Task 1:

=== Run information ===

Scheme:weka.classifiers.bayes.NaiveBayes

Relation: house-votes-84

Instances: 435

Attributes: 17

Test mode:5-fold cross-validation

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

Naive Bayes Classifier

=== Summary ===

Correctly Classified Instances 248 74.9245 %

Incorrectly Classified Instances 83 25.0755 %

Kappa statistic 0.4183

Mean absolute error 0.247

Root mean squared error 0.4784

Relative absolute error 80.7213 %

Root relative squared error 122.601 %

Total Number of Instances 331

Ignored Class Unknown Instances 104

=== Detailed Accuracy By Class ===

TP Rate FP Rate Precision Recall F-Measure ROC Area Class

0.721 0.129 0.96 0.721 0.824 0.598 y

0.871 0.279 0.419 0.871 0.565 0.869 n

Weighted Avg. 0.749 0.157 0.859 0.749 0.775 0.648

=== Confusion Matrix ===

a b <-- classified as

194 75 | a = y

8 54 | b = n

Task 2

=== Run information ===

Scheme:weka.classifiers.bayes.NaiveBayes

Relation: breast\_cancer\_92

Instances: 699

Attributes: 10

clump\_thickness

uniformity\_of\_cell\_size

uniformity\_of\_cell\_shape

marginal\_adhersion

single\_epithelial

bare\_nucleoli

bland\_chromatin

normal\_nucleoli

mitoses

class

Test mode:5-fold cross-validation

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

Naive Bayes Classifier

Class

Attribute 2 4

(0.65) (0.35)

=========================================

clump\_thickness

mean 2.9563 7.195

std. dev. 1.6725 2.4238

weight sum 458 241

precision 1 1

uniformity\_of\_cell\_size

mean 1.3253 6.5726

std. dev. 0.9067 2.7139

weight sum 458 241

precision 1 1

uniformity\_of\_cell\_shape

mean 1.4432 6.5602

std. dev. 0.9967 2.5567

weight sum 458 241

precision 1 1

marginal\_adhersion

mean 1.3646 5.5477

std. dev. 0.9957 3.2038

weight sum 458 241

precision 1 1

single\_epithelial

mean 2.1201 5.2988

std. dev. 0.9161 2.4465

weight sum 458 241

precision 1 1

bare\_nucleoli

mean 1.3468 7.6276

std. dev. 1.1765 3.1102

weight sum 444 239

precision 1 1

bland\_chromatin

mean 2.1004 5.9793

std. dev. 1.0792 2.2691

weight sum 458 241

precision 1 1

normal\_nucleoli

mean 1.2904 5.8631

std. dev. 1.0577 3.3437

weight sum 458 241

precision 1 1

mitoses

mean 1.1889 2.7401

std. dev. 0.4833 2.5138

weight sum 458 241

precision 1.125 1.125

Time taken to build model: 0.01 seconds

=== Stratified cross-validation ===

=== Summary ===

Correctly Classified Instances 672 96.1373 %

Incorrectly Classified Instances 27 3.8627 %

Kappa statistic 0.9159

Mean absolute error 0.0398

Root mean squared error 0.1961

Relative absolute error 8.8157 %

Root relative squared error 41.2581 %

Total Number of Instances 699

=== Detailed Accuracy By Class ===

TP Rate FP Rate Precision Recall F-Measure ROC Area Class

0.952 0.021 0.989 0.952 0.97 0.987 2

0.979 0.048 0.915 0.979 0.946 0.983 4

Weighted Avg. 0.961 0.03 0.963 0.961 0.962 0.986

=== Confusion Matrix ===

a b <-- classified as

436 22 | a = 2

5 236 | b = 4

**Discretize**

=== Run information ===

Scheme:weka.classifiers.bayes.NaiveBayes

Relation: breast\_cancer\_92-weka.filters.supervised.attribute.Discretize-Rfirst-last-weka.filters.unsupervised.attribute.Discretize-B10-M-1.0-Rfirst-last-weka.filters.unsupervised.attribute.Discretize-B10-M-1.0-Rfirst-last-weka.filters.unsupervised.attribute.Discretize-B10-M-1.0-Rfirst-last

Instances: 699

Attributes: 10

clump\_thickness

uniformity\_of\_cell\_size

uniformity\_of\_cell\_shape

marginal\_adhersion

single\_epithelial

bare\_nucleoli

bland\_chromatin

normal\_nucleoli

mitoses

class

Test mode:5-fold cross-validation

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

Naive Bayes Classifier

Class

Attribute 2 4

(0.65) (0.35)

=========================================

clump\_thickness

'(-inf-4.5]' 353.0 32.0

'(4.5-6.5]' 102.0 64.0

'(6.5-inf)' 6.0 148.0

[total] 461.0 244.0

uniformity\_of\_cell\_size

'(-inf-1.5]' 381.0 5.0

'(1.5-2.5]' 38.0 9.0

'(2.5-4.5]' 37.0 57.0

'(4.5-inf)' 6.0 174.0

[total] 462.0 245.0

uniformity\_of\_cell\_shape

'(-inf-1.5]' 352.0 3.0

'(1.5-2.5]' 53.0 8.0

'(2.5-4.5]' 47.0 55.0

'(4.5-inf)' 10.0 179.0

[total] 462.0 245.0

marginal\_adhersion

'(-inf-1.5]' 376.0 33.0

'(1.5-3.5]' 69.0 49.0

'(3.5-inf)' 16.0 162.0

[total] 461.0 244.0

single\_epithelial

'(-inf-2.5]' 410.0 25.0

'(2.5-3.5]' 30.0 44.0

'(3.5-inf)' 21.0 175.0

[total] 461.0 244.0

bare\_nucleoli

'(-inf-1.5]' 388.0 16.0

'(1.5-2.5]' 22.0 10.0

'(2.5-5.5]' 31.0 48.0

'(5.5-inf)' 7.0 169.0

[total] 448.0 243.0

bland\_chromatin

'(-inf-2.5]' 310.0 10.0

'(2.5-3.5]' 130.0 37.0

'(3.5-inf)' 21.0 197.0

[total] 461.0 244.0

normal\_nucleoli

'(-inf-2.5]' 433.0 48.0

'(2.5-9.5]' 27.0 134.0

'(9.5-inf)' 1.0 62.0

[total] 461.0 244.0

mitoses

'(-inf-1.5]' 446.0 135.0

'(1.5-inf)' 14.0 108.0

[total] 460.0 243.0

Time taken to build model: 0 seconds

=== Stratified cross-validation ===

=== Summary ===

Correctly Classified Instances 680 97.2818 %

Incorrectly Classified Instances 19 2.7182 %

Kappa statistic 0.9406

Mean absolute error 0.0284

Root mean squared error 0.1608

Relative absolute error 6.2734 %

Root relative squared error 33.8275 %

Total Number of Instances 699

=== Detailed Accuracy By Class ===

TP Rate FP Rate Precision Recall F-Measure ROC Area Class

0.965 0.012 0.993 0.965 0.979 0.992 2

0.988 0.035 0.937 0.988 0.962 0.992 4

Weighted Avg. 0.973 0.02 0.974 0.973 0.973 0.992

=== Confusion Matrix ===

a b <-- classified as

442 16 | a = 2

3 238 | b = 4