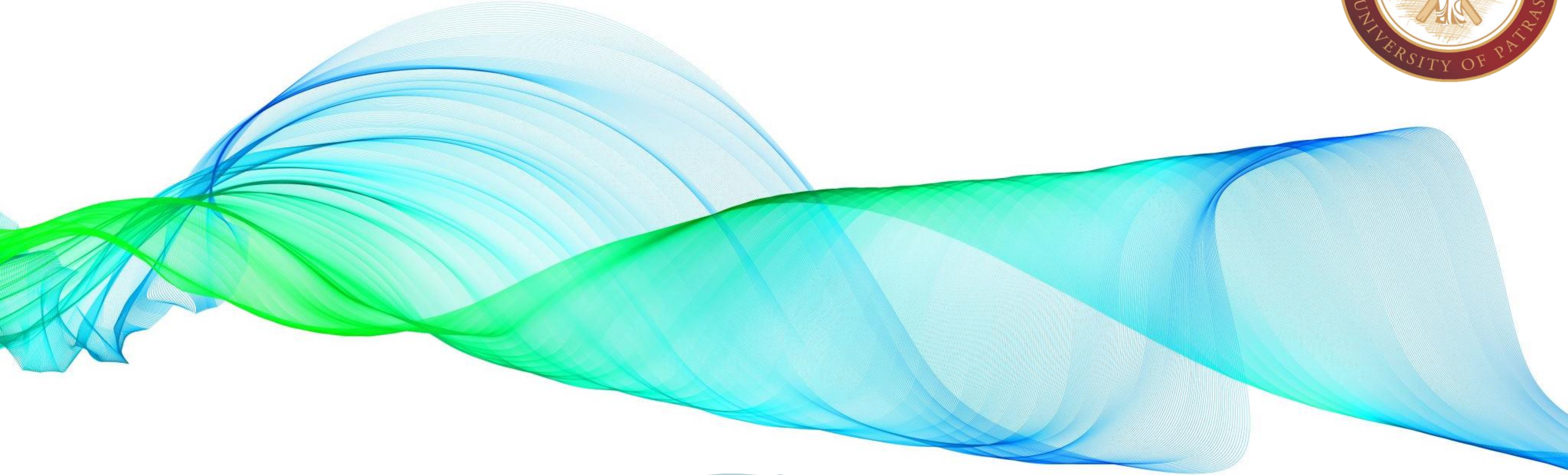


# WEKA CLASSIFICATION

**Ευφυή Συστήματα Λήψης Απόφασης στις Επιστήμες Υγείας**

Υπ. Διδάκτορες: Χασάπη Μαρία Κωνσταντίνα
Χασάπη Λαμπρινή

Waikato Environment for Knowledge Analysis
Version 3.8.3
(c) 1999 - 2018
The University of Waikato
Hamilton, New Zealand

Το WEKA είναι μια σουίτα λογισμικού για μηχανική μάθηση και εξόρυξη δεδομένων.

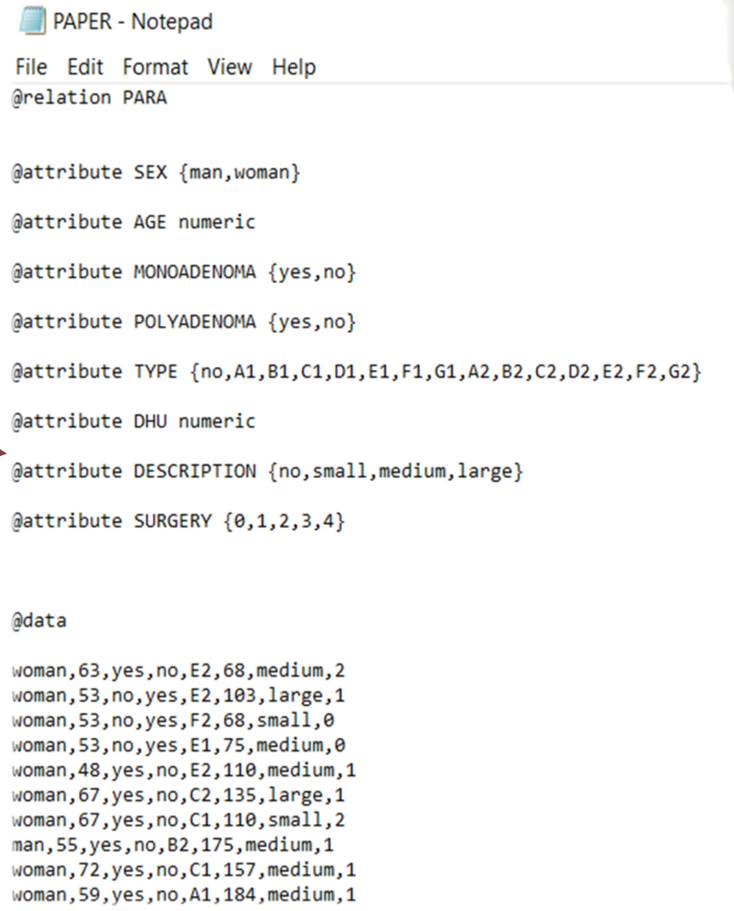
Μέσω του WEKA Explorer ο χρήστης μπορεί να εκτελέσει εργασίες προεπεξεργασίας δεδομένων, κατηγοριοποίησης, ανάλυσης συστάδων, ανάλυσης κανόνων συσχέτισης, επιλογής χαρακτηριστικών και οπτικοποίησης των δεδομένων.

**Για να δημιουργήσουμε το έμπειρο σύστημα στο weka απαιτείται ένα αρχείο το οποίο να έχει μορφή: ARFF, CSV, C4.5, Binary**

Η πιο συνηθισμένη μορφή αρχείων είναι τα ARFF.
Εντός του ARFF αρχείου πρέπει η πρώτη γραμμή να ξεκινά με τη λέξη @relation και το όνομα που περιγράφει το αρχείο.

Στη συνέχεια ακολουθεί η δήλωση των πεδίων ξεκινώντας κάθε πεδίο με τη λέξη @attribute <όνομα attribute> <τύπος attribute>.
Μετά τη δήλωση των παραμέτρων, ακολουθεί η δήλωση των δεδομένων, με τη σειρά που έχουν δηλωθεί τα πεδία.

Η δήλωση των δεδομένων πραγματοποιείται με @data και ακολουθούν οι τιμές οι οποίες χωρίζονται μεταξύ τους με κόμμα.



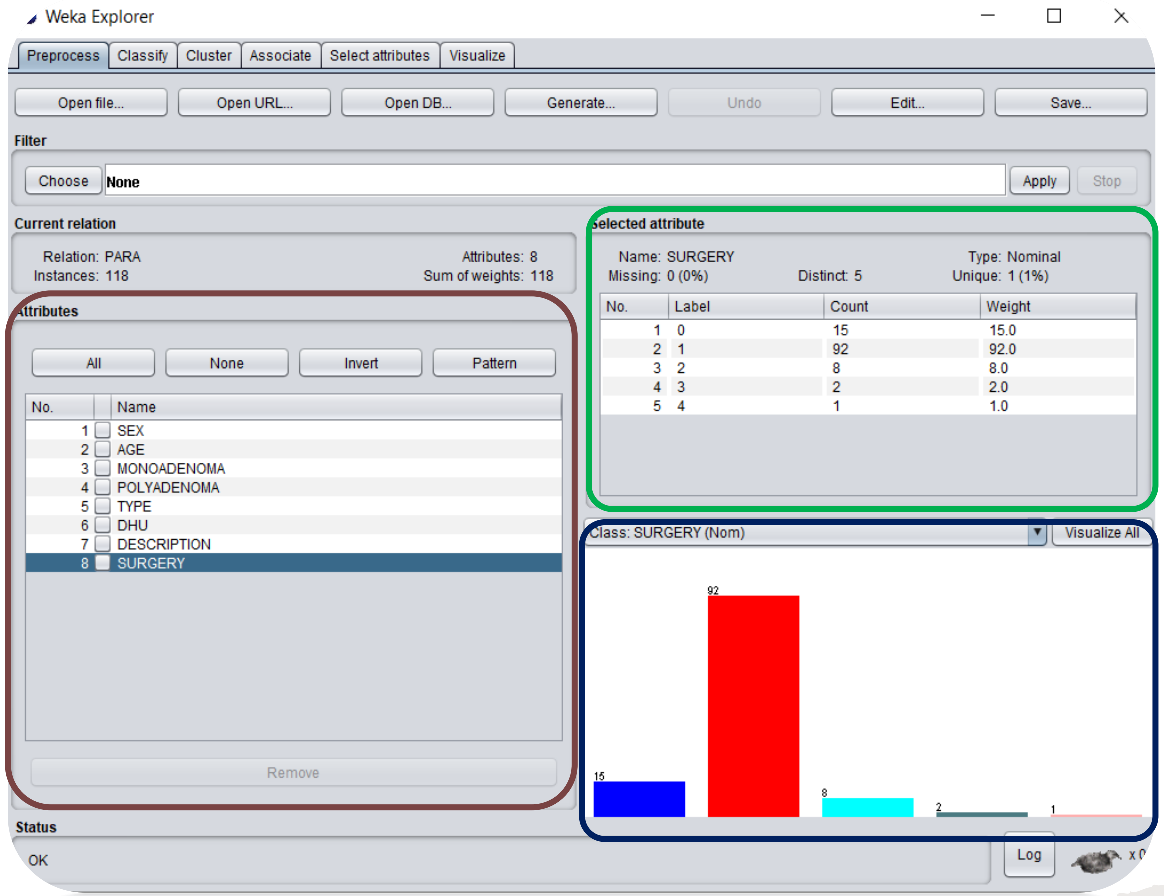
```
@relation PARA


@attribute SEX {man,woman}

@attribute AGE numeric

@attribute MONOADENOMA {yes,no}

@attribute POLYADENOMA {yes,no}

@attribute TYPE {no,A1,B1,C1,D1,E1,F1,G1,A2,B2,C2,D2,E2,F2,G2}

@attribute DHU numeric

@attribute DESCRIPTION {no,small,medium,large}

@attribute SURGERY {0,1,2,3,4}



@data

woman,63,yes,no,E2,68,medium,2
woman,53,no,yes,E2,103,large,1
woman,53,no,yes,F2,68,small,0
woman,53,no,yes,E1,75,medium,0
woman,48,yes,no,E2,110,medium,1
woman,67,yes,no,C2,135,large,1
woman,67,yes,no,C1,110,small,2
man,55,yes,no,B2,175,medium,1
woman,72,yes,no,C1,157,medium,1
woman,59,yes,no,A1,184,medium,1
```

**Open File**: επιλογή αρχείου ARFF των δεδομένων

Απεικόνιση των παραμέτρων του συνόλου δεδομένων.
Σε αυτό το σημείο μπορώ να αφαιρέσω παραμέτρους που
δεν χρειάζομαι καθώς επίσης και να επιλέξω μια παράμετρο

Απεικόνιση στιγμιότυπων της επιλεγμένης παραμέτρου

Οπτικοποίηση των δεδομένων της κλάσης εξόδου που έχω επιλέξει



Filter: None

Current relation
Relation: PARA
Instances: 118
Attributes: 8
Sum of weights: 118

Attributes

| No. | | Name |
|---|---|---|
| 1 | ☐ | SEX |
| 2 | ☐ | AGE |
| 3 | ☐ | MONOADENOMA |
| 4 | ☐ | POLYADENOMA |
| 5 | ☐ | TYPE |
| 6 | ☐ | DHU |
| 7 | ☐ | DESCRIPTION |
| 8 | ☐ | SURGERY |

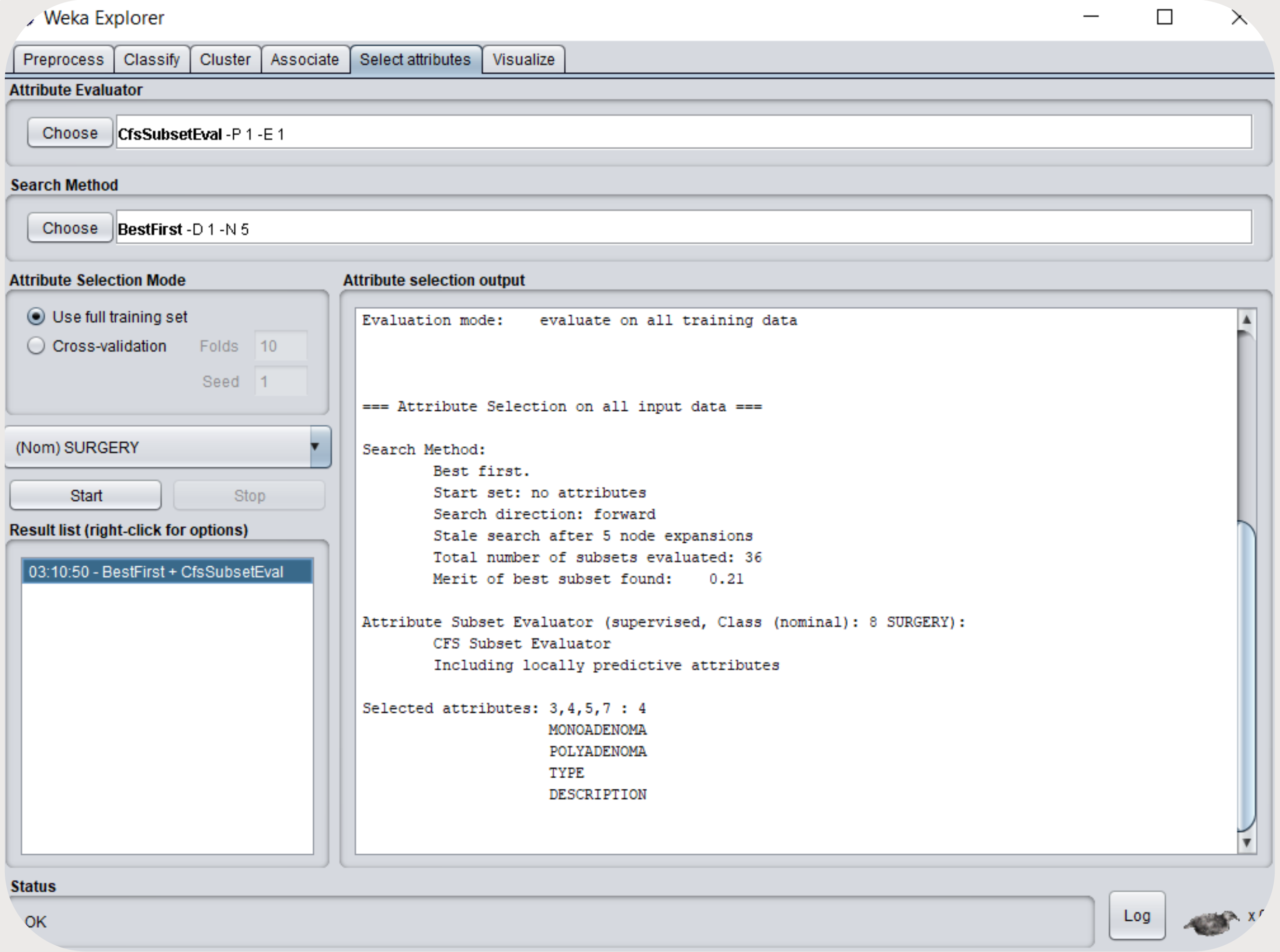
Selected attribute
Name: SURGERY
Missing: 0 (0%)
Distinct: 5
Type: Nominal
Unique: 1 (1%)

| No. | Label | Count | Weight |
|---|---|---|---|
| 1 | 0 | 15 | 15.0 |
| 2 | 1 | 92 | 92.0 |
| 3 | 2 | 8 | 8.0 |
| 4 | 3 | 2 | 2.0 |
| 5 | 4 | 1 | 1.0 |

Class: SURGERY (Nom)

Status
OK

Στην καρτέλα **Select Attributes** μπορώ να απεικονίσω τις πιο σημαντικές παραμέτρους των δεδομένων μου



Attribute Evaluator

**CfsSubsetEval** -P 1 -E 1

Search Method

**BestFirst** -D 1 -N 5

Attribute Selection Mode

● Use full training set
○ Cross-validation Folds 10 Seed 1

(Nom) SURGERY

Result list (right-click for options)

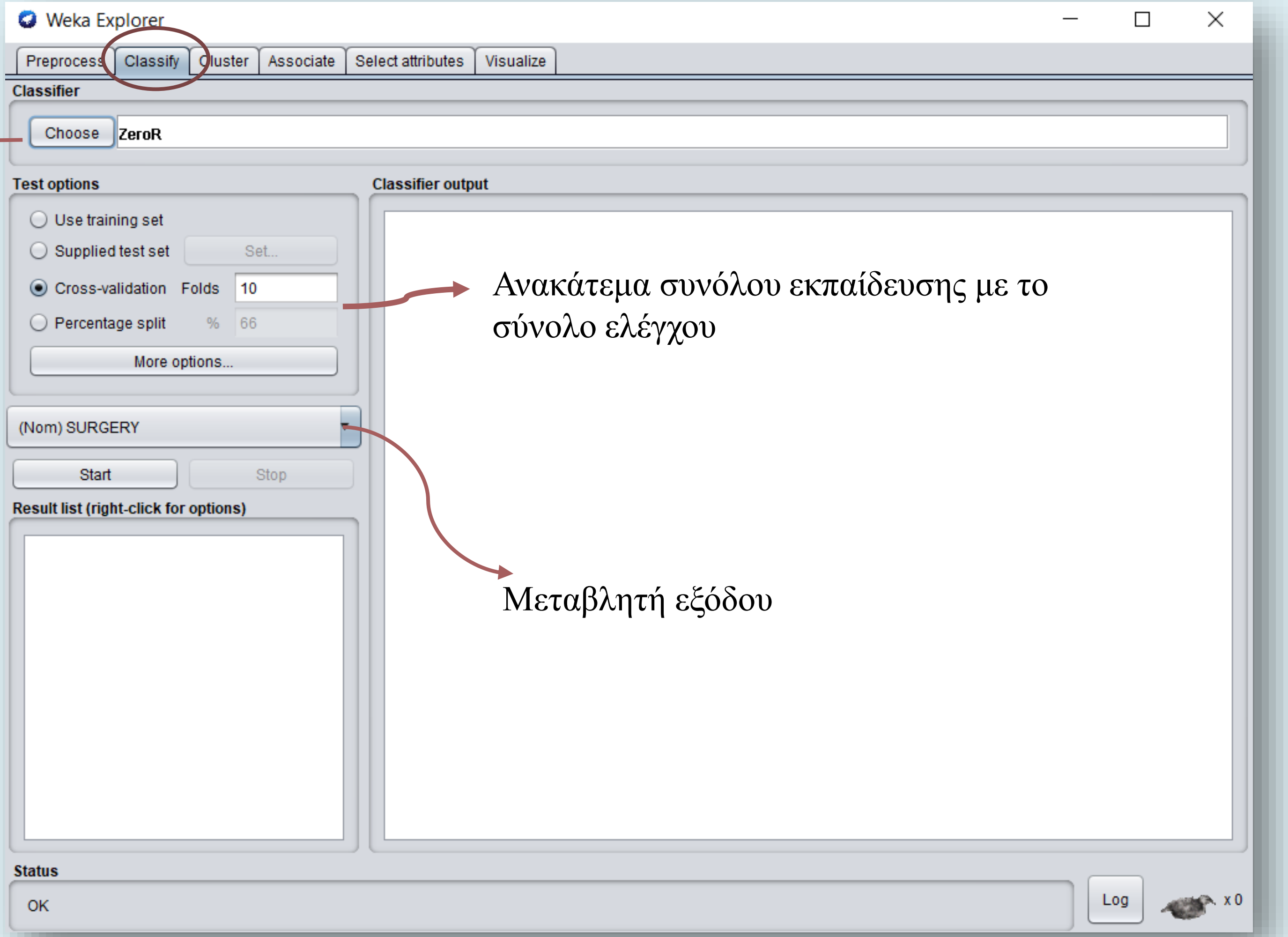
03:10:50 - BestFirst + CfsSubsetEval

Attribute selection output

```
Evaluation mode:    evaluate on all training data



=== Attribute Selection on all input data ===

Search Method:
        Best first.
        Start set: no attributes
        Search direction: forward
        Stale search after 5 node expansions
        Total number of subsets evaluated: 36
        Merit of best subset found:    0.21

Attribute Subset Evaluator (supervised, Class (nominal): 8 SURGERY):
        CFS Subset Evaluator
        Including locally predictive attributes

Selected attributes: 3,4,5,7 : 4
                     MONOADENOMA
                     POLYADENOMA
                     TYPE
                     DESCRIPTION
```

Status

OK



Classifier: ZeroR

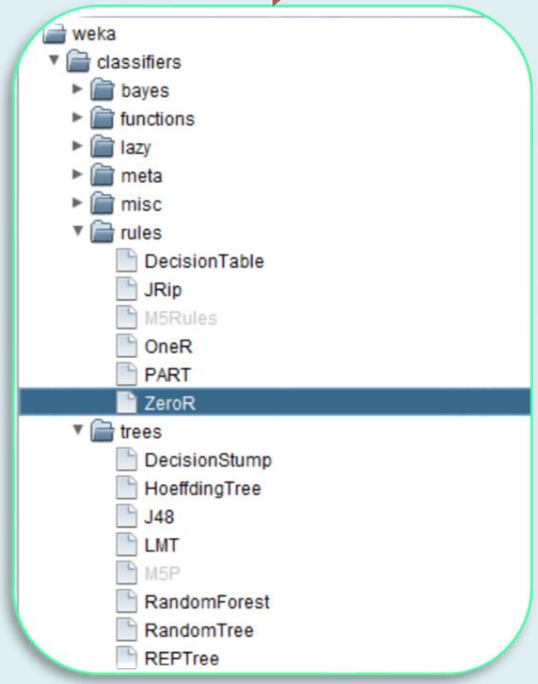
● Cross-validation Folds 10

(Nom) SURGERY

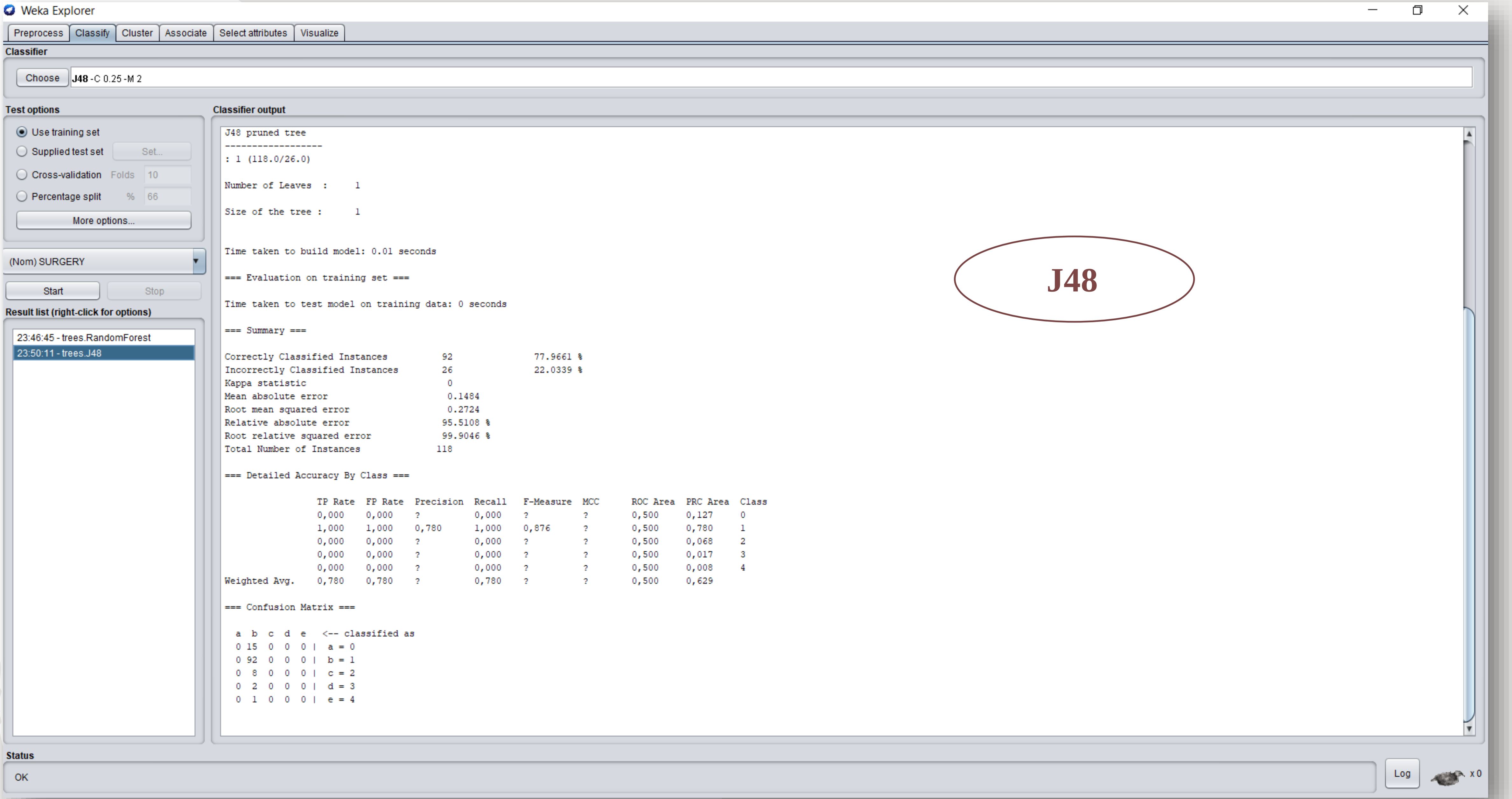
Status: OK

Ανακάτεμα συνόλου εκπαίδευσης με το σύνολο ελέγχου

Μεταβλητή εξόδου



Αλγόριθμος Κατηγοριοποίησης δεδομένων



Classifier: **J48** -C 0.25 -M 2

Test options:

- ● Use training set
- ○ Supplied test set
- ○ Cross-validation Folds 10
- ○ Percentage split % 66

(Nom) SURGERY

Result list (right-click for options):

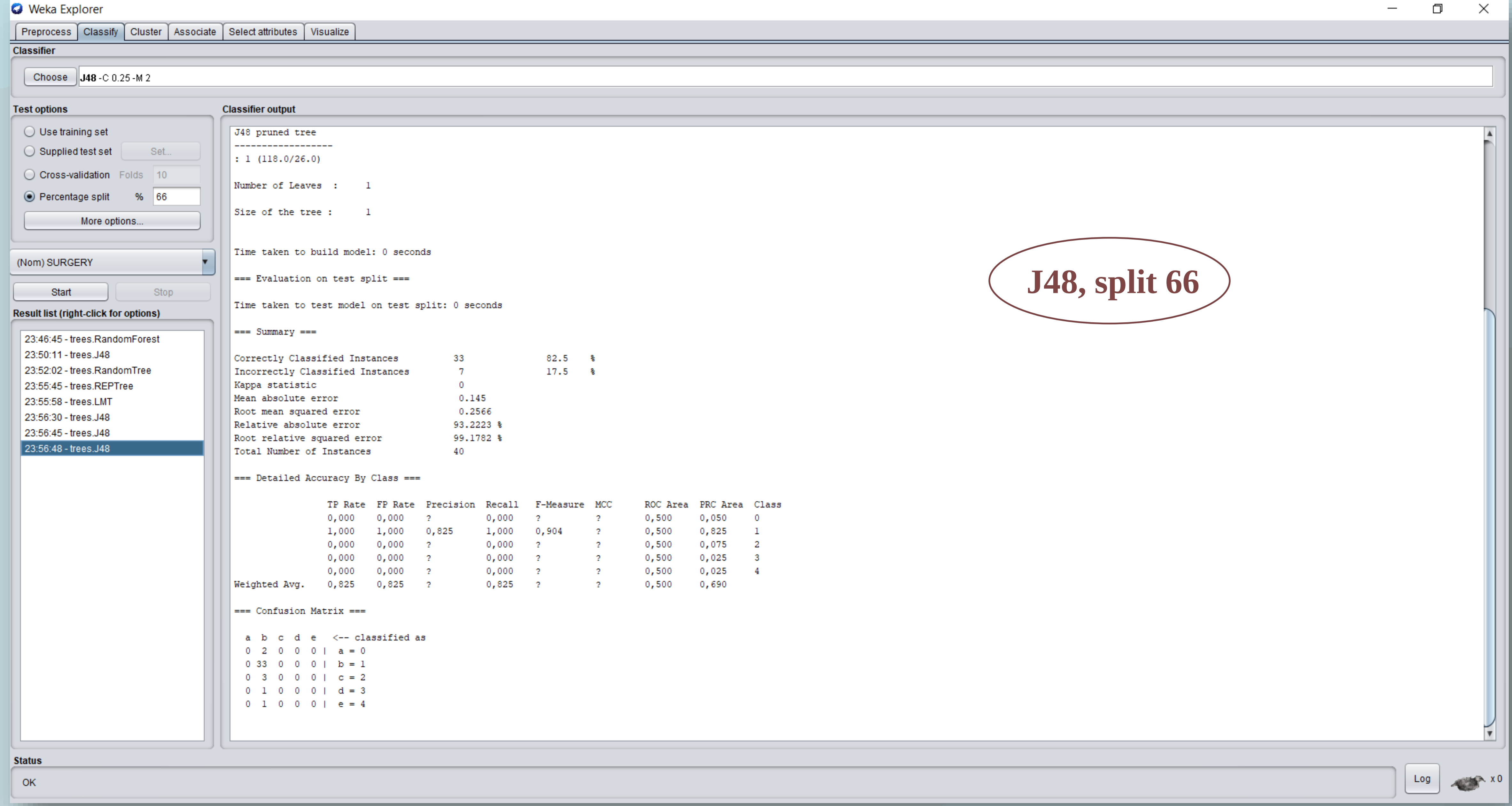
- 23:46:45 - trees.RandomForest
- 23:50:11 - trees.J48

Classifier output:

```
J48 pruned tree
------------------
: 1 (118.0/26.0)

Number of Leaves  :     1

Size of the tree :      1


Time taken to build model: 0.01 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0 seconds

=== Summary ===

Correctly Classified Instances          92               77.9661 %
Incorrectly Classified Instances        26               22.0339 %
Kappa statistic                          0
Mean absolute error                      0.1484
Root mean squared error                  0.2724
Relative absolute error                 95.5108 %
Root relative squared error             99.9046 %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,127     0
                 1,000    1,000    0,780      1,000    0,876      ?        0,500     0,780     1
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,068     2
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,017     3
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,008     4
Weighted Avg.    0,780    0,780    ?          0,780    ?          ?        0,500     0,629

=== Confusion Matrix ===

  a  b  c  d  e   <-- classified as
  0 15  0  0  0 |  a = 0
  0 92  0  0  0 |  b = 1
  0  8  0  0  0 |  c = 2
  0  2  0  0  0 |  d = 3
  0  1  0  0  0 |  e = 4
```

Status: OK

**J48**



**Classifier**

J48 -C 0.25 -M 2

**Test options**

○ Use training set
○ Supplied test set
○ Cross-validation Folds 10
● Percentage split % 66

(Nom) SURGERY

**Result list (right-click for options)**

- 23:46:45 - trees.RandomForest
- 23:50:11 - trees.J48
- 23:52:02 - trees.RandomTree
- 23:55:45 - trees.REPTree
- 23:55:58 - trees.LMT
- 23:56:30 - trees.J48
- 23:56:45 - trees.J48
- 23:56:48 - trees.J48

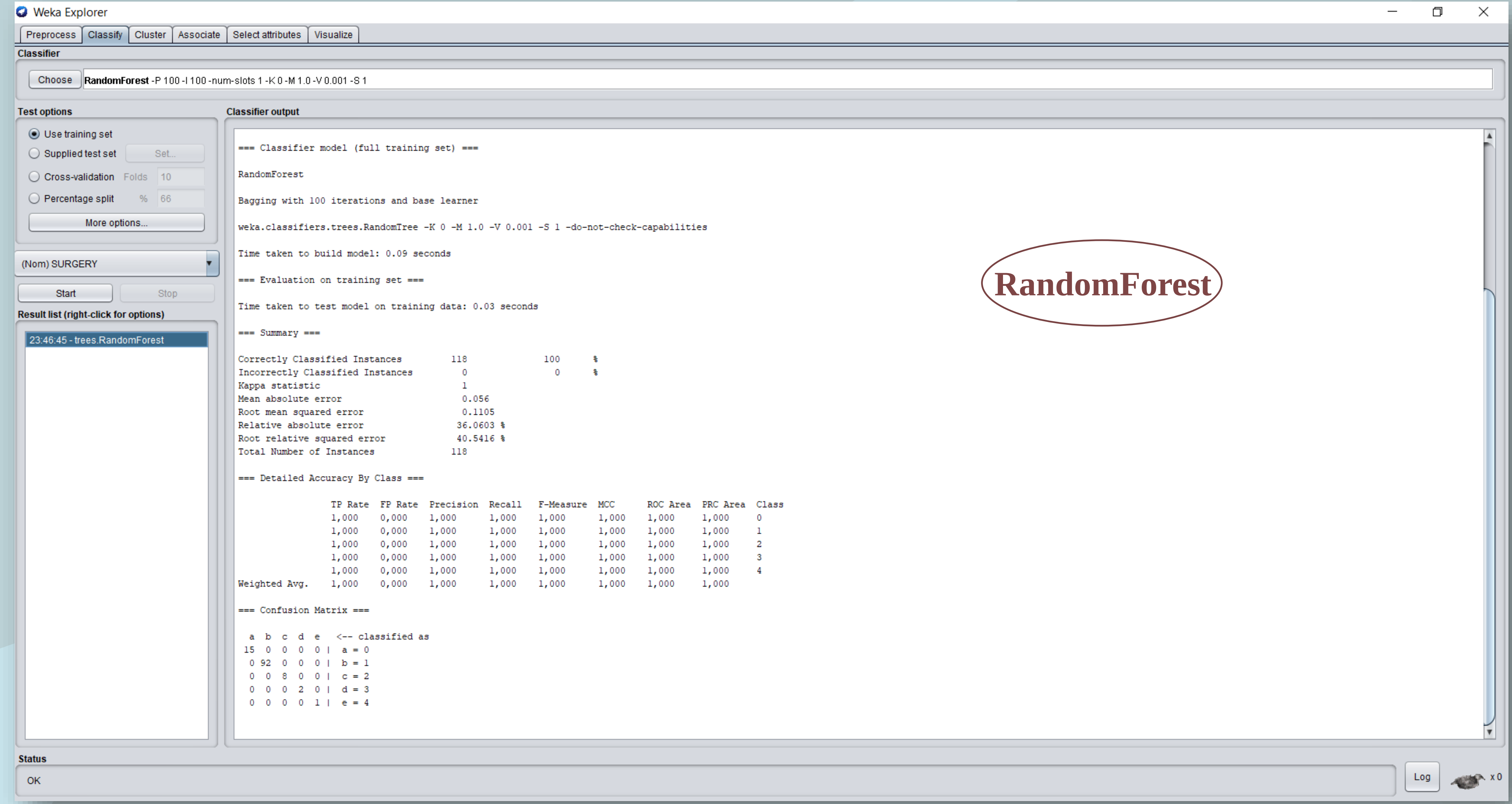
**Classifier output**

```
J48 pruned tree
------------------
: 1 (118.0/26.0)

Number of Leaves  :     1

Size of the tree :      1


Time taken to build model: 0 seconds

=== Evaluation on test split ===

Time taken to test model on test split: 0 seconds

=== Summary ===

Correctly Classified Instances          33               82.5    %
Incorrectly Classified Instances         7               17.5    %
Kappa statistic                          0
Mean absolute error                      0.145
Root mean squared error                  0.2566
Relative absolute error                 93.2223 %
Root relative squared error             99.1782 %
Total Number of Instances               40

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,050     0
                 1,000    1,000    0,825      1,000    0,904      ?        0,500     0,825     1
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,075     2
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,025     3
                 0,000    0,000    ?          0,000    ?          ?        0,500     0,025     4
Weighted Avg.    0,825    0,825    ?          0,825    ?          ?        0,500     0,690

=== Confusion Matrix ===

  a  b  c  d  e   <-- classified as
  0  2  0  0  0 |  a = 0
  0 33  0  0  0 |  b = 1
  0  3  0  0  0 |  c = 2
  0  1  0  0  0 |  d = 3
  0  1  0  0  0 |  e = 4
```

**J48, split 66**

**Status**

OK



**RandomForest** -P 100 -I 100 -num-slots 1 -K 0 -M 1.0 -V 0.001 -S 1

● Use training set
○ Supplied test set
○ Cross-validation Folds 10
○ Percentage split % 66

(Nom) SURGERY

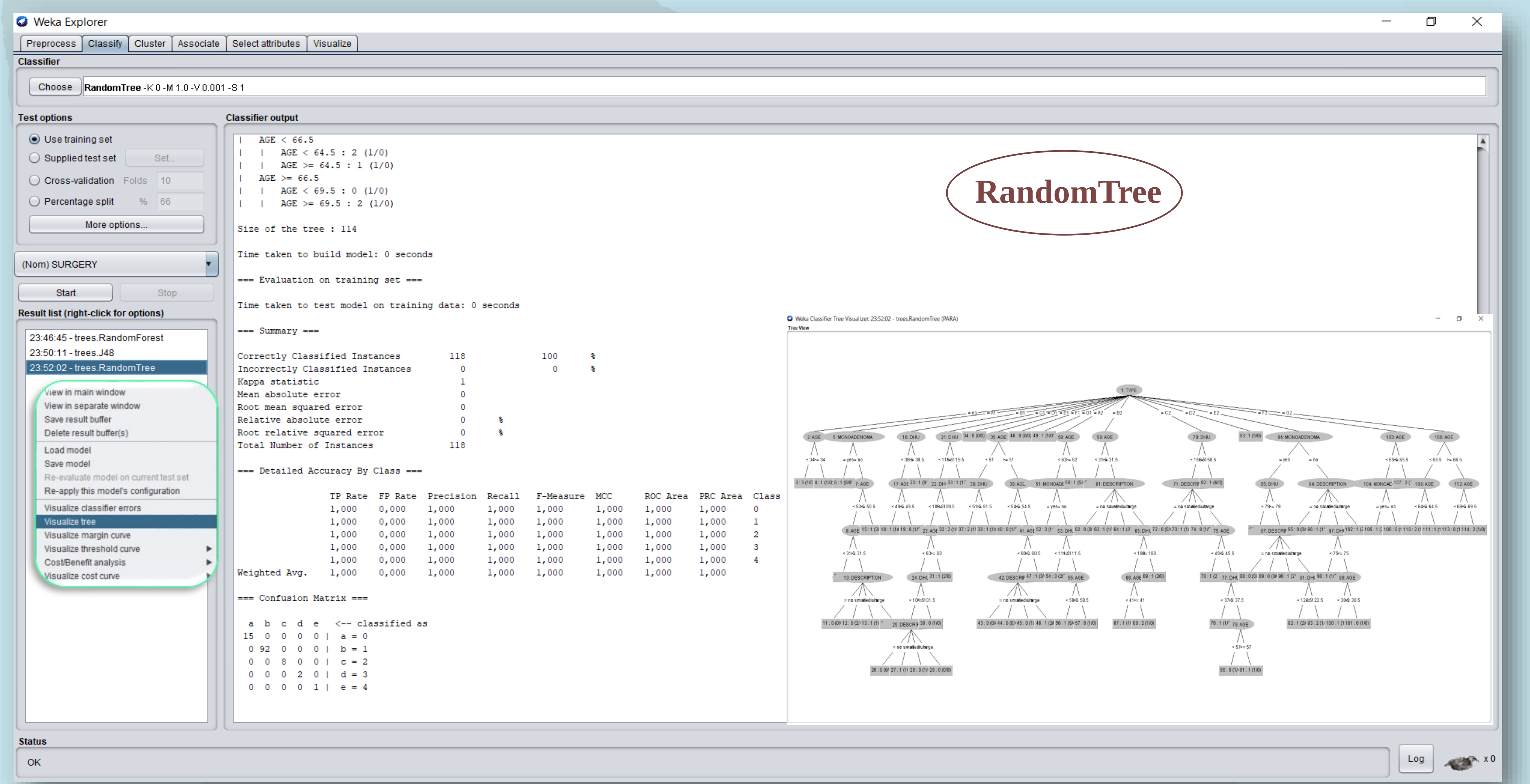
23:46:45 - trees.RandomForest

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

RandomForest

Bagging with 100 iterations and base learner

weka.classifiers.trees.RandomTree -K 0 -M 1.0 -V 0.001 -S 1 -do-not-check-capabilities

Time taken to build model: 0.09 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0.03 seconds

=== Summary ===

Correctly Classified Instances         118              100      %
Incorrectly Classified Instances         0                0      %
Kappa statistic                          1
Mean absolute error                      0.056
Root mean squared error                  0.1105
Relative absolute error                 36.0603 %
Root relative squared error             40.5416 %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     0
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     1
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     2
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     3
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     4
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000

=== Confusion Matrix ===

  a  b  c  d  e   <-- classified as
 15  0  0  0  0 |  a = 0
  0 92  0  0  0 |  b = 1
  0  0  8  0  0 |  c = 2
  0  0  0  2  0 |  d = 3
  0  0  0  0  1 |  e = 4
```

Status: OK

**RandomForest**

Υπ. Διδάκτορες: Χασάπη Μαρία Κωνσταντίνα
Χασάπη Λαμπρινή



**RandomTree**

Classifier: **RandomTree** -K 0 -M 1.0 -V 0.001 -S 1

Test options:
- ● Use training set
- ○ Supplied test set
- ○ Cross-validation Folds 10
- ○ Percentage split % 66

(Nom) SURGERY

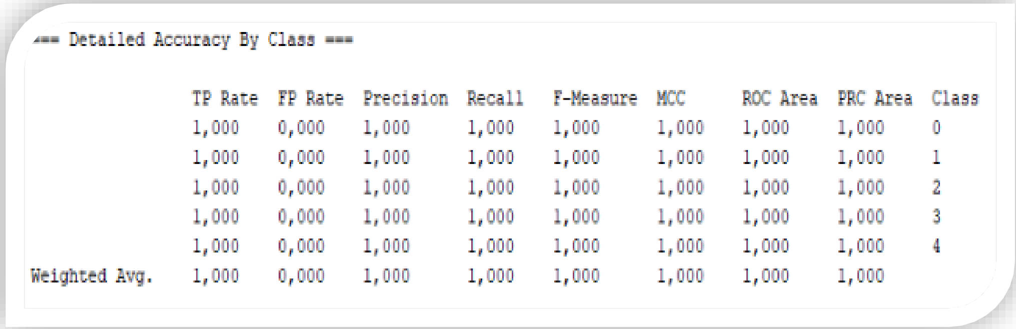
Result list (right-click for options):
- 23:46:45 - trees.RandomForest
- 23:50:11 - trees.J48
- 23:52:02 - trees.RandomTree

Classifier output:

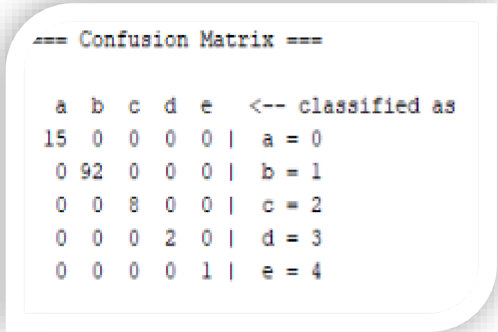
```
|   AGE < 66.5
|   |   AGE < 64.5 : 2 (1/0)
|   |   AGE >= 64.5 : 1 (1/0)
|   AGE >= 66.5
|   |   AGE < 69.5 : 0 (1/0)
|   |   AGE >= 69.5 : 2 (1/0)

Size of the tree : 114

Time taken to build model: 0 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0 seconds

=== Summary ===

Correctly Classified Instances         118              100      %
Incorrectly Classified Instances         0                0      %
Kappa statistic                          1
Mean absolute error                      0
Root mean squared error                  0
Relative absolute error                  0      %
Root relative squared error              0      %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     0
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     1
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     2
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     3
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     4
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000

=== Confusion Matrix ===

  a  b  c  d  e   <-- classified as
 15  0  0  0  0 |  a = 0
  0 92  0  0  0 |  b = 1
  0  0  8  0  0 |  c = 2
  0  0  0  2  0 |  d = 3
  0  0  0  0  1 |  e = 4
```

Status: OK

# Μετρικές αξιολόγησης ανά κλάση (WEKA)



```
=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     0
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     1
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     2
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     3
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     4
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000
```



```
=== Confusion Matrix ===

  a  b  c  d  e   <-- classified as
 15  0  0  0  0 |  a = 0
  0 92  0  0  0 |  b = 1
  0  0  8  0  0 |  c = 2
  0  0  0  2  0 |  d = 3
  0  0  0  0  1 |  e = 4
```

Accuracy: ορθότητα συστήματος

$$\frac{TP + TN}{TP + FP + FN + TN}$$

Precision: ακρίβεια συστήματος

$$\frac{TP}{TP + FP}$$

Sensitivity/Recall: ευαισθησία συστήματος

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

F-Measure: συνδυασμός precision και recall

$$\frac{2 * Precision * Recall}{Precision + Recall}$$

Για την κλάση εξόδου 0 έχουμε:

- Precision = 100% (Ακρίβεια)
- Recall = 100% (Ευαισθησία)
- F-Measure = 100% (Precision and Recall)

Για την κλάση εξόδου 1 έχουμε:

- Precision = 100%
- Recall = 100%
- F-Measure = 100%

Για την κλάση εξόδου 2 έχουμε:

- Precision = 100%
- Recall = 100%
- F-Measure = 100%

Για την κλάση εξόδου 3 έχουμε:

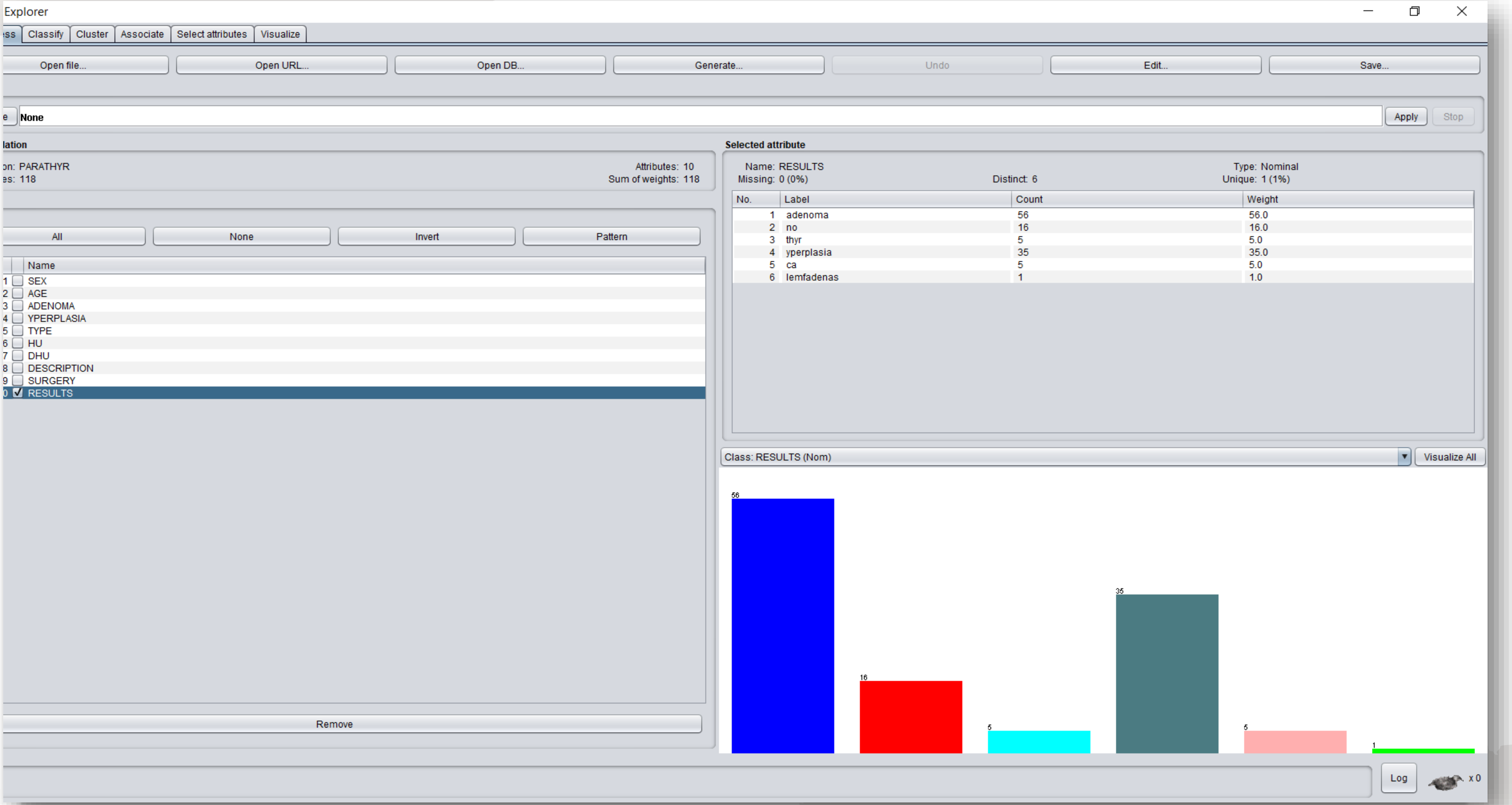
- Precision = 100%
- Recall = 100%
- F-Measure = 100%

Για την κλάση εξόδου 4 έχουμε:

- Precision = 100%
- Recall = 100%
- F-Measure = 100%

Και συνολικά για το μοντέλο δηλαδή για τους ασθενείς που είχαν χειρουργικά αποτελέσματα (0, 1, 2, 3, 4) , έχουμε:

- Accuracy = 100%
- Precision = 100%
- Recall = 100%
- F-Measure = 100%



e None

lation

on: PARATHYR
es: 118

Attributes: 10
Sum of weights: 118

|  |  | Name |
|---|---|---|
| 1 | ☐ | SEX |
| 2 | ☐ | AGE |
| 3 | ☐ | ADENOMA |
| 4 | ☐ | YPERPLASIA |
| 5 | ☐ | TYPE |
| 6 | ☐ | HU |
| 7 | ☐ | DHU |
| 8 | ☐ | DESCRIPTION |
| 9 | ☐ | SURGERY |
| 0 | ☑ | RESULTS |

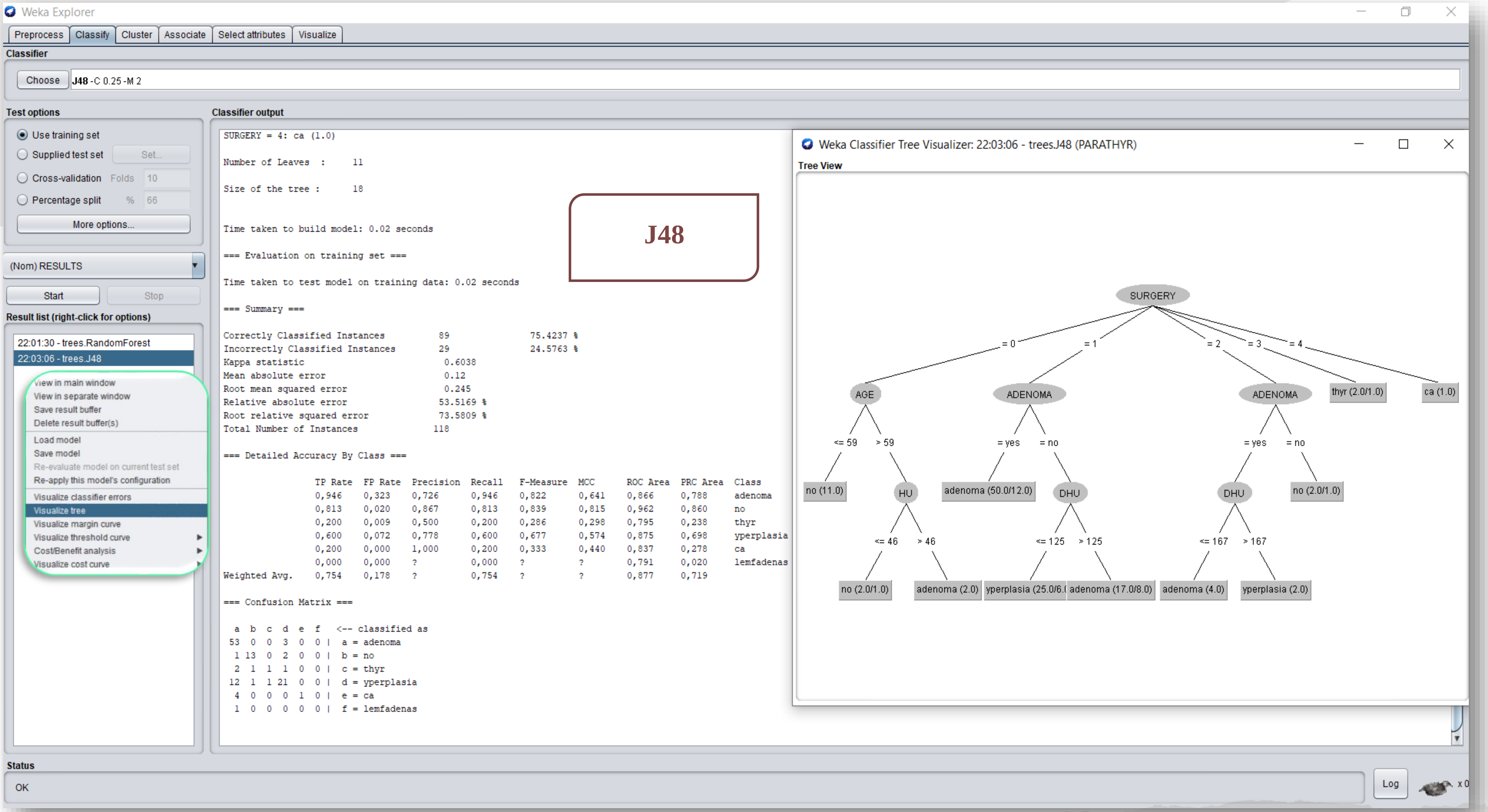
**Selected attribute**

Name: RESULTS
Missing: 0 (0%)
Distinct: 6
Type: Nominal
Unique: 1 (1%)

| No. | Label | Count | Weight |
|---|---|---|---|
| 1 | adenoma | 56 | 56.0 |
| 2 | no | 16 | 16.0 |
| 3 | thyr | 5 | 5.0 |
| 4 | yperplasia | 35 | 35.0 |
| 5 | ca | 5 | 5.0 |
| 6 | lemfadenas | 1 | 1.0 |

Class: RESULTS (Nom)

# J48



Classifier: J48 -C 0.25 -M 2

Test options:
- ● Use training set
- ○ Supplied test set
- ○ Cross-validation Folds 10
- ○ Percentage split % 66

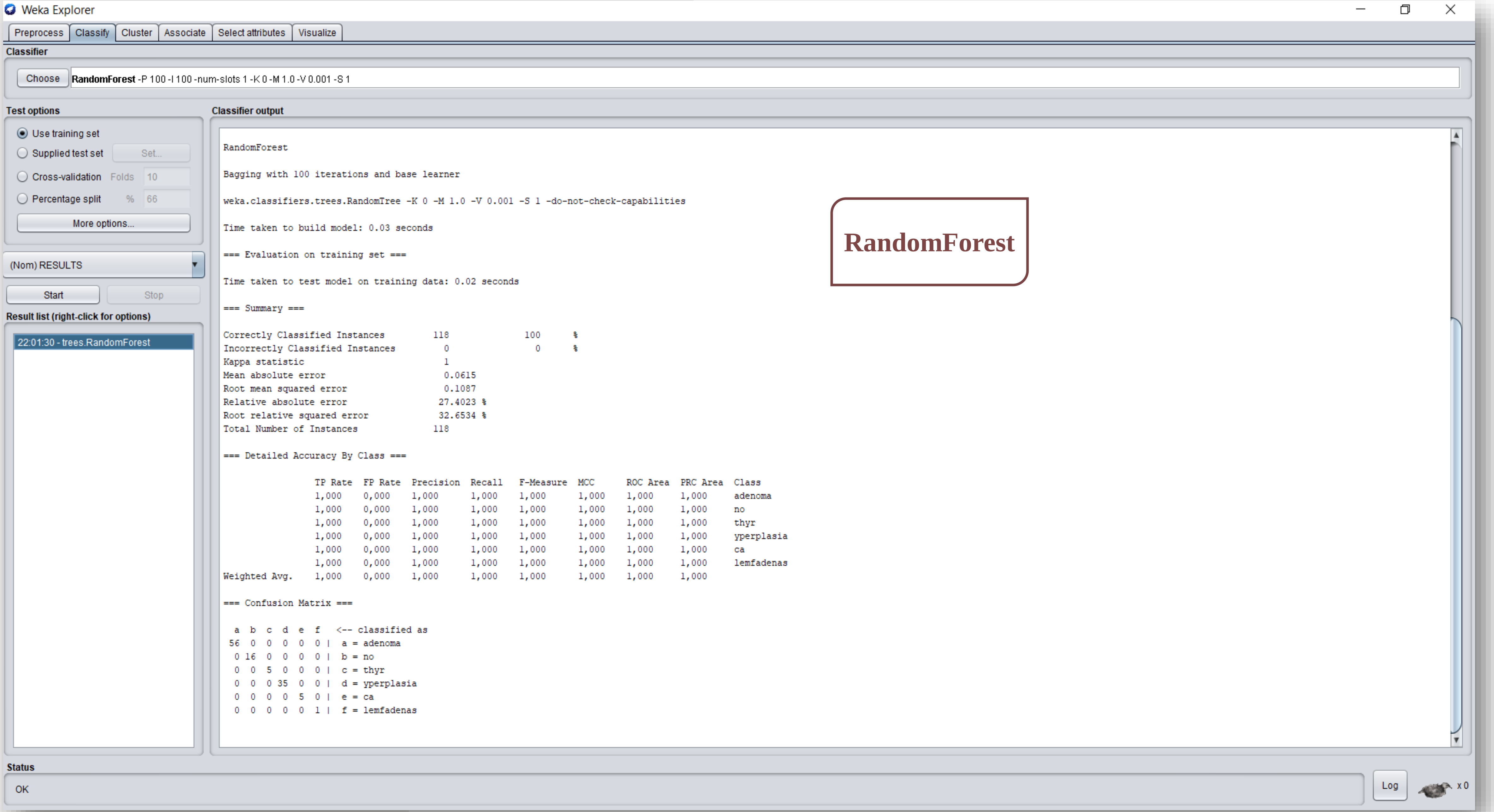
(Nom) RESULTS

Result list:
- 22:01:30 - trees.RandomForest
- 22:03:06 - trees.J48

```
SURGERY = 4: ca (1.0)

Number of Leaves  :     11

Size of the tree :      18


Time taken to build model: 0.02 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0.02 seconds

=== Summary ===

Correctly Classified Instances          89               75.4237 %
Incorrectly Classified Instances        29               24.5763 %
Kappa statistic                          0.6038
Mean absolute error                      0.12
Root mean squared error                  0.245
Relative absolute error                 53.5169 %
Root relative squared error             73.5809 %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0,946    0,323    0,726      0,946    0,822      0,641    0,866     0,788     adenoma
                 0,813    0,020    0,867      0,813    0,839      0,815    0,962     0,860     no
                 0,200    0,009    0,500      0,200    0,286      0,298    0,795     0,238     thyr
                 0,600    0,072    0,778      0,600    0,677      0,574    0,875     0,698     yperplasia
                 0,200    0,000    1,000      0,200    0,333      0,440    0,837     0,278     ca
                 0,000    0,000    ?          0,000    ?          ?        0,791     0,020     lemfadenas
Weighted Avg.    0,754    0,178    ?          0,754    ?          ?        0,877     0,719

=== Confusion Matrix ===

  a  b  c  d  e  f   <-- classified as
 53  0  0  3  0  0 |  a = adenoma
  1 13  0  2  0  0 |  b = no
  2  1  1  1  0  0 |  c = thyr
 12  1  1 21  0  0 |  d = yperplasia
  4  0  0  0  1  0 |  e = ca
  1  0  0  0  0  0 |  f = lemfadenas
```

Status: OK

**RandomForest**



Classifier: RandomForest -P 100 -I 100 -num-slots 1 -K 0 -M 1.0 -V 0.001 -S 1

Test options:
- ● Use training set
- ○ Supplied test set
- ○ Cross-validation Folds 10
- ○ Percentage split % 66

(Nom) RESULTS

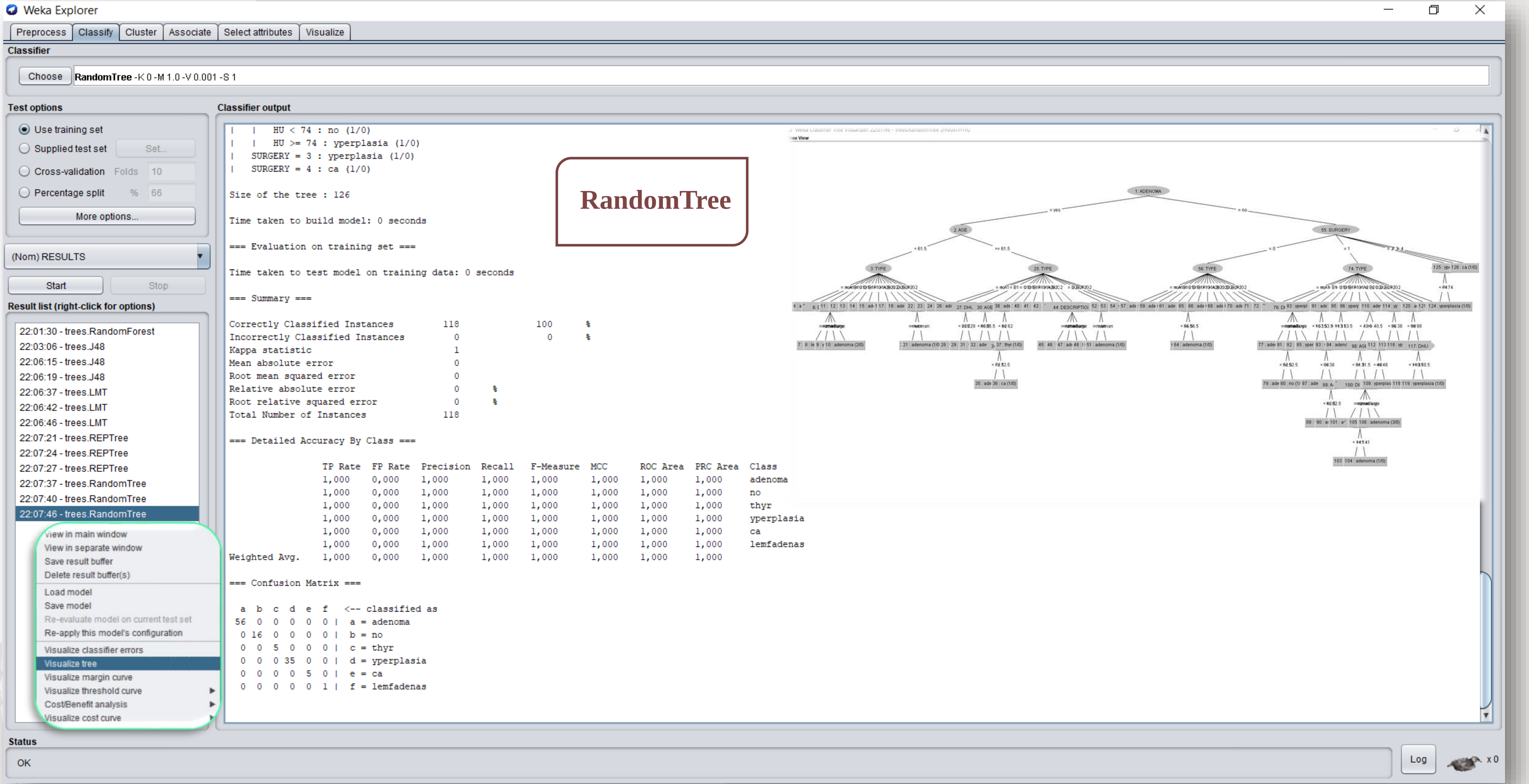
Result list (right-click for options): 22:01:30 - trees.RandomForest

Status: OK

Classifier output:

```
RandomForest

Bagging with 100 iterations and base learner

weka.classifiers.trees.RandomTree -K 0 -M 1.0 -V 0.001 -S 1 -do-not-check-capabilities

Time taken to build model: 0.03 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0.02 seconds

=== Summary ===

Correctly Classified Instances         118              100      %
Incorrectly Classified Instances         0                0      %
Kappa statistic                          1
Mean absolute error                      0.0615
Root mean squared error                  0.1087
Relative absolute error                 27.4023 %
Root relative squared error             32.6534 %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     adenoma
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     no
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     thyr
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     yperplasia
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     ca
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     lemfadenas
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000

=== Confusion Matrix ===

  a  b  c  d  e  f   <-- classified as
 56  0  0  0  0  0 |  a = adenoma
  0 16  0  0  0  0 |  b = no
  0  0  5  0  0  0 |  c = thyr
  0  0  0 35  0  0 |  d = yperplasia
  0  0  0  0  5  0 |  e = ca
  0  0  0  0  0  1 |  f = lemfadenas
```

# RandomTree



Classifier: **RandomTree** -K 0 -M 1.0 -V 0.001 -S 1

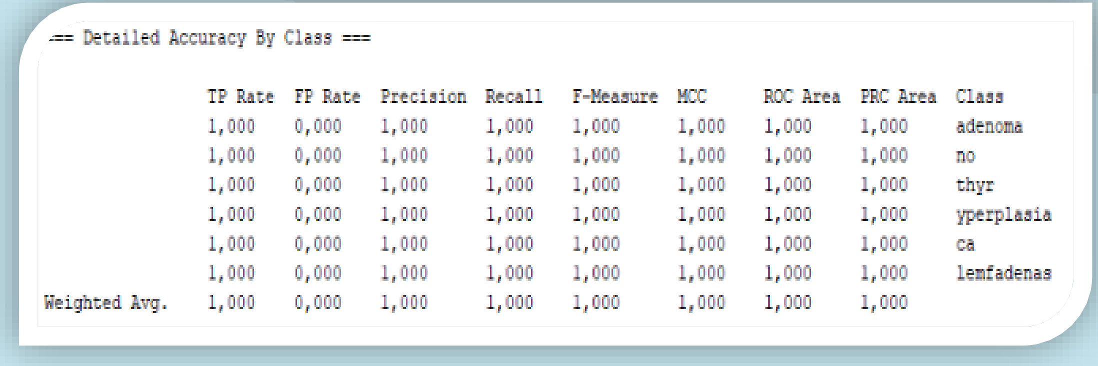
Test options: ● Use training set

(Nom) RESULTS

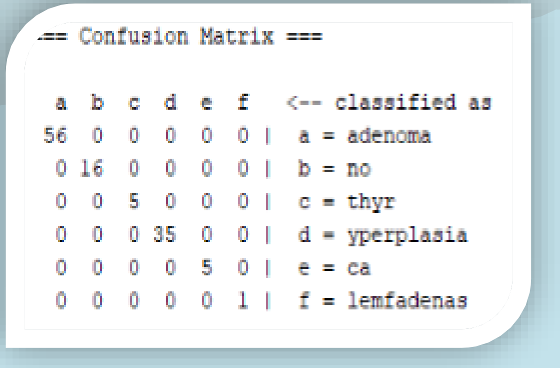
Status: OK

```
|   |   HU < 74 : no (1/0)
|   |   HU >= 74 : yperplasia (1/0)
|   SURGERY = 3 : yperplasia (1/0)
|   SURGERY = 4 : ca (1/0)

Size of the tree : 126

Time taken to build model: 0 seconds

=== Evaluation on training set ===

Time taken to test model on training data: 0 seconds

=== Summary ===

Correctly Classified Instances         118              100      %
Incorrectly Classified Instances         0                0      %
Kappa statistic                          1
Mean absolute error                      0
Root mean squared error                  0
Relative absolute error                  0      %
Root relative squared error              0      %
Total Number of Instances              118

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     adenoma
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     no
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     thyr
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     yperplasia
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     ca
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     lemfadenas
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000

=== Confusion Matrix ===

  a  b  c  d  e  f   <-- classified as
 56  0  0  0  0  0 |  a = adenoma
  0 16  0  0  0  0 |  b = no
  0  0  5  0  0  0 |  c = thyr
  0  0  0 35  0  0 |  d = yperplasia
  0  0  0  0  5  0 |  e = ca
  0  0  0  0  0  1 |  f = lemfadenas
```

# Μετρικές αξιολόγησης ανά κλάση (WEKA)



```
=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     adenoma
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     no
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     thyr
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     yperplasia
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     ca
                 1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000     lemfadenas
Weighted Avg.    1,000    0,000    1,000      1,000    1,000      1,000    1,000     1,000
```



```
=== Confusion Matrix ===

  a  b  c  d  e  f   <-- classified as
 56  0  0  0  0  0 |  a = adenoma
  0 16  0  0  0  0 |  b = no
  0  0  5  0  0  0 |  c = thyr
  0  0  0 35  0  0 |  d = yperplasia
  0  0  0  0  5  0 |  e = ca
  0  0  0  0  0  1 |  f = lemfadenas
```

Accuracy: ορθότητα συστήματος

$$\frac{TP + TN}{TP + FP + FN + TN}$$

Precision: ακρίβεια συστήματος

$$\frac{TP}{TP + FP}$$

Sensitivity/Recall: ευαισθησία συστήματος

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

F-Measure: συνδυασμός precision και recall

$$\frac{2 * Precision * Recall}{Precision + Recall}$$

Για την κλάση εξόδου adenoma έχουμε:

- ➢ Precision = 100% (Ακρίβεια)
- ➢ Recall = 100% (Ευαισθησία)
- ➢ F-Measure = 100% (Precision and Recall)

Για την κλάση εξόδου no έχουμε:

- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Για την κλάση εξόδου thyr έχουμε:

- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Για την κλάση εξόδου yperplasia έχουμε:

- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Για την κλάση εξόδου ca έχουμε:

- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Για την κλάση εξόδου lemfadenas έχουμε:

- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Και συνολικά για το μοντέλο δηλαδή για τους ασθενείς που είχαν ανατομοπαθολογικά αποτελέσματα (adenoma, no, thyr, yperplasia, ca, lemfadenas) , έχουμε:

- ➢ Accuracy = 100%
- ➢ Precision = 100%
- ➢ Recall = 100%
- ➢ F-Measure = 100%

Υπ. Διδάκτορες: Χασάπη Μαρία Κωνσταντίνα
Χασάπη Λαμπρινή