

Homework 7

Clustering with WEKA

Ομάδα G

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THESSALY

(2.1)

- We load the “*CardiologyCategorical.csv*” data file to build a neural network (using the MLP algorithm) that predicts whether a patient has a heart condition.

Preprocess Classify Cluster Associate Select attributes Visualize

Open file... Open URL... Open DB... Generate... Undo Edit... Save...

Filter
Choose **None** Apply Stop

Current relation
Relation: CardiologyCategorical
Instances: 303
Attributes: 14
Sum of weights: 303

Attributes
All None Invert Pattern

No.	Name
1	<input checked="" type="checkbox"/> age
2	<input type="checkbox"/> sex
3	<input type="checkbox"/> chest pain type
4	<input type="checkbox"/> blood pressure
5	<input type="checkbox"/> cholesterol
6	<input type="checkbox"/> Fasting blood sugar <120
7	<input type="checkbox"/> resting ecg
8	<input type="checkbox"/> maximum heart rate
9	<input type="checkbox"/> angina
10	<input type="checkbox"/> peak
11	<input type="checkbox"/> slope
12	<input type="checkbox"/> #colored vessels
13	<input type="checkbox"/> thal
14	<input type="checkbox"/> class

Remove

Selected attribute
Name: age
Missing: 0 (0%)
Distinct: 41
Type: Numeric
Unique: 4 (1%)

Statistic	Value
Minimum	29
Maximum	77
Mean	54.366
StdDev	9.082

Class: class (Nom) Visualize

Age Range	Frequency (Red)	Frequency (Blue)
29-33	11	1
33-37	33	1
37-41	38	1
41-45	45	1
45-49	52	1
49-53	63	1
53-57	43	1
57-61	14	1
61-65	3	1

- We choose “True” value on “normalizeAttributes” to normalize our features and set learning rate for weights updates to 0.01

normalizeAttributes	True
learningRate	0.01

- The 10-fold cross-validation accuracy of your model (A1) is 84.1584%

Preprocess Classify Cluster Associate Select attributes Visualize

Classifier

Choose **MultilayerPerceptron** -L 0.01 -M 0.2 -N 500 -V 0 -S 0 -E 20 -H a

Test options

☐ Use training set

☐ Supplied test set Set...

☒ Cross-validation Folds **10**

☐ Percentage split % 70

More options...

(Nom) class

Start Stop

Result list (right-click for options)

14:56:01 - functions.MultilayerPerceptron

Classifier output

Node 1

Time taken to build model: 1.3 seconds

=== Stratified cross-validation ===

=== Summary ===

Correctly Classified Instances	255	84.1584 %
Incorrectly Classified Instances	48	15.8416 %
Kappa statistic	0.6795	
Mean absolute error	0.2013	
Root mean squared error	0.345	
Relative absolute error	40.5837 %	
Root relative squared error	69.2689 %	
Total Number of Instances	303	

=== Detailed Accuracy By Class ===

	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	PRC Area	Class
	0,804	0,127	0,841	0,804	0,822	0,680	0,909	0,901	Sick
	0,873	0,196	0,842	0,873	0,857	0,680	0,909	0,908	Healthy
Weighted Avg.	0,842	0,165	0,842	0,842	0,841	0,680	0,909	0,905	

=== Confusion Matrix ===

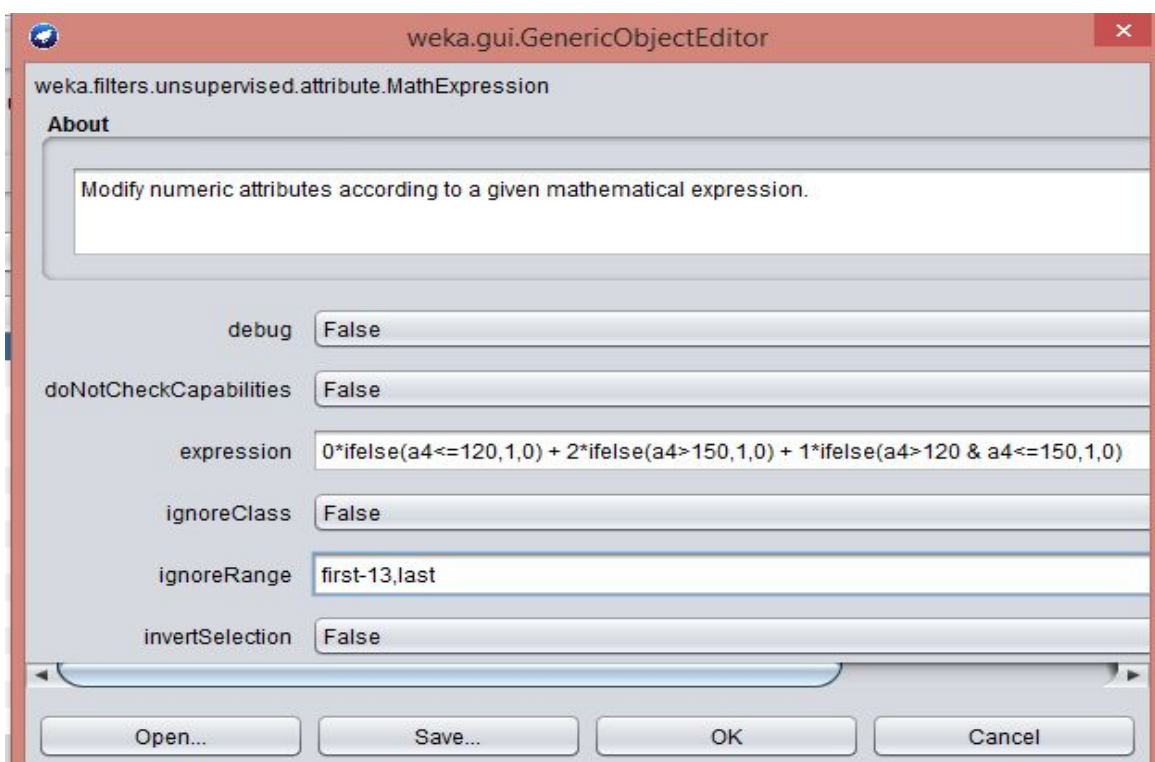
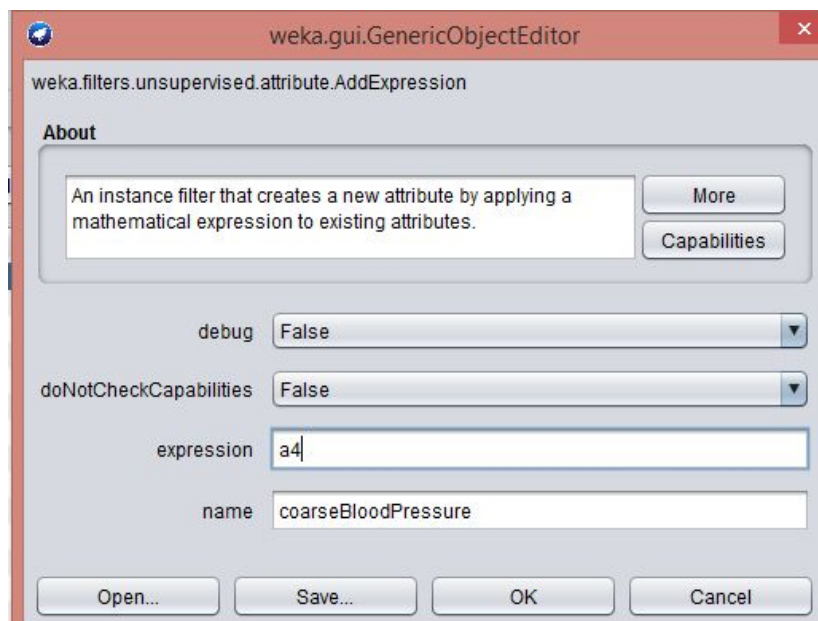
```

a b <-- classified as
111 27 | a = Sick
21 144 | b = Healthy

```

(2.2)

- We create a new attribute *coarseBloodPressure*, with values: Low if *blood pressure* is less than or equal to 120, Normal if *blood pressure* is greater than 120 but less than or equal to 150, and High if *blood pressure* is greater than 150
- First we create a copy of *blood pressure* with the new name using filter *AddExpression* and then with *MathExpression* we transform *blood pressure*'s values as follows :



1: age	2: sex	3: chest pain type	4: blood pressure	5: cholesterol	6: Fasting blood sugar 120	7: resting ecg	8: maximum heart rate	9: angina	10: peak	11: slope	12: #colored vessels	13: thal	14: coarseBloodPressure	15: class
Numeric	Nominal	Nominal	Numeric	Numeric	Nominal	Nominal	Numeric	Nominal	Numeric	Nominal	Numeric	Nominal	Numeric	Nominal
60.0	Male	Asymptomatic	130.0	266.0	FALSE	Hyp	132.0	TRUE	2.4	Flat	2.0	Rev	(Normal)	1.0 Sick
49.0	Male	Abnormal Angi...	130.0	266.0	FALSE	Normal	171.0	FALSE	0.6	Up	0.0	Nor...		1.0 Healthy
64.0	Male	Angina	110.0	244.0	FALSE	Hyp	144.0	TRUE	1.8	Flat	0.0	Nor...	(Low)	0.0 Healthy
63.0	Male	Asymptomatic	130.0	254.0	FALSE	Hyp	147.0	FALSE	1.4	Flat	1.0	Rev		1.0 Sick
53.0	Male	Asymptomatic	140.0	203.0	TRUE	Hyp	155.0	TRUE	3.1	Down	0.0	Rev		1.0 Sick
58.0	Fem...	Angina	150.0	283.0	TRUE	Hyp	162.0	FALSE	1.0	Up	0.0	Nor...		1.0 Healthy
58.0	Male	Abnormal Angi...	120.0	284.0	FALSE	Hyp	160.0	FALSE	1.8	Flat	0.0	Nor...		0.0 Sick
58.0	Male	NoTang	132.0	224.0	FALSE	Hyp	173.0	FALSE	3.2	Up	2.0	Rev		1.0 Sick
63.0	Male	Angina	145.0	233.0	TRUE	Hyp	150.0	FALSE	2.3	Down	0.0	Fix		1.0 Healthy
67.0	Male	Asymptomatic	160.0	286.0	FALSE	Hyp	168.0	TRUE	1.5	Flat	3.0	Nor...	(High)	2.0 Sick
67.0	Male	Asymptomatic	120.0	229.0	FALSE	Hyp	129.0	TRUE	2.6	Flat	2.0	Rev		0.0 Sick
37.0	Male	NoTang	130.0	250.0	FALSE	Normal	187.0	FALSE	3.5	Down	0.0	Nor...		1.0 Healthy
41.0	Fem...	Abnormal Angi...	130.0	204.0	FALSE	Hyp	172.0	FALSE	1.4	Up	0.0	Nor...		1.0 Healthy
56.0	Male	Abnormal Angi...	120.0	236.0	FALSE	Normal	178.0	FALSE	0.8	Up	0.0	Nor...		0.0 Healthy
62.0	Fem...	Asymptomatic	140.0	268.0	FALSE	Hyp	160.0	FALSE	3.6	Down	2.0	Nor...		1.0 Sick
57.0	Fem...	Asymptomatic	120.0	354.0	FALSE	Normal	163.0	TRUE	0.6	Up	0.0	Nor...		0.0 Healthy
57.0	Male	Asymptomatic	140.0	192.0	FALSE	Normal	148.0	FALSE	0.4	Flat	0.0	Fix		1.0 Healthy
56.0	Fem...	Abnormal Angi...	140.0	294.0	FALSE	Hyp	153.0	FALSE	1.3	Flat	0.0	Nor...		1.0 Healthy
56.0	Male	NoTang	130.0	256.0	TRUE	Hyp	142.0	TRUE	0.6	Flat	1.0	Fix		1.0 Sick
44.0	Male	Abnormal Angi...	120.0	263.0	FALSE	Normal	173.0	FALSE	0.0	Up	0.0	Rev		0.0 Healthy
50.0	Fem...	NoTang	120.0	219.0	FALSE	Normal	158.0	FALSE	1.6	Flat	0.0	Nor...		0.0 Healthy
58.0	Fem...	NoTang	120.0	340.0	FALSE	Normal	172.0	FALSE	0.0	Up	0.0	Nor...		0.0 Healthy
66.0	Fem...	Angina	150.0	226.0	FALSE	Normal	114.0	FALSE	2.6	Down	0.0	Nor...		1.0 Healthy
43.0	Male	Asymptomatic	150.0	247.0	FALSE	Normal	171.0	FALSE	1.5	Up	0.0	Nor...		1.0 Healthy
40.0	Male	Asymptomatic	110.0	167.0	FALSE	Hyp	114.0	TRUE	2.0	Flat	0.0	Rev		0.0 Sick
69.0	Fem...	Angina	140.0	239.0	FALSE	Normal	151.0	FALSE	1.8	Up	2.0	Nor...		1.0 Healthy
60.0	Male	Asymptomatic	117.0	230.0	TRUE	Normal	160.0	TRUE	1.4	Up	2.0	Rev		0.0 Sick
64.0	Male	NoTang	140.0	335.0	FALSE	Normal	158.0	FALSE	0.0	Up	0.0	Nor...		1.0 Sick
59.0	Male	Asymptomatic	135.0	234.0	FALSE	Normal	161.0	FALSE	0.5	Flat	0.0	Rev		1.0 Healthy
44.0	Male	NoTang	130.0	233.0	FALSE	Normal	179.0	TRUE	0.4	Up	0.0	Nor...		1.0 Healthy
42.0	Male	Asymptomatic	140.0	226.0	FALSE	Normal	178.0	FALSE	0.0	Up	0.0	Nor...		1.0 Healthy
43.0	Male	Asymptomatic	120.0	177.0	FALSE	Hyp	120.0	TRUE	2.5	Flat	0.0	Rev		0.0 Sick

(2.3)

- We build a neural network (using the MLP algorithm) that predicts whether a patient has a heart condition, using the new attribute *coarseBloodPressure* instead of the original *blood pressure*. The 10-fold cross-validation accuracy of your model (A2) is 83.1683%

No.		Name
1	<input type="checkbox"/>	age
2	<input type="checkbox"/>	sex
3	<input type="checkbox"/>	chest pain type
4	<input type="checkbox"/>	cholesterol
5	<input type="checkbox"/>	Fasting blood sugar <120
6	<input type="checkbox"/>	resting ecg
7	<input type="checkbox"/>	maximum heart rate
8	<input type="checkbox"/>	angina
9	<input type="checkbox"/>	peak
10	<input type="checkbox"/>	slope
11	<input type="checkbox"/>	#colored vessels
12	<input type="checkbox"/>	thal
13	<input type="checkbox"/>	coarseBloodPressure
14	<input type="checkbox"/>	class

Classifier
Choose **MultilayerPerceptron** -L 0.01 -M 0.2 -N 500 -V 0 -S 0 -E 20 -H a

Test options
☐ Use training set
☐ Supplied test set Set...
☒ Cross-validation Folds **10**
☐ Percentage split % 70
More options...
(Nom) class
Start Stop

Classifier output
Time taken to build model: 1.31 seconds
=== Stratified cross-validation ===
=== Summary ===
Correctly Classified Instances 252 **83.1683 %**
Incorrectly Classified Instances 51 **16.8317 %**
Kappa statistic 0.6601
Mean absolute error 0.2027
Root mean squared error 0.3474
Relative absolute error 40.8586 %
Root relative squared error 69.7447 %
Total Number of Instances 303
=== Detailed Accuracy By Class ===

	TP Rate	FP Rate	Precision	Recall	F-Measure	MCC	ROC Area	FRC Area	Class
	0,804	0,145	0,822	0,804	0,813	0,660	0,908	0,899	Sick
	0,855	0,196	0,839	0,855	0,847	0,660	0,908	0,907	Healthy
Weighted Avg.	0,832	0,173	0,832	0,832	0,832	0,660	0,908	0,903	

=== Confusion Matrix ===
a b <-- classified as
111 27 | a = Sick
24 141 | b = Healthy

Result list (right-click for options)
14:56:01 - functions.MultilayerPerceptron
14:59:59 - functions.MultilayerPerceptron

(2.4)

- The accuracies we achieve from using blood pressure in the first occasion and coarse blood pressure in the second do not have a significant difference (1%). The generalisation of the blood pressure feature does not seem to work better than raw values, but it usually depends to the problem.

(2.5)

- We remove all records (4 in total) whose value of the attribute *resting ecg* is Abnormal.

No.	1: age	2: sex	3: chest pain type	4: cholesterol	5: Fasting blood sugar	120	6: resting ecg	7: maximum heart rate	8: angina	9: peak	10: slope	11: #colored vessels	12:
	Numeric	Nominal	Nominal	Numeric	Nominal		Nominal	Numeric	Nominal	Numeric	Nominal	Numeric	Nominal
1	60.0	Male	Asymptomatic	206.0	FALSE		Hyp	132.0	TRUE	2.4	Flat	2.0	Re
2	49.0	Male	Abnormal Angi...	266.0	FALSE		Normal	171.0	FALSE	0.6	Up	0.0	No
3	64.0	Male	Angina	211.0	FALSE		Hyp	144.0	TRUE	1.8	Flat	0.0	No
4	63.0	Male	Asymptomatic	254.0	FALSE		Hyp	147.0	FALSE	1.4	Flat	1.0	Re
5	53.0	Male	Asymptomatic	203.0	TRUE		Hyp	155.0	TRUE	3.1	Down	0.0	Re
6	58.0	Fem...	Angina	283.0	TRUE		Hyp	162.0	FALSE	1.0	Up	0.0	No
7	58.0	Male	Abnormal Angi...	284.0	FALSE		Hyp	160.0	FALSE	1.8	Flat	0.0	No
8	58.0	Male	NoTang	224.0	FALSE		Hyp	173.0	FALSE	3.2	Up	2.0	Re
9	63.0	Male	Angina	233.0	TRUE		Hyp	150.0	FALSE	2.3	Down	0.0	Fix
10	67.0	Male	Asymptomatic	286.0	FALSE		Hyp	108.0	TRUE	1.5	Flat	3.0	No
11	67.0	Male	Asymptomatic	229.0	FALSE		Hyp	129.0	TRUE	2.6	Flat	2.0	Re
12	37.0	Male	NoTang	250.0	FALSE		Abnormal	187.0	FALSE	3.5	Down	0.0	No
13	41.0	Fem...	Undo	ALSE			Hyp	172.0	FALSE	1.4	Up	0.0	No
14	56.0	Male	Copy	ALSE			Normal	178.0	FALSE	0.8	Up	0.0	No
15	62.0	Fem...	Search...	ALSE			Hyp	160.0	FALSE	3.6	Down	2.0	No
16	57.0	Fem...	Clear search	ALSE			Normal	163.0	TRUE	0.6	Up	0.0	No
17	57.0	Male		ALSE			Normal	148.0	FALSE	0.4	Flat	0.0	Fix
18	56.0	Fem...	Delete selected instance	ALSE			Hyp	153.0	FALSE	1.3	Flat	0.0	No
19	56.0	Male	Delete ALL selected instances	TRUE			Hyp	142.0	TRUE	0.6	Flat	1.0	Fix
20	44.0	Male	Insert new instance	ALSE			Normal	173.0	FALSE	0.0	Up	0.0	Re
21	50.0	Fem...	Set instance weight	ALSE			Normal	158.0	FALSE	1.6	Flat	0.0	No
22	58.0	Fem...		ALSE			Normal	172.0	FALSE	0.0	Up	0.0	No
23	66.0	Fem...		ALSE			Normal	114.0	FALSE	2.6	Down	0.0	No
24	43.0	Male	Asymptomatic	247.0	FALSE		Normal	171.0	FALSE	1.5	Up	0.0	No
25	40.0	Male	Asymptomatic	167.0	FALSE		Hyp	114.0	TRUE	2.0	Flat	0.0	Re
26	69.0	Fem...	Angina	239.0	FALSE		Normal	151.0	FALSE	1.8	Up	2.0	No
27	60.0	Male	Asymptomatic	230.0	TRUE		Normal	160.0	TRUE	1.4	Up	2.0	Re
28	64.0	Male	NoTang	335.0	FALSE		Normal	158.0	FALSE	0.0	Up	0.0	No
29	58.0	Male	Asymptomatic	221.0	FALSE		Normal	164.0	FALSE	0.5	Flat	0.0	No

(2.6)

- We construct a decision tree (using the J48 Algorithm) that predicts whether a patient has a heart condition, given the attributes *age*, *sex*, *chest pain type*, *coarseBloodPressure*, *angina*, *peak*, and *slope*.

No.		Name
1	<input type="checkbox"/>	age
2	<input type="checkbox"/>	sex
3	<input type="checkbox"/>	chest pain type
4	<input type="checkbox"/>	angina
5	<input type="checkbox"/>	peak
6	<input type="checkbox"/>	slope
7	<input type="checkbox"/>	coarseBloodPressure
8	<input type="checkbox"/>	class

Preprocess Classify Cluster Associate Select attributes Visualize

Clusterer

Choose SimpleKMeans -init 0 -max-candidates 100 -periodic-pruning 10000 -min-density 2.0 -t1 -1.25 -t2 -1.0 -N 3 -A "weka.core.EuclideanDistance -R first-last" -i 500 -num-slots 3 -S 10

Cluster mode

☐ Use training set
☐ Supplied test set Set...
☒ Percentage split % 70
☐ Classes to clusters evaluation
 (Num) CHMAX
☒ Store clusters for visualization

Ignore attributes

Start Stop

Result list (right-click for options)

13:25:49 - SimpleKMeans
 13:29:25 - SimpleKMeans
 13:29:31 - SimpleKMeans
 13:29:37 - SimpleKMeans
 13:32:09 - SimpleKMeans
 13:32:19 - SimpleKMeans
 13:32:21 - SimpleKMeans
 13:32:24 - SimpleKMeans
 13:32:24 - SimpleKMeans_0
 13:32:25 - SimpleKMeans
 13:32:30 - SimpleKMeans
 13:33:18 - SimpleKMeans
 13:34:01 - SimpleKMeans
 13:34:05 - SimpleKMeans
 13:45:06 - SimpleKMeans
 13:45:07 - SimpleKMeans
 13:50:19 - SimpleKMeans
 13:50:23 - SimpleKMeans
 15:46:37 - SimpleKMeans
 18:51:01 - SimpleKMeans
 18:51:17 - SimpleKMeans

Clusterer output

Time taken to build model (full training data) : 0 seconds

=== Model and evaluation on test split ===

KMeans
 =====

Number of iterations: 8
 Within cluster sum of squared errors: 11.643418179272054

Initial starting points (random):

Cluster 0: 50,2000,16000,24,6,16
 Cluster 1: 167,524,2000,8,4,15
 Cluster 2: 320,256,6000,0,1,6

Missing values globally replaced with mean/mode

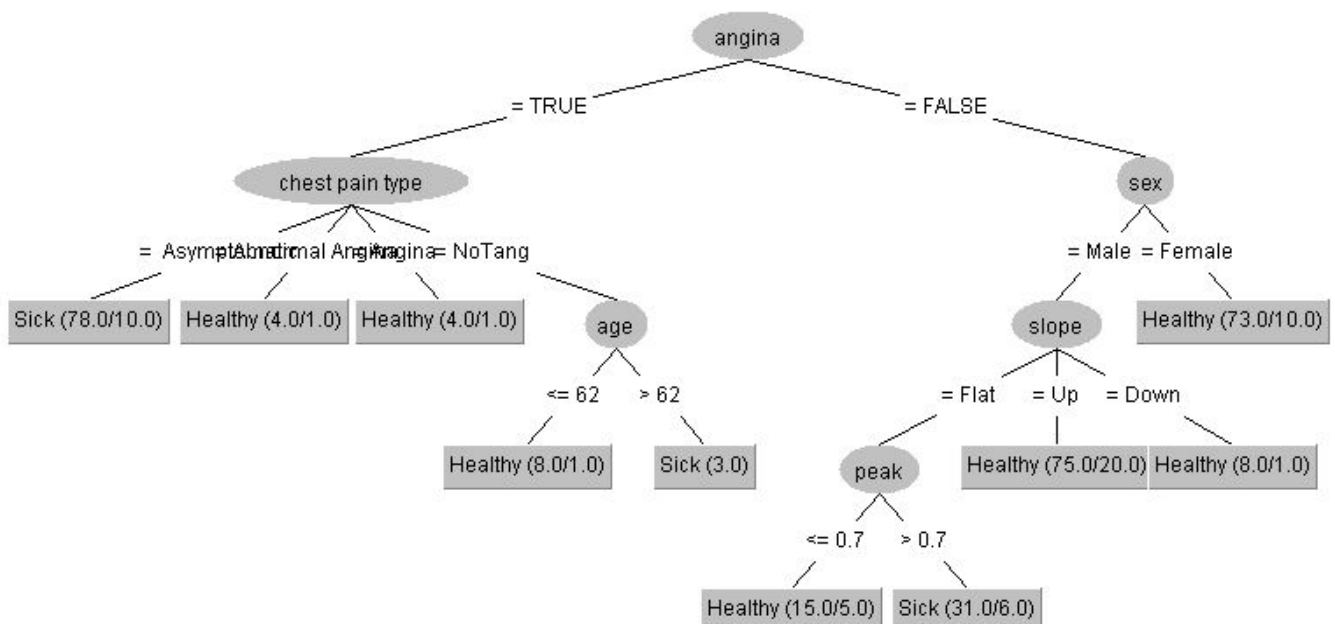
Final cluster centroids:

Attribute	Full Data (146.0)	Cluster# 0 (26.0)	1 (107.0)	2 (13.0)
MYCT	205.9658	45	155.9907	939.2308
MMIN	3184.7123	9356	1992.5981	654.1538
MMAX	12526.0685	32730.7692	8661.6262	3924
CACH	26.089	90.3846	13.486	1.2308
CRMIN	5.1575	15	3.271	1
CRMAX	20.2123	52.4615	14.5888	2

Time taken to build model (percentage split) : 0 seconds

Clustered Instances

0	6 (10%)
1	50 (79%)
2	7 (11%)



- Confusion matrix obtained with 10-fold cross-validation in our report.

=== Confusion Matrix ===

a b <-- classified as

23 8 | a = Sick

9 20 | b = Healthy

(3.1)

- We load the “*cpu.arff*” data file, cluster the data (using the simple k-Means algorithm, with k=3) and delete the attribute *class*.

The screenshot shows the Weka Clusterer window with the SimpleKMeans algorithm selected. The configuration includes a 70% percentage split for training and testing, and the option to store clusters for visualization is checked. The output panel displays the results of the clustering process.

Clusterer mode

- ☐ Use training set
- ☐ Supplied test set
- ☒ Percentage split % 70
- ☐ Classes to clusters evaluation
- (Num) CHMAX
- ☒ Store clusters for visualization

Clusterer output

Time taken to build model (full training data) : 0 seconds

=== Model and evaluation on test split ===

kMeans
=====

Number of iterations: 8
Within cluster sum of squared errors: 11.643418179272054

Initial starting points (random):

Cluster 0: 50,2000,16000,24,6,16
Cluster 1: 167,524,2000,8,4,15
Cluster 2: 320,256,6000,0,1,6

Missing values globally replaced with mean/mode

Final cluster centroids:

Attribute	Full Data	Cluster# 0	Cluster# 1	Cluster# 2
	(146.0)	(26.0)	(107.0)	(13.0)
MYCT	205.9658	45	155.9907	939.2308
MMIN	3184.7123	9356	1992.5981	654.1538
MMAx	12526.0685	32730.7692	8661.6262	3924
CACH	26.089	90.3846	13.486	1.2308
CHMIN	5.1575	15	3.271	1
CHMAX	20.2123	52.4615	14.5888	2

Time taken to build model (percentage split) : 0 seconds

Clustered Instances

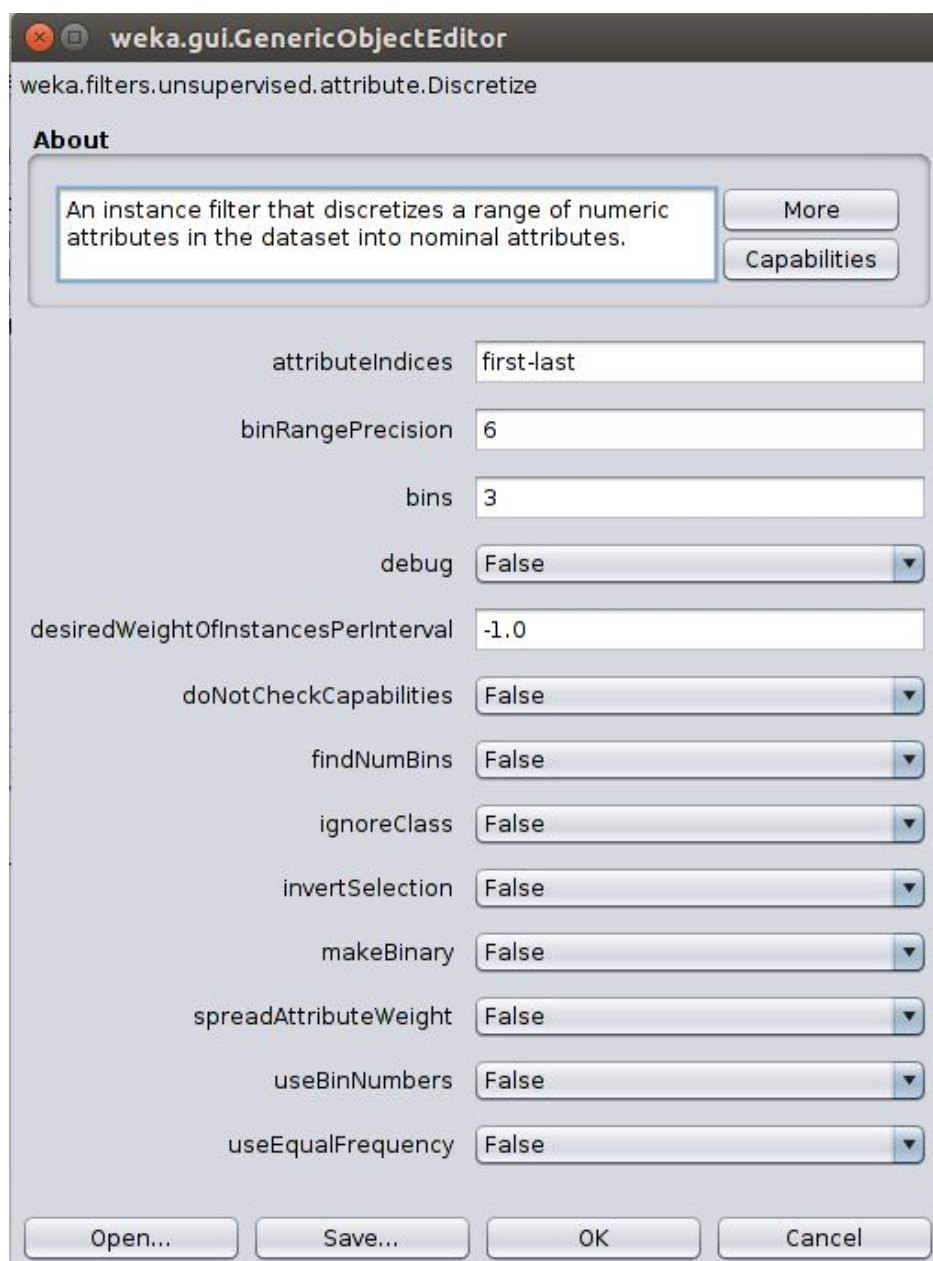
0	6 (10%)
1	50 (79%)
2	7 (11%)

- We can observe, that the main mass of the data instances belongs to one cluster (79%). The other two clusters include

a very small percentage of the examples that we can categorise as outliers.

(3.2)

- We discretize the attributes *MMIN*, *MMAX*, *CACH*, *CHMIN* and *CHMAX* using 3 buckets in one step and converting numeric values into nominal.



- Then, we apply the 'NumericToNominal' filter to every attribute in order to turn them to nominals.
- Then we find associations among these attributes using the Apriori algorithm, with support 0.2, confidence 0.95 and top 3 rules only being displayed. The result buffer :

=== Run information ===

Scheme: weka.associations.Apriori -N 3 -T 0 -C 0.95 -D 0.05 -U 1.0 -M 0.2 -S -1.0 -c -1

Relation:

cpu-weka.filters.unsupervised.attribute.Remove-R7-weka.filters.unsupervised.attribute.Remove-R1-weka.filters.unsupervised.attribute.Discretize-B3-M-1.0-Rfirst-last-precision1-weka.filters.unsupervised.attribute.NumericToNominal-Rfirst-last

Instances: 209

Attributes: 5

MMIN

MMAX

CACH

CHMIN

CHMAX

=== Associator model (full training set) ===

Apriori

=====

Minimum support: 0.9 (188 instances)

Minimum metric <confidence>: 0.95

Number of cycles performed: 2

Generated sets of large itemsets:

Size of set of large itemsets L(1): 3

Size of set of large itemsets L(2): 3

Size of set of large itemsets L(3): 1

Best rules found:

1. CACH='(-inf-85.3]' 194 ==> CHMIN='(-inf-17.3]' 193 <conf:(0.99)> lift:(1.02) lev:(0.02)
[3] conv:(2.32)
2. MMIN='(-inf-10709.3]' CACH='(-inf-85.3]' 189 ==> CHMIN='(-inf-17.3]' 188
<conf:(0.99)> lift:(1.02) lev:(0.02) [3] conv:(2.26)
3. MMIN='(-inf-10709.3]' 201 ==> CHMIN='(-inf-17.3]' 197 <conf:(0.98)> lift:(1) lev:(0)
[0] conv:(0.96)

(3.3)

- Using the original data, we list the eigenvalues associated with the attributes selected by the Principal Components Analysis method, when the amount of variance covered by the subset of attributes is 75%.

=== Run information ===

Evaluator: weka.attributeSelection.PrincipalComponents -R 0.75 -A 5
 Search: weka.attributeSelection.Ranker -T -1.7976931348623157E308 -N -1
 Relation: cpu
 Instances: 209
 Attributes: 7
 MYCT
 MMIN
 MMAX
 CACH
 CHMIN
 CHMAX
 class
 Evaluation mode: evaluate on all training data

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

Search Method:
 Attribute ranking.

Attribute Evaluator (unsupervised):

Principal Components Attribute Transformer

Correlation matrix

1	-0.34	-0.38	-0.32	-0.3	-0.25
-0.34	1	0.76	0.53	0.52	0.27
-0.38	0.76	1	0.54	0.56	0.53
-0.32	0.53	0.54	1	0.58	0.49
-0.3	0.52	0.56	0.58	1	0.55
-0.25	0.27	0.53	0.49	0.55	1

eigenvalue	proportion	cumulative
3.35674	0.55946	0.55946
-0.469MMAX-0.435CHMIN-0.429CACH-0.427MMIN-0.374CHMAX...		
0.82936	0.13823	0.69768
0.682MYCT+0.559CHMAX-0.333MMIN+0.275CHMIN+0.152CACH...		
0.73923	0.1232	0.82089
0.669MYCT+0.548MMIN-0.426CHMAX+0.264MMAX-0.03CHMIN...		

Eigenvectors

V1	V2	V3	
0.29	0.6822	0.6686	MYCT
-0.4274		-0.333 0.5477	MMIN
-0.4691		-0.1141	0.2643 MMAX
-0.4286		0.1516	0.0199 CACH
-0.4353		0.2746	-0.0302 CHMIN
-0.3742		0.5588	-0.4264 CHMAX

Ranked attributes:

0.441	1	-0.469MMAX-0.435CHMIN-0.429CACH-0.427MMIN-0.374CHMAX...
0.302	2	0.682MYCT+0.559CHMAX-0.333MMIN+0.275CHMIN+0.152CACH...
0.179	3	0.669MYCT+0.548MMIN-0.426CHMAX+0.264MMAX-0.03CHMIN...

Selected attributes: 1,2,3 : 3