An update of the J48Consolidated WEKA’s class: CTC algorithm enhanced with the notion of coverage

EHU-KAT-IK-02-14
Informe de Investigación

Igor Ibarguren
Jesús Mª Pérez
Javier Muguerza
Ibai Gurrutxaga
Olatz Arbelaitz

Ekaina 2014
An update of the J48Consolidated WEKA's class: CTC algorithm enhanced with the notion of coverage

Igor Ibarguren, Jesús Mª Pérez, Javier Muguerza, Ibai Gurutzaga, Olatz Arbelaitz

Dept. of Computer Architecture and Technology, University of the Basque Country (UPV/EHU)
M. Lardizabal, 1, 20018 Donostia, Spain
{igor.ibarguren, txus.perez, j.muguerza, i.gurutzaga, olatz.arbelaitz}@ehu.es
http://www.sc.ehu.es/aldapa

Index

An update of the J48Consolidated WEKA's class: CTC algorithm enhanced with the notion of coverage.................................................................1
Introduction.................................................................................................................................2
What is new?.................................................................................................................................2
Using the notion of coverage......................................................................................................3
Enabling the change of class distribution of the generated samples for multi-class datasets 3
Taking some exceptional characteristics of some datasets into account..............................4
Coverage.................................................................................................................................5
Bootstrap samples.....................................................................................................................5
Stratified samples....................................................................................................................5
Class distribution modified samples.....................................................................................6
Examples for a set of datasets...............................................................................................6
Using J48consolidated...............................................................................................................14
Graphical interface..................................................................................................................14
Command-line.........................................................................................................................14
New measures shown..............................................................................................................15
Source code.............................................................................................................................16
Downloading............................................................................................................................16
Citation policy........................................................................................................................19
Further work.............................................................................................................................19
Bibliography............................................................................................................................19
Appendix 1: Source code........................................................................................................21
J48Consolidated.java.............................................................................................................21
InstancesConsolidated.java.................................................................................................45

Index of Tables

Table 1: Characteristics of the datasets....................................................................................8
Table 2: Inferred characteristics of the datasets to determine the size of the subsamples to be
generated using balancing and maxSize..................................................................................9
Table 3: Number of samples to be generated over a spectrum of different coverage values for
balanced subsamples with maximum size............................................................................10
Table 4: Inferred characteristics of the datasets to determine the size of the subsamples to be
generated using balancing and sizeOfMinClass.....................................................................12
Table 5: Number of samples to be generated over a spectrum of different coverage values for
balanced subsamples with minority class’ size.......................................................................13
Table 6: Coverage value for N_S=3 and Number of samples to be generated over a spectrum of
different coverage values for bootstrap and stratified samples (with different sizes)........13

¥ If you want to refer to CTC in a publication, see “Citation policy” section.
* Corresponding author. E-mail address: txus.perez@ehu.es
Index of figures
Figure 1: New graphical interface of the Weka Explorer for J48Consolidated classifier.................14
Figure 2: Changes in J48Consolidated options through the command-line........................................15
Figure 3: Output of J48Consolidated for the german_credit dataset with the default parameters.....16
Figure 4: Main window of Weka stable 3.6.11 version.................................................................17
Figure 5: J48Consolidated Repository version package successfully installed in Weka dev-3-7-11...18
Figure 6: Main window of Weka development 3.7.11 version.......................................................18

Introduction
This document aims to describe an update of the implementation of the J48Consolidated class
within WEKA platform [1]. The J48Consolidated class implements the CTC algorithm [2][3] which
builds a unique decision tree based on a set of samples. The term “Inner Ensembles” was recently
coined in [4] for this kind of techniques, applying ensemble techniques to build single models.

The J48Consolidated class extends WEKA’s J48 class which implements the well-known C4.5
algorithm [5]. This implementation was described in the technical report "J48Consolidated: An
implementation of CTC algorithm for WEKA" [6].

The main, but not only, change in this update is the integration of the notion of coverage in order to
determine the number of samples to be generated to build a consolidated tree. We define coverage
as the percentage of examples of the training sample present in—or covered by— the set of generated
subsamples. So, depending on the type of samples that we use, we will need more or less samples in
order to achieve a specific value of coverage. More details about this issue can be seen in the
“Coverage” section.

Before examining the coverage issue in depth, in the next section, “What is new?”, we will describe
the rest of the changes in this update.

What is new?
All changes in this update are related to the way to generate the samples that will be used to build
consolidated trees. So, the implementation of the CTC algorithm does not vary from the previous
version.

We can classify the major changes in three sections:

• Using the notion of coverage
• Enabling the change of class distribution of the generated samples for multi-class datasets
• Taking some exceptional characteristics of some datasets into account

Using the notion of coverage
We have already described this concept briefly and we will devote the rest of the paper to deepen
this issue.

Regarding this concept, we have added two new measures to the J48Consolidated class. For this
purpose, we have redefined the enumerateMeasures() function which adds the two new measures
below to the enumeration of the measure names of the J48 class:

• measureNumberSamplesByCoverage: the number of samples necessary to achieve the
  coverage indicated by the corresponding option.
• measureTrueCoverage: the true coverage of the examples of the original sample achieved
  by the set of samples generated for the consolidated tree. Although a coverage value had
been indicated as a parameter to determine the number of samples to be generated, this value
is the minimum value to be guarantee in the least favored class, so the rest of classes would
be better covered. As a consequence, the achieved true coverage with the generated samples
should be bigger than the one indicated via parameter.

**Enabling the change of class distribution of the generated samples for multi-class
datasets**

In the implementation of the J48Consolidated class, three types of samples can be generated to
build consolidated trees according to the way the distribution of the minority class is changed (or is
not), i.e., the `newDistrMinClass` parameter:

- **Bootstrap samples** (-1 value): The instances will be randomly selected without taking their
classes into account. This type of sample is used by the well-known Bagging ensemble, for
example.

- **Stratified samples** (-2 value): The instances will be randomly selected but taking their
classes into account and, therefore, the original class distribution will be maintained. In
order to generate a set of different samples the size of these is reduced in a percentage value
(by `bagSizePercent` parameter).

- **Class distribution modified samples** (a value between 0 and 100): The instances will be
randomly selected taking their classes into account in order to achieve the specified
proportion of examples of the minority class into the new subsamples.

In the above implementation, the third option, class distribution modified samples, was restricted
to two-class datasets only. In this implementation we added the possibility to use multi-class datasets
also. However, since a unique value can be set and the dataset has more than two classes, the only
possibility accepted to change the original class distribution will be in order to balance all classes
into the generated samples.

When the dataset has two classes, the value used to balance the generated samples is 50 (the
proportion of the examples of the minority class). We will use this same value in order to indicate
that we want to balance the samples to be generated also when we use multi-class datasets.

**Taking some exceptional characteristics of some datasets into account**

Based on our experiments along different works, the CTC algorithm achieves the best results when
we use subsamples as big as possible and with a balanced class distribution using random sub-
sampling without replacement. This occurs, in general terms, for a wide set of classification
problems when the Area Under ROC Curve (AUC) is used as evaluation measure. Nowadays, AUC
is widely used and is considered as one of the most robust measures in order to evaluate the
classification capacity of classifiers [7][8]. Because of all this we set this kind of samples as default
parameters for J48Consolidated classifiers, that is, `newDistrMinClass` parameter is set to 50 and
`bagSizePercent` parameter is set to -2 (`maxSize`). This does not mean that other kind of sampling
could not achieve better results for a specific dataset, specially if the evaluation criterion used is
different, such as error rate, kappa or others.

When we use J48Consolidated classifier with the default parameters, that is to say, in order to
balance the subsamples of a multi-class dataset (the most general case), the size of each class into
the generated samples will be the same that the minority class has into the original sample. This
means the minority class into the original sample is entirely copied and, in the case of the rest of the
classes, random sub-sampling without replacement is used to complete the rest of the classes of the
subsample.
In this sampling process, we can find two exceptional situations:

- **The original dataset is already balanced**: If the original dataset is already balanced (for example, the well-known iris dataset from UCI repository [9]), this sampling process would generate a set of samples all identical to the original sample. Thus, the CTC algorithm would build the same decision tree the C4.5 algorithm would. The CTC algorithm works but the result does not make much sense.

In this situation, taking previous experiments into account, we decided to generate stratified samples (thus, in this case, balanced too) but reducing their size to 75% of the original sample size. This value is set in a member attribute of the J48Consolidated class, `m_bagSizePercentToReduce`, but it has not been considered a parameter (an option in WEKA's terminology) of J48Consolidated classifier in order to make easier the parameter's setting. Of course, the user will always have the possibility to set a different value indicating the corresponding value to use stratified samples.

- **The number of examples of the minority class is very low**: There are datasets which contain only one or two examples of the minority class (datasets such as hypothyroid or audiology from the UCI repository). If we generate balanced subsamples with this class size, we achieve very small samples and, as consequence, with very low knowledge, without forgetting the large amount of samples that would be required to cover most of examples.

To mitigate this effect, we determined a minimum value of examples that the classes have to contain into subsamples as a percentage related to the original sample's size. It has been declared as a member attribute of the J48Consolidated class, `m_minExamplesPerClassPercent`, and initialized with 2%. If any class does not have enough examples to achieve this value, the examples will be oversampled randomly in order to get it.

We carried out different trails comparing different values of this attribute, as well as with and without oversampling examples, and this choice seems a good option although we are aware a deeper work would be of interest.

**Coverage**

As we mentioned above, in this new version of the implementation of the J48Consolidated classifier, the user can determine the number of samples to be generated based on the percentage of examples of the original sample that is wanted to be covered, asymptotically, by the set of generated samples. We called this the **coverage** value. This value depends on the resampling method chosen to generate the samples. Therefore, we will have a different expression to calculate this value according to the kind of the obtained samples.

We want to know what percentage of examples from the original sample is contained in the set of generated samples. In other words, what probability has an example in the training sample of being in at least one sample of the set. Let us start with Bootstrap samples and, then, we will continue with the others.

**Bootstrap samples**

Bauer and Kohavi already determined in [10] the probability that an instance has of being selected at least once in a bootstrap sample as 63.2%. Let $n$ be the number of examples of the original sample. Bootstrap sampling consist of selecting randomly $n$ instances with replacement. So,

- The probability of an example being selected from the original sample: $1/n$
- The probability of an example not being selected from the original sample: $1-1/n$
The probability of an example not being selected from the original sample in \( n \) times: \((1 - 1/n)^n\)

At last, the probability of an example being selected from the original sample in \( n \) times is \(1 - (1 - 1/n)^n\). For large \( n \), this is about \(1 - 1/e \approx 63.2\%\).

In our case, we want to know the probability of being selected for the set of samples, that is, if we generate \( m \) samples, the probability of being selected in \( n \times m \) times, that is, \(1 - 1/e^m = 1 - e^{-m}\).

Therefore, the number of samples, \( m \), which we also denote \( N_S \), required to achieve a specific value of coverage is calculated by the next expression:

\[
N_S = -\ln (1 - \text{coverage}) \quad (1)
\]

**Stratified samples**

In this kind of samples, instances are randomly selected without replacement until the size of sample achieves a percentage (\texttt{bagSizePercent} parameter) of the training sample and, besides, taking into account that the class distribution has to be maintained. Let \( n \) be the number of examples of the original sample. Let \( s \) be the number of examples of the subsamples to be generated. We denote \( r \) as the ratio between the size the subsample and the size of the whole sample. Finally, let \( m \) be the number of samples to be generated. So,

- The probability of an example being selected from the original sample: \(1/n\)
- The probability of \( s \) examples being selected from the original sample: \(s/n = r\)
- The probability of an example not being selected from the original sample: \(1-r\)
- The probability of an example not being selected from the original sample in \( m \) samples: \((1-r)^m\)

At last, the probability of an example being selected from the original sample in \( m \) samples is \(1-(1-r)^m\).

We do not take into account that the class distribution should be maintained into the generated subsamples. However, if we subsample each of the classes using the same \( r \) ratio, we will get a stratified sub-sample and with the desired size \((r\times n)\). Thus, the expression of coverage for this kind of subsamples is the mentioned one.

Finally, we can calculate the number of samples, \( m \) or \( N_S \), required to achieve a specific value of coverage as:

\[
N_S = -\ln (1 - \text{coverage}) / r \quad (2)
\]

On the other hand, if we use replacement in the process of selection of instances, then:

- The probability of an example being selected from the original sample: \(1/n\)
- The probability of an example not being selected from the original sample: \(1-1/n\)
- The probability of an example not being selected from the original sample in \( r \times n \times m \) times: \((1-1/n)^{rm}\)

At last, the probability of an example being selected from the original sample in \( m \) samples is \(1-(1-r)^{rm}\). And for large \( n \), this is about \(1 - 1/e^{rm} \), that is, \(1 - e^{-rm}\).

And we can calculate the number of samples as below:

\[
N_S = -\ln (1 - \text{coverage}) / r \quad (3)
\]

That is, if the ratio between sample and sub-samples’ size is of 100\% (\( r = 1 \)), we have Bootstrap samples and (3) expression becomes (1).
**Class distribution modified samples**

We generate class distribution modified samples sub- or under-sampling the original sample without replacement. For this purpose, we have to subsample each class adequately based on the new class distribution and the indicated size. Anyway, in order to achieve a given coverage with a set of this kind of subsamples we have to guarantee this value in the least favored class, that is, the class whose ratio between the amount of examples in the subsamples and the amount of examples in the original sample is the lowest one. With a given number of samples, we get the corresponding coverage value in the least favored class and, as a consequence, the coverage value for the rest of the classes will be equal or higher.

So, this case becomes the same case we have with stratified samples but using the ratio of the size of the least favored class between the subsample and the whole sample, instead of the sizes of the whole subsample and sample. Then, let \( r_{lfc} \) be the ratio between the amount of examples of the least favored class from the subsamples and the amount of examples of the same class from the original sample and let \( m \) be the number of samples to be generated, we get that the probability of an example being selected from the original sample in the \( m \) samples is \( 1-(1-r_{lfc})^m \).

Therefore, the expression to calculate the number of samples, \( N_S \), is:

\[
N_S = \log_{1-r_{lfc}} \left(1-coverage\right) \tag{4}
\]

In this case, in contrast with the rest of the seen expressions, the value of number of samples varies, in addition with the coverage value, also with a characteristic of the dataset, that is, with the class distribution. For example, in order to generate balanced subsamples, the lower the proportion of the examples of the minority class is, the more subsamples will be necessary to achieve the same coverage (as we can observed in the next section).

**Examples for a set of datasets**

In this section we will present the values of number of samples to be generated to achieve a certain value of coverage which varies from 10% to 99.9% for the different expressions of coverage here presented. As we mentioned, when we use class distribution modified samples, since the number of subsamples changes based on the class distribution of the original sample, by way of example we have selected a well-known set of datasets whose subsample numbers for different coverage values will be shown in the next tables. In particular we downloaded the first jar file available in the section “Collections of Datasets” ([http://www.cs.waikato.ac.nz/ml/weka/datasets.html](http://www.cs.waikato.ac.nz/ml/weka/datasets.html)) from the website of Weka Data Mining Software\(^1\), containing 37 (actually 36!) classification problems, originally collected from the UCI repository [9].

Table 1 shows the characteristics of the datasets; name, number of instances, number of attributes and number of classes and, separately, number of instances and its proportion regarding with the size of the whole sample of minority and majority classes, respectively. The datasets are ordered based on the proportion of the number of examples into the minority class, from the smallest to the biggest. At the bottom of the table, a summary of these characteristics with the average value, the median, and the minimum and maximum values can be observed.

First of all, in order to determine the number of samples required for a specific coverage value, we need to know whether some of the exceptional situations mentioned in the above section (Taking some exceptional characteristics of some datasets into account) occur taking into account the characteristics of these datasets:

- **The original dataset is already balanced**: As it can be observed in Table 1 there are 3 datasets which have the same amount of examples in the minority class and in the majority

---

\(^1\) http://www.cs.waikato.ac.nz/ml/weka/index.html
class (these values are marked in bold in the table), thus, they are balanced. Specifically, these datasets are: Vowel, segment and iris, and there are marked with the symbol (*). So, as we mentioned before, in these datasets the generated samples will be under-sampled to 75% of the size of the whole dataset maintaining their class distribution, that is, being stratified, and in this situation, being balanced.

- The number of examples of the minority class is very low: There are 8 datasets whose minority class' size does not reach the determined minimum, 2% of the dataset's size. They are located in the first 8 positions of Table 1. As we mentioned before, when we want to change the class distribution of the subsamples to be generated and the dataset is multi-class, this implementation only accepts to balance the classes. In this set of datasets, there are 18 two-class datasets and the other 18 datasets are multi-class. In normal conditions, the minority class' size determines the size of all of the classes into the subsamples in order to be balanced. When the minority class' size of a dataset does not reach the 2% set, this latter value (2%) will determine the size of the classes. Table 2 contains some values inferred from the characteristics of the datasets in order to determine the size of the subsamples to be generated, when we want to balance the subsamples and using the maximum possible size, $maxSize$ value for $bagSizePercent$ parameter. So, “MinCoverByClass” column indicates the minimum amount of examples to be covered by each class into the subsamples. If the number of examples of the minority class is lower than this value, the latter one will be set as the size of all classes, “SizeOfClasses” column, in otherwise, it will be the minority class' size. The next column, “Size”, refers to the subsamples' size (SizeOfClasses value multiplied by the number of classes) and, finally, “%Size” is the proportion of this size with respect to the whole sample's size. As it can be observed at the end of Table 2, the subsamples size is, in average, around a 60% of the whole datasets' size.
<table>
<thead>
<tr>
<th>Dataset</th>
<th>#Instances</th>
<th>#Attributes</th>
<th>#Classes (Distinct)</th>
<th>Minority class</th>
<th>Majority class</th>
</tr>
</thead>
<tbody>
<tr>
<td>hypothyroid</td>
<td>3772</td>
<td>30</td>
<td>4</td>
<td>2</td>
<td>3481</td>
</tr>
<tr>
<td>primary-tumor</td>
<td>339</td>
<td>18</td>
<td>21</td>
<td>1</td>
<td>84</td>
</tr>
<tr>
<td>audiology</td>
<td>226</td>
<td>70</td>
<td>24</td>
<td>1</td>
<td>57</td>
</tr>
<tr>
<td>anneal</td>
<td>898</td>
<td>39</td>
<td>5</td>
<td>8</td>
<td>684</td>
</tr>
<tr>
<td>anneal.ORIG</td>
<td>898</td>
<td>39</td>
<td>5</td>
<td>8</td>
<td>684</td>
</tr>
<tr>
<td>soybean</td>
<td>683</td>
<td>36</td>
<td>19</td>
<td>8</td>
<td>92</td>
</tr>
<tr>
<td>lymphography</td>
<td>148</td>
<td>19</td>
<td>4</td>
<td>2</td>
<td>81</td>
</tr>
<tr>
<td>autos</td>
<td>205</td>
<td>26</td>
<td>6</td>
<td>3</td>
<td>67</td>
</tr>
<tr>
<td>letter</td>
<td>20000</td>
<td>17</td>
<td>26</td>
<td>734</td>
<td>813</td>
</tr>
<tr>
<td>zoo</td>
<td>101</td>
<td>18</td>
<td>7</td>
<td>4</td>
<td>41</td>
</tr>
<tr>
<td>Glass</td>
<td>214</td>
<td>10</td>
<td>6</td>
<td>9</td>
<td>76</td>
</tr>
<tr>
<td>sick</td>
<td>3772</td>
<td>30</td>
<td>2</td>
<td>231</td>
<td>3541</td>
</tr>
<tr>
<td>balance-scale</td>
<td>625</td>
<td>5</td>
<td>3</td>
<td>49</td>
<td>288</td>
</tr>
<tr>
<td>Vowel (*)</td>
<td>990</td>
<td>14</td>
<td>11</td>
<td>90</td>
<td>90</td>
</tr>
<tr>
<td>segment (*)</td>
<td>2310</td>
<td>20</td>
<td>7</td>
<td>330</td>
<td>330</td>
</tr>
<tr>
<td>hepatitis</td>
<td>155</td>
<td>20</td>
<td>2</td>
<td>32</td>
<td>123</td>
</tr>
<tr>
<td>vehicle</td>
<td>846</td>
<td>19</td>
<td>4</td>
<td>199</td>
<td>218</td>
</tr>
<tr>
<td>splice</td>
<td>3190</td>
<td>62</td>
<td>3</td>
<td>767</td>
<td>1655</td>
</tr>
<tr>
<td>breast-cancer</td>
<td>286</td>
<td>10</td>
<td>2</td>
<td>85</td>
<td>201</td>
</tr>
<tr>
<td>german_credit</td>
<td>1000</td>
<td>21</td>
<td>2</td>
<td>300</td>
<td>700</td>
</tr>
<tr>
<td>waveform</td>
<td>5000</td>
<td>41</td>
<td>3</td>
<td>1653</td>
<td>1692</td>
</tr>
<tr>
<td>iris (*)</td>
<td>150</td>
<td>5</td>
<td>3</td>
<td>50</td>
<td>50</td>
</tr>
<tr>
<td>wisconsin-breast-cancer</td>
<td>699</td>
<td>10</td>
<td>2</td>
<td>241</td>
<td>458</td>
</tr>
<tr>
<td>pima_diabetes</td>
<td>768</td>
<td>9</td>
<td>2</td>
<td>268</td>
<td>500</td>
</tr>
<tr>
<td>labor</td>
<td>57</td>
<td>17</td>
<td>2</td>
<td>20</td>
<td>37</td>
</tr>
<tr>
<td>ionosphere</td>
<td>351</td>
<td>35</td>
<td>2</td>
<td>126</td>
<td>225</td>
</tr>
<tr>
<td>hungarian-14-heart-diseas</td>
<td>294</td>
<td>14</td>
<td>2</td>
<td>106</td>
<td>188</td>
</tr>
<tr>
<td>horse-colic</td>
<td>368</td>
<td>23</td>
<td>2</td>
<td>136</td>
<td>232</td>
</tr>
<tr>
<td>vote</td>
<td>435</td>
<td>17</td>
<td>2</td>
<td>168</td>
<td>267</td>
</tr>
<tr>
<td>horse-colic.ORIG</td>
<td>368</td>
<td>28</td>
<td>2</td>
<td>152</td>
<td>214</td>
</tr>
<tr>
<td>heart-statlog</td>
<td>270</td>
<td>14</td>
<td>2</td>
<td>120</td>
<td>150</td>
</tr>
<tr>
<td>credit-rating</td>
<td>690</td>
<td>16</td>
<td>2</td>
<td>307</td>
<td>383</td>
</tr>
<tr>
<td>cleveland-14-heart-diseas</td>
<td>303</td>
<td>14</td>
<td>2</td>
<td>138</td>
<td>165</td>
</tr>
<tr>
<td>sonar</td>
<td>208</td>
<td>61</td>
<td>2</td>
<td>97</td>
<td>111</td>
</tr>
<tr>
<td>kr-vs-kp</td>
<td>3196</td>
<td>37</td>
<td>2</td>
<td>1527</td>
<td>1669</td>
</tr>
<tr>
<td>mushroom</td>
<td>8124</td>
<td>23</td>
<td>2</td>
<td>3916</td>
<td>4208</td>
</tr>
</tbody>
</table>

| Average               | 1720.53    | 24.64       | 5.47                | 330.22         | 662.64         |
| Median                | 530.00     | 19.50       | 2.50                | 113.00         | 221.50         |
| Min                   | 57         | 5           | 2                   | 1              | 37             |
| Max                   | 20000      | 70          | 26                  | 3916           | 4208           |

_table 1: Characteristics of the datasets_
<table>
<thead>
<tr>
<th>Dataset</th>
<th>MinCover</th>
<th>ByClass</th>
<th>SizeOfClasses</th>
<th>Size</th>
<th>%Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hypothyroid (*)</td>
<td>76</td>
<td>76</td>
<td>304</td>
<td>8.06%</td>
<td></td>
</tr>
<tr>
<td>primary-tumor (*)</td>
<td>7</td>
<td>7</td>
<td>147</td>
<td>43.36%</td>
<td></td>
</tr>
<tr>
<td>audiology (*)</td>
<td>5</td>
<td>5</td>
<td>120</td>
<td>53.10%</td>
<td></td>
</tr>
<tr>
<td>anneal (*)</td>
<td>18</td>
<td>18</td>
<td>90</td>
<td>10.02%</td>
<td></td>
</tr>
<tr>
<td>anneal.ORIG (*)</td>
<td>18</td>
<td>18</td>
<td>90</td>
<td>10.02%</td>
<td></td>
</tr>
<tr>
<td>soybean (*)</td>
<td>14</td>
<td>14</td>
<td>266</td>
<td>38.95%</td>
<td></td>
</tr>
<tr>
<td>lymphography (*)</td>
<td>3</td>
<td>3</td>
<td>12</td>
<td>8.11%</td>
<td></td>
</tr>
<tr>
<td>autos (*)</td>
<td>5</td>
<td>5</td>
<td>30</td>
<td>14.63%</td>
<td></td>
</tr>
<tr>
<td>letter</td>
<td>400</td>
<td>734</td>
<td>19084</td>
<td>95.42%</td>
<td></td>
</tr>
<tr>
<td>zoo</td>
<td>3</td>
<td>4</td>
<td>28</td>
<td>27.72%</td>
<td></td>
</tr>
<tr>
<td>Glass</td>
<td>5</td>
<td>9</td>
<td>54</td>
<td>25.23%</td>
<td></td>
</tr>
<tr>
<td>sick</td>
<td>76</td>
<td>231</td>
<td>462</td>
<td>12.25%</td>
<td></td>
</tr>
<tr>
<td>balance-scale</td>
<td>13</td>
<td>49</td>
<td>147</td>
<td>23.52%</td>
<td></td>
</tr>
<tr>
<td>vowel</td>
<td>20</td>
<td>67.5</td>
<td>742.5</td>
<td>75.00%</td>
<td></td>
</tr>
<tr>
<td>segment</td>
<td>47</td>
<td>247.5</td>
<td>1732.5</td>
<td>75.00%</td>
<td></td>
</tr>
<tr>
<td>hepatitis</td>
<td>4</td>
<td>32</td>
<td>64</td>
<td>41.29%</td>
<td></td>
</tr>
<tr>
<td>vehicle</td>
<td>17</td>
<td>199</td>
<td>796</td>
<td>94.09%</td>
<td></td>
</tr>
<tr>
<td>splice</td>
<td>64</td>
<td>767</td>
<td>2301</td>
<td>72.13%</td>
<td></td>
</tr>
<tr>
<td>breast-cancer</td>
<td>6</td>
<td>85</td>
<td>170</td>
<td>59.44%</td>
<td></td>
</tr>
<tr>
<td>german_credit</td>
<td>20</td>
<td>300</td>
<td>600</td>
<td>60.00%</td>
<td></td>
</tr>
<tr>
<td>waveform</td>
<td>100</td>
<td>1653</td>
<td>4959</td>
<td>99.18%</td>
<td></td>
</tr>
<tr>
<td>iris</td>
<td>3</td>
<td>37.5</td>
<td>112.5</td>
<td>75.00%</td>
<td></td>
</tr>
<tr>
<td>wisconsin-breast-cancer</td>
<td>14</td>
<td>241</td>
<td>482</td>
<td>68.96%</td>
<td></td>
</tr>
<tr>
<td>pima_diabetes</td>
<td>16</td>
<td>268</td>
<td>536</td>
<td>69.79%</td>
<td></td>
</tr>
<tr>
<td>labor</td>
<td>2</td>
<td>20</td>
<td>40</td>
<td>70.18%</td>
<td></td>
</tr>
<tr>
<td>ionosphere</td>
<td>8</td>
<td>126</td>
<td>252</td>
<td>71.79%</td>
<td></td>
</tr>
<tr>
<td>hungarian-14-heart-diseas</td>
<td>6</td>
<td>106</td>
<td>212</td>
<td>72.11%</td>
<td></td>
</tr>
<tr>
<td>horse-colic</td>
<td>8</td>
<td>136</td>
<td>272</td>
<td>73.91%</td>
<td></td>
</tr>
<tr>
<td>vote</td>
<td>9</td>
<td>168</td>
<td>336</td>
<td>77.24%</td>
<td></td>
</tr>
<tr>
<td>horse-colic.ORIG</td>
<td>8</td>
<td>152</td>
<td>304</td>
<td>82.61%</td>
<td></td>
</tr>
<tr>
<td>heart-statlog</td>
<td>6</td>
<td>120</td>
<td>240</td>
<td>88.89%</td>
<td></td>
</tr>
<tr>
<td>credit-rating</td>
<td>14</td>
<td>307</td>
<td>614</td>
<td>88.99%</td>
<td></td>
</tr>
<tr>
<td>cleveland-14-heart-diseas</td>
<td>7</td>
<td>138</td>
<td>276</td>
<td>91.09%</td>
<td></td>
</tr>
<tr>
<td>sonar</td>
<td>5</td>
<td>97</td>
<td>194</td>
<td>93.27%</td>
<td></td>
</tr>
<tr>
<td>kr-vs-kp</td>
<td>64</td>
<td>1527</td>
<td>3054</td>
<td>95.56%</td>
<td></td>
</tr>
<tr>
<td>mushroom</td>
<td>163</td>
<td>3916</td>
<td>7832</td>
<td>96.41%</td>
<td></td>
</tr>
<tr>
<td><strong>Average</strong></td>
<td><strong>34.83</strong></td>
<td><strong>330.10</strong></td>
<td><strong>1304.32</strong></td>
<td><strong>60.06%</strong></td>
<td></td>
</tr>
<tr>
<td><strong>Median</strong></td>
<td><strong>11.00</strong></td>
<td><strong>113.00</strong></td>
<td><strong>269.00</strong></td>
<td><strong>70.99%</strong></td>
<td></td>
</tr>
</tbody>
</table>

Table 2: Inferred characteristics of the datasets to determine the size of the subsamples to be generated using balancing and maxSize

Based on the values of Table 2, we know the amount of examples that the subsamples will have into each class, so, we can determine which class is the least favored class and, thus, we can calculate the ratio \( r_{lf} \), and, finally, the expression (4), the number of samples required according to a specific coverage value. Table 3 shows, in the first column, the obtained \( r_{lf} \) ratio, and then, the required number of samples in order to achieve the indicated coverage value related to each column.

The number of samples in the table is rounded up to the next integer and it has been set to 3 when
the obtained value was lower than this because this is the minimum number of samples required to build a consolidated tree.

<table>
<thead>
<tr>
<th>Dataset</th>
<th>( \hat{r}_{IC} )</th>
<th>10%</th>
<th>20%</th>
<th>30%</th>
<th>40%</th>
<th>50%</th>
<th>75%</th>
<th>90%</th>
<th>95%</th>
<th>99%</th>
<th>99.9%</th>
</tr>
</thead>
<tbody>
<tr>
<td>hypothyroid</td>
<td>2.18%</td>
<td>5</td>
<td>11</td>
<td>17</td>
<td>24</td>
<td>32</td>
<td>63</td>
<td>105</td>
<td>136</td>
<td>209</td>
<td>313</td>
</tr>
<tr>
<td>primary-tumor</td>
<td>8.33%</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>8</td>
<td>16</td>
<td>27</td>
<td>35</td>
<td>53</td>
<td>80</td>
</tr>
<tr>
<td>audiology</td>
<td>8.77%</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>16</td>
<td>26</td>
<td>33</td>
<td>51</td>
<td>76</td>
</tr>
<tr>
<td>anneal</td>
<td>2.63%</td>
<td>4</td>
<td>9</td>
<td>14</td>
<td>20</td>
<td>26</td>
<td>52</td>
<td>87</td>
<td>113</td>
<td>173</td>
<td>260</td>
</tr>
<tr>
<td>anneal.ORIG</td>
<td>2.63%</td>
<td>4</td>
<td>9</td>
<td>14</td>
<td>20</td>
<td>26</td>
<td>52</td>
<td>87</td>
<td>113</td>
<td>173</td>
<td>260</td>
</tr>
<tr>
<td>soybean</td>
<td>15.22%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>9</td>
<td>14</td>
<td>19</td>
<td>28</td>
<td>42</td>
</tr>
<tr>
<td>lymphography</td>
<td>3.70%</td>
<td>3</td>
<td>6</td>
<td>10</td>
<td>14</td>
<td>19</td>
<td>37</td>
<td>62</td>
<td>80</td>
<td>123</td>
<td>184</td>
</tr>
<tr>
<td>autos</td>
<td>7.46%</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>7</td>
<td>9</td>
<td>18</td>
<td>30</td>
<td>39</td>
<td>60</td>
<td>90</td>
</tr>
<tr>
<td>letter</td>
<td>90.28%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>zoo</td>
<td>9.76%</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>14</td>
<td>23</td>
<td>30</td>
<td>45</td>
<td>68</td>
</tr>
<tr>
<td>Glass</td>
<td>11.84%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>11</td>
<td>19</td>
<td>24</td>
<td>37</td>
<td>55</td>
</tr>
<tr>
<td>sick</td>
<td>6.52%</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>11</td>
<td>21</td>
<td>35</td>
<td>45</td>
<td>69</td>
<td>103</td>
</tr>
<tr>
<td>balance-scale</td>
<td>17.01%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>8</td>
<td>13</td>
<td>17</td>
<td>25</td>
<td>38</td>
</tr>
<tr>
<td>vowel</td>
<td>75.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
</tr>
<tr>
<td>segment</td>
<td>75.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
</tr>
<tr>
<td>hepatitis</td>
<td>26.02%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>vehicle</td>
<td>91.28%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>splice</td>
<td>46.34%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>8</td>
<td>12</td>
</tr>
<tr>
<td>breast-cancer</td>
<td>42.29%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>german_credit</td>
<td>42.86%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>waveform</td>
<td>97.70%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>iris</td>
<td>75.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
</tr>
<tr>
<td>wisconsin-brest-cancer</td>
<td>52.62%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>10</td>
</tr>
<tr>
<td>pima_diabetes</td>
<td>53.60%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>labor</td>
<td>54.05%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>ionosphere</td>
<td>56.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>hungarian-14-heart-diseas</td>
<td>56.38%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>9</td>
</tr>
<tr>
<td>horse-colic</td>
<td>58.62%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
</tr>
<tr>
<td>vote</td>
<td>62.92%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
</tr>
<tr>
<td>horse-colic.ORIG</td>
<td>71.03%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>6</td>
</tr>
<tr>
<td>heart-statlog</td>
<td>80.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
</tr>
<tr>
<td>credit-rating</td>
<td>80.16%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>cleveland-14-heart-diseas</td>
<td>83.64%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>sonar</td>
<td>87.39%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>kr-vs-kp</td>
<td>91.49%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>mushroom</td>
<td>93.06%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

Median: 53.83% 3.00 3.00 3.00 3.00 3.00 3.00 4.00 6.00 9.00

Table 3: Number of samples to be generated over a spectrum of different coverage values for balanced subsamples with maximum size

As it can be observed in Table 3, the lower the ratio of the least favored class is, the higher is the required number of samples to achieve a specific coverage value. In the case of the dataset which has the smallest ratio, the number of samples required to obtain a 99.9% of coverage is 313. At the
bottom of the table, the ratios are close to 90% and, thus, 3 samples will be enough to achieve this coverage (likely even more).

This implementation has another preconfigured option to generate balanced samples but, in this case, the size of the samples will be the same that minority class' size has in the original sample (sizeOfMinClass value for bagSizePercent parameter). This kind of samples were used by Weiss and Provost in [11] in order to guarantee that the proportion of the minority class may vary from 0% to 100% without using replacement for two-class problems. Regarding the CTC algorithm, this kind of subsampling was used in [12] and [13] in order to analyze the effect of changes in class distribution over this algorithm.

For this update, we have also adapted this kind of subsampling in order to be able to use it with multi-class datasets and, also, taking into account the minimum number of examples which determines classes size into the subsamples. Regarding the latter issue, nothing new in this case, that is, the same criterion will be used that we used for maxSize samples. On the other hand, for the multi-class datasets, we decided not to strictly use the size of the minority class into the training sample to generate the subsamples with this size (such as we do with two-class datasets). This would make impossible to build a subsample when the number of examples of the minority class in the training sample were lower than the number of classes (hypothyroid, for example, with 2 instances in its minority class and 4 classes or audiology with only one instance and 24 classes, in the most extreme case). Besides, in other cases, although it were possible, the representation of each class into the subsamples could be ridiculous. Because of this, we decided determine the size of all classes into the subsamples as half the minority class' size in the training sample. This makes that the size for the subsample in two-class datasets being the minority class' size in the sample, and getting a reasonable representation for multi-class datasets, in normal conditions.

Table 4 shows the values inferred for sizeMax samples in Table 2 but for sizeOfMinClass samples. As it can be seen, the same first 8 datasets continue to be where the minority class' size does not reach the required minimum, however, 3 more datasets do not satisfy this condition.

On the other hand, in this case, the average subsample size is around 34%, when it was around 60% for maxSize samples.

At last, Table 5 shows the number of samples to be generated for balanced and sizeOfMinClass sized samples using different values of coverage. Like in Table 3, the first column refers the ratio of the least favored class in this case. This values decrements, in average, to 26.14% (in contrast with 48.30% in the case of maxSize samples) and, so, the obtained values for number of samples are bigger than above. For example, for the most balanced datasets of the list more than 3 samples are required to achieve values of coverage equal or greater than 90%.

Regarding the other types of used resampling techniques (bootstrap and stratified samples), it is worth noting that, for bootstrap samples, the number of samples required for a specific coverage value does not depend on any dataset's characteristic and, for stratified samples, only the ratio between both samples (the original one's and the generated one's) will be taken into account. As a consequence, Table 6 summarizes the number of samples to be generated for both types of samples. In the case of stratified samples, four different percentages have been used indicating the size of the subsamples, S%, respect to the original sample's size: 90%, 75%, 50% and 25%. Besides, in order to notice the amount of coverage obtained with these kind of samples, we also have added in the second column the coverage value that would be obtained whether we use only three samples, the minimum number of samples necessary to build a consolidated tree.

Finally, we want to note that an extensive analysis of the results obtained by CTC algorithm with these resampling strategies has been reported in [14].
<table>
<thead>
<tr>
<th>Dataset</th>
<th>MinCover ByClass</th>
<th>SizeOfClasses</th>
<th>Size</th>
<th>%Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>hypothyroid (*)</td>
<td>76</td>
<td>76</td>
<td>304</td>
<td>8.06%</td>
</tr>
<tr>
<td>primary-tumor (*)</td>
<td>7</td>
<td>7</td>
<td>147</td>
<td>43.36%</td>
</tr>
<tr>
<td>audiology (*)</td>
<td>5</td>
<td>5</td>
<td>120</td>
<td>53.10%</td>
</tr>
<tr>
<td>anneal (*)</td>
<td>18</td>
<td>18</td>
<td>90</td>
<td>10.02%</td>
</tr>
<tr>
<td>anneal.ORIG (*)</td>
<td>18</td>
<td>18</td>
<td>90</td>
<td>10.02%</td>
</tr>
<tr>
<td>soybean (*)</td>
<td>14</td>
<td>14</td>
<td>266</td>
<td>38.95%</td>
</tr>
<tr>
<td>lymphography (*)</td>
<td>3</td>
<td>3</td>
<td>12</td>
<td>8.11%</td>
</tr>
<tr>
<td>autos (*)</td>
<td>5</td>
<td>5</td>
<td>30</td>
<td>14.63%</td>
</tr>
<tr>
<td>letter (*)</td>
<td>400</td>
<td>400</td>
<td>10400</td>
<td>52.00%</td>
</tr>
<tr>
<td>zoo (*)</td>
<td>3</td>
<td>3</td>
<td>21</td>
<td>20.79%</td>
</tr>
<tr>
<td>Glass (*)</td>
<td>5</td>
<td>5</td>
<td>30</td>
<td>14.02%</td>
</tr>
<tr>
<td>sick</td>
<td>76</td>
<td>116</td>
<td>232</td>
<td>6.15%</td>
</tr>
<tr>
<td>balance-scale</td>
<td>13</td>
<td>25</td>
<td>75</td>
<td>12.00%</td>
</tr>
<tr>
<td>vowel</td>
<td>20</td>
<td>45</td>
<td>495</td>
<td>50.00%</td>
</tr>
<tr>
<td>segment</td>
<td>47</td>
<td>165</td>
<td>1155</td>
<td>50.00%</td>
</tr>
<tr>
<td>hepatitis</td>
<td>4</td>
<td>16</td>
<td>32</td>
<td>20.65%</td>
</tr>
<tr>
<td>vehicle</td>
<td>17</td>
<td>100</td>
<td>400</td>
<td>47.28%</td>
</tr>
<tr>
<td>splice</td>
<td>64</td>
<td>384</td>
<td>1152</td>
<td>36.11%</td>
</tr>
<tr>
<td>breast-cancer</td>
<td>6</td>
<td>43</td>
<td>86</td>
<td>30.07%</td>
</tr>
<tr>
<td>german_credit</td>
<td>20</td>
<td>150</td>
<td>300</td>
<td>30.00%</td>
</tr>
<tr>
<td>waveform</td>
<td>100</td>
<td>827</td>
<td>2481</td>
<td>49.62%</td>
</tr>
<tr>
<td>iris</td>
<td>3</td>
<td>25</td>
<td>75</td>
<td>50.00%</td>
</tr>
<tr>
<td>wisconsin-breast-cancer</td>
<td>14</td>
<td>121</td>
<td>242</td>
<td>34.62%</td>
</tr>
<tr>
<td>pima_diabetes</td>
<td>16</td>
<td>134</td>
<td>268</td>
<td>34.90%</td>
</tr>
<tr>
<td>labor</td>
<td>2</td>
<td>10</td>
<td>20</td>
<td>35.09%</td>
</tr>
<tr>
<td>ionosphere</td>
<td>8</td>
<td>63</td>
<td>126</td>
<td>35.90%</td>
</tr>
<tr>
<td>hungarian-14-heart-diseas</td>
<td>6</td>
<td>53</td>
<td>106</td>
<td>36.05%</td>
</tr>
<tr>
<td>horse-colic</td>
<td>8</td>
<td>68</td>
<td>136</td>
<td>36.96%</td>
</tr>
<tr>
<td>vote</td>
<td>9</td>
<td>84</td>
<td>168</td>
<td>38.62%</td>
</tr>
<tr>
<td>horse-colic.ORIG</td>
<td>8</td>
<td>76</td>
<td>152</td>
<td>41.30%</td>
</tr>
<tr>
<td>heart-statlog</td>
<td>6</td>
<td>60</td>
<td>120</td>
<td>44.44%</td>
</tr>
<tr>
<td>credit-rating</td>
<td>14</td>
<td>154</td>
<td>308</td>
<td>44.64%</td>
</tr>
<tr>
<td>cleveland-14-heart-diseas</td>
<td>7</td>
<td>69</td>
<td>138</td>
<td>45.54%</td>
</tr>
<tr>
<td>sonar</td>
<td>5</td>
<td>49</td>
<td>98</td>
<td>47.12%</td>
</tr>
<tr>
<td>kr-vs-kp</td>
<td>64</td>
<td>764</td>
<td>1528</td>
<td>47.81%</td>
</tr>
<tr>
<td>mushroom</td>
<td>163</td>
<td>1958</td>
<td>3916</td>
<td>48.20%</td>
</tr>
</tbody>
</table>

Average 34.83 169.81 703.31 34.06%
Median 11.00 61.50 142.50 36.53%

Table 4: Inferred characteristics of the datasets to determine the size of the subsamples to be generated using balancing and sizeOfMinClass
<table>
<thead>
<tr>
<th>Dataset</th>
<th>( r_{ic} )</th>
<th>10%</th>
<th>20%</th>
<th>30%</th>
<th>40%</th>
<th>50%</th>
<th>75%</th>
<th>90%</th>
<th>95%</th>
<th>99%</th>
<th>99.9%</th>
</tr>
</thead>
<tbody>
<tr>
<td>hypothyroid</td>
<td>2.18%</td>
<td>5</td>
<td>11</td>
<td>17</td>
<td>24</td>
<td>32</td>
<td>63</td>
<td>105</td>
<td>136</td>
<td>209</td>
<td>313</td>
</tr>
<tr>
<td>primary-tumor</td>
<td>8.33%</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>8</td>
<td>16</td>
<td>27</td>
<td>35</td>
<td>53</td>
<td>80</td>
</tr>
<tr>
<td>audiology</td>
<td>8.77%</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>16</td>
<td>26</td>
<td>33</td>
<td>51</td>
<td>76</td>
</tr>
<tr>
<td>anneal</td>
<td>2.63%</td>
<td>4</td>
<td>9</td>
<td>14</td>
<td>20</td>
<td>26</td>
<td>52</td>
<td>87</td>
<td>113</td>
<td>173</td>
<td>260</td>
</tr>
<tr>
<td>anneal.ORIG</td>
<td>2.63%</td>
<td>4</td>
<td>9</td>
<td>14</td>
<td>20</td>
<td>26</td>
<td>52</td>
<td>87</td>
<td>113</td>
<td>173</td>
<td>260</td>
</tr>
<tr>
<td>soybean</td>
<td>15.22%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>9</td>
<td>14</td>
<td>19</td>
<td>28</td>
<td>42</td>
</tr>
<tr>
<td>lymphography</td>
<td>3.70%</td>
<td>3</td>
<td>6</td>
<td>10</td>
<td>14</td>
<td>19</td>
<td>37</td>
<td>62</td>
<td>80</td>
<td>123</td>
<td>184</td>
</tr>
<tr>
<td>autos</td>
<td>7.46%</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>7</td>
<td>9</td>
<td>18</td>
<td>30</td>
<td>39</td>
<td>60</td>
<td>90</td>
</tr>
<tr>
<td>letter</td>
<td>49.20%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>11</td>
</tr>
<tr>
<td>zoo</td>
<td>7.32%</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>7</td>
<td>10</td>
<td>19</td>
<td>31</td>
<td>40</td>
<td>61</td>
<td>91</td>
</tr>
<tr>
<td>Glass</td>
<td>6.58%</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>11</td>
<td>21</td>
<td>34</td>
<td>45</td>
<td>68</td>
<td>102</td>
</tr>
<tr>
<td>sick</td>
<td>3.28%</td>
<td>4</td>
<td>7</td>
<td>11</td>
<td>16</td>
<td>21</td>
<td>42</td>
<td>70</td>
<td>90</td>
<td>139</td>
<td>208</td>
</tr>
<tr>
<td>balance-scale</td>
<td>8.68%</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>16</td>
<td>26</td>
<td>33</td>
<td>51</td>
<td>77</td>
</tr>
<tr>
<td>vowel</td>
<td>50.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>10</td>
</tr>
<tr>
<td>segment</td>
<td>50.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>10</td>
</tr>
<tr>
<td>hepatitis</td>
<td>13.01%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>10</td>
<td>17</td>
<td>22</td>
<td>34</td>
<td>50</td>
</tr>
<tr>
<td>vehicle</td>
<td>45.87%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>8</td>
<td>12</td>
</tr>
<tr>
<td>splice</td>
<td>23.20%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>6</td>
<td>9</td>
<td>12</td>
<td>18</td>
</tr>
<tr>
<td>breast-cancer</td>
<td>21.39%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>6</td>
<td>10</td>
<td>13</td>
<td>20</td>
</tr>
<tr>
<td>german_credit</td>
<td>21.43%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>6</td>
<td>10</td>
<td>13</td>
<td>20</td>
</tr>
<tr>
<td>waveform</td>
<td>48.88%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>11</td>
</tr>
<tr>
<td>iris</td>
<td>50.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>7</td>
<td>10</td>
</tr>
<tr>
<td>wisconsin-breast-cancer</td>
<td>26.42%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>8</td>
<td>10</td>
<td>16</td>
</tr>
<tr>
<td>pima_diabetes</td>
<td>26.80%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>8</td>
<td>10</td>
<td>15</td>
<td>23</td>
</tr>
<tr>
<td>labor</td>
<td>27.03%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>8</td>
<td>10</td>
<td>15</td>
<td>22</td>
</tr>
<tr>
<td>ionosphere</td>
<td>28.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>8</td>
<td>10</td>
<td>15</td>
</tr>
<tr>
<td>hungarian-14-heart-diseas</td>
<td>28.19%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>7</td>
<td>10</td>
<td>14</td>
<td>21</td>
</tr>
<tr>
<td>horse-colic</td>
<td>29.31%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>7</td>
<td>9</td>
<td>14</td>
<td>20</td>
</tr>
<tr>
<td>vote</td>
<td>31.46%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>7</td>
<td>8</td>
<td>13</td>
<td>19</td>
</tr>
<tr>
<td>horse-colic.ORIG</td>
<td>35.51%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>7</td>
<td>11</td>
<td>16</td>
</tr>
<tr>
<td>heart-statlog</td>
<td>40.00%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>10</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td>credit-rating</td>
<td>40.21%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>9</td>
<td>14</td>
</tr>
<tr>
<td>cleveland-14-heart-diseas</td>
<td>41.82%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>6</td>
<td>9</td>
<td>13</td>
<td></td>
</tr>
<tr>
<td>sonar</td>
<td>44.14%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>6</td>
<td>8</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>kr-vs-kp</td>
<td>45.78%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>8</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td>mushroom</td>
<td>46.53%</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>8</td>
<td>12</td>
</tr>
<tr>
<td><strong>Average</strong></td>
<td><strong>26.14%</strong></td>
<td><strong>3.14</strong></td>
<td><strong>3.78</strong></td>
<td><strong>4.72</strong></td>
<td><strong>5.86</strong></td>
<td><strong>7.14</strong></td>
<td><strong>12.83</strong></td>
<td><strong>20.97</strong></td>
<td><strong>27.06</strong></td>
<td><strong>41.36</strong></td>
<td><strong>61.81</strong></td>
</tr>
<tr>
<td><strong>Median</strong></td>
<td><strong>26.91%</strong></td>
<td><strong>3.00</strong></td>
<td><strong>3.00</strong></td>
<td><strong>3.00</strong></td>
<td><strong>3.00</strong></td>
<td><strong>5.00</strong></td>
<td><strong>6.00</strong></td>
<td><strong>10.00</strong></td>
<td><strong>15.00</strong></td>
<td><strong>22.50</strong></td>
<td></td>
</tr>
</tbody>
</table>

Table 5: Number of samples to be generated over a spectrum of different coverage values for balanced subsamples with minority class' size

<table>
<thead>
<tr>
<th>N,S</th>
<th>Coverage</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>10%</td>
</tr>
<tr>
<td></td>
<td>3</td>
</tr>
<tr>
<td>Bootstrap</td>
<td>0.9502</td>
</tr>
<tr>
<td>Stratified S%=90</td>
<td>0.9990</td>
</tr>
<tr>
<td>Stratified S%=75</td>
<td>0.9844</td>
</tr>
<tr>
<td>Stratified S%=50</td>
<td>0.8750</td>
</tr>
<tr>
<td>Stratified S%=25</td>
<td>0.5781</td>
</tr>
</tbody>
</table>

Table 6: Coverage value for N,S=3 and Number of samples to be generated over a spectrum of different coverage values for bootstrap and stratified samples (with different sizes)
Using J48consolidated

The major changes done in this update of the J48consolidated class has been already mentioned in the above sections. However, this has also implied some changes in the user interfaces of this class. The main change is related to the way about how to determine the number of samples to be generated. We have added a new option, \texttt{RMnumberSamplesHowToSet} (\texttt{m\_RMnumberSamplesHowToSet} member), which can be set to two values: "using a fixed value" (\texttt{NumberSamples\_FixedValue} tag) or "based on a coverage value (%)" (\texttt{NumberSamples\_BasedOnCoverage} tag).

The "using a fixed value" tag maintains the same semantic of the \texttt{RMnumberSamples} parameter that it had above, that is, the user can directly specify a particular value of number of samples to be generated for the consolidated tree's construction. On the other hand, if the user chooses the "based on a coverage value (%)" tag for the \texttt{RMnumberSamplesHowToSet} parameter, the value of the \texttt{RMnumberSamples} parameter must be the coverage value that the user wants to achieve with the generated set of samples (as a percentage; a value between 0 and 100). By default, the option based on a coverage value is selected and the default value for the coverage is 99%.

Graphical interface

The figure below shows the new graphical interface for J48Consolidated. As mentioned above, the \texttt{RMnumberSamplesHowToSet} option has been added. Only the options started by the “RM” prefix (Resampling Method) are specifically related to the CTC algorithm (J48Consolidated class); the rest of options (partially shown in the figure) are derived from the implementation of the C4.5 algorithm (J48 class in Weka).

![New graphical interface of the Weka Explorer for J48Consolidated classifier.](image)

Command-line

Regarding the use of the J48Consolidated class from the command-line, a new option has been added in order to determine how to set the number of samples to be used. Actually, if the user wants
to set a fixed value of number of samples, nothing changes; only -RM-N option will have to be set followed by the specific value. However, if we want to determine the number of samples based on a coverage value, the new -RM-C option will have to be set followed by the -RM-N option and the desired coverage value. The figure below shows the help information related to both options.

![Figure 2: Changes in J48Consolidated options through the command-line](image)

**New measures shown**

As it has been mentioned, two new measures has been implemented on the J48Consolidated class (see “Using the notion of coverage” section), both related to the coverage concept: measureNumberSamplesByCoverage and measureTrueCoverage. The values related to these measures will be shown with the built tree, as well as a brief summary of the used resampling method.

Figure 3 shows an example of the output achieved by J48Consolidated class with the default parameters for the *german_credit* dataset (“credit-g.arff”). As it can be seen, the used resampling method ([RM]) is to change the class distribution (-RM-D 50.0), in particular, balancing the classes, and using the maximum size for the subsamples (-RM-B -2) taking into account replacement is not selected (not -RM-R used). The number of samples is determined based on a coverage value (-RM-C appears) and the coverage value is 99.0% (-RM-N 99.0).

Regarding the new measures, the necessary number of samples to obtain a 99% of coverage is 9 ($N_S=f(99\% \text{ of coverage})=9$) and the actual coverage achieved based on the dataset's characteristics, taking into account the mentioned resampling method, is around 99.5453%.

If an exceptional situation occurred, like those mentioned in the “Taking some exceptional characteristics of some datasets into account” section (for example, if the original dataset is already balanced), a brief message would also be added here in order to notice this situation.
The implementation of the CTC algorithm for Weka consists on the `J48Consolidated` class and the `j48Consolidated` package which includes other 5 classes, all of them derived from its corresponding `j48`'s original class (for more details see [6]). All changes done in the source code to achieve the functionality mentioned in this report were done, mainly, in the `J48Consolidated` class. Only two functions were added to the `InstancesConsolidated` class, basically for debugging purposes. The complete source code of both classes, “`J48Consolidated.java`” and “`InstancesConsolidated.java`” files, has been included in “Appendix 1: Source code” (page 21).

**Source code**

A website exists containing the complete material related to the J48Consolidated classifier:

[http://www.sc.ehu.es/aldapa/weka-ctc](http://www.sc.ehu.es/aldapa/weka-ctc)

Regarding this update, the material below can be found:

- **Documentation:**
  
  This technical report:

  [Weka-CTC-v2.pdf](http://www.sc.ehu.es/aldapa/weka-ctc/Weka-CTC-v2.pdf)
Weka maintains two primary versions: the stable version corresponding to the latest edition of the data mining book and the development version, which exhibits a package management system that makes it easy for the Weka community to add new functionality to Weka (See Downloading and installing Weka).

Thus, we also offers both versions for J48Consolidated package:

**Stable version**

The source code of the six classes that implement the J48Consolidated classifier can be found in (tested for weka-3-6-11):

- J48Consolidated-v2-stb.java.tar.gz

In order to complete the whole source code of the implementation, download Weka source code from http://www.cs.waikato.ac.nz/ml/weka/downloading.html.

And, finally, the whole executable file of Weka for stable-3-6-11 including J48Consolidated package can be found in:

- Weka-CTC-v2-stb.jar

**Development version**

The Weka package containing the J48Consolidated classifier (including compiled code, source code, javadocs and package description files) can be found in (tested for weka-3-7-11):

- J48Consolidated-v2.zip

Also, this package has recently become an “official” Weka package and is accessible in the central package repository of Weka, as it can be seen in Figure 5.

In order to better understand how packages are structured for the package management system see here.

This package can be installed through the package management system of the development 3.7.11 version of Weka. However, since J48Consolidated class extends J48 class, some J48's members and functions have to be 'protected' (instead 'private') in order to be able to use them. Because of this and based on a question done in Wekalist, the Weka mailing list, Eibe Frank, one of the authors and developers of Weka platform, changed the access modifiers for (almost all) private member variables to protected in J48 and all classes in the j48 package (See “[Wekalist] How to build a package with a new classifier if I changed an original class of weka?”).
These changes were done on Tue Apr 1 2014, therefore to be able to install the J48Consolidated package a version of dev-3-7-11 generated later than that date is required.

And, finally, the whole executable file of Weka for dev-3-7-11 including the J48Consolidated class (not the package) can be found in:

Weka-CTC-v2-dev.jar

Figure 5: J48Consolidated Repository version package successfully installed in Weka dev-3-7-11

Figure 6: Main window of Weka development 3.7.11 version
Citation policy

If you want to refer to CTC in a publication, please cite one of these papers:


We have also recently written this paper which explores the results of consolidated trees using the notion of coverage introduced in this technical report but it is pending for publication:


Further work

There are some things that can be done related to this work. All of them have been marked as //TODO in the source code:

- Implement the options binarySplits and reducedErrorPruning of the J48 implementation.
- Set the different options to generate the samples as a filter of Weka. In this way other strategies, already implemented in Weka, could be used for the generation of samples, as for example SMOTE method.
- Generalize the process of changing the class distribution to multi-class datasets. In this update it was enabled the possibility of balancing the classes of the subsamples to be generated, but not in a more general way.
- Make possible the use of replacement when changing the class distribution, even though we have not used this option in our previous works.

Bibliography


Appendix 1: Source code

This appendix contains the source code of the two only java classes that were changed in this update: “J48Consolidated.java” and “InstancesConsolidated.java”. The rest of classes that compose the implementation of the J48Consolidated classifier (C45ConsolidatedPruneableClassifierTree.java, C45ConsolidatedModelSelection.java, C45ConsolidatedSplit.java and DistributionConsolidated.java) can be found in the previous technical report [6].

J48Consolidated.java

```java
package weka.classifiers.trees;

import java.util.Enumeration;
import java.util.Random;
import java.util.Vector;
import weka.classifiers.Sourcable;
import weka.classifiers.trees.j48.C45PruneableClassifierTree;
import weka.classifiers.trees.j48.ModelSelection;
import weka.classifiers.trees.j48Consolidated.C45ConsolidatedModelSelection;
import weka.classifiers.trees.j48Consolidated.C45ConsolidatedPruneableClassifierTree;
import weka.classifiers.trees.j48Consolidated.InstancesConsolidated;
import weka.core.AdditionalMeasureProducer;
import weka.core.Capabilities;
import weka.core.Drawable;
import weka.core.Instance;
import weka.core.Instance;
import weka.core.Matchable;
import weka.core.Option;
import weka.core.OptionHandler;
import weka.core.SelectedTag;
import weka.core.Summarizable;
import weka.core.Tag;
import weka.core.TechnicalInformation;
import weka.core.TechnicalInformationHandler;
import weka.core.Utils;
import weka.core.WeightedInstancesHandler;
import weka.core.TechnicalInformation.Field;
import weka.core.TechnicalInformation.Type;

/**
 * Class for generating a pruned or unpruned C4.5 consolidated tree. Uses the Consolidated Tree Construction (CTC) algorithm: a single tree is built based on a set of subsamples. New options are added to the J48 class to set the Resampling Method (RM) for the generation of samples to be used in the consolidation process. For more
**/
```

<!-- globalinfo-start -->

/* Class for generating a pruned or unpruned C4.5 consolidated tree. Uses the Consolidated Tree Construction (CTC) algorithm: a single tree is built based on a set of subsamples. New options are added to the J48 class to set the Resampling Method (RM) for the generation of samples to be used in the consolidation process. For more
```
information, see:

* Jesús M. Pérez and Javier Muguerza and Olatz Arbelaitz and Ibai Gurrutxaga and José I. Martín.
  * <a href="http://dx.doi.org/10.1016/j.patrec.2006.08.013" target="_blank">doi:10.1016/j.patrec.2006.08.013</a>

A new way has been added to determine the number of samples to be used in the consolidation process which guarantees the minimum percentage, the coverage value, of the examples of the original sample to be contained by the set of built subsamples. For more information, see:

* Igor Ibarguren and Jesús M. Pérez and Javier Muguerza and Ibai Gurrutxaga and Olatz Arbelaitz.

BibTeX:
```
@article{Perez2007,
  title = "Combining multiple class distribution modified subsamples in a single tree",
  journal = "Pattern Recognition Letters",
  volume = "28",
  number = "4",
  pages = "414 - 422",
  year = "2007",
  doi = "10.1016/j.patrec.2006.08.013",
  author = "Jesús M. Pérez and Javier Muguerza and Olatz Arbelaitz and Ibai Gurrutxaga and José I. Martín"
}
```
```
@article{Ibarguren2014,
  title = "An extensive analysis of consolidated trees with a new resampling strategy to establish their robustness across multiple classification contexts againsts a wide set of rule induction algorithms",
  journal = "Knowledge Based Systems (submitted)",
  year = "2014",
  author = "Igor Ibarguren and Jesús M. Pérez and Javier Muguerza and Ibai Gurrutxaga and Olatz Arbelaitz"
}
```

Valid options are: <pre>
J48 options <br/> ==========
<p>-U<br/> Use unpruned tree.</p>
<p>-C &lt;pruning confidence&gt;
Set confidence threshold for pruning.
(default 0.25)</p>
<p>-M &lt;minimum number of instances&gt;
Set minimum number of instances per leaf.
(default 2)</p>
<p>-S
Don't perform subtree raising.</p>
<p>-L
Do not clean up after the tree has been built.</p>
<p>-A
Laplace smoothing for predicted probabilities.</p>
<p>-0 &lt;seed&gt;
Seed for random data shuffling (default 1).</p>
```

22
Options to set the Resampling Method (RM) for the generation of samples to use in the consolidation process:

- **RM-C**: Determines the way to set the number of samples to be generated will be based on a coverage value as a percentage. In the case this option is not set, the number of samples will be determined using a fixed value. (set by default)

- **RM-N**: Number of samples to be generated for the use in the construction of the consolidated tree. It can be set as a fixed value or based on a coverage value as a percentage, when -RM-C option is used, which guarantees the number of samples necessary to adequately cover the examples of the original sample. (default 5 for a fixed value or 99% for the case based on a coverage value)

- **RM-R**: Determines whether or not replacement is used when generating the samples. (default false)

- **RM-B**: Size of each sample, as a percentage of the training set size. Combined with the option -distribution minority class&gt; accepts:
  - 1 (sizeOfMinClass): The size of the minority class
  - 2 (Max): Maximum size taking -distribution minority class&gt; into account and using no replacement (default -2)

- **RM-D**: Determines the new value of the distribution of the minority class, if we want to change it. It can be one of the following values:
  - A value between 0 and 100 to change the portion of minority class instances in the new samples (this option can only be used with binary problems (two-class datasets))
  - -1 (free): Works with the instances without taking their class into account
  - -2 (stratified): Maintains the original class distribution in the new samples (default 50.0)

*Author: Jesús M. Pérez (txus.perez@ehu.es)
*Author: Igor Ibarguren (igor.ibarguren@ehu.es)
(based on the previous version written in collaboration with Fernando Lozano)
(based on J48.java written by Eibe Frank)
*Version $Revision: 3.0 $
```java
private static float m_minExamplesPerClassPercent = (float)2.0;

/** String containing a brief explanation of exceptional situations, if occur */
String m_stExceptionalSituationsMessage = "";

/** Ways to set the numberSamples option */
public static final int NumberSamples_FixedValue = 1;
public static final int NumberSamples_BasedOnCoverage = 2;

/** Strings related to the ways to set the numberSamples option */
public static final Tag[] TAGS_WAYS_TO_SET_NUMBER_SAMPLES = {
    new Tag(NumberSamples_FixedValue, "using a fixed value"),
    new Tag(NumberSamples_BasedOnCoverage, "based on a coverage value (%)"),
};

/** Options to set the Resampling Method (RM) for the generation of samples
* to use in the consolidation process
* (Prefix RM added to the option names in order to appear together in the graphical interface)
********************************************************************************/
/** Selected way to set the number of samples to be generated; or using a fixed value;
* or based on a coverage value as a percentage (by default). */
private int m_RMnumberSamplesHowToSet = NumberSamples_BasedOnCoverage;

/** Number of samples to be generated for the use in the construction of the consolidated tree.
* If m_RMnumberSamplesHowToSet = NumberSamples_BasedOnCoverage, the value of number of
* the number of samples necessary to adequately cover the examples of the original sample. */
private float m_RMnumberSamples = (float)m_coveragePercent; // default: f(99% of coverage)

/** Determines whether or not replacement is used when generating the samples.**/
private boolean m_RMreplacement = false;

/** Size of each sample(bag), as a percentage of the training set size.
* Combined with the option &lt;distribution minority class&gt; accepts:
* -1 (sizeOfMinClass): The size of the minority class
* -2 (maxSize): Maximum size taking &lt;distribution minority class&gt; into account
* and using no replacement */
private int m_RMbagSizePercent = -2; // default: maxSize

/** Value of the distribution of the minority class to be changed.
* It can be one of the following values: <br>
* - A value between 0 and 100 to change the portion of minority class instances in the new samples
* - (If the dataset is multi-class, only the special value 50.0 will be accepted to balance the classes)
* -1 (free): Works with the instances without taking their class into account
* -2 (stratified): Maintains the original class distribution in the new samples */
private float m_RMnewDistrMinClass = (float)50.0;

public String globalInfo() {
    return "Class for generating a pruned or unpruned C45 consolidated tree. Uses the Consolidated 
    + "Tree Construction (CTC) algorithm: a single tree is built based on a set of subsamples. 
    + "New options are added to the J48 class to set the Resampling Method (RM) for 
    + "the generation of samples to be used in the consolidation process.\n"
    + "Recently, a new way has been added to determine the number of samples to be used 
    + "in the consolidation process which guarantees the minimum percentage, the coverage value, 
    + "of the examples of the original sample to be contained by the set of built subsamples. 
    + "For more information, see:\n"
    + getTechnicalInformation().toString();
}

public TechnicalInformation getTechnicalInformation() {
    TechnicalInformation result;
    result = new TechnicalInformation(Type.ARTICLE);
}
```
result.setValue(Field.AUTHOR, "Jesús M. Pérez and Javier Muguerza and Olatz Arbelaitz and Ibai Gurrutxaga and José I. Martín");
result.setValue(Field.YEAR, "2007");
result.setValue(Field.TITLE, "Combining multiple class distribution modified subsamples in a single tree");
result.setValue(Field.JOURNAL, "Pattern Recognition Letters");
result.setValue(Field.VOLUME, "28");
result.setValue(Field.NUMBER, "4");
result.setValue(Field.PAGES, "414-422");
result.setValue(Field.URL, "http://dx.doi.org/10.1016/j.patrec.2006.08.013");

TechnicalInformation additional = new TechnicalInformation(Type.ARTICLE);
additional.setValue(Field.AUTHOR, "Igor Ibarguren and Jesús M. Pérez and Javier Muguerza and Ibai Gurrutxaga and Olatz Arbelaitz");
additional.setValue(Field.YEAR, "2014");
additional.setValue(Field.TITLE, "An extensive analysis of consolidated trees with a new resampling strategy to establish their robustness across multiple classification contexts againsts a wide set of rule induction algorithms");
additional.setValue(Field.JOURNAL, "Knowledge Based Systems (submitted)");
result.add(additional);
return result;
}

/**
 * Returns default capabilities of the classifier.
 *
 * @return the capabilities of this classifier
 */
public Capabilities getCapabilities() {
   Capabilities result;
   try {
        result = new C45PruneableClassifierTree(null, !m_unpruned, m_CF, m_subtreeRaising, !m_noCleanup, m_collapseTree).getCapabilities();
    } catch (Exception e) {
        result = new Capabilities(this);
    }
    result.setOwner(this);
    return result;
}

/**
 * Generates the classifier.
 * (Implements the original CTC algorithm, so it does not implement the options binarySplits and reducedErrorPruning of J48, only what is based on C4.5 algorithm)
 *
 * @param instances the data to train the classifier with
 * @throws Exception if classifier can't be built successfully
 */
public void buildClassifier(Instances instances) throws Exception {
    ModelSelection modSelection;
    // TODO Implement the option binarySplits of J48
    modSelection = new C45ConsolidatedModelSelection(m_minNumObj, instances, m_useMDLcorrection, m_doNotMakeSplitPointActualValue);
    // TODO Implement the option reducedErrorPruning of J48
    m_root = new C45ConsolidatedPruneableClassifierTree(modSelection, !m_unpruned, m_CF, m_subtreeRaising, !m_noCleanup, m_collapseTree);
    // remove instances with missing class before generating samples
    instances = new Instances(instances);
    instances.deleteWithMissingClass();

    //Generate as many samples as the number of samples with the given instances
    Instances[] samplesVector = generateSamples(instances);
    //if (m_Debug)
    //   printSamplesVector(samplesVector);
    ((C45ConsolidatedPruneableClassifierTree)m_root).buildClassifier(instances, samplesVector);
protected Instances[] generateSamples(Instances instances) throws Exception {
    Instances[] samplesVector = null;
    // can classifier tree handle the data?
    getCapabilities().testWithFail(instances);
    // remove instances with missing class
    InstancesConsolidated instancesWMC = new InstancesConsolidated(instances);
    instancesWMC.deleteWithMissingClass();
    if (m_Debug) {
        System.out.println("=== Generation of the set of samples ===");
        System.out.println(toStringResamplingMethod());
    }
    /**
     * Original sample size */
    int dataSize = instancesWMC.numInstances();
    if(dataSize==0)
        System.err.println("Original data size is 0! Handle zero training instances!");
    else
        if (m_Debug)
            System.out.println("Original data size: "+ dataSize);
    /** Size of samples(bags) to be generated */
    int bagSize = 0;
    // Some checks done in set-methods
    //@ requires 0 <= m_RMnumberSamples
    //@ requires -2 <= m_RMbagSizePercent && m_RMbagSizePercent <= 100
    //@ requires -2 <= m_RMnewDistrMinClass && m_RMnewDistrMinClass < 100
    if(m_RMbagSizePercent >= 0 ) {
        bagSize =  dataSize * m_RMbagSizePercent / 100;
        if(bagSize==0)
            System.err.println("Size of samples is 0 (" + m_RMbagSizePercent + "+ of " + dataSize
                             + ")! Handle zero training instances!");
    } else if (m_Debug)
        System.out.println("Original data size: "+ dataSize);
    return samplesVector;
}

/** * Generate a set of stratified samples * * @param instances the training data which will be used to generate the sample set * @param dataSize Size of original sample (instances) * @param bagSize Size of samples(bags) to be generated
@param random a random number generator
@throws Exception if something goes wrong
*/

private Instances[] generateStratifiedSamples(
    InstancesConsolidated instances, int dataSize, int bagSize, Random random) throws Exception{
    int numClasses = instances.numClasses();
    // Get the classes
    InstancesConsolidated[] classesVector = instances.getClasses();
    // What is the minority class?
    /** Vector containing the size of each class */
    int classSizeVector[] = instances.getClassesSize(classesVector);
    /** Index of the minority class in the original sample */
    int iMinClass = Utils.minIndex(classSizeVector);
    if (m_Debug)
        instances.printClassesInformation(dataSize, iMinClass, classSizeVector);
    // Determine the sizes of each class in the new samples
    /** Vector containing the size of each class in the new samples */
    int newClassSizeVector[] = new int[numClasses];
    // Check the bag size
    int bagSizePercent;
    if((dataSize == bagSize) & !m_RMreplacement){
        System.out.println("It doesn't make sense that the original sample's size and " + "the size of samples to be generated are the same without using replacement" + "because all the samples will be entirely equal!!!
        m_bagSizePercentToReduce + "% will be used as the bag size percentage!!");
        bagSizePercent = m_bagSizePercentToReduce;
        bagSize =  dataSize * m_bagSizePercentToReduce / 100;
    } else 
        bagSizePercent = m_RMBagSizePercent;
    // Partial bag size
    int localBagSize = 0;
    for(int iClass = 0; iClass < numClasses; iClass++)
        if(iClass != iMinClass){
            /** Value for the 'iClass' -th class size of the samples to be generated */
            int newClassSize = Utils.round(classSizeVector[iClass] * (double)bagSizePercent / 100); 
            newClassSizeVector[iClass] = newClassSize;
            localBagSize += newClassSize;
        }
    /** Value for the minority class size of the samples to be generated */
    // (Done in this way to know the exact size of the minority class in the generated samples)
    newClassSizeVector[iMinClass] = bagSize - localBagSize;
    if (m_Debug) {
        System.out.println("New bag size: " + bagSize);
        System.out.println("Classes sizes of the new bag: ");
        for(int iClass = 0; iClass < numClasses; iClass++)
            System.out.print(newClassSizeVector[iClass] + (iClass == iMinClass) ? "(*) The most disfavored class based on coverage") + 
        System.out.println(" ");
    }
    System.out.println(" ");
    // Determine the size of samples' vector; the number of samples
    int numberSamples;
    // Calculate the ratio of the sizes for each class between the sample and the subsample */
    double bagBySampleClassRatioVector[] = new double[numClasses];
    for(int iClass = 0; iClass < numClasses; iClass++)
        if(classSizeVector[iClass] > 0)
            bagBySampleClassRatioVector[iClass] = newClassSizeVector[iClass] / (double)classSizeVector[iClass];
        else // The size of the class is 0
            // This class won't be selected
            bagBySampleClassRatioVector[iClass] = Double.MAX_VALUE;
    if(m_RMNumberOfSamplesHowToSet == NumberSamples_BasedOnCoverage) {
        // The number of samples depends on the coverage to be guaranteed for the most disfavored class.
        double coverage = m_RMNumberOfSamples / (double)100;
        /** Calculate the most disfavored class in respect of coverage */
        int iMostDisfavorClass = Utilities.minIndex(bagBySampleClassRatioVector);
        if (m_Debug) {
            System.out.println("Ratio bag:sample by each class:");
            System.out.println("(*) The most disfavored class based on coverage");
            for (int iClass = 0; iClass < numClasses; iClass++)
                System.out.println(Utilities. &frac10;ToString(bagBySampleClassRatioVector[iClass],2));
            if(iClass == iMostDisfavorClass)
System.out.print("(*)");
if(iClass < numClasses - 1)
    System.out.print(",");
}
System.out.println(";");
}
if(m_RMreplacement)
    numberSamples = (int)Math.ceil((-1) * Math.log(1 - coverage) / 
        bagBySampleClassRatioVector[iMostDisfavorClass]);
else
    numberSamples = (int)Math.ceil(Math.log(1 - coverage) / 
        Math.log(1 - bagBySampleClassRatioVector[iMostDisfavorClass]));
System.out.println("The number of samples to guarantee at least a coverage of " + 
    Utils.doubleToString(100*coverage,0) + "% is " + numberSamples + ");

m_numberSamplesByCoverage = numberSamples;
if (numberSamples < 3){
    numberSamples = 3;
    System.out.println("(*) Forced the number of samples to be 3!!!");
    m_stExceptionalSituationsMessage += " (*) Forced the number of samples to be 3!!!\n";
} else // m_RMNumberSamplesHowToSet == NumberSamples_FixedValue
    // The number of samples has been set by parameter
    numberSamples = (int)m_RMNumberSamples;

    // Calculate the true coverage achieved
    m_trueCoverage = (double)0.0;
    for (int iClass = 0; iClass < numClasses; iClass++){
        double trueCoverageByClass;
        if(classSizeVector[iClass] > 0){
            if(m_RMreplacement)
                trueCoverageByClass = 1 - Math.pow(Math.E, 
                    (-1) * bagBySampleClassRatioVector[iClass] * numberSamples);
            else
                trueCoverageByClass = 1 - Math.pow((1 - bagBySampleClassRatioVector[iClass]), numberSamples);
        } else
            trueCoverageByClass = (double)0.0;
        double ratioClassDistr = classSizeVector[iClass] / (double)dataSize;
        m_trueCoverage += ratioClassDistr * trueCoverageByClass;
    }

    // Set the size of the samples' vector
    Instances[] samplesVector = new Instances[numberSamples];

    // Generate the vector of samples
    for(int iSample = 0; iSample < numberSamples; iSample++){
        InstancesConsolidated bagData = null;
        InstancesConsolidated bagClass = null;
        for(int iClass = 0; iClass < numClasses; iClass++){
            // Extract instances of the iClass-th class
            if(m_RMreplacement)
                bagClass = new InstancesConsolidated(classesVector[iClass].resampleWithWeights(random));
            else
                bagClass = new InstancesConsolidated(classesVector[iClass]);
            // Shuffle the instances
            bagClass.randomize(random);
            if(newClassSizeVector[iClass] < classSizeVector[iClass]) {
                InstancesConsolidated newBagData = new InstancesConsolidated(bagClass, 0,
                    newClassSizeVector[iClass]);
                bagClass = newBagData;
                newBagData = null;
            } else
                bagData = bagClass;
        } if(bagData == null)
            bagData = bagClass;
        else
            bagData.add(bagClass);
        bagClass = null;
    } // Shuffle the instances
    bagData.randomize(random);
    samplesVector[iSample] = (Instances)bagData;
    bagData = null;
    classesVector = null;
    classSizeVector = null;
    newClassSizeVector = null;
return samplesVector;
}
/**
 * Generate a set of samples without taking the class distribution into account
 * (like in the meta-classifier Bagging)
 */
@parameters
@name instances the training data which will be used to generate the sample set
@name dataSize Size of original sample (instances)
@name bagSize Size of samples (bags) to be generated
@name random a random number generator
@returns
Instances[] the vector of generated samples
@throws Exception if something goes wrong
*/
private Instances[] generateFreeDistrSamples(
InstancesConsolidated instances, int dataSize, int bagSize, Random random) throws Exception{
    // Check the bag size
    if(dataSize == bagSize && !m_RMreplacement){
        System.out.println("It doesn't make sense that the original sample's size and " + "the size of samples to be generated are the same without using replacement" + "because all the samples will be entirely equal!!!\n" + m_bagSizePercentToReduce + "% will be used as the bag size percentage!!!");
        bagSize = dataSize * m_bagSizePercentToReduce / 100;
    }
    if(m_Debug)
        System.out.println("New bag size: " + bagSize);
    // Determine the size of samples' vector; the number of samples
    int numberSamples;
    double bagBySampleRatio = bagSize / (double) dataSize;
    if(m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage) {
        // The number of samples depends on the coverage to be guaranteed for the most disfavored class.
        double coverage = m_RMnumberSamples / (double)100;
        if(m_RMreplacement)
            numberSamples = (int) Math.ceil((-1) * Math.log(1 - coverage) / bagBySampleRatio);
        else
            numberSamples = (int) Math.ceil(Math.log(1 - coverage) / Math.log(1 - bagBySampleRatio));
        System.out.println("The number of samples to guarantee at least a coverage of " + "Utils.doubleToString(100*coverage,0) + "% is " + numberSamples + ".");
        m_numberSamplesByCoverage = numberSamples;
        if(numberSamples < 3){
            numberSamples = 3;
            System.out.println("(*) Forced the number of samples to be 3!!!");
            m_stExceptionalSituationsMessage += " (*) Forced the number of samples to be 3!!!\n";
        }
    } else // m_RMnumberSamplesHowToSet == NumberSamples_FixedValue
    // The number of samples has been set by parameter
    numberSamples = (int)m_RMnumberSamples;
    // Calculate the true coverage achieved
    if(m_RMreplacement)
        m_trueCoverage = 1 - Math.pow(Math.E, (-1) * bagBySampleRatio * numberSamples);
    else
        m_trueCoverage = 1 - Math.pow(1 - bagBySampleRatio, numberSamples);
    // Set the size of the samples' vector
    Instances[] samplesVector = new Instances[numberSamples];
    // Generate the vector of samples
    for(int iSample = 0; iSample < numberSamples; iSample++){
        Instances bagData = null;
        if(m_RMreplacement)
            bagData = new Instances(instances.resampleWithWeights(random));
        else
            bagData = new Instances(instances);
        // Shuffle the instances
        bagData.randomize(random);
        if(bagSize < dataSize) {
            Instances newBagData = new Instances(bagData, 0, bagSize);
            bagData = newBagData;
            newBagData = null;
        }
        samplesVector[iSample] = bagData;
    }
/**
 * Generate a set of samples changing the distribution of the minority class
 *
 * @param instances the training data which will be used to generate the sample set
 * @param dataSize Size of original sample (instances)
 * @param bagSize Size of samples(bags) to be generated
 * @param random a random number generator
 * @return Instances[] the vector of generated samples
 * @throws Exception if something goes wrong
 */
private Instances[] generateSamplesChangingMinClassDistr(
    InstancesConsolidated instances, int dataSize, int bagSize, Random random)
throws Exception{
    int numClasses = instances.numClasses();
    // Some checks
    if ((numClasses > 2) && (m_RMnewDistrMinClass != (float)50.0))
        throw new Exception("In the case of multi-class datasets, the only possibility to change the
distribution of classes is to balance them!!!\n" +
        "Use the special value '50.0' in <distribution minority class> for this purpose!!!");
    // TODO Generalize the process to multi-class datasets to set different new values of distribution for
each class.
    // Some checks done in set-methods
    //@ requires m_RMreplacement = false
    // TODO Accept replacement
    // Get the classes
    InstancesConsolidated[] classesVector = instances.getClasses();

    // What is the minority class?
    /** Vector containing the size of each class */
    int classSizeVector[] = instances.getClassesSize(classesVector);
    /** Index of the minority class in the original sample */
    int iMinClass, i_iMinClass;
    /** Prevent the minority class from being empty (we hope there is one non-empty!) */
    int iClassSizeOrdVector[] = Utils.sort(classSizeVector);
    for(i_iMinClass = 0; ((i_iMinClass < numClasses) &&
        (classSizeVector[iClassSizeOrdVector[i_iMinClass]] == 0)); i_iMinClass++);
    if(i_iMinClass < numClasses)
        iMinClass = iClassSizeOrdVector[i_iMinClass];
    else // To be OK when testing to Handle zero training instances!
        iMinClass = 0;

    /** Index of the majority class in the original sample */
    int iMajClass = Utils.maxIndex(classSizeVector);
    /** Determines whether the original sample is balanced or not */
    boolean isBalanced = false;
    if (iMinClass == iMajClass){
        isBalanced = true;
        // If the sample is balanced, it is determined, by convention, that the majority class is the last one
        iMajClass = numClasses-1;
    }
    if (m_Debug)
        instances.printClassesInformation(dataSize, iMinClass, classSizeVector);

    /** Distribution of the minority class in the original sample */
    float distrMinClass;
    if (dataSize == 0)
        distrMinClass = (float)0;
    else
        distrMinClass = (float)100 * classSizeVector[iMinClass] / dataSize;

    /** Guarantee the minimum number of examples in each class based on m_minExamplesPerClassPercent */
    int minExamplesPerClass = (int) Math.ceil(dataSize * m_minExamplesPerClassPercent / (double)100.0);
    /** Guarantee to be at least m_minNumObj */
    if (minExamplesPerClass < m_minNumObj)
        minExamplesPerClass = m_minNumObj;
    if (m_Debug)
        System.out.println("Minimum number of examples to be guaranteed in each class: "+
            minExamplesPerClass);
    for(int iClass = 0; iClass < numClasses; iClass++)
        if((classSizeVector[iClass] < minExamplesPerClass) &
            // if number of examples is smaller than the
            // Guarantee the minimum number of examples in each class based on m_minExamplesPerClassPercent */
            minExamplesPerClass = (int) Math.ceil(dataSize * m_minExamplesPerClassPercent / (double)100.0);
(classSizeVector[iClass] > 0)) {  // but, at least, it has to exist any example.
    // Oversample the class randomly
    System.out.println("The " + iClass + "-th class has too few examples (" +
    classSizeVector[iClass] + ")!!!\n" +
    "It will be oversampled randomly up to " + minExamplesPerClass + "!!!");
    m_stExceptionalSituationsMessage += "  (+) Forced the " + iClass +
    "-th class to be oversampled!!!\n";
    // based on the code of the function `resample(Random)` of the class `Instances`
    InstancesConsolidated bagClass = classesVector[iClass];
    while (bagClass.numInstances() < minExamplesPerClass) {
        bagClass.add(classesVector[iClass].instance(random.nextInt(classSizeVector[iClass])));
    }
    // Update the vectors with classes' information and the new data size
    dataSize = dataSize - classSizeVector[iClass] + minExamplesPerClass;
    classesVector[iClass] = bagClass;
    classSizeVector[iClass] = minExamplesPerClass;
}

/** Maximum values for classes' size on the samples to be generated taking RMnewDistrMinClass into account
*   and without using replacement */
int maxClassSizeVector[] = new int[numClasses];
if (numClasses == 2) {
    // the dataset is two-class
    if (m_RMnewDistrMinClass > distrMinClass) {
        // Maintains the whole minority class
        maxClassSizeVector[iMinClass] = classSizeVector[iMinClass];
        maxClassSizeVector[iMajClass] = Util.round(classSizeVector[iMajClass] *
            (100 - m_RMnewDistrMinClass) / m_RMnewDistrMinClass);
    } else {
        // Maintains the whole majority class
        maxClassSizeVector[iMajClass] = classSizeVector[iMajClass];
        maxClassSizeVector[iMinClass] = Util.round(classSizeVector[iMinClass] *
            m_RMnewDistrMinClass / (100 - m_RMnewDistrMinClass));
    }
} else {
    // the dataset is multi-class
    /** The only accepted option is to change the class distribution is to balance the samples */
    for (int iClass = 0; iClass < numClasses; iClass++)
        maxClassSizeVector[iClass] = classSizeVector[iClass];

    // Determine the sizes of each class in the new samples
    /** Vector containing the size of each class in the new samples */
    int newClassSizeVector[] = new int[numClasses];
    /** Determines whether the size of samples to be generated will be forced to be reduced in exceptional situations */
    boolean forceToReduceSamplesSize = false;
    if (m_RMBagSizePercent == -2) {
        // maxSize : Generate the biggest samples according to the indicated distribution (RMnewDistrMinClass),
        // that is, maintaining the whole minority (majority) class
        if (numClasses == 2) {
            // the dataset is two-class
            if (Util.eq(m_RMnewDistrMinClass, distrMinClass)) {
                System.out.println("It doesn't make sense that the original distribution and " +
                    "the distribution to be changed (RMnewDistrMinClass) are the same and " +
                    "the size of samples to be generated is maximum (RMBagSizePercent=-2) " +
                    "(without using replacement) " +
                    "because all the samples will be entirely equal!!!\n" +
                    "m_bagSizePercentToReduce + % will be used as the bag size percentage!!!");
                forceToReduceSamplesSize = true;
            } else {
                // the dataset is multi-class
                if (isBalanced) {
                    System.out.println("In the case of multi-class datasets, if the original sample is balanced, " +
                        "it doesn't make sense that " +
                        "the size of samples to be generated is maximum (RMBagSizePercent=-2) " +
                        "(without using replacement) " +
                        "because all the samples will be entirely equal!!!\n" +
                        "m_bagSizePercentToReduce + % will be used as the bag size percentage!!!");
                    forceToReduceSamplesSize = true;
                }
            }
        } else {
            // the dataset is multi-class
            if (isBalanced) {
                System.out.println("In the case of multi-class datasets, if the original sample is balanced, " +
                    "it doesn't make sense that " +
                    "the size of samples to be generated is maximum (RMBagSizePercent=-2) " +
                    "(without using replacement) " +
                    "because all the samples will be entirely equal!!!\n" +
                    "m_bagSizePercentToReduce + % will be used as the bag size percentage!!!");
                forceToReduceSamplesSize = true;
            }
        }
    } else {
        // the dataset is multi-class
        if (isBalanced) {
            System.out.println("In the case of multi-class datasets, if the original sample is balanced, " +
                "it doesn't make sense that " +
                "the size of samples to be generated is maximum (RMBagSizePercent=-2) " +
                "(without using replacement) " +
                "because all the samples will be entirely equal!!!\n" +
                "m_bagSizePercentToReduce + % will be used as the bag size percentage!!!");
            forceToReduceSamplesSize = true;
        }
    }
}
if(!forceToReduceSamplesSize){
    bagSize = 0;
    for(inticlass = 0;iclass < numClasses;iclass++)
        if(classSizeVector[iClass] == 0)
            newClassSizeVector[iClass] = 0;
    else{
        newClassSizeVector[iClass] = maxClassSizeVector[iClass];
        bagSize += maxClassSizeVector[iClass];
    }
}
else{
    if(m_RMbagSizePercent == -1)
        // sizeOfMinClass: the generated samples will have the same size that the minority class
        bagSize = classSizeVector[iMinClass];
    else
        // m_RMbagSizePercent is between 0 and 100. bagSize is already set.
        if(dataSize == bagSize){
            System.out.println("It doesn't make sense that the original sample's size and " +
"the size of samples to be generated are the same" +
"(without using replacement)" +
"because all the samples will be entirely equal!!!\n" +
m_bagSizePercentToReduce + "% will be used as the bag size percentage!!!");
            forceToReduceSamplesSize = true;
        }
    }
    if((m_RMbagSizePercent != -2) || forceToReduceSamplesSize)
    {
        if(numClasses == 2){
            // the dataset is two-class
            if(forceToReduceSamplesSize){
                bagSize = dataSize * m_bagSizePercentToReduce / 100;
                m_stExceptionalSituationsMessage += " (*) Forced to reduce the size of the generated
samples!!!\n";
            }
            newClassSizeVector[iMinClass] = Utils.round(m_RMnewDistrMinClass * bagSize / 100);
            newClassSizeVector[iMajClass] = bagSize - newClassSizeVector[iMinClass];
        }
        else{
            // the dataset is multi-class
            /** The only accepted option is to change the class distribution is to balance the samples */
            /** All the classes will have the same size, classSize, based on bagSizePercent applied
            * on minority class, that is, the generated samples will be bigger than expected,
            * neither sizeofMinClass nor original sample's size by bagSizePercent. Otherwise,
            * the classes of the samples would be too unpopulated */
            int bagSizePercent;
            if(m_RMbagSizePercent == -1)
                /** sizeOfMinClass (-1) is a special case, where the bagSizePercent to be applied will be
                * the half of the minority class, the same that it would be achieved if the dataset was two-
                * class */
                bagSizePercent = 50;
            else
                if(forceToReduceSamplesSize)
                    bagSizePercent = m_bagSizePercentToReduce;
                else
                    bagSizePercent = m_RMbagSizePercent;
            int classSize = (int)(bagSizePercent * classSizeVector[iMinClass]) / (float)100;
            bagSize = 0;
            for(inticlass = 0;iclass < numClasses;iclass++)
                if(classSizeVector[iClass] == 0)
                    newClassSizeVector[iClass] = 0;
                else{
                    newClassSizeVector[iClass] = classSize;
                    bagSize += classSize;
                }
        }
    }
    if(m_Debug) {
        System.out.println("New bag size: " + bagSize);
        System.out.println("New minority class size: " + newClassSizeVector[iMinClass] + " (" +
(int)newClassSizeVector[iMinClass] / (double)bagSize * 100) + ") obstruction: " +
(int)newClassSizeVector[iMajClass] / (double)bagSize * 100) + ");
    }
    if(numClasses > 2)
        System.out.println("New majority class size: " + newClassSizeVector[iMajClass]);
}
// Some checks
for (int iClass = 0; iClass < numClasses; iClass++)
    if (newClassSizeVector[iClass] > classSizeVector[iClass])
        throw new Exception("There aren't enough instances of the " + iClass + "-th class (" + classSizeVector[iClass] + ") to extract " + newClassSizeVector[iClass] + " for the new samples without replacement!!!");

// Determine the size of samples' vector; the number of samples
int numberSamples;
/** Calculate the ratio of the sizes for each class between the sample and the subsample */
double bagBySampleClassRatioVector[] = new double[numClasses];
for (int iClass = 0; iClass < numClasses; iClass++)
    if (classSizeVector[iClass] > 0)
        bagBySampleClassRatioVector[iClass] = newClassSizeVector[iClass] / (double)classSizeVector[iClass];
    else // The size of the class is 0
        bagBySampleClassRatioVector[iClass] = Double.MAX_VALUE;

if (m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage) {
    // The number of samples depends on the coverage to be guaranteed for the most disfavored class.
    double coverage = m_RMnumberSamples / (double)100;
    **/ Calculate the most disfavored class in respect of coverage */
    int iMostDisfavorClass = Utils.minIndex(bagBySampleClassRatioVector);
    if (m_Debug) {
        System.out.println("Ratio bag:sample by each class:");
        System.out.println("(*) The most disfavored class based on coverage");
        for (int iClass = 0; iClass < numClasses; iClass++){
            System.out.println(Utils.doubleToString(bagBySampleClassRatioVector[iClass], 2));
            if (iClass == iMostDisfavorClass)
                System.out.println("(*)");
            if (iClass < numClasses - 1)
                System.out.println(",");
        }
        System.out.println("\n");
    }
    numberSamples = (int) Math.ceil(Math.log(1 - coverage) / Math.log(1 - bagBySampleClassRatioVector[iMostDisfavorClass]));
    System.out.println("The number of samples to guarantee at least a coverage of " +
        Utils.doubleToString(100*coverage, 0) + "+% is " + numberSamples + ".");
    m_numberSamplesByCoverage = numberSamples;
    if (numberSamples < 3){
        numberSamples = 3;
        System.out.println("(*) Forced the number of samples to be 3!!!");
        m_stExceptionalSituationsMessage += " (*) Forced the number of samples to be 3!!!\n";
    }
} else // m_RMnumberSamplesHowToSet == NumberSamples_FixedValue
    // The number of samples has been set by parameter
    numberSamples = (int)m_RMnumberSamples;

// Calculate the true coverage achieved
m_trueCoverage = (double)0.0;
for (int iClass = 0; iClass < numClasses; iClass++)
    double trueCoverageByClass;
    if (classSizeVector[iClass] > 0){
        trueCoverageByClass = 1 - Math.pow(Math.E, (-1) * bagBySampleClassRatioVector[iClass] * numberSamples);
        if (m_RMreplacement)
            trueCoverageByClass = 1 - Math.pow(Math.E, (-1) * bagBySampleClassRatioVector[iClass], numberSamples);
        else
            trueCoverageByClass = 1 - Math.pow((1 - bagBySampleClassRatioVector[iClass]), numberSamples);
    }
    else
        trueCoverageByClass = (double)0.0;
    double ratioClassDistr = classSizeVector[iClass] / (double) dataSize;
    m_trueCoverage += ratioClassDistr * trueCoverageByClass;
}

// Set the size of the samples' vector
Instances[] samplesVector = new Instances[numberSamples];

// Generate the vector of samples
for (int iSample = 0; iSample < numberSamples; iSample++)
    InstancesConsolidated bagData = null;
    InstancesConsolidated bagClass = null;
    for (int iClass = 0; iClass < numClasses; iClass++)
if (classSizeVector[iClass] > 0) {
    // Extract instances of the i-th class
    bagClass = new InstancesConsolidated(classesVector[iClass]);
    // Shuffle the instances
    bagClass.randomize(random);
    if (newClassSizeVector[iClass] < classSizeVector[iClass]) {
        InstancesConsolidated newBagData = new InstancesConsolidated(bagClass, 0,
                                                                        newClassSizeVector[iClass]);

        bagClass = newBagData;
        newBagData = null;
    }
    // Add the bagClass (i-th class) to bagData
    if (bagData == null) {
        bagData = bagClass;
    } else {
        bagData.add(bagClass);
        bagClass = null;
    }
    // Shuffle the instances
    if (bagData == null) // To be OK when testing to Handle zero training instances!
        bagData = instances;
    else
        bagData.randomize(random);

    samplesVector[iSample] = (Instances) bagData;
    bagData = null;
}

classesVector = null;
classSizeVector = null;
maxClassSizeVector = null;
newClassSizeVector = null;

return samplesVector;
}

/**
 * Print the generated samples. Only for testing purposes.
 * @param samplesVector the vector of samples
 */
protected void printSamplesVector(Instances[] samplesVector){
    for (int iSample=0; iSample<samplesVector.length; iSample++){
        System.out.println("==== SAMPLE "+ iSample + " ====");
        System.out.println(samplesVector[iSample]);
        System.out.println(" ");
    }
}

/**
 * Returns an enumeration describing the available options.
 * Valid options are:<br/>
 * J48 options<br/>
 * =============<br/>
 * -U Use unpruned tree.<br/>
 * -C confidence<br/>
 * Set confidence threshold for pruning. (Default: 0.25)<br/>
 * -M number<br/>
 * Set minimum number of instances per leaf. (Default: 2)<br/>
 * -S<br/>
 * Don't perform subtree raising.<br/>
 * -L<br/>
 * Do not clean up after the tree has been built.<br/>
 * -A<br/>
 * If set, Laplace smoothing is used for predicted probabilities.<br/>
 * -Q seed
 */
* Seed for random data shuffling (Default: 1)

* Options to set the Resampling Method (RM) for the generation of samples to use in the consolidation process

---

* `-RM-C`
- Determines the way to set the number of samples to be generated will be based on a coverage value as a percentage. In the case this option is not set, the number of samples will be determined using a fixed value.

* `-RM-N &lt;number of samples&gt;`
- Number of samples to be generated for the use in the construction of the consolidated tree.
It can be set as a fixed value or based on a coverage value as a percentage, when `-RM-C` option is used, which guarantees the number of samples necessary to adequately cover the examples of the original sample.
((Default 5 for a fixed value or 99% for the case based on a coverage value)

* `-RM-R`
- Determines whether or not replacement is used when generating the samples.
(Default: false)

* `-RM-B percentage`
- Size of each sample (bag), as a percentage of the training set size.
Combined with the option `<distribution minority class>` accepts:
  * `-1 (sizeOfMinClass)`: The size of the minority class
  * `-2 (maxSize)`: Maximum size taking `<distribution minority class>` into account and using no replacement.
(Default: `-2(maxSize)`)

* `-RM-D distribution minority class`
- Determines the new value of the distribution of the minority class, if we want to change it.
It can be one of the following values:
  * A value between 0 and 100 to change the portion of minority class instances in the new samples
  * (If the dataset is multi-class, only the special value 50.0 will be accepted to balance the classes)
  * `-1 (free)`: Works with the instances without taking their class into account
  * `-2 (stratified)`: Maintains the original class distribution in the new samples
((Default: `-1(free)`)

@return an enumeration of all the available options.

```java
public Enumeration listOptions() {
    Vector<Option> newVector = new Vector<Option>();
    // J48 options
    Enumeration en;
    en = super.listOptions();
    while (en.hasMoreElements())
        newVector.addElement((Option) en.nextElement());
    // Options to set the Resampling Method (RM) for the generation of samples to use in the consolidation process
    newVector.addElement(new Option("\tSet the number of samples to be generated based on a coverage value\nas a percentage (by default)\n\"RM-C\", 0, "-RM-C"));
    newVector.addElement(new Option("\tNumber of samples to be generated for the use in the construction of the\nconsolidated tree\n\"RM-N\", 1, \\
\"-RM-N <Number of samples>\"));
    newVector.addElement(new Option("\tUse replacement to generate the set of samples\n\"RM-R\", 0, "-RM-R"));
    newVector.addElement(new Option("\tSize of each sample(bag), as a percentage of the training set size\n\"RM-B\", 1, "-RM-B percentage")
And using no replacement.
(\default: \-2(maxSize))
\)`
```
"| RM | Description |
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>-RM-C</strong></td>
<td>Determines the way to set the number of samples to be generated will be based on a coverage value as a percentage. In the case this option is not set, the number of samples will be determined using a fixed value. (set by default)</td>
</tr>
<tr>
<td><strong>-RM-N</strong></td>
<td>Number of samples to be generated for the use in the construction of the consolidated tree. It can be set as a fixed value or based on a coverage value as a percentage, when -RM-C option is used, which guarantees the number of samples necessary to adequately cover the examples of the original sample</td>
</tr>
<tr>
<td><strong>-RM-R</strong></td>
<td>Determines whether or not replacement is used when generating the samples. (default true)</td>
</tr>
<tr>
<td><strong>-RM-B</strong></td>
<td>Size of each sample(bag), as a percentage of the training set size. Combined with the option &lt;distribution minority class&gt; selects:</td>
</tr>
<tr>
<td><strong>-RM-D</strong></td>
<td>Determines the new value of the distribution of the minority class, if we want to change it.</td>
</tr>
</tbody>
</table>

*Valid options are:*

- **-RM-C**: Determines the way to set the number of samples to be generated will be based on a coverage value as a percentage. In the case this option is not set, the number of samples will be determined using a fixed value. (set by default)
- **-RM-N**: Number of samples to be generated for the use in the construction of the consolidated tree. It can be set as a fixed value or based on a coverage value as a percentage, when -RM-C option is used, which guarantees the number of samples necessary to adequately cover the examples of the original sample (default 5 for a fixed value or 99% for the case based on a coverage value)
- **-RM-R**: Determines whether or not replacement is used when generating the samples. (default true)
- **-RM-B**: Size of each sample(bag), as a percentage of the training set size. Combined with the option &lt;distribution minority class&gt; selects:
  - **-1** (sizeOfMinClass): The size of the minority class
  - **-2** (maxSize): Maximum size taking &lt;distribution minority class&gt; into account and using no replacement
  (default -2(maxSize))
- **-RM-D**: Determines the new value of the distribution of the minority class, if we want to change it. * It can be one of the following values:
  - A value between 0 and 100 to change the portion of minority class instances in the new samples
  - (If the dataset is multi-class, only the special value 50.0 will be accepted to balance the classes)
  - **-1** (free): Works with the instances without taking their class into account
  - **-2** (stratified): Maintains the original class distribution in the new samples
  (default 50.0)
if (Utils.getFlag("RM-C", options))
    setRMnumberSamplesHowToSet(new SelectedTag(NumberSamples_BasedOnCoverage,
        TAGS_WAYS_TO_SET_NUMBER_SAMPLES));
else
    setRMnumberSamplesHowToSet(new SelectedTag(NumberSamples_FixedValue,
        TAGS_WAYS_TO_SET_NUMBER_SAMPLES));
String RMnumberSamplesString = Utils.getOption("RM-N", options);
if (RMnumberSamplesString.length() != 0) {
    setRMnumberSamples(new Float(RMnumberSamplesString).floatValue());
} else {
    if (m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage)
        setRMnumberSamples((float)m_coveragePercent); // default: f(99% of coverage)
    else
        setRandNumberSamples((float)5.0); // default: 5 samples
}
String RMbagSizePercentString = Utils.getOption("RM-B", options);
if (RMbagSizePercentString.length() != 0)
    setRMbagSizePercent(Integer.parseInt(RMbagSizePercentString), false);
else
    setRandbagSizePercent(-2, false); // default: maxSize
String RMnewDistrMinClassString = Utils.getOption("RM-D", options);
if (RMnewDistrMinClassString.length() != 0)
    setRMnewDistrMinClass(new Float(RMnewDistrMinClassString).floatValue(), false);
else
    setRandnewDistrMinClass((float)50.0, false); // Only checking the combinations of the three options RMreplacement, RMbagSizePercent and
// RMnewDistrMinClass when they all are set.
    setRMreplacement(Utils.getFlag("RM-R", options), true);
    // J48 options
    // ============
    super.setOptions(options);
}

public String[] getOptions() {  
    Vector<String> result = new Vector<String>();
    // J48 options
    // =============
    String[] options = super.getOptions();
    for (int i = 0; i < options.length; i++)
        result.add(options[i]);
    // In J48 m_Seed is added only if m_reducedErrorPruning is true,
    // but in J48Consolidated it is necessary to the generation of the samples
    result.add("-Q");
    result.add("" + m_Seed);
    // Options to set the Resampling Method (RM) for the generation of samples
    // to use in the consolidation process
    // ===========
    if (m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage)
        result.add("-RM-C");
    result.add("-RM-N");
    result.add("" + m_RMnumberSamples);
    if (m_RMreplacement)
        result.add("-RM-R");
    result.add("-RM-B");
    result.add("" + m_RMcsizePercent);
    result.add("-RM-D");
    result.add("" + m_RMnewDistrMinClass);
    return (String[]) result.toArray(new String[result.size()]);
}

/**
 * Returns a description of the classifier.
 * @return a description of the classifier
 */
public String toString() {
    if (m_root == null) {
        return "No classifier built";
    }
    if (m_unpruned)
        return "J48Consolidated unpruned tree\n" +
        toStringResamplingMethod() +
        m_root.toString();
    else
        return "J48Consolidated pruned tree\n" +
        toStringResamplingMethod() +
        m_root.toString();
}

/**
 * Returns a description of the Resampling Method used in the consolidation process.
 * @return a description of the used Resampling Method (RM)
 */
public String toStringResamplingMethod() {
    String st;
    st = "[RM] N_S=
";
    if (m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage)
        st += "f(" + Utils.doubleToString(m_RMnumberSamples,2) + "% of coverage)"
            + m_numberSamplesByCoverage;
    else // m_RMnumberSamplesHowToSet == NumberSamples_FixedValue
        st += (int)m_RMnumberSamples;
    if (m_RMnewDistrMinClass == -2)
        st += " stratified"
    else if (m_RMnewDistrMinClass == -1)
        st += " free distribution"
    else {
        st += " %Min=
";
        if (Utils.eq(m_RMnewDistrMinClass, (float)50))
            st += "balanced"
        else
            st += m_RMnewDistrMinClass;
    }
    st += " Size=
";
    if (m_RMbagSizePercent == -2)
        st += "maxSize"
    else if (m_RMbagSizePercent == -1)
        st += "sizeOfMinClass"
    else
        st += m_RMbagSizePercent + "%"
    if (m_RMreplacement)
        st += " (with replacement)"
    else
        st += " (without replacement)"
    st += "\n";
    st += m_stExceptionalSituationsMessage;
    // Add the true coverage achieved
    st += "True coverage achieved: " + m_trueCoverage + "\n";
    // Add a separator
    char[] ch_line = new char[st.length()];
    for (int i = 0; i < ch_line.length; i++)
        ch_line[i] = '-';
    String line = String.valueOf(ch_line);
    line += "\n";
    st += line;
    return st;
}

/**
 * Returns the tip text for this property
 * @return tip text for this property suitable for
 * displaying in the explorer/experimenter gui
 */
public String RMnumberSamplesHowToSetTipText() {
    return "Way to set the number of samples to be generated:\n" +
    " * using a fixed value which directly indicates the number of samples to be generated\n" +

public SelectedTag getRMnumberSamplesHowToSet() {
    return new SelectedTag(m_RMnumberSamplesHowToSet, TAGS_WAYS_TO_SET_NUMBER_SAMPLES);
}

public void setRMnumberSamplesHowToSet(SelectedTag newWayToSetNumberSamples) throws Exception {
    if (newWayToSetNumberSamples.getTags() == TAGS_WAYS_TO_SET_NUMBER_SAMPLES)
    {
        int newEvWay = newWayToSetNumberSamples.getSelectedTag().getID();
        if (newEvWay == NumberSamples_FixedValue || newEvWay == NumberSamples_BasedOnCoverage)
            m_RMnumberSamplesHowToSet = newEvWay;
        else
            throw new IllegalArgumentException("Wrong selection type, value should be: " + "between 1 and 2");
    }
}

public String RMnumberSamplesTipText() {
    return "Number of samples to be generated for the use in the consolidation process (fixed value) or based
    on a coverage value as a %.
    * if RMnumberSamplesHowToSet == " + (new
    SelectedTag(NumberSamples_FixedValue, TAGS_WAYS_TO_SET_NUMBER_SAMPLES)).getSelectedTag().getReadable() + "\n    * A positive value which directly indicates the number of samples to be generated\n    * if RMnumberSamplesHowToSet == " + (new
    SelectedTag(NumberSamples_BasedOnCoverage, TAGS_WAYS_TO_SET_NUMBER_SAMPLES)).getSelectedTag().getReadable() + "\n    * A positive value as a percentage, the coverage value, which guarantees the number of samples
    necessary\n    * to adequately cover the examples of the original sample\n    * (default: 5 for a fixed value or " + Utils.doubleToString(m_coveragePercent,0) + ") for the case
    based on a coverage value");
}

public float getRMnumberSamples() {
    return m_RMnumberSamples;
}

public void setRMnumberSamples(float v) throws Exception {
    if (m_RMnumberSamplesHowToSet == NumberSamples_FixedValue) {
        if (v < 0)
            throw new Exception("Number of samples has to be greater than zero!");
        if (v == (float)0)
            return 0;
    }
}
System.err.println("Number of samples is 0. It doesn't make sense to build a consolidated tree without set of samples. Handle zero training instances!");
if ((v == (float)1) || (v == (float)2))
    System.out.println("It doesn't make sense to build a consolidated tree with 1 or 2 samples, but it's possible!");
} else { // m_RNumberSamplesHowToSet == NumberSamples_BasedOnCoverage
    if (v < -1)
        throw new Exception("Coverage value has to be greater than zero!");
    if (v == (float)0)
        System.err.println("Coverage value is 0. It doesn't make sense to build a consolidated tree without set of samples. Handle zero training instances!");
}
m_RNumberSamples = v;

/**
 * Returns the tip text for this property
 * @return tip text for this property suitable for displaying in the explorer/experimenter gui
 */
public String RMreplacementTipText() {
    return "Whether replacement is performed to generate the set of samples."
;
}

/**
 * Get the value of RMreplacement
 * @return Value of RMreplacement
 */
public boolean getRMreplacement() {
    return m_RMreplacement;
}

/**
 * Set the value of RMreplacement.
 * Checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass
 * @param v Value to assign to RMreplacement.
 * @throws Exception if an option is not supported
 */
public void setRMreplacement(boolean v) throws Exception {
    setRMreplacement(v, true);
}

/**
 * Set the value of RMreplacement, but, optionally,
 * checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass.
 * This makes possible only checking in the last call of the method setOptions().
 * @param v Value to assign to RMreplacement.
 * @param checkComb true to check some combinations of options
 * @throws Exception if an option is not supported
 */
public void setRMreplacement(boolean v, boolean checkComb) throws Exception {
    if (checkComb)
        checkBagSizePercentAndReplacementAndNewDistrMinClassOptions(v, m_RmbagSizePercent,
            m_RMnewDistrMinClass);
    m_RMreplacement = v;
}

/**
 * Returns the tip text for this property
 * @return tip text for this property suitable for displaying in the explorer/experimenter gui
 */
public String RMBagSizePercentTipText() {
    return "Size of each sample(bag), as a percentage of the training set size/-1=sizeOfMinClass/-2=maxSize."
+ "Combined with the option <distribution minority class>, RMnewDistrMinClass, accepts:
" + " * -1 (sizeOfMinClass): The size of the minority class
" + " * -2 (maxSize): Maximum size taking <distribution minority class> into account \n" + " and using no replacement." +
/**
* Get the value of RMbagSizePercent.
*
* @return Value of RMbagSizePercent.
*/
public int getRMbagSizePercent() {
    return m_RMbagSizePercent;
}

/**
* Set the value of RMbagSizePercent.
* Checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass
*
* @param v Value to assign to RMbagSizePercent.
* @throws Exception if an option is not supported
*/
public void setRMbagSizePercent(int v) throws Exception {
    setRMbagSizePercent(v, true);
}

/**
* Set the value of RMbagSizePercent, but, optionally,
* checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass.
* This makes possible only checking in the last call of the method setOptions().
*
* @param v Value to assign to RMbagSizePercent.
* @param checkComb true to check some combinations of options
* @throws Exception if an option is not supported
*/
public void setRMbagSizePercent(int v, boolean checkComb) throws Exception {
    if ((v < -2) || (v > 100))
        throw new Exception("Size of sample (%) has to be greater than zero and smaller " +
                "than or equal to 100 " +
                "(or combining with the option <distribution minority class> -1 for 'sizeOfMinClass' " +
                "or -2 for 'maxSize')!");
    else if (v == 0)
        throw new Exception("Size of sample (%) has to be greater than zero and smaller " +
                "than or equal to 100!");
    else {
        if (checkComb)
            checkBagSizePercentAndReplacementAndNewDistrMinClassOptions(m_RMreplacement, v,
                m_RMnewDistrMinClass);
        m_RMbagSizePercent = v;
    }
}

/**
* Returns the tip text for this property
* @return tip text for this property suitable for
* displaying in the explorer/experimenter gui
*/
public String RMnewDistrMinClassTipText() {
    return "Determines the new value of the distribution of the minority class, if we want to change it/-
1=free/-2=stratified.\n" +
    "It can be one of the following values:\n" +
    "A value between 0 and 100 to change the portion of minority class instances in the new" +
    "samples.\n" +
    "(If the dataset is multi-class, only the special value 50.0 will be accepted to balance the" +
    "classes).\n" +
    "-1 (free): Works with the instances without taking their class into account.\n" +
    "-2 (stratified): Maintains the original class distribution in the new samples.\n" +
    "(default: 50.0)";
}

/**
* Get the value of RMnewDistrMinClass
* @return Value of RMnewDistrMinClass
*/
public float getRMnewDistrMinClass() {
    return m_RMnewDistrMinClass;
}

/**
 * Set the value of RMnewDistrMinClass
 * Checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass
 * @param v Value to assign to RMnewDistrMinClass
 * @throws Exception if an option is not supported
 */
public void setRMnewDistrMinClass(float v) throws Exception {
    setRMnewDistrMinClass(v, true);
}

/**
 * Set the value of RMnewDistrMinClass, but, optionally,
 * checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass.
 * This makes possible only checking in the last call of the method setOptions().
 * @param v Value to assign to RMnewDistrMinClass
 * @param checkComb true to check
 * @throws Exception if an option is not supported
 */
public void setRMnewDistrMinClass(float v, boolean checkComb) throws Exception {
    if ((v < -2) || (v >= 100))
        throw new Exception("Minority class distribution has to be greater than zero and smaller " +
        "than 100 (or -1 for 'sizeOfMinClass' or -2 for 'maxSize')!");
    else {
        if (checkComb)
            checkBagSizePercentAndReplacementAndNewDistrMinClassOptions(m_RMreplacement,
            m_RMbagSizePercent, v);
        m_RMnewDistrMinClass = v;
    }
}

/**
 * Checks the combinations of the options RMreplacement, RMbagSizePercent and RMnewDistrMinClass
 * @throws Exception if an option is not supported
 */
private void checkBagSizePercentAndReplacementAndNewDistrMinClassOptions(
    boolean replacement, int bagSizePercent, float newDistrMinClass) throws Exception{
    if ((newDistrMinClass > (float)0) && (newDistrMinClass < (float)100))
        // NewDistrMinClass is a valid value to change the distribution of the sample
    if(replacement)
        throw new Exception("Using replacement isn't contemplated to change the distribution of minority
        class!");
    if((newDistrMinClass == (float)-1) || (newDistrMinClass == (float)-2)){
        // NewDistrMinClass = free OR stratified
    if(bagSizePercent < 0)
        throw new Exception("Size of sample (%) has to be greater than zero and smaller " +
        "than or equal to 100!");
    if(!replacement) && (bagSizePercent==100))
        System.err.println("It doesn't make sense that size of sample (%) is 100, when replacement is
        false!");
    }
}

/**
 * Returns the tip text for this property
 * (Rewritten to indicate this option is not implemented for J48Consolidated)
 * @return tip text for this property suitable for
 * displaying in the explorer/experimenter gui
 */
public String reducedErrorPruningTipText() {
    return "J48 option not implemented for J48Consolidated";
}

/**
 * Set the value of reducedErrorPruning. Turns
 * unpruned trees off if set.
 */
public void setReducedErrorPruning(boolean v) {
    m_reducedErrorPruning = false;
    throw new RuntimeException("J48 option not implemented for J48Consolidated");
}
stNumberSamplesByCoverage = "Number of samples based on coverage: " + measureNumberSamplesByCoverage() + "\n";
else
stNumberSamplesByCoverage = "";
return super.toString() +
stNumberSamplesByCoverage +
"True coverage: " + measureTrueCoverage() + "\n";
}
/**
* Returns the number of samples necessary to achieve the indicated coverage
* @return number of samples based on coverage
*/
public double measureNumberSamplesByCoverage() {
return m_numberSamplesByCoverage;
}
/**
* Returns the true coverage of the examples of the original sample
* achieved by the set of samples generated for the consolidated tree
* @return the true coverage achieved
*/
public double measureTrueCoverage() {
return m_trueCoverage;
}
/**
* Returns an enumeration of the additional measure names
* produced by the J48 algorithm, plus the true coverage achieved
* by the set of samples generated
* @return an enumeration of the measure names
*/
public Enumeration enumerateMeasures() {
Enumeration enm = super.enumerateMeasures();
Vector measures = new Vector();
while (enm.hasMoreElements())
measures.add(enm.nextElement());
if (m_RMnumberSamplesHowToSet == NumberSamples_BasedOnCoverage)
measures.add("measureNumberSamplesByCoverage");
measures.add("measureTrueCoverage");
return measures.elements();
}
/**
* Returns the value of the named measure
* @param additionalMeasureName the name of the measure to query for its value
* @return the value of the named measure
*/
public double getMeasure(String additionalMeasureName) {
if (additionalMeasureName.compareToIgnoreCase("measureTrueCoverage") == 0)
return measureTrueCoverage();
else if (additionalMeasureName.compareToIgnoreCase("measureNumberSamplesByCoverage") == 0)
return measureNumberSamplesByCoverage();
else
return super.getMeasure(additionalMeasureName);
}
/**
* Main method for testing this class
* @param argv the commandline options
*/
public static void main(String[] argv){
runClassifier(new J48Consolidated(), argv);
}
InstancesConsolidated.java

package weka.classifiers.trees.j48Consolidated;

import weka.core.Instance;
import weka.core.Instances;
import weka.core.Utils;

/**
 * Class for extending the Instances class in order to add some methods
 * (These methods can be added to the class 'Instances').
 * ************************************************************************
 * @author Jesús M. Pérez (txus.perez@ehu.es)
 * @version $Revision: 2.0 $
 */
public class InstancesConsolidated extends Instances {

    private static final long serialVersionUID = 8452710983684965074L;

    /** Constructor calling the constructor of the superclass
     * (Not necessary if the above methods are moved to the official class 'Instances')
     */
    public InstancesConsolidated(Instances dataset) {
        super(dataset);
    }

    /** Constructor calling the constructor of the superclass
     * (Not necessary if the above methods are moved to the official class 'Instances')
     */
    public InstancesConsolidated(Instances source, int first, int toCopy) {
        super(source, first, toCopy);
    }

    /**
     * Gets the vector of classes of the dataset like a set of samples
     * @return the vector of classes
     */
    public InstancesConsolidated[] getClasses(){
        int numClasses = numClasses();
        InstancesConsolidated[] classesVector = new InstancesConsolidated[numClasses];
        // Sort instances based on the class to extract the set of classes
        sort(classIndex());
        // Determine where each class starts in the sorted dataset
        int[] classIndices = getClassIndices();

        for (int iClass = 0; iClass < numClasses; iClass++) {
            int classSize;
            if (iClass == numClasses - 1) // if the last class
                classSize = numInstances() - classIndices[iClass];
            else
                classSize = classIndices[iClass + 1] - classIndices[iClass];

            classesVector[iClass] = new InstancesConsolidated(this, classIndices[iClass], classSize);
            classIndices = null;
            return classesVector;
        }

        /**
         * Creates an index containing the position where each class starts in
         * the dataset. The dataset must be sorted by the class attribute.
         * (based on the method 'createSubsample()' of the class 'SpreadSubsample'
         */

}
private int[] getClassIndices() {

    // Create an index of where each class value starts
    int[] classIndices = new int[numClasses() + 1];
    int currentClass = 0;
    classIndices[currentClass] = 0;
    for (int i = 0; i < numInstances(); i++) {
        Instance current = instance(i);
        if (current.classIsMissing()) {
            for (int j = currentClass + 1; j < classIndices.length; j++) {
                classIndices[j] = i;
            }
            break;
        } else if (current.classValue() != currentClass) {
            for (int j = currentClass + 1; j <= current.classValue(); j++) {
                classIndices[j] = i;
            }
            currentClass = (int) current.classValue();
        }
    }
    if (currentClass <= numClasses()) {
        for (int j = currentClass + 1; j < classIndices.length; j++) {
            classIndices[j] = numInstances();
        }
    }
    return classIndices;
}

/**
 * Gets the vector with the size of each class of the dataset
 * @return the vector of classes' size
 */
public int[] getClassesSize(InstancesConsolidated[] classesVector) {
    int numClasses = numClasses();
    int[] classSizeVector = new int[numClasses];
    for (int iClass = 0; iClass < numClasses; iClass++) {
        classSizeVector[iClass] = classesVector[iClass].numInstances();
    }
    return classSizeVector;
}

/**
 * Adds a set of instances to the end of the set.
 * @param instances the set of instances to be added
 */
public void add(InstancesConsolidated instances) {
    for (int i = 0; i < instances.numInstances(); i++) {
        add(instances.instance(i));
    }
}

/**
 * Prints information about the size of the classes and their proportions
 * and indicates which is the minority class of the sample
 * @param dataSize the size of original sample
 * @param iMinClass the index of the minority class in the original sample
 * @param classSizeVector the vector with the size of each class of the dataset
 */
public void printClassesInformation(int dataSize, int iMinClass, int[] classSizeVector) {
    int numClasses = numClasses();
    System.out.println(“Minority class value (” + iMinClass + “): “ + classAttribute().value(iMinClass));
    System.out.println(“Classes sizes:”);
    for (int iClass = 0; iClass < numClasses; iClass++) {
        float distrClass;
        if (dataSize == 0)
            distrClass = (float)0;
        else
            distrClass = (float)classSizeVector[iClass] / (float)dataSize;
    }
distrClass = (float)100 * classSizeVector[iClass] / dataSize;
System.out.print(classSizeVector[iClass] + " (" + Utils.doubleToString(distrClass, 2) + ")");
if(iClass < numClasses - 1)
    System.out.print(",");
System.out.println(";");
}