ECT_HW8

2019

第一大題

- 利用 Weka 對 DeerHunter.arff 進行前處理，依序完成以下步驟及問題：
  - Replace Missing Value，需列出補上的值為何 (10%)
  - Outlier Detection& Remove (10%)
  - Attribute Selection，請篩選出適合的屬性 (10%)

Replace Missing Value

: gender Numeric	11: age Numeric	12: hunte Numeric
1.0	18.0	11
1.0	18.0	8
1.0	18.0	6
1.0	18.0	10
1.0	18.0	5
1.0	19.0	8
1.0	19.0	9
1.0		6
1.0	19.0	8
1.0	19.0	2
1.0	19.0	3

harried meric	9: income Numeric	10: ger Nume
1.0	15000.0	
1.0	5000.0	
1.0	40000.0	
1.0	15000.0	
0.0	40000.0	
0.0	15000.0	
0.0	15000.0	
0.0		
1.0	22500.0	
1.0	15000.0	

以平均值代替

e 10: gender Numeric	11: age Numeric	1
0	1.0	18.0
0	1.0	18.0
0	1.0	18.0
0	1.0	18.0
0	1.0	18.0
0	1.0	19.0
0	1.0	19.0
0	1.0	38.3...

ried ric	9: income Numeric	10: Nu
1.0	15000.0	
1.0	5000.0	
1.0	40000.0	
1.0	15000.0	
0.0	40000.0	
0.0	15000.0	
0.0	15000.0	
0.0	37678....	
1.0	22500.0	
1.0	15000.0	

Name: age
Missing: 5 (0%)
Distinct: 68
Type: Numeric
Unique: 3 (0%)

Statistic	Value
Minimum	18
Maximum	90
Mean	38.316
StdDev	12.875

Selected attribute

Name: income
Missing: 5 (0%)
Distinct: 7
Type: Numeric
Unique: 0 (0%)

Statistic	Value
Minimum	5000
Maximum	85000
Mean	37678.394
StdDev	20096.855

Filter

Choose: ReplaceMissingValues

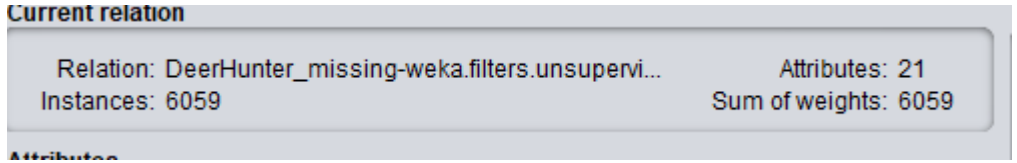
Current relation

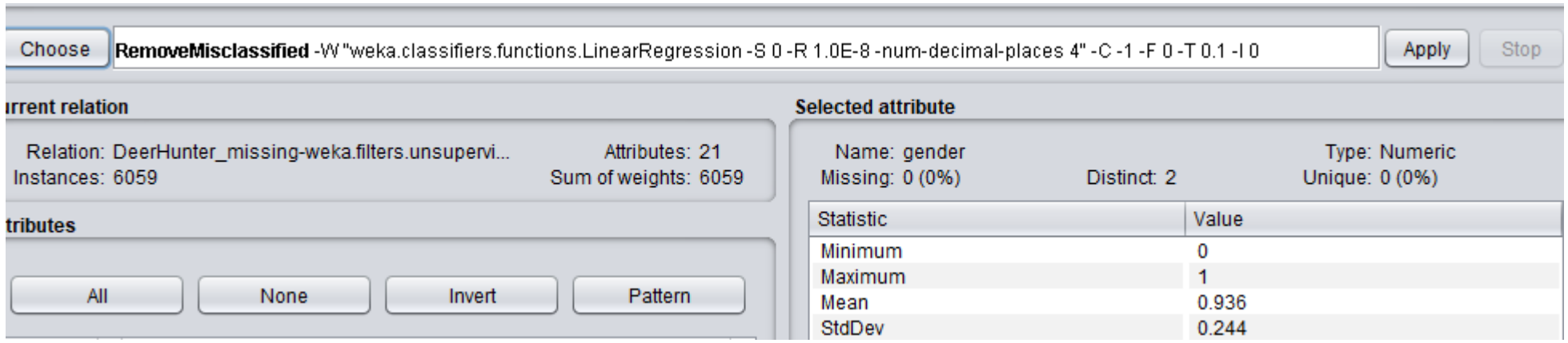
Relation: DeerHunter_missing-weka.filters.unsupervi...
Instances: 6059
Attributes: 21
Sum of weights: 6059

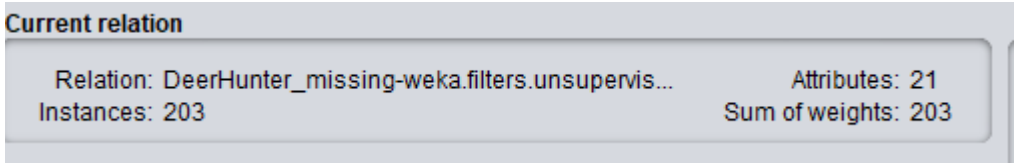
Attributes

All | None | Invert | Pattern

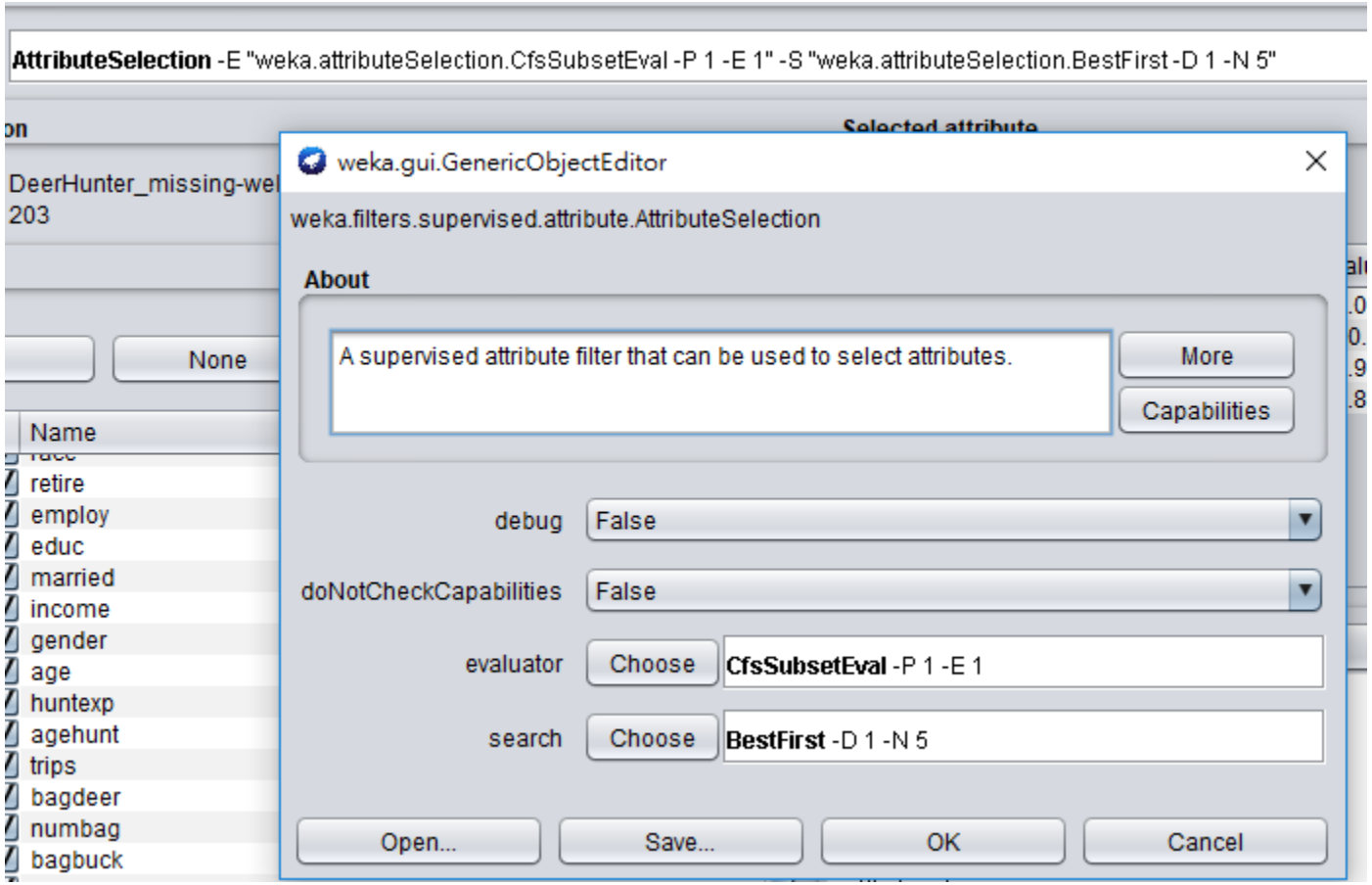
Outlier Detection& Remove







Attribute Selection



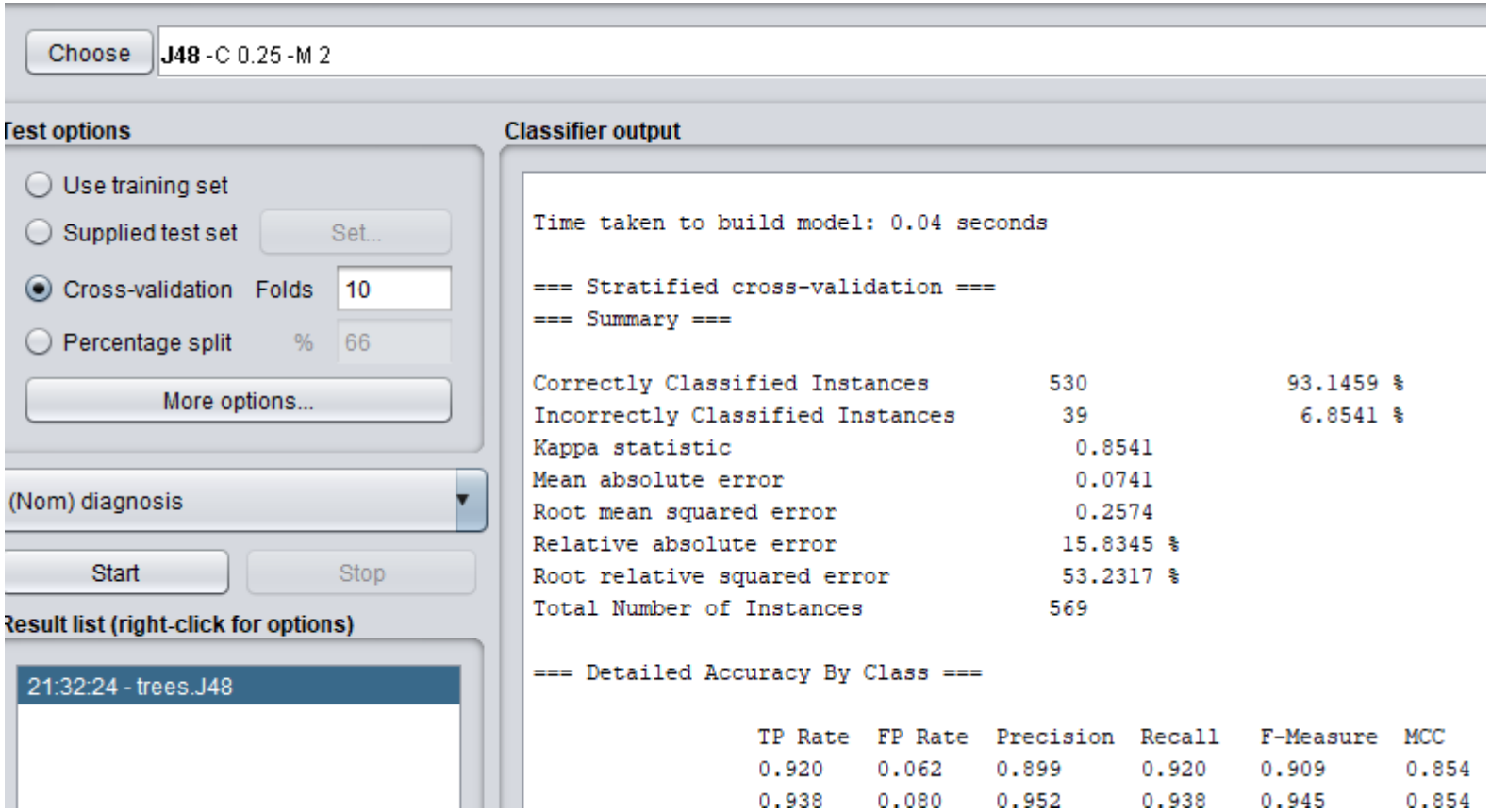
Attributes: 21
Sum of weights: 203

Attributes: 15
Sum of weights: 203

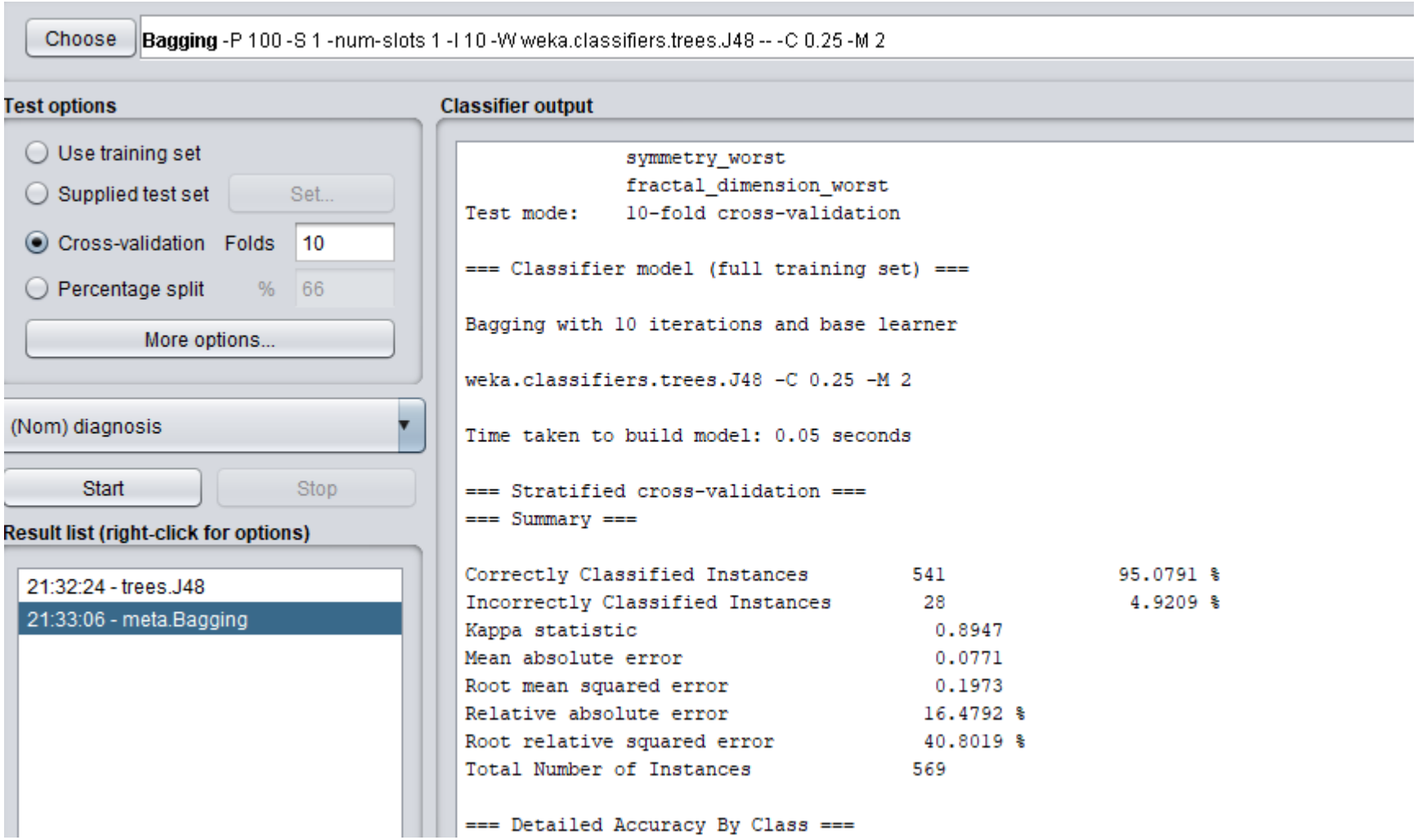
第二大題

- 請用weka對BreastCancer.csv對目標diagnosis進行Ensemble learning並與未使用的結果進行比較(請列出重要過程及適當說明)：
  - 以10 Folds cross-validation進行J48分類(5%)
  - 以10 Folds cross-validation進行Bagging分類並選擇J48 classifier進行分類(10%)
  - 以10 Folds cross-validation進行Bagging分類並選擇Randomforest進行分類(10%)
  - 以10 Folds cross-validation進行AdaBoost分類並選擇DecisionStump進行分類(10%)

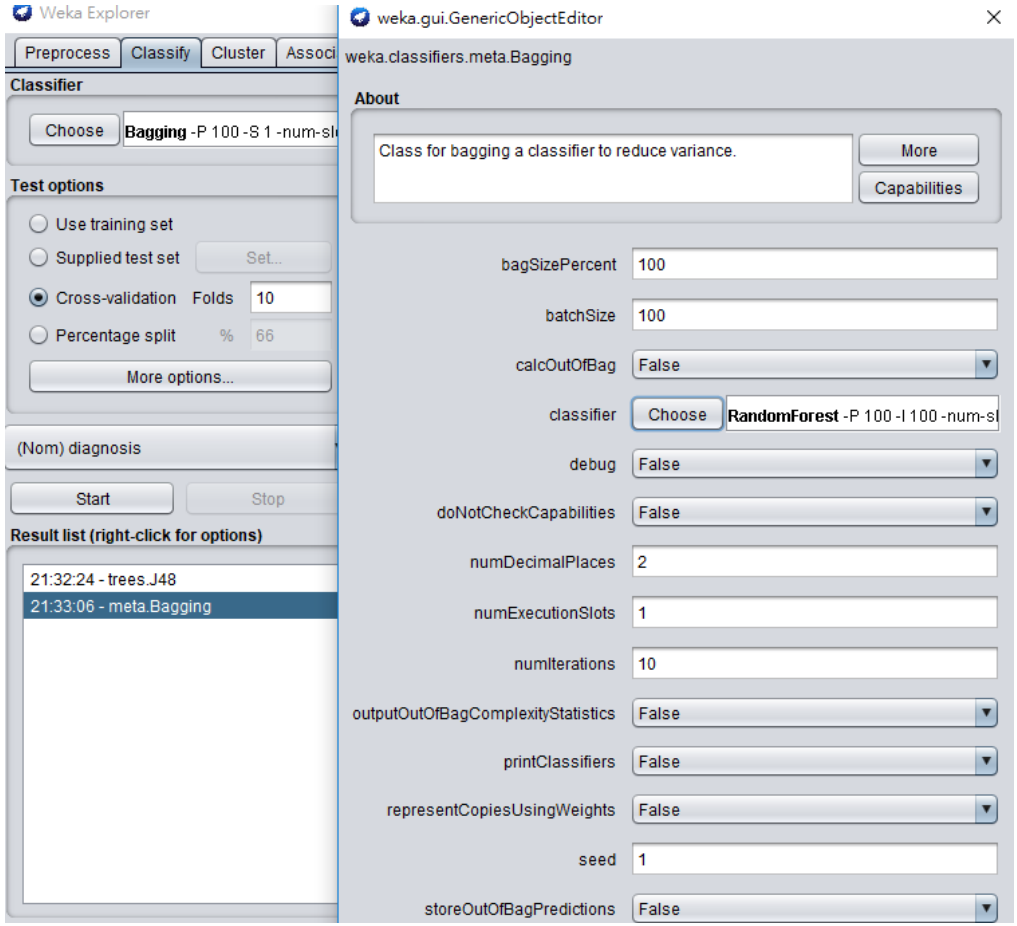
J48分類

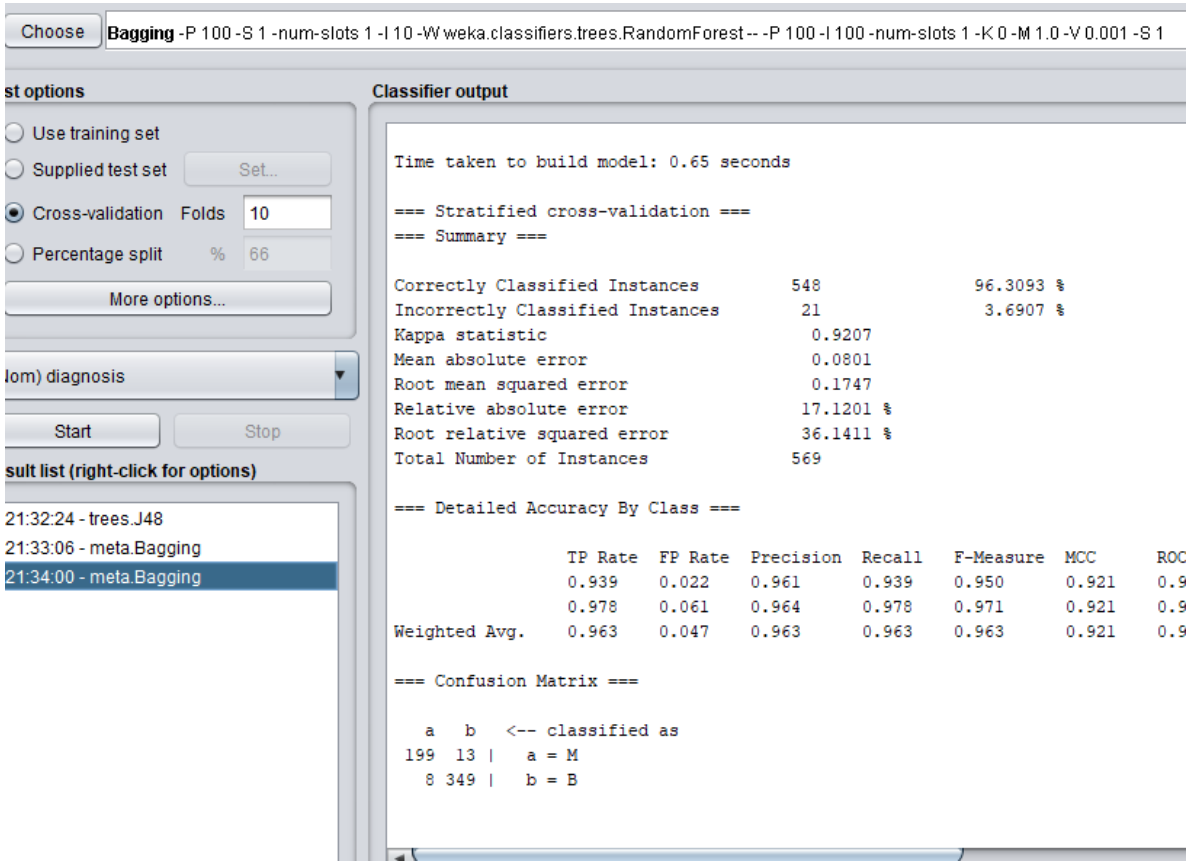

Choose
J48 -C 0.25 -M 2
Test options
Use training set
Supplied test set
Set...
Cross-validation
Folds
10
Percentage split
%
66
More options...
(Nom) diagnosis
Start
Stop
Result list (right-click for options)
21:32:24 - trees.J48
Classifier output
Time taken to build model: 0.04 seconds
=== Stratified cross-validation ===
=== Summary ===
Correctly Classified Instances 530 93.1459 %
Incorrectly Classified Instances 39 6.8541 %
Kappa statistic 0.8541
Mean absolute error 0.0741
Root mean squared error 0.2574
Relative absolute error 15.8345 %
Root relative squared error 53.2317 %
Total Number of Instances 569
=== Detailed Accuracy By Class ===
TP Rate FP Rate Precision Recall F-Measure MCC
0.920 0.062 0.899 0.920 0.909 0.854
0.938 0.080 0.952 0.938 0.945 0.854

Bagging J48

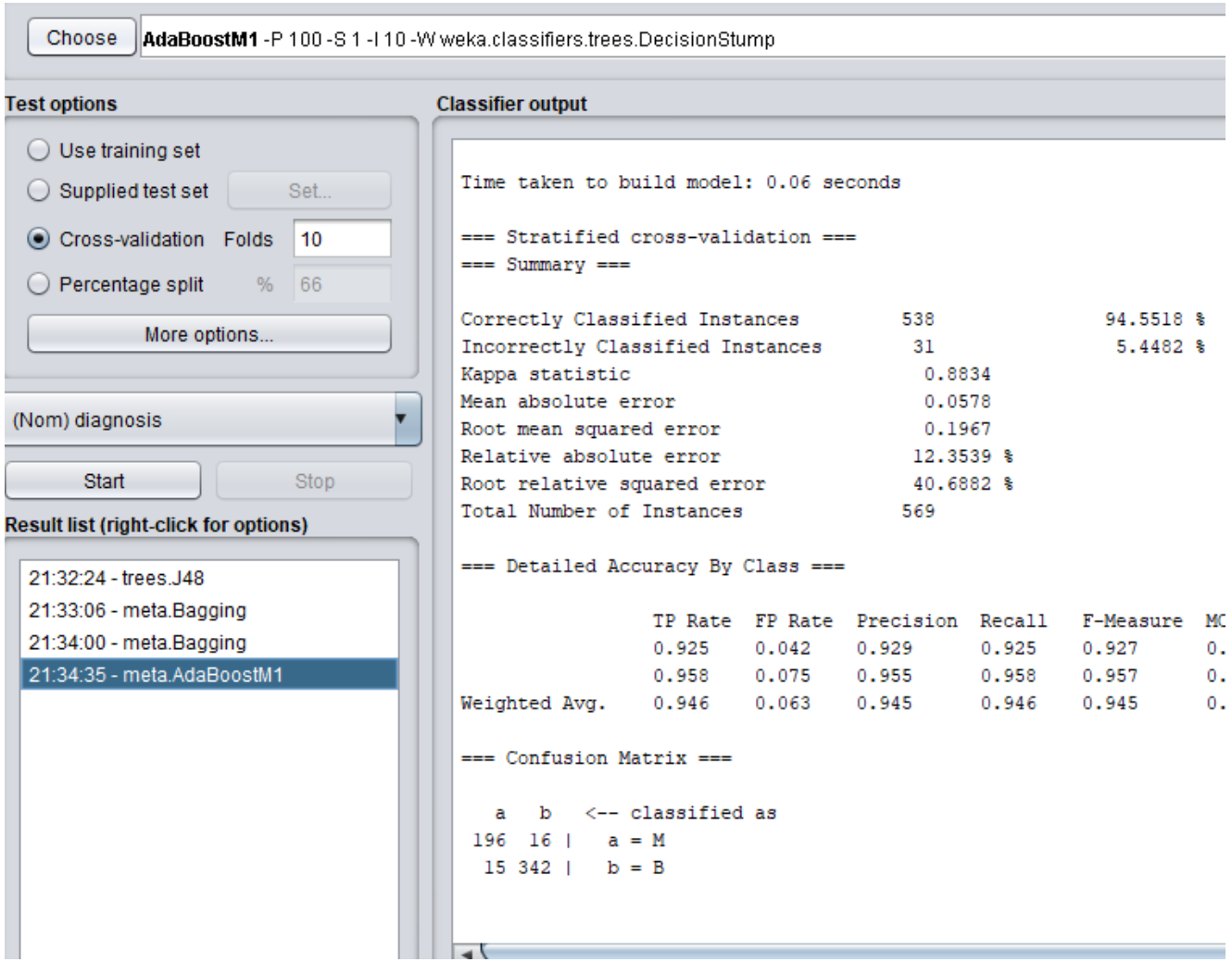

Choose
Bagging -P 100 -S 1 -num-slots 1 -I 10 -W weka.classifiers.trees.J48 -- -C 0.25 -M 2
Test options
Use training set
Supplied test set
Set...
Cross-validation
Folds
10
Percentage split
%
66
More options...
(Nom) diagnosis
Start
Stop
Result list (right-click for options)
21:32:24 - trees.J48
21:33:06 - meta.Bagging
Classifier output
symmetry_worst
fractal_dimension_worst
Test mode: 10-fold cross-validation
=== Classifier model (full training set) ===
Bagging with 10 iterations and base learner
weka.classifiers.trees.J48 -C 0.25 -M 2
Time taken to build model: 0.05 seconds
=== Stratified cross-validation ===
=== Summary ===
Correctly Classified Instances 541 95.0791 %
Incorrectly Classified Instances 28 4.9209 %
Kappa statistic 0.8947
Mean absolute error 0.0771
Root mean squared error 0.1973
Relative absolute error 16.4792 %
Root relative squared error 40.8019 %
Total Number of Instances 569
=== Detailed Accuracy By Class ===

Bagging Randomforest





AdaBoost DecisionStump



第三大題

- 請用python對BreastCancer.csv對目標diagnosis進行Ensemble learning並與未使用的結果進行比較(請列出重要過程及適當說明)：
  - 以10 Folds cross-validation進行DecisionTreeClassifier分類(5%)
  - 以10 Folds cross-validation進行Bagging，n_estimators=10分類(10%)
  - 以10 Folds cross-validation進行RandomForest分類(10%)
  - 以10 Folds cross-validation進行AdaBoost, n_estimators=10分類(10%)

Import/data processing

In [1]:
```
import pandas as pd
from sklearn import preprocessing
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import train_test_split
from sklearn.ensemble import BaggingClassifier
from sklearn.ensemble import AdaBoostClassifier
from sklearn import metrics
from sklearn import tree
from sklearn.ensemble import RandomForestClassifier
```

In [2]:
```
data = pd.read_csv('BreastCancer.csv')
```

In [3]:
```
data.dropna()
label=data.iloc[:,1]
```

In [4]:
```
data = data.drop('diagnosis',axis=1)
```

In [5]:
```
le = preprocessing.LabelEncoder()
encodedlabel = le.fit_transform(label)
```

In [6]:
```
train_X, test_X, train_y, test_y = train_test_split(data, encodedlabel, test_size = 0.3)
```

DecisionTree

```
clf = tree.DecisionTreeClassifier(criterion = 'entropy',max_depth=3,max_leaf_nodes = 4)

scores = cross_val_score(clf, data, encodedlabel, cv=10)
scores.mean()
```

```
0.9016744447325209
```

Bagging

```
bagging = BaggingClassifier(n_estimators = 10)

scores = cross_val_score(bagging, data, encodedlabel, cv=10)
scores.mean()
```

```
0.9509938639702705
```

RandomForest

```
Rndclf = RandomForestClassifier(n_estimators=10)

scores = cross_val_score(Rndclf, data, encodedlabel, cv=10)
scores.mean()
```

```
0.9684480598046841
```

AdaBoost

```
adaBoost = AdaBoostClassifier(n_estimators = 100)

scores = cross_val_score(adaBoost, data, encodedlabel, cv=10)
scores.mean()
```

```
0.9702326938034741
```

python cross-validation

- sklearn.model_selection. cross_val_score

```
scores = cross_val_score(分類方法, 屬性, 目標, fold量)
scores.mean()
```

- sklearn.ensemble(**base_estimator(default=decision tree)**)
  - BaggingClassifier (**n_estimators**)
  - AdaBoostClassifier(**n_estimators**)