrectly Classified Instances	4	5.5556 %
Kappa statistic	0.88	
Mean absolute error	0.0556	
Root mean squared error	0.2357	
Relative absolute error	11.6637 %	
Root relative squared error	48.3082 %	
Total Number of Instances	72	

=== Detailed Accuracy By Class ===

	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area	Class
	1.000	0.143	0.917	1.000	0.957	0.886	0.942	0.933	ALL
	0.857	0.000	1.000	0.857	0.923	0.886	0.978	0.976	AML
Weighted Avg.	0.944	0.087	0.949	0.944	0.944	0.886	0.956	0.949	

=== Confusion Matrix ===

```
a b <-- classified as
44 0 | a = ALL
 4 24 | b = AML
```

KNN

=== Run information ===

```
Scheme:      weka.classifiers.lazy.IBk -K 5 -W 0 -A "weka.core.neighboursearch.LinearNNSearch -A
\"weka.core.EuclideanDistance -R first-last\"
Relation:     leukemia gene expression data names changed
Instances:    72
Attributes:    151
               [list of attributes omitted]
Test mode:    5-fold cross-validation
```

=== Classifier model (full training set) ===

IB1 instance-based classifier
using 5 nearest neighbour(s) for classification

Time taken to build model: 0 seconds

=== Stratified cross-validation ===
=== Summary ===

Correctly Classified Instances	68	94.4444 %
Incorrectly Classified Instances	4	5.5556 %
Kappa statistic	0.88	
Mean absolute error	0.0917	
Root mean squared error	0.2235	
Relative absolute error	19.2509 %	
Root relative squared error	45.7979 %	
Total Number of Instances	72	

=== Detailed Accuracy By Class ===

	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area	Class
	1.000	0.143	0.917	1.000	0.957	0.886	0.976	0.978	ALL
	0.857	0.000	1.000	0.857	0.923	0.886	0.976	0.967	AML
Weighted Avg.	0.944	0.087	0.949	0.944	0.944	0.886	0.976	0.973	

=== Confusion Matrix ===

```
 a  b  <-- classified as
44  0  |  a = ALL
 4 24  |  b = AML
```