Cortana Manual

August 15, 2012

1 Before you start

Although Cortana is written in Java, and therefore platform independent, it will behave slightly different on different operation systems and/or platforms. These differences arise from small variations in the Java Virtual Machines, used in different situations. The main issue is with 32-bit operating systems (OS). On such systems the maximum amount of memory the Java Virtual Machine (JVM) can use is around 1600 MegaBytes. However, the actual amount depends on the amount of RAM available. The cortana.bat and cortana.sh file included in the Cortana.zip set the maximum amount of memory the JVM can use to 1600 MegaBytes, through the -Xmx option. The value should, at most, be set to half the amount of available RAM, meaning eg. for a 2GB machine to -Xmx1000m. For 64-bit OSes no such limit exists, and it should be save to remove the -Xmx. Note that the above means that, especially for 32-bit OSes, not all datasets will fit into memory. This is a problem particularly relevant to the bioinformatics setting (see section 9.2), as some of the background sources used for enrichment are relatively large.

2 Preliminaries

Before giving a detailed description of the functionalities of *Cortana*, it is beneficial to first clarify some of the terms used in the rest of this manual.

2.1 Dataset

First there is the data that will be used as input. The data can often best be visualised as a table, or matrix, containing *columns* and *rows*. The first *row* of the data, the *header*, contains all the names of the columns. The remaining rows form the so-called *instances*, and describe, for each *instance*, the values for each *column*. Different authors use different names for the same concepts. To be clear, a *dataset* describes all data under investigation, and is referred to by some authors as *population*. The members that constitute a *dataset* are referred to as *instances* or *examples*. Columns will be referred to as *attributes*, and the *column name* is the *attribute name*.

Currently, two types of files can be loaded into *Cortana*, *arff* files and plain (comma separated) text files. Both file types provide the data in a matrix form. *arff* (*Attribute-Relation File Format*) files, however, additionally define the data type, or *attribute type*, of each *attribute* in a section preceding the actual data. *arff* files are very common in data mining. More on them can be found at http://www.cs.waikato.ac.nz/~ml/weka/arff.html.

2.2 Attribute Type

Each attribute has an attribute type that indicates what kind of data is associated with the attribute. Currently, Cortana distinguishes three attribute types: nominal, numeric and binary. This is less than the number of attribute types that can be declared in an arff file. Some of the valid 'arff types' are mapped to a valid Cortana attribute type. For instance, the 'arff types' numeric, real and integer are all handled by Cortana as the numeric attribute type. An attribute with the nominal attribute type is said to be a nominal attribute, and likewise for the other attribute types.

2.3 Subgroup

A subgroup is a selected number of instances from the dataset. As returned by Cortana, it will both be non-empty, and will not contain all instances in the dataset. Any Subgroup Discovery process will try to find subgroups that, on a characteristic of interest, show a statistically unusual deviation from the whole dataset.

2.4 Subgroup Discovery

Cortana is a generic Subgroup Discovery tool. However, it differs from other such tools in some respects. Traditionally, Subgroup Discovey could be described as a heuristic search process in which one tries to optimise for a single target attribute, or target value, using some quality measure. A target attribute, or target for short, should be understood as one of the attributes available in the dataset, and the target value, then, is one of the valid values for that attribute.

Note that for *nominal targets* the *target value* is contained in the data as one of its values. For a *numeric target* however, one does not set a *target value* in *Cortana*, and the underlying *Subgroup Discovery* algorithm will, within the range determined for that *target*, infer its own boundaries to create *subgroups*.

2.5 Condition

A condition is a description, or the intension, of a subgroup, while the actual instances that form a subgroup constitute its extension. The simplest, or atomic, condition consists of three parts: an attribute, an operator and a value. More complex conditions can be formed from conjunctions of atomic conditions. Conjunctions formed this way are sometimes also referred to as condition lists. An

example of an atomic *condition* would be: $age \le 18$, a more complex one would be $age \le 18 \land length \le 1.8$.

2.6 Quality Measure

In Subgroup Discovery, one uses a quality measure to asses the quality of the subgroups found. Here, quality should be understood as a score obtained by appying the quality measure to, the characteristics of, the subgroup. It depends on the actual quality measure, and/or the goal the researcher has in mind, whether such a quality should evaluate high or low. For example, if the very simple quality measure 'average' is used, it depends on the domain specific goal whether one would try to obtain a very high or low score. Cortana features more than 40 quality measures, most based on statistical tests. This manual currently does not provide a description of them, and the user is referred to any statistical handbook, or relevant papers from the data mining community, e.g. [1, 2].

2.7 Target Attribute vs. Target Concept

Traditionally, Subgroup Discovery focussed only on optimising for a single target, or target value. Obviously, this is a setting that can still be used in Cortana. However, since Cortana can also be used in a novel setting referred to as Exceptional Model Mining (EMM) [3, 4], the object of optimisation need no longer be singular, and hence non-plural terms like target and target value are no longer applicable. Therefore the term target concept is introduced. In better describes what is the object of the optimisation effort used in the Subgroup Discovery process. There are a number of target types related to target concepts. Section Target Type 2.8 describes them in more detail, including their influence on the Subgroup Discovery algorithm used by Cortana.

2.8 Target Type

2.8.1 Single Nominal

The first target type is single nominal. It may very well be the best known, and most used, target type in the Subgroup Discovery discipline. In this setting, the target concept is simply one of the values of the target attribute, more commonly known as target value. For most quality measures, Cortana will optimise the quality of subgroups by considering the proportion of positive and negative examples in the dataset. Instances count as positive examples if their value for the target attribute is identical to the target concept, they are negative otherwise. Note that this yields a binary distinction, such that, for any target attribute, only that value that coincides with the target concept is considered positive, all other values, including missing values, are considered negative.

2.8.2 Single Numeric

The second target type is single numeric. This is another simple target type, however, it substantially differs from the single nominal type. Most importantly, one does set a single target attribute, but one does not set a target value when using this setting.

This target type can only be used for numeric attributes. All values of such attributes are numeric, and thus define a range. The goal of the Subgroup Discovery process will then, most often, be to find a certain threshold value, within that range, that best separates the whole dataset into a subgroup and its complement, such that the distribution, on the target attribute, of that subgroup differs most from the distribution of the whole dataset. Here the quality measure plays an important role, since it determines whether Cortana should try to find subgroups that have a much higher or lower average value for the target attribute than the average value for the whole dataset. The simple quality measure 'average' would try to miximise this value, while 'inverse average' would try to minimise it.

As alluded to above, in this target type setting, threshold values are inferred to form subgroups. For a numeric attribute, Cortana will test various threshold values to set apart instances, constituting a new subgroup, from the rest of the dataset. Instead of an (in)equality test, as used in the single nominal setting, Cortana uses can use, a combination of, different tests ('<=', '>=' and '=') to form subgroups in the single numeric setting. So, for a numeric attribute, a threshold value is selected, and then, for each instance in the dataset, it is determined whether this instance is to be regarded as a positive or a negative example, based on the value of that instance and the actual test performed. Eg., when using the '<=' test, an instance counts as a positive example if its value is less than, or equal to, the selected threshold, and negative otherwise. Obviously, in case of the '>=' test an instance is regarded a positive example if its value is greater than, or equal to, the selected threshold, and considered a negative example otherwise.

The final point to address for this target type is to clarifying how Cortana actually determines the thresholds it uses. Unfortunately, there is no short answer to this question, as it depends on the actual search strategy selected by the end user. However, for all three best numeric search strategy types, Cortana selects as threshold a value from the data range of the numeric attribute under consideration. For more details on search strategy, see section 4.4.

2.8.3 Double Correlation

This target type is used in one of Cortana's implementations of possible Exceptional Model Mining extentions of traditional Subgroup Discovery. More on Exceptional Model Mining in general, and some of its possible implementations, can be found in Leman, Feelders, Knobbe (2008) [3], and the ideas presented there will not be reiterated in this manual. However, as the purpose of this manual is to provide some useful, or necessary, information about, parts of, Cortana,

a little will be said about this *target type*, its use, and the way it influences the *Subgroup Discovery* process used by *Cortana* to form candidate *subgroups*.

2.8.4 Multi-label

3 Starting Cortana

After obtaining and unpacking a copy of *Cortana* from http://datamining.liacs.nl/cortana.html, navigate to the Cortana directory. There you will find a cortana.jar file. One could start *Cortana* by double clicking the jar, however, it is recommended to start *Cortana* from the command line. This way, a lot more information about the *Subgroup Discovery* process is fed back to the user. To start *Cortana* this way, open a terminal or command window, navigate to the Cortana directory containing cortana.jar, and type: *java -jar cortana.jar*. Alternatively one can use either cortana.bat (for Windows) or cortana.sh (Bash shell script). Be sure to read Section 1 *Before you start* if you do.

After starting *Cortana* one is asked to select the file that contains the dataset to be analysed, after which *Cortana*'s main screen is shown.

Currently, two types of files can be loaded into *Cortana*, *arff* files and plain (comma seperated) text files. The first is very common in data mining and describes the data and additionally defines the *attribute type* of each *attribute*. As such, *arff* files are preferred over plain text files. For text files, *Cortana* wil try to infer the correct attribute type of each attribute. Unfortunately, this may fail, so to check whether Cortana was able to infer the correct attribute type, or change the attribute type anyway, the *Meta Data...* button on the main screen gives access to the *Meta Data Window* (section 6).

4 Cortana - Main Screen

The main screen of *Cortana* is devided into four major panels, *Dataset*, *Target Concept*, *Search Conditions*, and *Search Strategy*. The following subsections will address them all.

4.1 Dataset

As can be expected from the name, this panel gives some information about the dataset that is currently loaded.

target table shows the name of the data file used, which for text files is just the filename, and for ARFF files is the name defined in the '@relation' field.

examples shows the number of example in the dataset.

columns shows the number of columns in the dataset. Remember that columns are also be referred to as attributes.

Finally, there is a number of fields that indicate the number of attributes from each data type. The type of an attribute determines the sort of mining

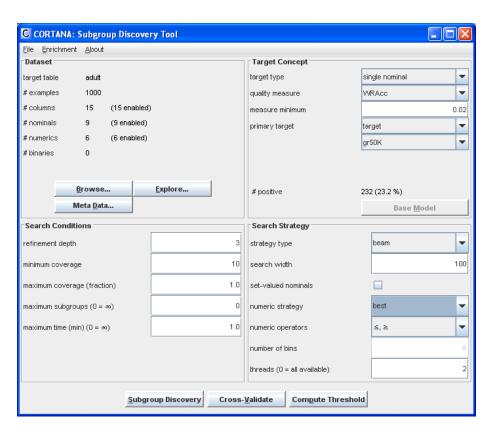


Figure 1: Cortana's main window.

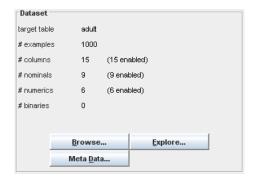


Figure 2: Dataset details in the main window.

algorithm or quality measure that is applicable to it. More about this can be found in section 2.2.

In addition to the fields described above, there are three buttons present on the Dataset panel, **Browse...**, **Meta Data...** and **Explore...**.

By clicking the **Browse...** button, a **Browse Window** (section 5) is presented, showing a table with the data in the state that it is currently in. Additionally, in the table header, it shows the number of distinct values for each attribute. Note that the data may not be in the same state as when it was loaded, as it can be modified using functionalities of the **Meta Data Window**, presented after pressing the **Meta Data...** button, which is also present on the **Dataset** panel. Section 6 describes the Meta Data Window, its components, and the data manipulation functionalities, in more detail. To be able to explain them more thoroughly though, it is benefical to describe the various fields of the **Target Concept** panel first.

Explore button.

4.2 Target Concept

The fields of this panel serve to manipulate the target concept-related search settings used during the Subgroup Discovery process. Traditionally, Subgroup Discovery focussed only on optimising for a single target or target value. Obviously, this is a setting that can still be used in Cortana. However, since Cortana can also be used in a novel setting referred to as *Exceptional Model Mining (EMM)* [3], the term target value is no longer applicable, hence the term *Target Concept*. Section 2.8 describes the various target types in more detail, including its relation to the type of search strategy (section 4.4) adopted by the Subgroup Discovery algorithm used by Cortana. In this section only a short description of the various fields will be given.

The first field is **target type**, that, obviously, is used to change the target type for which one wants to do the Subgroup Discovery. Selecting another target type from the drop down box will force Cortana to consider other attributes as

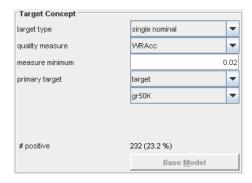


Figure 3: The target concept specification details in the main window.

target concept. For example, when changing the target type from the default single nominal to single numeric, the first attribute having the numeric attribute type is selected, and subsequently displayed in the **primary target** drop down box (see below).

Based on the target type selected, a number of quality measures is available. These are listed in the quality measure drop down box. After changing the target type, the quality measures listed in the quility measure drop down box are automatically updated, to fit the new target type.

The text field next to measure minimum will, by default, show a minimum threshold value for the selected quality measure, that, based on historical observations, is considered to be sensible. One might consider lowering this value if a Subgroup Discovery experiment, run with the default value, did not return any, or only few, subgroups. On the other hand, one can increase this value to force Cortana to only report subgroups that have a quality, as calculated by the selected quality measure, that lies above this threshold. Also, it is worth mentioning that if the search depth is greater than one, leading to conjunctions of conditions to be used to select instances from the dataset to form subgroups, the number of intermediate results, when going from one search depth to a higher one, can be lower when using a higher threshold. This, naturally, aleviates the computational burden of the Subgroup Discovery process. However, the recommended way of controling the amount of (intermediate) results, is through the maximum subgroups setting in Search Conditions. More on search depth, or refinement depth, and maximum subgroups can be found in section 4.3 below.

The items described in the remainder of this section will not be available in every target type setting, as the various target types are related to the attribute type of the target concept. For each item, it will be mentioned to which attribute type it applies.

primary target is available in the following target type settings: single nominal, single numeric and double correlation. The primary target drop down box lists all attributes available in the dataset.

target value is available only in the single nominal setting. The target

value drop down box lists all values of the attribute set as primary target, which can be of the nominal and binary attribute type.

secondary target is available only in the *double correlation* setting. In this setting only *attributes* of the *numeric attribute type* will be listed in both the *primary target* and *secondary target* drop down box.

targets and settings is available only in the *multi-label* setting. If this target type is selected, the Targets and Settings button will be enabled, and this gives access to the Multi-label details. The upper part of which shows some input fields related to multi-label search settings. The lower part lists all attributes of the binary attribute type. More on the multi-label can be found in section 7 and in [3, 4].

Then, there is an information field that shows information relevant to the selected $target\ type$. The number of positives, $\#\ positives$ is shown for the $single\ nominal\ target\ type$, $average\ for\ single\ numeric$, $correlation\ for\ double\ correlation\ and\ \#\ binary\ targets\ for\ multi-label$.

The Base Model button will only be enabled if the target type is double correlation or multi-label. It gives access to a Base Model Window, showing a correlation plot for the selected primary target and secondary target, if the target type is double correlation. For the multi-label target type, it will show a bayesian network, connecting the various binary attributes.

4.3 Search Conditions

The fields on this panel allow setting the *search conditions* used in the *Subgroup Discovery* process. For all fields the default values are also given.

refinement depth controls the number of conditions that is used to create subgroups. A refinement depth of 1 would lead to conditions like $[x \le 9.11]$, while a refinement depth of 2 would allow for the creation of conditions like $[x \le 1.2 \land y \ge 3.4]$. It is not recommended to set the refinement depth to very high values. In Subgroup Discovery, often a depth greater than 4 or 5 does not lead to significant improvements of the measure score any more, and just increases both the risk if overfitting, and the computational time needed to calculate the result. The default value is 1.

minimum coverage sets the lower bound for the size of the *subgroups* that should be reported by Cortana, meaning all reported *subgroups* have at least this size. The default value is set to 10% of the total dataset size, which is shown as # examples, see section 4.1 Dataset above.

coverage fraction sets the upper bound for the size of the *subgroups* that should be reported by Cortana, meaning all reported subgroups have at most this size. The default value is set to 100% of the total dataset size, which is shown as #examples, see section 4.1 Dataset above.

maximum subgroups is used to control the maximum number of *subgroups* in the result list generated by *Cortana*. First, this means that the *Result Window* (section 8) will show at most this number of *subgroups*.

But also, as alluded to in the *Dataset* section (4.1 on *measure minimum*, this number also controls the number of intermediate results retained by *Cortana*

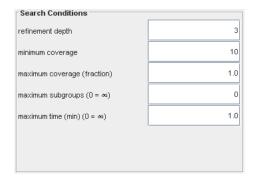


Figure 4: Specification of the search conditions in the main window.

to form the pool out of which the generation for the next refinement depth is formed. As such, this Search Condition parameter has significant influence on the computational demands, as it directly controls the number of combinatorial candidates to be tested during Cortana's Subgroup Discovery process. Without going into the actual algorithm, a small example probably suffices to make this clear. For a dataset consisting of only nominal attributes, assume $n = maximum \ subgroups$, and $m = number \ of \ attribute-value \ pairs$, then the number of candidates c to be tested by Cortana for the next refinement depth iteration is: $c = n \cdot m$. The default value is 50.

maximum time (min) will determine the maximum time, measured in minutes, Cortana is allowed to search for new subgroups. After this periode Cortana will abort the Subgroup Discovery process and report all subgroups found up until that point. This means that especially for the search strategy (section 4.4) strategy type depth first a large of the search space will not be explored at all, if the search proces is aborted. More precisely, only the first attributes will have been addressed at that time. The default value is 1.

4.4 Search Strategy

This is an intro. It describes strategy type, best numeric and number of bins. strategy type beam, cover-based beam selection, best first, depth first and breadth first. The default value is beam.

search width This parameter can not be set for the best first strategy type. The default value is 100.

numeric operators The default value is $\langle =, \rangle =$.

best numeric bins, best and all. The default value is bins.

number of bins Only available for the $best\ numeric$ setting of bins. Default value is 8.

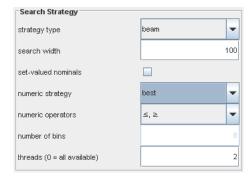


Figure 5: Search strategy specification in the main window.

5 Browse Window

6 Meta Data Window

The Meta Data... button gives access to a new window that, next to displaying some additional information about the dataset loaded, also allows changing some of the (characteristics of) the data. The upper part of the Meta Data Window shows a table with six columns. The lower part contains a number of panels that allow modification of the data as it is in memory, note that no modifications are made to the original data file. First the properties shown in the table in the upper part will be described, the purpose of the various data manipulations will be explained after that.

6.1 Meta Data Table

The first column in this table, Attribute, lists all attribute names of the attributes in the dataset. The remaining columns show some information for each of these attributes. Cardiality gives the number of distinct values for an attribute. Type shows its attribute type. Enabled indicates whether the attribute is enabled or disabled. Values Missing indicates whether the attribute contains missing values or not. And finally, Missing Value shows the value that is currently used for missing values in the data. Obviously, this field is blank if there are no values missing for the attribute.

6.2 Meta Data Functions

The panels in the lower part of the *Meta Data Window* all allow selecting or changing the data. The first, *Select*, allows selecting all *attributes* of a certain type. This is a conveiniance method to be used in combination with the functionalities available in other panels.

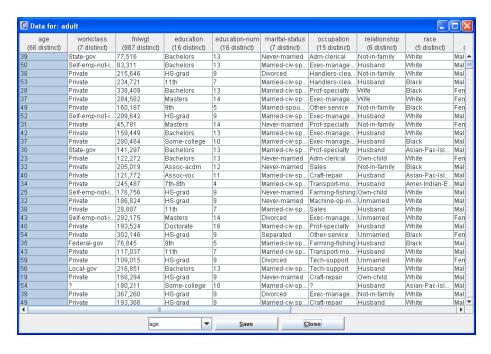


Figure 6: The browse window.

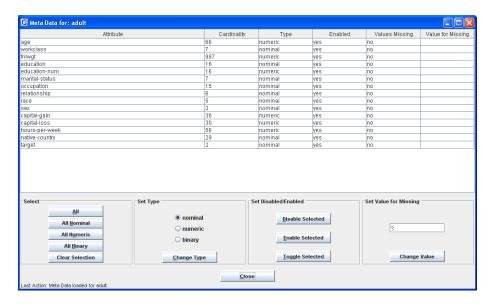


Figure 7: Meta data window.

Set Type allows changing the *attribute type*. This can be useful for various reasons. The first is that, after loading a plain text file, it is observed that Cortana was not capable to infer the correct type for an attribute. Related to this is the possiblity to change the type of an attribute to allow other quality measures to be used in the Subgroup Discovery process. An example of this would be an attribute that describes the number of doors in a car dataset. If this value is used as a target value, one might treat it as a nominal property, forcing the Subgroup Discovery process to only perform equality tests on this attribute value for the creation of the conditions used to form subgroups. Instances in the dataset are then either in the target set if they have the same value for the 'doors' attribute as the selected target value, or are in the complement of the set formed by those instances. If the 'doors' attribute is treated as numeric, any, combination, of the '<=', '>=' and '=' tests can used to create conditions to perform on the attribute values. This means that the size of the set of instances selected using an attribute value might be bigger than in the nominal case. A condition using [doors >= 2] will select all cars having two or more doors. In the nominal case it would not be possible to select this group using only one condition (assuming the set of cars having more than two doors is not empty). Obviously, it would be possible to select the same group using a set of conditions like [doors equals '2' \lor doors equals '3'...], but, among other negative characteristics, creating such *conditions* would be computationally more demanding, and less intuitive. Note that if there are missing values for an attribute, the missing value value for this attribute might be automatically changed to a value that is relevant to the attribute type. See Set Value for Missing below for more on the missing value values for the different attribute types.

Set Disabled/Enabled allows to disable or enable an *attribute*. When an *attribute* is disabled, it will not be considered by the mining algorithm to form *conditions* with to create *subgroups*. Note that disabling an *attribute* does not affect the possibility to select it as a *target concept* (see section 2.7 for more on *target concepts*).

Set Value for Missing can be used to change the value that is curently used for values that were missing in the data. The value that is used for missing values depends on the type of the attribute. If, in an arff file, values are declared missing, using the '?' directive, Cortana's file loader might replace this value with one that makes more sense in its Subgroup Discovery setting. For nominal types it will leave this value as is. This will result in '?' being one of the possible target values one can select for the corresponding attribute. However, one can assign a differ value to the missing values. One than has two options, either assign the *missing values* a value that is an existing one for the *attribute*, or a non-exiting one. In the first case one effectively assigns all instances that have a missing value for the corresponding attribute to one of the other attribute values. In the latter case, one just changes the value. When changing the missing value value of an attribute, the Cardinality column is updated accordingly. For numeric and binary attribute types Cortana's file loader will replace '?' values with 0.0 and false, respectively. Again, if this is incorrect, or one wishes to assign the missing values another attribute value, either existing or non-existing,

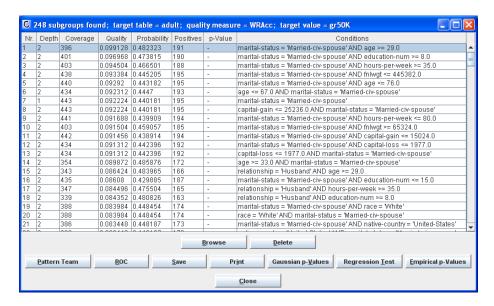


Figure 8: The result window.

this can be done analogously to the *nominal* case.

7 Multi-label

8 Result Window

When a mining run terminates, a Result Window is shown. The titlebar of this window shows some basic information about the search settings that were used to obtain the result displayed. The top half of a Result Window shows a table with the subgroups found, the lower half contains two rows of buttons. Some of the buttons on this Button Panel will be presented only in certain search settings. Also, a number of buttons is used for post-processing, others just give access to additional information. Finally, the buttons in the lower row will execute operations on the whole Result Set, that is all results shown in the Result Window, while those in the upper row operate only on the selected subgroup(s).

The following subsections will go into detail about the use of the various components of the *Result Window*.

8.1 Result Set Table

The top half of the *Result Window* consists of a *Result Set Table*, showing all subgroups in the result set. Form left to right the columns in this table are:

Nr., Depth, Coverage, Measure, p-Value and Conditions, and they all reveil a characteristic of the subgroup found. This section will address all columns, and explains how to interpret the information they display.

Nr. shows the rank of the subgroup. Note, however, that Cortana does not use a partial ranking for ties, and, as a result, subgroups that attain the same measure score, will not receive equal ranks. Rather, if such an event occurs, Cortana assigns the value, displayed by Nr., based on where in the Subgroup Discovery process the subgroup was found.

Depth shows the refinement depth at which the subgroup was found. As explained in the section on Search Conditions (4.3), the refinement depth controls the number of conditions that is used to create a subgroup. So, a subgroup that is formed by using only one condition is said to have been found at depth 1. The number displayed at Depth is the same as the number of conjuncts in the Conditions column of the Result Set Table.

Note that in Subgroup Discovery it often happens that one condition already selects a highly valuable, high scoring, subgroup. Adding extra conditions to this first one may improve the measure score, but only by a, possibly very, limited amount. This will lead to a result set containing a number of subgroups that all consist of the same 'base' condition, which is then refined with additional conditions using another attribute. If these extra conditions do not substantially increase the measure score, all of these variations will attain consecutive ranks in the final result set.

Coverage shows the number of instances in the subgroup. Depending on the target type used, this number can consist of both true positives and false positives, or just indicates the total size of the subgroup.

Measure shows the score of the subgroup, according to the quality measure used. Different quality measures have different ranges for the scores they assign to the worst and best possible subgroups. As a result, measure scores resulting from applying different quality measures can not be compared directly in any sensible manner.

p-Value is initially blank. But it will show the p-value of the subgroup after additional user input. In Subgroup Discovery, quality measures are used that are based on, or insired by, well known, standard, statistical tests. However, Cortana does not allow calculation of p-values in a fashion that is customary in statistics. To be able to do so, the dataset under investigation should be considered a sample of the total population itself. But, as the dataset is not treated as such, the calculation of the p-value is done using a different paradigm. The major benefit of this paradigm is that it is agnostic to the target type used in the Subgroup Discovery process. Section 8.3.2 Compute p-Value below describes how the p-value is calculated in Cortana.

Conditions shows the condition(s) used to form a subgroup. As explained in section 2.5 Condition, a condition consists of an attribute, an operator, and a value. For depths greater than 1 Conditions shows a conjunction of such conditions.

8.2 Subgroup Buttons

The following subsections describe the various buttons that can appear on the upper row of the lower part of the Result Window. These buttons operate only on the subgroup(s) that are selected, or highlighted, in the Result Set Table. The selection can be changed using the mouse or pressing (Shift) and the Down/Up arrow of the keyboard. The target type setting used for the Subgroup Discovery experiment determines which buttons will be shown. For all buttons it will be indicated for what target type setting it is applicable.

8.2.1 Show Model

Show Model is available only for the multi-label target type. For all subgroups selected in the Result Set Table, it will show a new Model Window, depicting the bayesian network connecting the binary attributes, according to the model that was inferred through the Subgroup Discovery process.

8.2.2 Browse Subgroup

Browse Subgroup is available for all target types and will show a Browse Window as described in the Browse Window section (5). For all subgroups selected in the Result Set Table, it will show such a window, depicting all instances that constitude the subgroup. For the single nominal target type one additional button is available, the True Positives button. Clicking it will highlight only those instances that count as true positives.

8.2.3 Delete Subgroup

Delete Subgroup is available for all target types and deletes a subgroup from the Result Set. Note that this means that the subgroup is removed both from the visible Result Set Table, as from the underlying result set. This means that, after deletion, the subgroup will no longer show up in the results of the Save and Print actions described below. Also, in the single nominal setting, this point is no longer used for any ROC plot created after deletion. ROC plots created before deletion are unaffected. This is intended behaviour, as in this way it allows comparison of ROC plots of the same result set in a way that would not be possible if pre-existing ROC plots are update after any deletion.

8.3 Result Set Buttons

The following subsections describe the various buttons that can appear on the lower row of the lower part of the *Result Window*. These buttons operate on the whole *result set*, that is, on all *subgroups* in the *result set*. As such, the results of these operations are unaffected by, changes in, the selection of *subgroups* in the *Result Set Table*. The *target type* setting used for the *Subgroup Discovery* experiment determines which buttons will be shown. For all buttons it will be indicated for what *target type* setting it is applicable.

8.3.1 ROC

ROC is only available for the single nominal target type. All subgroups in the Result Set Table will be taken into account to show a ROC Curve Window. ROC (Receiver Operating Characteristic) curves have their origin in electrival engeneering, where they are used to show the performance of classifiers. In the single nominal setting some of the members of a subgroup are true positives, while others are false positives. In a ROC plot the true positive rate (TPR) of each subgroup is plotted against its false positive rate (FPR). When this is done, a line, the ROC curve, can be draw that forms a convex hull connecting the outer most points. A straight diagonal from the lower left corner to the upper right indicates complete randomness of the result, and the furher the line approaches the upper left corner the better the result. For a subgroup to reach the upper left corner, its TPR must be 1, and its FPR 0.

8.3.2 Compute p-Values

To calculate the p-values for the *subgroups* found, the end user clicks the *Compute p-Value* button on the *Button Panel*. In short the calculation of p-values is done by creating n random subgroups ...

8.3.3 Regression Test

TBI.

8.3.4 Empirical p-Values

This functionality may be removed.

8.3.5 Fold

TBI.

8.4 Save

Save is available for all target types. It allows saving of the whole result set to a file. The user will be asked for a name and location of this file. The file will contain the information as it is depicted in the Result Set Table, and the values for the various columns will be comma separated. Currently, there is no method of changing this separator.

8.4.1 Print

Print is available for all target types. It allows printing of the whole Result Set Table. Note that it does not have a maximum amount of result it prints, the Result Set Table will be printed as-is. Therefore, it is not recommended to use this functionality on large Result Sets/Result Set Tables.

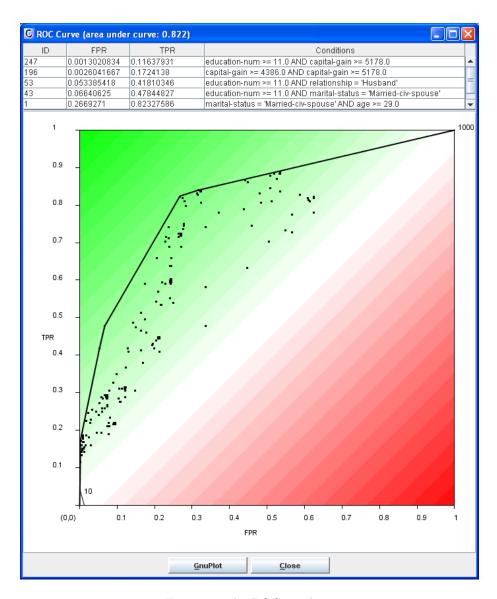


Figure 9: The ROC window.



Figure 10: Choosing the type of randomization to be used for any significance testing.

8.4.2 Close

Close is available for all target types, and it will close the Result Window. Note that it can not be reopened. Therefore, all necessary actions like, saving or printing the results, should be done before closing the Result Window. All results will be lost, and the only way to get a new Result Window is to run the same Subgroup Discovery process again. As this may be a very lengthy process, be sure to finish all operations before closing the Result Window.

9 Usage

9.1 Orinary Subgroup Discovery

java -jar Cortana.jar

9.2 Bioinformatics Setting

10 Autorun

Cortana comes with the ability to run experiments in an unsupervised setting. This is a mode that is specifically created to allow so-called batch mining. This section will explain how Cortana accomplishes this, and how to set up an autorun or batch mining experiment.

In normal usage mode, the end user can set all search settings using the graphical user interface (GUI). After loading a data file and setting the search settings one usually clicks the *Subgroup Discovery* button, and the *Subgroup Discovery* process begins. However, *Cortana*'s menu bar on the top of the main window gives access to two options that allow saving the search parameters to a XML-file. This file can then be used to start the *Subgroup Discovery* process, using the defined search settings, at some other time.

The two autorun related options can be found under *File*, and are named *Create Autorun File* and *Add to Autorun File*. The first will ask the user for a name and location for the new file that will be created, containing all information, as shown in the main window, needed to do an unsupervised *Subgroup*

Discovery experiment. The second option allows to add all information currently presented by the main window to an already existing autorun file. By using this last option one can create a large file, containing multiple experiments. An example usage would be running several experiments on a single data file, where each experiment uses a different quality measure.

The paragraph above refers to information, and not solely search settings, as the XML-file used in the autorun setting also needs to know the name of the data file to use. That name is not part of the search settings, but it is important to state how Cortana looks for this data file. When loading the autorun XML-file, Cortana will remember the directory in which this autorun file resides. It will then parse the XML-file, and retrieve the name of the data file to use. Cortana will then try to load the data file from the directory in which the autorun resides, and that directory only. This means no relative paths can be used for the location of the data file, and the autorun file should always reside in the same directory as the data file(s) for which it describes experiments. Although this limits its use, it keeps it easily portable, as, in this way, one can simply exchange directories containing autorun file(s) and accompanying data file(s), without having to worry about setting paths correctly in the autorun file, or placing the directories in the correct relative location, before being able to run an experiment.

When *Cortana* runs an experiment defined in an *autorun* file, the *Subgroup Discovery* process is exactly the same as when the experiment would be started from the GUI. However, at the end of the *Subgroup Discovery* process, there are a few deviations from the normal GUI situation.

First of all, when the Subgroup Discovery process terminates, the Result Set will be automatically saved, as it would happen when the end used clicks the Save button in the Result Window. The result file will have a name indicative of the search settings used, and starts with the data file name. Also, it will contain a time stamp as part of its name, so that identical runs on, updated versions of, the data file will not overwrite older results. The result file will be saved to the directory in which the autorun file resides.

Second, a Result Window may or may not be shown. Whether it is, is controlled by a command line parameter, as shown at the end of this section. Omitting this command line parameter will cause Cortana to default to always showing a Result Window after an experiment finishes. Showing the Result Window is necessary if one wishes to perform additional actions on the result set, be it plotting ROC Curve Windows, calculating p-Values or any of the other actions described in section 8 Result Window.

Third, if the *autorun* file defined multiple experiments, the next experiment will be run automatically. This will go on until all the experiments in the *autorun* file are executed. In case of any errors, for example when *Cortana* can not locate a data file, some efforts are made to resume execution by discarding the erroneous experiment and continuing with the next.

A final, more technical, word about the *autorun* files. The preferred way to create *autorun* files is through the *Cortana*'s main GUI. In most cases this is the most convenient way, eliminating the chance of errors that could occur

when one were to craft an *autorun* file by hand. The XML-parser parsing the *autorun* file uses a very strict *autorun* definition file, and will throw errors when any of the XML tags are not present in the *autorun* file. This means that, even for XML-tags that define settings that are not relevant to the experiment for which they are defined, they should be present, although they will be so-called empty tags in such a case.

Note that some efforts were taken to allow *Cortana* to run in a headless environment, as is customary for the majority of servers. If all goes well, this should not be a problem. However, if an error occurs, it may cause an error message windows or dialogs to be shown. Obviously, showing this in a headless environment will fail, and may lead to additional errors. This is a known problem, but will not be addressed any time soon.

To use *Cortana* in *autorun* mode start it as shown below, where *file.xml* is the *autorun* file to use, and the optional *false* controls whether a *Result Window* should be shown after each experiment finishes. Remember that the default is *true*, and the second parameter can thus be omitted if one wishes to see the *Result Window*.

java -jar Cortana.jar file.xml [false]

References

- [1] Author, Statistical Handbook.
- [2] Lavrac, Flach, Zupan, Rule Evaluation Measures, a unifying View, .
- [3] Leman, Feelders, Knobbe, Exeptional Model Mining, .
- [4] Wouterd, Subgroup Discovery meets Bayesian Networks, an EMM approach .