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# Visual Data Mining System Architecture (Architettura del sistema integrato di data mining e visualizzazione)

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## Sommario

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### Abstract

In this report we present the architecture of the overall data mining system and detail the main functionalities of its visual interface. The semantics of the visual operators is formally given in terms of the language of the corresponding mining techniques, namely metarules, association rules, clustering, approximate similarity queries.

# Contents

1	Introduction	3
Ι	System Architecture (Vincenzo Curci and Giuseppe Santucci)	4
<b>2</b>	Introduction	4
3	The GUI architecture	4
4	The Abstract DMengine architecture	6
II	Visual Interface (Tiziana Catarci, Stephen Kimani, Giuseppe Santucci)	9
5	Proposed Interface	9
6	Usability	<b>25</b>
7	Future Work	26
II] Pa	I Formal Semantics(Paolo Ciaccia, Giovambattista Ianni, Stefano Lodi, L Ilopoli, Marco Patella, Claudio Sartori)	Luigi 27
8	Metarules interchange format	<b>27</b>
9	Clustering	32
10	Approximate Similarity Queries	37

# 1 Introduction

It can neither be underestimated nor overestimated that the vast amounts of data still present formidable challenges to the effective and efficient acquisition of knowledge. The knowledge discovery process entails more than just the application of data mining strategies. There are many other aspects including, but not limited to: planning, data pre-processing, data integration, evaluation and presentation. In fact, the discovery process is both a domain-centered process and a human-centered process. On the whole, there is a need for an overall framework that can support the entire discovery process. Of special interest, is the role and place of visualization in such a framework. Visualization enables or triggers the user to use his/her outstanding visual and mental capabilities, thereby gaining insight and understanding of data. The foregoing points to the pivotal role that visualization can play in supporting the user throughout the entire knowledge discovery process. Whereas, traditionally visualization has been placed at the beginning and at the end of the knowledge discovery process.

The proposed Data Mining system is intended to provide an avenue for the discovery and acquisition of knowledge from data through exploiting visual strategies during the mining process. The system provides the user with a consistent, uniform and flexible interaction environment across the entire mining activity. The interface employs various visual strategies that can effectively enable the user to exploit his/her powerful visual capabilities with a view to discovering knowledge through metarules and association rules. This is accomplished through enabling more visual interaction with the target dataset and its schema in a bid to formulate rules to be used in searching for matching rules from the target data. In an effort to make the system more interactive, the interface provides optional support for the approximate evaluation of similarity queries. The environment also allows the user to visualize rules along with related tuples. Moreover, the interface provides controls and mechanisms that enable the user to specify parameters that the Data Mining system would use in the generation of clusters from the target dataset. The environment also enables the user to visualize and interact with the clustering output. It is worth noting that the visual operators have associated a formal semantics given in terms of the underlying mining operations.

The report is organized as follows. Section I presents the overall system architecture; Section II describes the visual environment and Section III deals with the formal semantics of the visual operators.

# Part I System Architecture (Vincenzo Curci and Giuseppe Santucci)

# 2 Introduction

The overall system architecture is based on the following guidelines:

- the system must be thought to present the user an heterogeneous set of tasks in the most homogeneous and integrated way;
- the system must be multi platform;
- the system must be open;
- the system must have a modular structure with well defined change/extension points;
- the system must provide the end user with the maximum flexibility during his data mining tasks.

The main problem lies in the extremely heterogeneous data mining methods that the system must support in this very moment (cluster analysis, metaqueries, and association rules) and possibly in the future. That affects both the the internal system behaviour (e.g., algorithm activation, result exchange) and the user interface (e.g., goal description, result presentation).

To overcome these difficulties, a deep abstraction effort has been necessary in the development of the architecture. Beside this, some architectural best practice guidelines has been followed:

- the system is internally multi layer;
- specific extension points have been defined in the architecture where the additions or changes of data mining user interactions, procedures, and algorithms concentrate.

The overall system architecture is depicted in Figure 1 and presents two main layers:

- 1. the first one, the graphical user interface (Gui in what follows), is intended for handling the user interaction in all data mining activities, from data definition to result understanding;
- 2. the second one is the data mining engine (DMengine, in what follows), i.e., the implementation of the data mining processes.

The other modules have orthogonal purposes, like the metadata management and the inter system communication mechanisms.

The metadata management and support module is normally accessed by both the Gui and the DMengine. The intersystem communication subsystem is a specific set of communication primitives able to manage all the possible interactions and data transfer of different data mining techniques in a uniform way.

# 3 The GUI architecture

As from the previous schema, the Gui architecture is organized around a Gui container, which will host the specific Gui extensions cartridges that contain the knowledge to access the respective underlying data mining engines. The container Gui registers, for each Gui extension, the specific data mining technique and configures the user interaction accordingly. Each extension, e.g., the association rules discovery, knows how to access the association rules engine and how to interact with the user in the submission of input data.

# Main DM System Architecture



Figure 1: The overall system architecture

Summarizing, the Gui container gives the data mining system a common set of services, both infrastructural and end user oriented.

The infrastructural services are:

- to register extensions, each of them implementing a specific interaction contract;
- to load on the Gui the specific extension options/commands;
- to route user commands to the active extension;
- to allow the user to select and access new extensions;
- to add specific controls for input insertion and result management.

The general end user added value services are:

- to provide the user with uniform presentation of the elaboration phases;
- to give access to general services like: to save, start, stop, load, and see the progress of data mining analysis.

The main characteristics of a Gui extension are:

• the extension implements a set of commands, that are loaded at runtime by the container Gui and made available to the end user;

- the extension implements the specific input/output modalities of the underlying data mining algorithm;
- the specific modalities can be added to the general pre-existing ones, or can substitute part of them.

# 4 The Abstract DMengine architecture

The DMengine architecture is the real soul of the system. It is completely decoupled from the presentation layer, but its internal structure shows a strong similarity with the one of the container Gui:

- there are some global services available to every specific data mining engine;
- there is a general reference abstract model of the engine (a conceptual framework);
- there are specific implementations of the real engines based on the type of data mining analysis to perform.

The global services are used by every engine implementation, and are relate to:

- metadata management;
- configuration saving/restoring;
- data access and DB connection management;
- internal data interchange and intersystem communication;
- data reduction.

The DM engine reference model is structured around a basic set of concepts:

- the global dataset, that contains all the needed information to perform and apply a data mining technique: data and metadata. Normally it will contain tables, fields and join metadata, along with the data itself. The internal structure of the engine has been kept very simple, collapsing the two abstraction levels (data and metadata) in a single data structure, to give ease and uniform access to only the needed data. Roughly speaking, a dataset is a relational subschema;
- the command manager is the DM engine interface towards the Gui. It is the interpreter of user commands coming from the Gui and manages the access to internal data structure. It is the unique point of contact between the Gui (both the container and the extension Gui) and the engine. Typical operations performed through the manager are, at a very high abstraction level:
  - to define the initial set of data to operate on;
  - to define , if any, some initialization data on the data mining technique in use;
  - to define, if necessary, some starting hypotheses on the data to be mined;
  - to apply the algorithm to discover data mining hypotheses;
  - to store the hypotheses;
  - to verify the hypotheses on the same or different, data.
- the hypothesis verifier that verifies a set of hypotheses on a dataset. The verifier gives a more accurate feedback of the hypothesis validity on data;

- the hypothesis discoverer, whose purpose is to discover hypotheses from the data, possibly using hint hypotheses given directly by the user or as a result of a previous analysis.
- the data mining hypotheses that is the real piece of information the user needs from a data mining analyses, whose content and format depends on the specific data mining algorithm used.



## **Dm Engine Structure**

Figure 2: The data mining engine structure

## 4.1 General DMengine behavior

The general engine behavior is the following:

- 1. the user selects a dataset;
- 2. the user defines one or more data mining techniques to be applied on such a dataset;
- 3. possibly the user gives hints to the engine to drive the hypothesis search;
- 4. the user starts the engine, which use the discoverer to generate hypotheses that, in turn, may be reanalyzed by the verifier.

### 4.2 Specific DMengine implementation

The general DMengine behavior is an abstraction, which must be specialized by specific engines, one for each available data mining method. So it is possible to envisage as many engines as the different techniques implemented by the system. The engines are made dynamically available to the general engine framework and consequently to the user and are accessed through the specific interaction Gui extension that must accompany each specific engine. The common data structure used by all the specialized engines is the global dataset, which contains all the information (data and metadata) needed by a data mining algorithm.

# Part II Visual Interface (Tiziana Catarci, Stephen Kimani, Giuseppe Santucci)

# 5 Proposed Interface

The system provides the user with a consistent, uniform and flexible interaction environment across the entire process of mining knowledge. The visual environment is intended to support the user in the entire data mining process.

The Data Mining interface enables the user to intuitively interact with data schema and the actual data toward visually defining a task relevant dataset.

The interface employs various visual strategies that can effectively enable the user to exploit his/her powerful visual capabilities with a view to discovering knowledge through metarules and association rules. This is accomplished through enabling more visual interaction with the target dataset and its schema in a bid to formulate rules to be used in searching for matching rules from the target data. In an effort to make the system more interactive, the interface provides optional support for the approximate evaluation of similarity queries. The environment also allows the user to visualize rules along with related tuples. Moreover, the interface provides controls and mechanisms that enable the user to specify parameters that the Data Mining system would use in the generation of clusters from the target dataset. The environment also enables the user to visualize and interact with the clustering output.

## 5.0.1 Visual Construction of a Target Dataset

One of the major tasks/phases in the knowledge discovery process is the selection of a task relevant dataset. In our data mining system, the target dataset may comprise one or more relations. In the following, a description of the visual environment and the main operations that are supported is given.

## The Interface

Toward supporting the user in the specification of a task relevant dataset, the Data Mining system does provide an intuitive visual environment through which the user can define each of such relations in a generic way. Moreover, the same environment enables the user to introduce constraints on each such relation. The constraints include the type of relation (which could be a standard database relation or otherwise), the name of the relation, the type of attributes to be included in the target relation, and the number of attributes that the target relation should have.

The environment is backed with drag-and-drop mechanisms and tools. In the context of defining a relation to include in the target dataset, there are two main interaction components namely the specification space and the target space as seen in Figure 1.

The specification space supports the user in performing the specification task. Through the component, the user can specify a *new* relation to be included in the set of task relevant data. Moreover, the component enables the user to *edit* the specifications/particulars of a relation that is already in the target data set. The component acts as the workshop from which the user "constructs" the desired relation. When through with the "construction", the user may forward/send the resultant relation to the target space.

The target space acts as a container for the relations that the user specifies. It should be mentioned that the set of all the resultant relations constitutes the target dataset. The component also enables the user to forward/send the relation to the specification space for editing. Within the target space, it is also possible to directly remove/*delete* a relation from the target dataset. The two interaction components are complementary. Therefore, the user operates by appropriately moving between the two components. Since the interface supports drag-and-drop mechanisms, the user may intuitively move elements (such as relations and relation items) from one component to the other as appropriate.



Figure 3: The Environment for Constructing a Set of Target Data

#### **Main Operations**

Essentially, the user may introduce a new relation into the set of target data, edit or even delete a relation that is already part of the target dataset. Specification of a New Relation The environment enables the user to specify a new relation. The specification operation may be commenced either by clicking on the icon for New Relation in the specification space window or by an interaction with the input widget Relation Type or Name of Relation in the same window. The type of relation can be specified through a list-box. Among others, the list includes Any type and Database. The name of relation can be selected from (or typed in using) a combo-box. If the type of relation has already been specified, then the list of relation names in the combo-box is restricted to the specified relation type. It should be pointed out that the combo-box also allows the user to specify a generic relation through choosing the combo-box entry Any Relation (\*). In such a case, the system returns all relations that satisfy the rest of the specifications (relation type and attributes).

The user can select the type of attributes to be included in the relation. There are two main options namely All/Any types or *Some* types. The selection can be carried out using radio/option buttons. With regard to the option *Some* types, the user may specify the attributes of interest through their respective check boxes. The types that are offered are *String*, *Numeric*, *Alphanumeric*, *Logical*, and *Date/Time*. Corresponding to each type are spin-boxes and a text-box through which the user could specify the number of attributes of that type the target relation would have.

Specifying the type of attributes helps the system to have some knowledge about the at-

tributes that are of interest to the user. However, given that the user might also have input the number of attributes, there is a possibility that the system might not be able to figure out which attributes, of the type that was specified, to include or to leave out. To address this complication, the interface offers the user the freedom to decide which attributes to include and in what order. Fundamentally, the system renders this through the generation of "resource" relation(s) and a "skeleton" relation, which it puts in the specification space.

"Resource" relation(s) are relations of the specified relation type and attribute types. Each such relation has a handle corresponding to the relation's name (upper handle). Moreover, each of the relation's attributes has a handle (attribute handle). The "skeleton" relation is a blank relation which the user works on as s/he desires. "Resource" relations act as the resource from which the user gets the materials for building the "skeleton" relation. The "skeleton" relation provides the structure/skeleton on which the user builds a target relation.

The "skeleton" relation comes with a name and with slots into which attributes can be slotted in. If there are multiple "resource" relations, then the "skeleton" relation takes on a generic name. In the case where there is only one "resource" relation, then the "skeleton" relation acquires a name similar to the "resource" relation. Figure 1 shows the environment with multiple "resource" relations and a "skeleton" relation that has a generic name (X).

The number of slots corresponds to the number of attributes that was specified. If the number that was specified is greater than the actual number of attributes, then the system uses the actual number of attributes and generates a corresponding number of slots. Like the "resource" relations, the "skeleton" relation also has a handle corresponding to the name (upper handle). Moreover, each slot that has been filled with an attribute also has a handle (attribute handles). It is worth mentioning that in the environment the user can hold/pick and drag a relation's name by the upper handle and an attribute by the attribute handle, using the hand tool.

In the case where there are multiple "resource" relations, the user may pick and drag an attribute from any of the relations and slot it in where s/he wants in the "skeleton" relation. If the user would like to use attributes only from one of the multiple "resource" relations, s/he could pick the relation's upper handle (relation's name) and overlay it on the "skeleton" relation's name. The operation sets up the "skeleton" relation to receive attributes only from the one "resource" relation of interest. As for the case where there is only one "resource" relation, the user may drag attributes from the relation and insert them into the "skeleton" relation's slots in a straightforward manner.

The user may also drag attributes up and down (rearranging the attributes) in the "skeleton" relation itself. The user uses the hand tool to hold the attribute handles thereby picking the respective attributes and therefore s/he can move the attributes up and down as s/he wishes.

When dealing with multiple "resource" relations, it is possible to delete or change a name that the user may have assigned to the "skeleton" relation. To delete the relation's name, the user selects the hand tool, uses the tool to pick the name by its handle and drops the name into the trash-bin or presses the delete key. Alternatively, the user may select the name by using the pointer tool and then press the delete key. The immediate result of the deletion is that the "skeleton" relation assumes a generic name. With regard to changing the name of the "skeleton" relation, the user may drag another relation's name from the pool of "resource" relations and overlay the current "skeleton" relation's name with the new name.

The user may also delete an attribute from the "skeleton" relation. Toward that, the user picks the attribute by its handle and drops it into the trash-bin or presses the delete key. The same operation can be accomplished by selecting the attribute using the pointer tool and then pressing the delete key.

Once the user is satisfied with the "skeleton" relation s/he has built, s/he may forward it to the target space. This indicates that the relation becomes part of the target dataset. The forwarding may be accomplished either by drag and drop or by iconic commands. With respect to drag and drop approach, the hand tool can be used to hold the ("skeleton") relation's upper handle. Then the user can drag the relation and drop it into the target space. In regard to iconic commands, the user selects the pointer tool, clicks the upper handle and clicks the icon for *To Target Space*. The interface gets ready for another task e.g. specification of another new relation.

#### Editing a Relation

The user can edit a relation that is already in the target space. With the hand tool, the user holds the relation of interest by the upper handle, drags the relation and drops it into the specification space. As an alternative, the user may pick the pointer tool, click the upper handle of the relation of interest, and then click on the icon for *To Specification Space* in the target space window. This causes the relation to be made available in the specification space for editing.

Once the relation of interest gets back to the specification space, the interface gets updated to support the anticipated editing. The relation of interest becomes the "skeleton" relation with "delicate" (subject-to- change) attributes. The system reloads the respective specifications and "resource" relation(s). At this level, editing operations then resemble the specification operations in the previous discussion on *Specification of a New Relation*.

#### Deleting a Relation

The user can delete/remove a relation from the target space. With the hand tool, the user holds the relation of interest by using the relation's upper handle. The user then drags the relation and drops it in the trash-bin or presses the delete key. Alternatively, the user could accomplish the same by using the pointer tool and the delete key. The user selects the pointer tool. With the tool, the user clicks the upper handle of the relation of interest. This causes the relation to be selected. With the relation selected, the user presses the delete key.

It is important to keep in mind that all the mentioned relation operations do not affect the original relations/data in any way. The operations define the set of data that is of interest to the user for the data mining task at hand.

## 5.1 Approximate Similarity Queries

In order to make the data mining more interactive, the interface provides an optional avenue through which the user can specify approximate similarity queries.

#### **Parameter Specification**

The system provides support for approximate similarity queries across all the implementations of data mining strategies. In the each of the environments, the input widgets for similarity query parameters are placed just below where the input widgets for the other data mining strategy-specific parameters are placed.

It is worth mentioning that approximate similarity query support is especially useful where clustering inputs or outputs are involved.

In [6, Part III], PAC queries are proposed as a search paradigm for quality-controlled approximate similarity search. In particular, PAC (range and k-NN) queries allow the error on the query result to exceed a certain threshold (indicated by an accuracy parameter  $\epsilon$ ) with a probability not higher than the value of the reliability parameter  $\delta$ . In order to perform a PAC query, the user has therefore to specify a value for the accuracy and the reliability parameters  $\epsilon$  and  $\delta$ . The environment provides two sliders to adjust the values of both accuracy and reliability parameters from a maximum of 100% (exact query) to a minimum application-specific value (e.g. 50% for both parameters).

Each similarity query requires a reference point to be expressed. The interface provides a text-box through which the coordinates of the reference point may be input. When the user clicks inside the text-box, the "coordinate selector" tool in the output window blinks. It should

be pointed out that blinking occurs only when there is already some visualization of results. The user may simply type in the text-box the coordinate values of a reference point thereby causing the blinking to stop. Alternatively, the user may move to the output window and directly click the point of interest. The blinking stops and the values of the clicked point get automatically recorded in the *Reference point* input widget. In the latter way of specifying the reference point, the user relies on the visualization of results from previous data mining tasks. In particular, since results of clustering are more likely to be used than those of meta-querying or association rules, the supposition is that the output window is the scatter plot of the *Overview* + *Details* visualization of clusters. The foregoing visualization is discussed later in this Section under *Visualizing Clustering Output* within the clustering environment.

The last parameter requested by a PAC query is dependent on the query type. In particular, for k-NN queries the user has to specify the number k of requested result, whereas for range queries the user fixes the distance threshold that points in the result should not exceed. The interface provides a spin-box and an alternate text-box for each of the two values. As for the query type, the interface offers two radio buttons that allow the user to specify either k-NN type or *Range* type. Moreover, selecting a query type activates the corresponding text-box and spin-box. Upon clicking the radio button for k-NN, the user may directly type in the value of k or use the spin-box. On the hand, when the user selects the radio button for Range or clicks inside the respective and already activated text-box, the "circle drawing" tool in the output window blinks. In a manner similar to the interactive specification of a reference point, blinking occurs only when there is already some output from previous data mining tasks. The user may manually enter the query radius in the text-box or use the spin-box. The specification causes the blinking to stop. Alternatively, the user may specify the radius by dragging within the output window, which is essentially the scatter plot of clusters. The dragging operation causes a circle to be drawn on the scatter plot with the respective radius being dynamically reflected in the text-box. When satisfied with the radius of the circle instance, the user releases the mouse button. The radius gets recorded in the text-box as the query radius and the blinking stops.

It should be mentioned that the user can always interrupt or even cancel an interactive specification process by clicking anywhere outside the context of the process or by simply pressing the escape key.

The "torch" icon is used to instruct the underlying system to actually perform the PAC query on the target dataset based on the specified approximate similarity query parameters (and data mining strategy-specific parameters).

## 5.2 Metaqueries

In the following, a discussion on how the system supports the formulation of metaqueries and visualization of metaquery results is given.

## **Designing Metaqueries**

Pattern Formulation

We introduce an interesting approach that can be exploited in the formulation of metapatterns. Assume that the task relevant dataset comprises the relations UsCa, CaMo and UsMo as shown in Table 1.

Consider that the user performs links/"joins"<sup>1</sup> on the fields:

<sup>&</sup>lt;sup>1</sup>As far as our Design of Metaqueries is concerned, "joins" do not refer to table joins; a "join" refers to a link between attributes that is aimed at generating a consequent pattern

UsCa	UsCa		$\operatorname{CaMo}$			$\mathrm{UsMo}$	
User	Carrier	]	Carrier	Model	]	User	Model
John K.	Omnitel	] [	Tim	Nokia	] [	John K.	Siemens
John K.	Tim		Omnitel	Siemens		John K.	Nokia
Anastasia A.	Omnitel		Wind	Nokia		Anastasia A.	Siemens

 Table 1: The Task Relevant Dataset

UsMo.User	$\operatorname{and}$	UsCa.User
UsMo.Model	$\operatorname{and}$	CaMo.Model
UsCa.Carrier	and	CaMo.Carrier

with constraints:

UsMo.User and UsCa.User = "JohnK." UsMo.Model and CaMo.Model = "Nokia"

Having linked the fields, we have the following:

UsMo(User, Model), UsCa(User, Carrier), CaMo(Carrier, Model)

Introducing the constraints, we get:

UsMo("JohnK.", "Nokia"), UsCa("JohnK.", Carrier), CaMo(Carrier, "Nokia")

which resembles:

R(x, z), P(x, y), Q(y, z)where P, Q, R are relations and x, y, z are attributes or literal values.

Intuitively, there appears to be a general transitive pattern/rule of the form:

 $R(x,z) \leftarrow P(x,y), Q(y,z)$ 

In fact the pattern is a metaquery. Therefore, from the discussion, a possible instantiation  $\sigma$  of the metaquery is such that:

 $\sigma = < R(x, z), UsMo("JohnK.", "Nokia") >, < P(x, y), \\ UsCa("JohnK.", Carrier) >, < Q(y, z), CaMo(Carrier, "Nokia") >$ 

and thus the following horn rule:

 $UsMo("JohnK.", "Nokia") \leftarrow UsCa("JohnK.", Carrier), CaMo(Carrier, "Nokia")$ 

The Metaquery Environment

Consider that the user visually constructs a task relevant dataset<sup>2</sup> thereby defining a dataset

 $<sup>^{2}</sup>$  The construction refers to the approach that was described earlier in the section on Visual Construction of a Task Relevant Dataset

consisting of the relations in Table 1.



Figure 4: The Environment for Formulating Metaqueries



Figure 5: The System Generates a Metapattern Corresponding to the "Joins"

The Design of Metaqueries environment enables the user to either define links/"joins" manually (Manual Joins) or have them defined automatically by the system (Automatic Joins) by selecting the relevant option button.

In the automated option, the user does not need to perform any linking operation. The system automatically analyses the metadata of the relations for any possible or applicable links/connections. The user may proceed and click the "Add Pattern" command button to have the system generate metapatterns that correspond to the links. The system puts the metapatterns into some "pool" (of metaqueries) located just below the command button.

As regards the manual specification of links, the user selects an attribute of interest by using its "hook". The operation is realized through the use of the mouse-pointer or the "pointer" tool. The operation causes the "join" tool to blink, demanding attention. The user picks the "join" tool from the tool-box causing the tool to stop blinking. The relations blink, demanding attention. With the "join" tool, the user selects an attribute (by its "hook") of another relation causing the relations to stop blinking. The two attributes ("hooks") get linked/connected with some "chain". An alternative way of accomplishing the linking operation is by using the "hand" tool. In this case, the user selects the "hand" tool from the tool-box, causing the relations to blink. The user uses the "hand" tool to hold attribute of interest (by its "hook"). The user drags and drops it on the "hook" of an attribute of another relation causing the relations to stop blinking. The two respective attributes get connected with a "chain".

The environment also offers mechanisms for introducing constraints on the linked fields. The user selects a defined link/connection by using the mouse-pointer or the "pointer" tool. The "disconnect" and "edit" tools blink, demanding attention. The user picks the "edit" tool from the tool-box causing the "disconnect" and "edit" tools to stop blinking. The selected connection provides some combo-box through which the user may type in some constraint or get a list of attribute values to select from. Entering or clicking anywhere else causes the combo-box inputs to be taken. An optional way of introducing a (or editing the) constraint is by double-clicking the respective connection (or defined constraint).

The user may wish to delete a defined connection or constraint. In regard to deleting a defined connection, the user selects it by using the mouse-pointer or the "pointer" tool. The "disconnect" and "edit" tools blink. The user either picks the "disconnect" tool from the tool-box or simply presses the delete key. The "disconnect" and "edit" tools stop blinking. The connection of interest gets broken. With respect to deleting a defined constraint, the user selects it thereby causing the "delete" and "edit" tools to blink. The user either picks the "delete" tool from the tool-box or presses the delete key. The "delete" and "edit" tools stop blinking. The constraint that was selected gets deleted. It should be mentioned that a more intuitive and straightforward way of deleting a connection or constraint is by holding, dragging, and dropping it in the trash-bin.

Figure 2 shows the initial status of the interface with the task relevant dataset.

When satisfied with the links/"joins" defined, the user may instruct the system to generate a metapattern (*Add Pattern*) corresponding to the links. It should be pointed out that, at this point, the system does not need to use/search the database. At the current level of operation, the generation of a metapattern is simply an analysis that relies only on metadata and link/"join" information. The generated pattern is put in a pool. The user may repeat the same process for the design of another or other metapatterns. It can be observed that the user has "direct" interaction with the target data and also has "direct" control over the metapatterns that are put in the pool. The patterns in the pool constitute a major parameter of the query that will be used to search for specific rules in the database corresponding to the patterns. Consider that the user introduces the links:

UsMo.User	and	UsCa.User
UsMo.Model	$\operatorname{and}$	CaMo.Model
UsCa.Carrier	and	CaMo.Carrier

Assuming that the user is satisfied with the "joins", and instructs the system to generate a corresponding metapattern, Figure 3 shows the interface at the current level of operation.

The user may also specify the threshold values for confidence and support measures. There are sliders and text-boxes to support the specification. Moreover, the user may specify the approximate similarity query parameters. The user may instruct the system to search for specific rules from the dataset that correspond to the metapatterns in the pool and that satisfy the specified threshold levels, by clicking the "torch" icon. The system returns the obtained metarules and provides various visualizations for the same. It should be mentioned that the system supports dynamic "updates" in that any subsequent changes to the metaquerying parameters are directly reflected in the visualization(s). Consequently, the user does not need to click the "torch" icon every time the parameters are changed. The dynamic functionality holds as long as the target dataset has not been modified.

## **Visualizing Metaqueries**

The system provides visualizations for the metarules that are obtained from the dataset. For any metarule, the parameters that are of principal interest are:

- Measures of interestingness (such as confidence and support)
- Relationship/association between the head part and the body part
- Number of items participating in the rule (total number in the rule; number in the head, number in the body)

The interface offers two main visualization mechanisms: Rules + Tuples (Overview + Detail) and *Dedicated View*.

#### Rules + Tuples

This is a visualization that displays rules, and also presents tuples that correspond to some selected rule(s). All the rules in the dataset that satisfy the user's query are presented on a scatter plot. Practically, the user would often ultimately need to access or handle the actual data i.e. the tuples themselves. In this scenario, the user would be interested in accessing or handling tuples related to some rule(s). This process may be envisaged as performing a more detailed analysis on the rules. With a view to supporting the detailed analysis, the interface offers, among other interaction facilities, a mechanism for selecting the rule(s) to be analyzed further. Moreover, the interface invokes a system-driven mechanism which chooses an appropriate presentation style for tuples corresponding to the selected rule(s). The scatter plot may be envisaged as the "overview" window and the tuples window may be taken to be the "detail" window.

In visualization, it is crucial that conceptually important aspects or dimensions be made perceptually important. With regard to rules, their (relative) confidence and support values are conceptually important. In the scatter plot, the two variables have been mapped to grayscale and Y-axis respectively. On the whole, the scatter plot mapping is as follows: a rule is represented by a point, the confidence value of a rule is represented by grayscale, the support value of a rule is represented by the y value, and the number of attributes in a rule is represented by the x value. Consider that the metaquery search based on the ongoing example returns the following metarules:

 UsMo("JohnK.", "Siemens") ← UsCa("JohnK.", Carrier), CaMo(Carrier, "Siemens") Support = 50% and Confidence = 66.66%



Figure 6: Rules + Tuples Visualization

- 2.  $UsMo("JohnK.", "Nokia") \leftarrow UsCa("JohnK.", Carrier), CaMo(Carrier, "Nokia")$ Support = 66.66% and Confidence = 50%
- 3. UsMo("AnastasiaA.", "Siemens") ← UsCa("AnastasiaA.", Carrier), CaMo(Carrier, "Siemens") Support = 33.33% and Confidence = 100%

Figure 4 shows the visualization with the foregoing results.

#### Dedicated View

Like the foregoing visualization, the *Dedicated View* enables the user to visualize all the metarules satisfying the query. However, in this case the rules are visualized in a more elaborate manner. The visualization shows; the confidence and support values of each rule, the relationship/association between the consequent and the antecedent parts of each rule, and the individual items/components that make up each rule.

This visualization uses a simple 2D floor with a perspective view. The floor has rows and columns. A rule is represented by a column on the floor. The rule is made up of the items/components which have entries in the column. The rows represent the items (e.g. attributes or values). Associated with each column/rule is a "bucket". The "bucket" represents two measures; the gray value of the contents of the "bucket" represents the confidence value of the rule, and the level of the contents of the "bucket" represents the support value of the rule. Rule items that form the antecedent are represented using a "key" icon, whereas rule items that form the consequent are represented using a "padlock" icon.

Figure 5 shows a *Dedicated View* presentation of the same metarules that were shown in



Figure 7: Dedicated View: Elaborate Rule Visualization

Figure 4. The handle of the "bucket" can be used to select the corresponding rule. The visualization has a scale for the support measure, and a grayscale key for the confidence measure.

One of the problems with a perspective view is the determination of size of far objects. Nonetheless, in our visualization, the icons/"objects" on the floor represent either the antecedent or the consequent of a rule. As such, their size is not a major issue in interpreting the visualization; as long as they are visually distinguishable as representations of the head or of the body.

## 5.3 Association Rules

In the following is a description of the environment through which the user can construct association rules and view corresponding results.

### **Designing Association Rules**

The proposed system provides an interface with intuitive tools and mechanisms which the user can use to construct association rules. In particular, the *Design of Association Rules* environment offers "baskets" and also supports "drag and drop" mechanisms.

In most cases, association rules deal with data stored on a single table. Nonetheless, if the relevant data are composed of more than one relation, the user may perform table joins<sup>3</sup>. The system should generate one table based on the table joins the user defines (a single joined table/view). The interface caters for both situations i.e. it provides:

- *Define Joins*: The user may either perform table joins manually or instruct the system to define the joins automatically.
- Skip Joins: The user may opt not to define any table joins.

$\operatorname{OrdProd}$					
OrderID	ProdID				
121	P002				
121	P003				
122	P004				
123	P001				
123	P004				
124	P003				
125	P001				
126	P001				
126	P005				

Product				
ProdID	ProdName			
P001	Shirt			
P002	Shoes			
P003	Socks			
P004	Sweater			
P005	Tie			

 Table 2: Relations OrdProd and Product



Figure 8: The Interface for Designing Association Rules

Consider that the user *visually constructs* a set of target data that comprises the relations in Table 2. Moreover, assume that the user has the following high-level questions:

- 1. How true is it that when a pair of "Shoes" is ordered, then a pair of "Socks" is also in the same order?
- 2. How true is it that when a "Shirt" is ordered, then a "Tie" is also in the same order?

<sup>&</sup>lt;sup>3</sup>Table joins or simply joins refer to table joins as known and used in database technology



Figure 9: Basket-based Construction of Association Rules

With our Data Mining system, the interface allows the user to formulate the questions/query without having to understand the details of the orders. Consequently, it is enough for the user to formulate the questions using only the *Product* table. In this case, the user does not have to define any table joins since the task relevant data comprise one relation, *Product*. Figure 6 shows the interface after the user opts to skip the joins.

Through the supported "drag and drop" mechanisms, the user may pick items from the relation and drop them into the relevant "basket". For the first question, the user needs to drag and drop the tuple Products = "Shoes" into the first "basket" and the tuple Products = "Socks" into the second "basket". Figure 7 shows the interface after the user has put the items in the "baskets" and emptied the "baskets", thereby constructing the rule:

$$IFProducts = "Shoes" THEN Products = "Socks"$$

The interface also provides sliders and text-boxes. Through either, the user may specify confidence and support levels. In addition, the user may specify the approximate similarity query parameters.

A search would analyze the dataset and return any rules that correspond to the user-defined ones and that satisfy the measures of interestingness.

#### Visualizing Association Rules

Toward visualizing the association rules found in the target data, the system exploits the same visualization mechanisms that are used for visualizing metarules. Consequently, association rules are displayed using two main visualization mechanisms: Rules + Tuples (Overview + Detail) and *Dedicated View*. The mechanisms were discussed in the previous discussion on *Visualizing Metaqueries*.

## 5.4 Clustering

The clustering environment does provide controls and mechanisms that enable the user to specify parameters that the Data Mining system would use in the generation of clusters from the target dataset. Moreover, the environment also enables the user to visualize and interact with various clustering results.

Consider that the user is interested in a database used at a tourist information point and in particular a relation that contains information about towns and how far the towns are from the airport. The distances are expressed in terms of x and y coordinates with respect to the airport (i.e. with the airport as the origin). Table 3 shows a tabular view of the relation. As it can be seen from the same figure, the relation also contains other details such as the identity of the town (TwID), the name of the town (TwName), and the year when the town was established (TwYEst). Consider that the user visually constructs a task relevant dataset that corresponds to Table 3. As seen in Figure 8, the user is interested in only four attributes of that relation i.e. TwName, TwX, TwY, and TwYEst.

	i	Town		
TwID	TwName	TwX	TwY	TwYEst
T001	Skyland	-3	5	1878
T002	Highview	-2	4	1886
T003	Terrace	-2	-3	1767
T004	Downside	-1	-2	1903
T005	Hilltown	-1	-4	1915
T006	Jollyscape	4	3	1943
T007	Lakeside	3	2	1840
T008	Ancient	5	-1	1494

Table 3: Relation Town

#### **Parameter Specification**

The user may specify various parameters to be used by the Data Mining system in the generation of clusters from the defined task relevant dataset.

The user may specify a similarity measure and/or a dissimilarity measure. There is a checkbox for each of the two measures to enable the user express interest in specifying the corresponding measure. Each of the measures is presented on an ordinal scale that runs from 0 to 100. There is a slider control for either scale. The user can set a measure by dragging the slider to some value/position of interest on the scale.

The system also provides interaction widgets for specifying the number of clusters desired in the output. There are spin-boxes (and alternatively a text-box) through which the user may provide the input.

It should be pointed out that hierarchical clustering algorithms essentially require an input of some distance measure (similarity or dissimilarity). However, the algorithms do not require the number of clusters as input. On the other hand, partitional clustering algorithms take in as input the number of clusters but do not require a distance measure. In line with the foregoing, the system activates the similarity and dissimilarity interaction widgets and inactivates the ones for the number of clusters if the target algorithm is hierarchical. The reverse activation and inactivation occur when the target algorithm is partitional.

The system allows the user to specify the variables/attributes that will directly participate in cluster analysis/computations. This specification takes the form of "checking" attributes of a relation(s) in the target space. As seen in Figure 8, a relation in the target space possesses

CLUSTERING INPUT				
□ Specif	ication Space 🛛 🕏			
Relation Type	Attribute Type Number of Attributes			
Name of Relation	r String Γ 🚖			
Any Relation 💌	└ Numeric └ 🚖			
	🗖 AlphaNumeric 🗍 🚍			
	🗖 Logical 🕅 🚍			
	☐ Date/Time ☐ 🛨			
Park Town	Town			
Г	arget Space 🤌			
ि () () () () () () () () () () () () ()	Town     TwName     Twx     Twy     TwyEst			
Level of	Approximate Similarity Query			
🔽 Similarity 🛛 🗐	- 10% Accuracy - 10%			
🔽 Dissimilarity	⊐ 10% Reliability d= 10%			
Number of Clusters ਤਾਂ ਦੀ Label for Cases ਸਿਆਪ	Reference point PAC Query Type ame ⓒ k-NN 용 편 ⓒ Range F 편			

Figure 10: Specifying Clustering Parameters

features such as a "handle" and a "check-box" for each attribute. "Checking" the "check-boxes" means that the corresponding attribute has been chosen to directly participate in cluster analysis. On the other hand, the user may undo ("uncheck" attributes) the operation. These operations are realized through standard "point-and-click" functionalities. In Figure 8, the attributes TwX and TwY have been selected ("checked").

The user may also select the variable that will serve to identify/label entities or components of a cluster in the output. This functionality is available through a combo-box that holds a list of attributes of the relation(s) in the target dataset. In Figure 8, the user has chosen the attribute representing the names of towns (i.e. TwName).

In this environment, the user may also specify the approximate similarity query parameters. When through with the clustering and approximate similarity query parameter specification, the user may instruct the system to undertake clustering on the target dataset based on all the inputs by clicking the "torch" icon. At present, the system determines the clustering algorithm to use on the constructed target dataset for the task at hand. It then carries out cluster analysis and returns the clustering output to the user. In case there are any subsequent changes to the input parameters, the changes are directly reflected in the output since the dynamic "updates" functionality is also supported in the clustering environment.

At the moment, the clustering environment is intended to at least support a typical data mining user. In line with the foregoing, it is aimed that the offered parameter widgets will be reasonably fundamental/basic, interpretable and useful to such a generic user.

#### Visualizing Clustering Output

The clustering interface component provides tools and mechanisms for interacting with and visualizing clustering results. The system provides two main visualization mechanisms: Clusters + Details (Overview + Detail) and Separation View.



Figure 11: The Environment for Visualizing Clustering Output

#### Clusters + Details

In this visualization mechanism, there are two display components. The first one is a display of the clusters on some space. In particular, the display uses a scatter plot. The second one is a display of the details of a selected element (cluster or point) from the first display. The scatter plot may be regarded as an "overview" window and the other display as a "detail" window.

In the scatter plot, cases in the target dataset are mapped to points on the scatter plot, whereby each point takes some x, y, and z values. The system offers two alternative methods of visualizing clusters using the scatter plot. In the first method, points in the same cluster are enclosed in a bounded region. Outliers are plotted lying outside such regions. Each region is shaded with some grayscale level depending on the accuracy/quality level of the respective cluster. The focus (currently selected) cluster or point is drawn with an outline around it. Figure 9 shows a visualization that uses this type of view. In the second method, points that belong to the same cluster are drawn with the same color. The latter method is appropriate in the case where the process of enclosing points would lead to overlapping regions. All outliers are coded with color blue. The color is reserved for this purpose and therefore is not used in the representation of clusters. Cluster points of the focus cluster or individually selected points are drawn with an outline around them. The system chooses the method to use based on the distribution of points belonging to the same cluster. There are many operations that are supported within the scatter plot such as selection and projection. The user may select a cluster or a point for exposition on the *Details* display. The scatter plot also enables the user project selected cluster(s) to a virtual 2D plane at the rear of the display. If the target data is already in 2D, then the system does not display the virtual 2D plane since the user does not need to perform any projection.

The *Details* display enables the user to visualize the details of an element selected in the scatter plot. At the moment, the system supports the exposition of a selected point. In line with the foregoing, the interface invokes a system-driven mechanism which chooses an appropriate

presentation style for the point/tuple. In Figure 9, a point from the most populated cluster has been selected. It is worth mentioning that it would be interesting to offer a display of the contents/cases of a selected cluster. In such a display, frequency counts of the cases with respect to the cluster and with respect to the entire target dataset could be displayed.

## Separation View

This view displays various measures pertaining to the clustering operation. As seen in Figure 9, the system draws a graph depicting how far the selected cluster (or the cluster containing the currently selected point) is from the other clusters and outliers. A circle is used to represent a cluster. The size of the circle represents the density of the cluster. The y-axis is used to represent the separation. The grayscale level of the circle represents the quality of the corresponding cluster. The circles are arranged along the x-axis.

# 6 Usability

To determine the usability of interfaces, it is necessary to subject them to rigorous evaluation tests. It should be pointed out that our system primarily targets users who are acquainted with data mining. It would arguably be easier to design an interface for a specific type of users than for a mixed audience. Nonetheless, the need to carry out usability tests remains. As a way of getting started, we carried out usability heuristics. The term "usability heuristics" refers to a more informal evaluation where the interface is assessed in terms of more generic features. This informal evaluation presents reasonably concise and generic principles that apply to virtually any kind of user interface. In the following discussion, we analyze how some of the principles have been applied in the design of the Data Mining system.

- The interface dialogue should be simple and natural. Moreover, the interface design should be based on the user's language/terms. In general, there should be an effective mapping between the interface and the user's conceptual model. In our system, the interface primarily uses data mining terms. It is worth recalling that our target audience comprises users who are conversant with data mining concepts. Furthermore, the provision of "hooks" and "chains" for linking attributes, "baskets" for designing association rules, "drag and drop" mechanisms, "buckets" for measures of interestingness, and "keys" and "padlocks" for antecedents and consequents are part of the effort aimed at getting effective mappings between the interface and the user's conceptual model.
- The interface should shift the user's mental workload from the cognitive processes to the perceptual processes. Our Data Mining interface supplies various mechanisms to support the shift. For practically all inputs, the user does not have to supply the units of measurement. Moreover, the system offers interaction controls (e.g. sliders) for helping the user get familiar with the range of valid values and also for helping him/her input within the range. Furthermore, visually presenting query parameters (e.g. data relations) minimizes the possibility of making mistakes while formulating a query.
- There should be consistent usage and placement of interface design elements. Consistency builds confidence in using the system and also facilitates exploratory learning of the system. In our interface, the same information is presented in the same location on all the screens. In fact, the Data Mining interface is uniform across the various environments for metaqueries, association rules, and clustering.
- The system should provide continuous and valuable feedback. One of the mechanisms our Data Mining system uses to provide feedback is realized when the user puts some item into the "baskets" or empties the "baskets". The "baskets" respond to reflect the insertion or

the removal. Moreover, the visualization dynamically updates itself as the user changes (or interacts with) data mining parameters.

- There is a need to provide shortcuts especially for frequently used operations. In the Data Mining interface, there are various shortcut mechanisms. For instance double clicking and single key press commands. The anticipated incorporation of a visual query language is expected to also help with respect to shortcuts.
- There are many situations that could potentially lead to errors. Adopting an interface design that prevents error situations from occurring would be of great benefit. In fact, the need for error prevention mechanisms arises before (but does not eliminate) the need to provide valuable error messages. Our Data Mining interface offers mechanisms to prevent invalid inputs (e.g. specification by selection, specification through sliders). It also provides some status indicators (e.g. when an item is put in a "basket", the status of the "basket" changes to indicate containment).

Moreover, we carried out some informal user tests on a previous version of the prototype with data mining experts. We got encouraging results from the tests and even suggestions on how to improve the interface.

For instance, with respect to clustering, the data mining experts suggested that the system should provide an optional interaction environment specifically designed for the expert user and still leave the user with the freedom to switch between the two. The optional environment would allow the user to specify more specific clustering parameters (such as choosing an algorithm, specifying the number of iterations, and putting weights on cases).

# 7 Future Work

As was suggested by the data mining experts, we are considering the provision of an optional clustering interaction environment specifically designed for the expert user and still leave the user with the freedom to switch as s/he desires. There is also an intention to include support for displaying clustering output using a non-Euclidean space. Moreover, as observed earlier, the incorporation of an optional display for showing the contents of a selected cluster with their frequency counts is worth consideration.

The current interface and the various data mining visualizations will later be subjected to formal usability tests. The results obtained from the tests would be instrumental in determining further relevant interface improvements and modifications.

Work aimed at widening the spectrum of data mining strategies supported by the current system is also going on. Toward providing more user support in the data mining process, plans are underway to incorporate a visual query language, including its syntax and semantics. At present, there is a partial prototype of the Data Mining system. The complete implementation of the same is underway.

# Part III Formal Semantics (Paolo Ciaccia, Giovambattista Ianni, Stefano Lodi,

Luigi Palopoli, Marco Patella, Claudio Sartori

# 8 Metarules interchange format

The meta-language nature of XML allows to easily define interchange formats and new languages. Developers are able to design structured, yet easily readable, formats without difficulty. Nonetheless, XML data may be exchanged through the Internet allowing the introduction of many distributed applications (e.g. SOAP based applications [7]).

The herein introduced MIF (Metarules Interchange Format), is conceived to exchange metarules and metarules' answers, to and from applications intended to deal with metarules for any purpose. The MIF format will be employed in order to allow Visual Interface to easily communicate with Metaquery Evaluation Engine (MEE in the following). Figure 8 depicts the role played by MIF in this context. The Visual Interface produces XML documents, written in MIFIn format. A MIFIn document specifies an evaluation request for a given metaquery. MEE answers to metarules and produces set of instantiated rules in MIFOut format, which can be displayed by the Visual Interface. It is assumed that instantiated rules are generated using type-2 instantiations (see Report D3.R1).



Figure 12: Interaction between Visual Interface and Metaquery Evaluation Engine

**MIF Overview.** Assume a metaquery has to be evaluated. A document in MIFIn format is produced, and submitted for evaluation. For instance, it might look like the following:

```
</variable>
   </metaatom>
 </head>
 <body>
   <metaatom name="Q">
       <unfitRelation>StudDep</unfitRelation>
       <unfitRelation>CourseDep</unfitRelation>
       <variable name="X">
         <fitDataType>integer</fitDataType>
       </variable>
       <variable name="Z">
         <fitAttributeName>Course</fitAttributeName>
       </variable>
   </metaatom>
   <metaatom name="R">
       <fitRelation>StudDep</fitRelation>
       <fitRelation>CourseDep</fitRelation>
       <variable name="Z">
         <fitDataType>integer</fitDataType>
       </variable>
       <variable name="Y">
         <fitAttributeName>Course</fitAttributeName>
       </variable>
   </metaatom>
 </body>
</metaquery>
```

The above MIFIn document expresses the metarule

$$P(X,Y) \Leftarrow Q(X,Z), R(Z,Y) \tag{1}$$

enriched with additional constraints, e.g.

- The minimum required threshold for support and confidence is, 88.35% and 34.23%, respectively;
- The predicate variables P and R may be assigned to the relations StudDep and CourseDep only, whereas the predicate variable Q cannot be matched to the aforementioned relations.
- The variables X and Z can be associated only to integer attributes.
- The occurrences of the variables Y and Z within third and second atom, respectively, can be associated to the attribute Course only.

In general, each MIFIn document contains a <metaquery> tag, which contains two subelements, <head> and <body>. <head> and <body> may contain, respectively, one or many <metaatom> tags, which specify single literal patterns. A <metaatom> tag contains a list of variables denoted by the <variable> tag.

Each tag carries some specific attribute. The <metaquery> tag has the attributes "support" and "confidence", whose value expresses the required threshold level for support and confidence on instantiated answers.

A <metaatom> tag may contain either a sequence of elements of the kind <fitRelation> or a sequence of elements of the kind <unfitRelation>. A sequence of <fitRelation> elements specifies a set of relation names to which the predicate variable at hand can be matched to. A sequence of <unfitRelation> elements specifies a set of relation names to which the predicate variable at hand cannot be matched to, instead. If none of the above sequences are present, a predicate variable may be freely matched to any relation. A <metaatom> contains anyway a list of <variable> tags, which specifies the set of ordinary variables associated to the metaatom at hand.

The meaning of the elements <fitAttributeName> and <unfitAttributeName> contained within the <variable> element is symmetric to the elements <fitRelation> and <unfitRelation> of the <metaatom> tag.

The element <fitDataType> (resp. <unfitDataType>) may be employed in order to specify which data type the variable at hand could be matched to (resp. not matched to). Note that it is possible to employ these statement within any occurrence of the tag <variable>, referring to the variable at hand.

An example of document written in MIFOut format is

```
<?xml version="1.0" encoding="UTF-8"?>
<result xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
    xsi:noNamespaceSchemaLocation="metaOut.xsd">
<rule support="91.00" confidence="38.23">
 <head>
  <atom name="StudDep" >
    <variable name="X" attributeName="Student"/>
    <variable name="Y" attributeName="Dept"/>
  </atom>
  </head>
  <body>
    <atom name="CourseDep" >
      <variable name="X" attributeName="Course"/>
      <variable name="Z" attributeName="Dept"/>
    </atom>
    <atom name="Course">
      <variable name="Z" attributeName="Course"/>
      <variable name="Y" attributeName="CourseName"/>
    </atom>
  </body>
 </rule>
<rule support="95.20" confidence="52.00">
 <head>
  <atom name="Student" >
    <variable name="X" attributeName="Dept"/>
    <variable name="Y" attributeName="Student"/>
  </atom>
  </head>
  <body>
    <atom name="CourseDep" >
     <variable name="X" attributeName="Course"/>
     <variable name="Z" attributeName="CourseID"/>
   </atom>
    <atom name="StudDep">
        <variable name="Z" attributeName="Student"/>
        <variable name="Y" attributeName="Dept"/>
   </atom>
```

```
</body>
</rule>
</result>
```

The MIFOut format is simpler than MIFIn, since it is designed to transport sets of instantiated rules giving necessary details on how instantiations were performed. For instance, the above document encodes the following set of instantiated rules:

$$studDep(X,Y) \iff courseDep(X,Z), course(Z,Y).$$
 (2)

$$student(X,Y) \iff courseDep(X,Z), studDep(Z,Y).$$
 (3)

Additional information are provided in order to specify how variables are matched to attributes. For example, considering rule 2 the occurrence of the variable X within the atom studDep(X, Y) is bound to the attribute Dept of the studDep table.

In general, a document in MIFOut format contains a sequence of rules. Each rule carries a list of variables, and for each variable, it is specified which is the bound attribute. A full specification for the two formats follows.

XML Schemes definition. Two XML Schemes are introduced for the MIFIn and MIFOut format respectively. The two schemes are employed in order to make applications able to easily validate MIFIn and MIFOut formats, using standard parsing tools. The XML-Schema to which the MIFIn format is compliant is:

```
<?xml version='1.0'?>
<xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema">
<rs:element name="metaquery" type="metaqueryType"/>
 <xs:complexType name="metaqueryType">
  <rs:sequence>
   <xs:element name="head" type="headType" minOccurs="1" />
   <rs:element name="body" type="bodyType" minOccurs="0" maxOccurs="1"/>
  </r></r>
  <re><rs:attribute name="support" type="percentageRange"/></re>
  <rs:attribute name="confidence" type="percentageRange"/>
 </xs:complexType>
 <!-- percentageRange is the type of support and confidence allowed -->
 <xs:simpleType name="percentageRange">
 <xs:restriction base="xs:decimal">
    <xs:minInclusive value="0.00"/>
    <rs:maxInclusive value="100.00"/>
  </xs:restriction>
</rs:simpleType>
 <xs:complexType name="headType">
  <rs:sequence>
  <xs:element name="metaatom" type="metaatomType"</pre>
   minOccurs="1" maxOccurs="1" />
  </xs:sequence>
 </xs:complexType>
 <rs:complexType name="bodyType">
```

```
<rs:sequence>
  <xs:element name="metaatom" type="metaatomType"</pre>
   minOccurs="0" maxOccurs="unbounded" />
  </rs:sequence>
</xs:complexType>
<xs:complexType name="metaatomType">
  <xs:attribute name="name" type="xs:NMTOKEN" use="required"/>
  <xs:choice minOccurs="0" maxOccurs="1">
      <xs:element name="fitRelation" type="xs:NMTOKEN"</pre>
        minOccurs="1" maxOccurs="unbounded" />
      <rs:element name="unfitRelation" type="xs:NMTOKEN"
        minOccurs="1" maxOccurs="unbounded" />
  </rs:choice>
  <rs:sequence>
   <rs:element name="variable" type="variableType"
   minOccurs="1" maxOccurs="unbounded" />
  </rs:sequence>
   </xs:complexType>
<rs:complexType name="variableType">
  <xs:attribute name="name" type="xs:NMTOKEN" use="required"/>
  <xs:choice minOccurs="0" maxOccurs="1">
      <xs:element name="fitAttributeName" type="xs:NMTOKEN"</pre>
        minOccurs="1" maxOccurs="unbounded"/>
      <xs:element name="unfitAttributeName" type="xs:NMTOKEN"</pre>
        minOccurs="1" maxOccurs="unbounded"/>
  </rs:choice>
  <xs:choice minOccurs="0" maxOccurs="1">
      <xs:element name="fitDataType" type="xs:NMTOKEN"</pre>
        minOccurs="1" maxOccurs="unbounded"/>
      <xs:element name="unfitDataType" type="xs:NMTOKEN"</pre>
        minOccurs="1" maxOccurs="unbounded"/>
  </rs:choice>
</xs:complexType>
</xs:schema>
  The specification for the MIFOut format is very similar:
<?xml version='1.0'?>
<xs:schema xmlns:xs="http://www.w3.org/2001/XMLSchema">
<rs:element name="result" type="resultType"/>
<xs:complexType name="resultType">
  <xs:sequence>
   <xs:element name="rule" type="ruleType"</pre>
   minOccurs="0" maxOccurs="unbounded" />
  </r></r>
```

</xs:complexType>

```
<rs:complexType name="ruleType">
<rs:sequence>
```

```
<xs:element name="head" type="headType"</pre>
        minOccurs="1" maxOccurs="1" />
   <rs:element name="body" type="bodyType"
        minOccurs="0" maxOccurs="1"/>
  </xs:sequence>
  <re><rs:attribute name="support" type="percentageRange"/></re>
  <rs:attribute name="confidence" type="percentageRange"/>
</xs:complexType>
<!-- percentageRange is the type of support and confidence allowed -->
<xs:simpleType name="percentageRange">
  <xs:restriction base="xs:decimal">
    <rs:minInclusive value="0.00"/>
    <xs:maxInclusive value="100.00"/>
  </xs:restriction>
</rs:simpleType>
<xs:complexType name="headType">
  <xs:sequence>
  <rs:element name="atom" type="atomType"
   minOccurs="1" maxOccurs="1" />
  </xs:sequence>
</xs:complexType>
<rs:complexType name="bodyType">
  <xs:sequence>
  <rs:element name="atom" type="atomType"
   minOccurs="0" maxOccurs="unbounded" />
  </xs:sequence>
</xs:complexType>
<rs:complexType name="atomType">
  <rs:sequence>
  <rs:element name="variable" type="variableType"
     minOccurs="1" maxOccurs="unbounded" />
  </xs:sequence>
  <xs:attribute name="name" type="xs:NMTOKEN" use="required"/>
</xs:complexType>
<rs:complexType name="variableType">
  <xs:attribute name="name" type="xs:NMTOKEN" use="required"/>
  <xs:attribute name="attributeName" type="xs:NMTOKEN" use="required"/>
</xs:complexType>
</xs:schema>
```

The reader may refer to [8] for a detailed reference of the XML-Schema syntax.

# 9 Clustering

In this section we map the visual operators of Part II to abstract clustering functions. The mapping will be associated to an XML-based protocol for exchanging information between the visual component and the clustering component.

The Data Mining Group has recently developed a industrial XML-based standard for the exchange of results between mining applications, named *Predictive Model Markup Language*. The standard is published as a XML DTD specification allowing for the description of a variety of data models, including descriptive statistics, trees, regression, and clustering. Although the specification is almost entirely satisfactory w.r.t. the description of the *result* of a mining task, no provision is made for the description of the input to a mining task, which is by nature algorithm-dependent.

In Section 9.1 we define a XML DTD for the specification of parameters and other information as input by the clustering component. In Section 9.2 we evaluate PMML 2.0 and describe an update which allows for the representation of the results of a clustering task.

## 9.1 An XML DTD for Specifying Clustering Parameters

```
<!ELEMENT D2IClusteringInput ( Header, DataDictionary, MiningSchema,
ClusteringSchema, ComparisonMeasure,
Parameters, AccuracyFunction,
WindowFunction? ) >
```

Figure 13: A DTD for specifying clustering input (root element).

In Figure 13 the root element, D2IClusteringInput, of the DTD for clustering input, is described. The definitions of the elements Header, DataDictionary, and MiningSchema are borrowed from the elements with the same name defined in PMML 2.0, with appropriate changes. Here we will briefly explain the syntax and meaning of such elements. (See the PMML 2.0 specification for more details.)

Header contains optional information about the application which generated the document, such as the application name, annotations, and a timestamp. DataDictionary is a modified version the PMML DataDictionary element and contains information about all the variables of the data set. (See Fig. 14.) DataDictionary is a sequence of one or more DataFields, followed by an IdField element whose name must equal the name of one DataField. For each DataField the data type (categorical, ordinal, or continuous) and the domain of the field, either as interval or by enumeration, are described.<sup>4</sup>

MiningSchema selects the variables that must be present in the result of the clustering task. Notice that this is not the set of active variables; the attribute usageType serves to the purpose of marking active variables, which influence the grouping of objects, and supplementary variables, which do not influence the grouping of objects, but are present in the result for evaluation purposes (e.g. to inspect their statistics). Other attributes of a MiningField describe the treatment of outliers and missing values. Notice that some elements and attributes of DataDictionary and MiningSchema cannot currently be manipulated by the visual interface. However, we include them for in case future versions of the interface support functionalities suited to advanced users.

Now we examine the DTDs which are specific to clustering input. The final elements in D2IClusteringInput allow for the representation of the following parametric information.

- 1. A list of fields which are used in the clustering task (element ClusteringSchema).
- 2. The form of the similarity or dissimilarity function between objects of the data set (element ComparisonMeasure).

<sup>&</sup>lt;sup>4</sup>We omit the element taxonomy, required in PMML 2.0.

```
<! ENTITY
                  % FIELD-NAME
                                               "CDATA" >
<!ELEMENT DataDictionary ( DataField+ , IdField ) >
<! ATTLIST DataDictionary
     numberOfFields
                        %INT-NUMBER;
                                      #IMPLIED
<!ELEMENT DataField ( Interval*| Value* ) >
<! ATTLIST DataField
                   %FIELD-NAME;
                                                        #REQUIRED
     name
                  CDATA
                                                        #IMPLIED
     displayName
     optype
                   (categorical|ordinal|continuous)
                                                        #REQUIRED
     isCyclic
                   (0 | 1)
                                  "0"
<! ELEMENT Value EMPTY >
<! ATTLIST Value
                                CDATA
                                                                 #REQUIRED
     value
     displayValue
                                CDATA
                                                                 #IMPLIED
     property
                                 (valid | invalid | missing)
                                                                 "valid"
<! ELEMENT Interval
                    EMPTY>
<! ATTLIST Interval
     closure
                      (openClosed|openOpen|closedOpen|closedClosed)
                                                                         #REQUIRED
                      %NUMBER;
                                                                         #IMPLIED
     leftMargin
     rightMargin
                      %NUMBER;
                                                                         #IMPLIED
<! ELEMENT IdField EMPTY>
<! ATTLIST Id
                                                           #REQUIRED
                      %FIELD-NAME;
 name
>
```

Figure 14: Data dictionary DTD for clustering input.

- 3. The form and parameters of the clustering problem (element Parameters).
- 4. The accuracy function for clusters (element AccuracyFunction).

ClusteringField (see Fig. 16) specifies, for field named field, the importance fieldWeight to be used in the clustering task, the function compareFunction used to compare the values of field. Notice that extensionally defined compare functions are representable by using the value table of compareFunction and specifying a list of Comparisons elements (not shown here for brevity, see [13]). The elements of ComparisonMeasure (euclidean, squaredEuclidean, chebychev,...) refer to well-known similarity or dissimilarity functions and will not be discussed here.

In Fig. 17 the DTD for the **Parameters** element is described. Clustering can be formally defined as an optimization problem [14] which commonly arises in one of the following two forms. Let  $\mathcal{P}$  be a partition of the data set S and f a function on the set of all partitions of S into  $\mathbb{R}^+$ .

- 1. Given a positive integer K > 1, find the partition  $\mathcal{P}$  of S such that  $f(\mathcal{P})$  is optimal.
- 2. Given a real number  $\theta \in \mathbb{R}^+$ , find the partition  $\mathcal{P}$  of S of minimum cardinality such that  $f(\mathcal{P}) \leq \theta$ .

One of FixedNumberOfClusters and MinimumNumberOfClusters must be specified as elements of Parameters. The attribute numberOfClusters will store the integer K above, as

```
<! ENTITY % FIELD-USAGE-TYPE "(active | predicted | supplementary)">
<!ENTITY % OUTLIER-TREATMENT-METHOD "( asIs | asMissingValues |
                                        asExtremeValues )">
<!ENTITY % MISSING-VALUE-TREATMENT-METHOD "( asIs | asMean | asMode |asMedian |
                                              asValue )">
<!ELEMENT MiningSchema (Extension*, MiningField+)>
<! ELEMENT MiningField (Extension*)>
<! ATTLIST MiningField
     name
                                 %FIELD-NAME;
                                                                     #REQUIRED
     usageType
                                 %FIELD-USAGE-TYPE;
                                                                     "active"
     outliers
                                 %OUTLIER-TREATMENT-METHOD;
                                                                     "asIs"
     lowValue
                                 %NUMBER;
                                                                     #IMPLIED
     highValue
                                 %NUMBER;
                                                                     #IMPLIED
     missingValueReplacement
                                 CDATA
                                                                     #IMPLIED
     missingValueTreatment
                                 %MISSING-VALUE-TREATMENT-METHOD;
                                                                     #IMPLIED
```

Figure 15: DTD for mining schema.

read from the variable in the visual interface's data space which is controlled by the Number of Clusters spin-box. The attribute threshold stores the bound on the value of the function to be optimized ( $\theta$  above). Its value depends on the numeric variables controlled by the sliders Similarity and Dissimilarity in the interface. The value is read from the numeric variable controlled by the slider that is active. The active slider will also determine the choice of the accuracy function. (See below.)

The function f to be optimized usually expresses a measure of either homogeneity or separation. For instance, worst-case (maximum) diameter over all clusters is a measure of homogeneity, whereas worst-case (minimum) split over all clusters is a measure of separation. (The *split* of a cluster is the minimum distance between an object in the cluster and an object not in the cluster.) The Homogeneity element is present whenever the active slider is the Similarity slider. The Separation element is present whenever the active slider is the Dissimilarity slider. Notice that, due to the dependencies between various measures of homogeneity and separation, the clustering component will not accept both specifications (as implied by the syntax). The value attribute of Homogeneity and Separation is used only in representing clustering output (see

```
<!ENTITY % CMP-FCT "(absDiff | gaussSim | delta | equal |
                                                           table)" >
<!ELEMENT ClusteringSchema (ClusteringField+)>
<!ELEMENT ClusteringField ( Extension*, Comparisons? ) >
<!ATTLIST ClusteringField
  field
                                     %FIELD-NAME;
                                                                     #REQUIRED
  fieldWeight
                                     %REAL-NUMBER;
                                                                     #IMPLIED
  compareFunction
                                     %CMP-FCT;
                                                                     #IMPLIED
>
<! ELEMENT ComparisonMeasure (Extension*,
        ( euclidean
                                                | chebychev
                          | squaredEuclidean
        | cityBlock
                          minkowski
                                                | simpleMatching
                                                | binarySimilarity ) )>
        | jaccard
                           tanimoto
```

Figure 16: DTD for clustering fields and comparison measure (simplified).

```
<!ELEMENT Parameters ( FixedNumberOfClusters | MinimumNumberOfClusters ) >
<!ELEMENT FixedNumberOfClusters EMPTY >
<!ATTLIST FixedNumberOfClusters  %INT-NUMBER; #REQUIRED
>
<!ELEMENT MinimumNumberOfClusters EMPTY >
<!ATTLIST MinimumNumberOfClusters
threshold  %REAL-NUMBER; #REQUIRED
>
```

Figure 17: Parameters specification DTD for clustering input.

Section 9.2).

The quantifiers partQuant, clusterQuant, objQuant define the accuracy function in terms of the operators minimum, maximum, sum and average. Not all combinations of the operators are meaningful. The meaningful ones are defined by the entities HOMO-PARTITION-QUANTIFIER, HOMO-CLUSTER-QUANTIFIER, etc. (The definitions operators are not shown for brevity.) For instance, the worst-case diameter function is selected by the element

```
<Homogeneity partQuant="Min" clusterQuant="Min" objQuant="Min"/>
```

and the worst-case split function is selected by the element

<Separation partQuant="Min" clusterQuant="Min" objQuant="Min"/>.

# 9.2 Specifying Clustering Results

Effective visualization of clustering output includes display components auch as scatter plots, object exposition tools, and quality displays (see Fig. ??.)

All information required to draw scatter plots is conveyed by a simple integer function called *clustering array*. A clustering array specifies, for each object identifier, the identifier of the cluster the object has been classified into. To this representation, we may add an optional grouped representation of all the objects in a cluster.

Concerning displays of quality, when evaluating the quality of a clustering task, both interpretability and accuracy have to be considered. The evaluation of interpretability often requires statistical descriptions of clusters, whereas accuracy evaluation is influenced both by the number of clusters and the value of accuracy functions.

The PMML 2.0 ClusteringModel DTD [13] defines two clustering models, a *center based* clustering model, and a *distribution based* clustering model (the latter for demographic clustering). Both models are a sequence of Cluster elements, plus parametric and statistical information. We describe here simple changs in the definition of the ClusteringModel element which support the required information.

**Clustering Array** In Fig. 20 a modified **ClusteringModel** PMML element is represented, which makes provision for an optional clustering array. The **ClusteringArray** is a integer array storing the clustering array of the model. All the values in the array must occur in the target data set as values of the **IdField** which is specified in the clustering input document for the task that generated the model. The **sortType** attribute specifies if the array is sorted. In most applications **ClusteringArray** will be unsorted to facilitate the drawing of a scatter plot. In the cluster display component, objects at positions  $\bar{p}$  and  $\bar{q}$  in the visualization space are depicted in the same cluster if the *i*th and *j*th integers in **ClusteringArray** are equal and the *i*th and *j*th objects in the target dataset (w.r.t. the ordering of **IdField**) are in position  $\bar{p}$  and  $\bar{q}$ . **Descriptive Statistics** Although statistical descriptions are currently not supported by the system, they are already present in PMML. Both in center-based and distribution-based models, the specification allows for utilizing a large number of descriptive statistics. For any mining field, background/per cluster discrete and continuous statistics can be represented, including mean, standard deviation, quantiles, and case frequencies. As a result, the specification supports the comparison of relative frequency counts with respect to a cluster and the entire target data set in the visual interface, e.g. by overlapping pie charts or histograms.

Accuracy Feedback The specification of the Cluster element does not include explicit support of accuracy functions. Consequently, the PMML standard has to be extended to support homogeneity or separation measures. (The computation of these functions in the visual interface would be inefficient.) To this purpose we introduce a new optional element AccuracyFeedback in the Cluster DTD of the PMML specification (see Fig. 21). Notice that it is legal to list an arbitrary number of accuracy functions. This can be helpful in situations where the user is searching for a compromise between different measures of accuracy. The system currently supports only a separation function per clustering task. Therefore, the content of the visual interface variable storing the position on the Separation axis of cluster named name in the Separation View has to be set according to the value attribute of the first AccuracyFeedback | Separation of the Cluster having name = name.

#### 9.3 Example

In Part II a simple example of a data set for the clustering task is presented. Here we extend the example, specifying an XML file for clustering input, which conforms to the D2IClusteringInput DTD, and an XML file for clustering output, which conforms to the modified PMML DTD, whose root element we name D2IClusteringOutput.

In the input document (see Fig. 22), the active variables are the towns' coordinates TwX and TwY. The supplementary variable TwYEst will not influence clustering, but will be in the output document. In ClusteringSchema, we select absolute difference as the function to compare values of each variable. ComparisonMeasure selects Euclidean distance. Parameters and AccuracyFunction select a separation function defined as the worst-case case split over the clusters in the partition.

The output document (see Fig. 23) is the result of applying the well-known single link hierarchical algorithm to the data set, halting at the topmost partition whose single link value is less than three. (It is well known that the single link algorithm finds the optimum solution for the worst-case split function at any level of the hierarchy [14].) For brevity, we omit the background statistics ModelStats and all information which is copied unchanged from the input document. The model describes four clusters named from 1 to 4 in the Cluster elements. Each cluster contains its split value and the maximum distance between its objects, i.e. the cluster's diameter. Finally, a clustering array assigns each object to its cluster: objects that are first and second in TwId to cluster named 1, third, fourth and fifth to 2, sixth and seventh to 3, and the eigth object to the singleton cluster 4.

# 10 Approximate Similarity Queries

The current trend in data mining is to make the data mining process much more interactive. In this light, approximate evaluation of similarity queries can dramatically reduce the time required by the data mining algorithm to produce its results. Quoting from [4]:

The current process is to select parameters, to run a data mining algorithm and, finally, to visualize the result of the algorithm. (The) dramatic performance gains

could open the potential to make this process so fast that a user may change parameters and immediately see the resulting changes in the visualization. Here, it could be beneficial to apply new concepts in database systems which evaluate queries approximately or produce first results in an early stage of processing.

In the following, we will specify how the system is able to support the formulation of approximate similarity queries, whereas, for the visualization of results, the (Overview + Detail) view used for clustering can be adopted. In order to specify the semantics of the visual interface, we adopt the syntax of XUL (XML-based User-interface Language) [24]

#### **Parameter Specification**

In [6, Part III], PAC queries are proposed as a search paradigm for quality-controlled approximate similarity search. In particular, PAC (range and k-NN) queries allow the error on the query result to exceed a certain threshold (indicated by an accuracy parameter  $\epsilon$ ) with a probability not higher than the value of the reliability parameter  $\delta$ . In order to perform a PAC query, the user has therefore to specify a value for the accuracy and the reliability parameters  $\epsilon$  and  $\delta$ . The environment provides two sliders to adjust the values of both accuracy and reliability parameters from a maximum of 100% (exact query) to a minimum application-specific value (e.g. 50% for both parameters).

Each similarity query requires a reference point to be expressed. The choice of a reference point can be performed by using two different modalities:

- 1. By manually entering the coordinates of the point.
- 2. By clicking on a point within a window.

For the former input modality, the system presents a text box where the user can type the coordinates of the point he/she is interested in. As for the latter way of specifying the query point, we rely on the visualization of results from previous data mining tasks. In particular, since results of clustering are more likely to be used than those of meta-querying or association rules, we suppose that the user can select the reference point by clicking on it within the "Clusters" component of the Clustering Output environment (see previous Section).

Finally, the last parameter requested by a PAC query is dependent on the query type. In particular, for k-NN queries the user has to specify the number k of requested result, whereas for range queries he/she has to fix the distance threshold that points in the result should not exceed. The component provides a spin-box for each value, with an alternate input/text-box where the user can type the requested value. Two radio buttons allow the user to specify the type of query he/she is interested in, and to activate the corresponding input box, the other being grayed out. In case that the reference point is graphically chosen by the user by clicking on a point in the Clustering Output environment, the range query threshold can also be specified by dragging within the window to specify the query radius: In this modality, a circle is drawn on the scatter plot, and the value within the input box is changed accordingly, until the user releases the mouse button. Finally, the torch icon is used to specify to the underlying system to actually perform the PAC query on the target dataset based on the specified parameters.

#### Definition of the Interface using XUL

In the following we provide a simple definition of the interface using XUL [24]. It is supposed that the underlying system supplies two methods, namely PAC\_kNN and PAC\_range: In particular:

• PAC\_kNN takes as input a reference point, an integer value k representing the required result cardinality, and the values of the accuracy and reliability parameters  $\epsilon$  and  $\delta$ , and returns a vector of k points.

• PAC\_range takes as input a reference point, a distance value r representing query radius, and the values of the accuracy and reliability parameters  $\epsilon$  and  $\delta$ , and returns a set of points.

In the following, we suppose that the corresponding XBL (eXtensible Bindings Language) file chrome://PAC/content/PAC.xbl is available, containing the code to communicate with the PAC\_kNN and PAC\_range methods. Note that, in this specification, the component defaults to range queries.

The next figure shows the content of the chrome://PAC/content/PAC.xbl file: Three basic event handler are provided:

- kNN This code is executed whenever the user selects the k best matches radio button, and activates the correspondent n. of results input box, while graying out the threshold value input box.
- range This code is executed whenever the user selects the max distance radio button, and activates the correspondent threshold value input box, while graying out the n. of results input box.
- go This code is used to communicate with the underlying system, invoking the PAC\_kNN and PAC\_range methods (that we suppose to be included in the file) with appropriate values for each parameter.

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ELEMENT AccuracyFunction ( Homogeneity   Separation )				
ELEMENT Homogeneity EMPTY				
ATTLIST Homogeneity</th <th></th> <th></th>				
partQuant	%HOMO-PARTITION-QUANTIFIER;	#IMPLIED		
clusterQuant	%HOMO-CLUSTER-QUANTIFIER;	#IMPLIED		
objQuant	%HOMO-OBJECT-QUANTIFIER;	#IMPLIED		
>				
ELEMENT Separation EM</td <td>PTY&gt;</td> <td></td>	PTY>			
ATTLIST Separation</th <th></th> <th></th>				
partQuant	%SEP-PARTITION-QUANTIFIER;	#IMPLIED		
clusterQuant	%SEP-CLUSTER-QUANTIFIER;	#IMPLIED		
objQuant	%SEP-OBJECT-QUANTIFIER;	#IMPLIED		
>				

Figure 18: Accuracy function DTD for clustering input (simplified).

```
<!ENTITY % HOMO-PARTITION-QUANTIFIER "( Max | Sum | Avg )" >
<!ENTITY % SEP-PARTITION-QUANTIFIER "( Min | Sum | Avg )" >
<!ENTITY % HOMO-CLUSTER-QUANTIFIER "( Min | Max | Sum | Avg )" >
<!ENTITY % SEP-CLUSTER-QUANTIFIER "( Min | Max | Sum | Avg )" >
<!ENTITY % HOMO-OBJECT-QUANTIFIER "( Max | Sum | Avg )" >
<!ENTITY % SEP-OBJECT-QUANTIFIER "( Min | Sum | Avg )" >
```

Figure 19: Allowed combinations of quantifiers.

ELEMENT ClusteringModel ( Extension*, MiningSchema, ModelStats?,</th				
:+,				
#IMPLIED				
#REQUIRED				
#REQUIRED				
"unsorted"				

Figure 20: A modified clustering model DTD.

```
<! ELEMENT Cluster (Extension*, (%NUM-ARRAY;)?, Partition?,
                                %Covariances?, AccuracyFeedback?) >
<!ATTLIST Cluster
                                                 CDATA
                      name
                                                                  #IMPLIED >
<!ELEMENT AccuracyFeedback ( Homogeneity | Separation )+ >
<! ELEMENT Homogeneity EMPTY>
<! ATTLIST Homogeneity
  value
                        %REAL-NUMBER
                                                                  #REQUIRED
  clusterQuant
                        %HOMO-CLUSTER-QUANTIFIER;
                                                                  #REQUIRED
  objQuant
                        %HOMO-OBJECT-QUANTIFIER;
                                                                  #REQUIRED
>
<! ELEMENT Separation EMPTY>
<!ATTLIST Separation
                                                                  #REQUIRED
  value
                        %REAL-NUMBER
  clusterQuant
                        %SEP-CLUSTER-QUANTIFIER;
                                                                  #REQUIRED
  objQuant
                        %SEP-OBJECT-QUANTIFIER;
                                                                  #REQUIRED
>
<! ENTITY Objects "( %INT-ARRAY; )">
<!ELEMENT Partition ( PartitionFieldStats+, Objects? ) >
<! ATTLIST Partition
     name
                              CDATA
                                                          #REQUIRED
      size
                              %NUMBER;
                                                          #IMPLIED
>
<!ELEMENT PartitionFieldStats ( %AGGREGATE;, (%NUM-ARRAY;)* ) >
<!ATTLIST PartitionFieldStats
                                field
                                              %FIELD-NAME;
                                                                  #REQUIRED >
```

Figure 21: Accuracy feedback and modified cluster DTD.

```
<?xml version="1.0" ?>
<!DOCTYPE D2IClusteringInput PUBLIC "D2IClusteringInput 1.0" "D2Ici.dtd" >
<D2IClusteringInput version="1.0">
  <Header copyright="The D2I Project. (http://www.dis.uniroma1.it/~lembo/D2I)"/>
  <DataDictionary numberOfFields="5">
    <DataField name="TwID" optype="ordinal"/>
    <DataField name="TwName" optype="categorical"/>
    <DataField name="TwX" optype="continuous"/>
    <DataField name="TwY" optype="continuous"/>
    <DataField name="TwYEst" optype="ordinal"/>
  </DataDictionary>
  <MiningSchema>
     <MiningField name="TwX"/>
     <MiningField name="TwY"/>
     <MiningField name="TwYEst" usageType="supplementary"/>
  </MiningSchema>
  <ClusteringSchema>
    <ClusteringField field="TwX" compareFunction="absDiff"/>
    <ClusteringField field="TwY" compareFunction="absDiff"/>
  </ClusteringSchema>
  <ComparisonMeasure kind="distance">
    <euclidean/>
  </ComparisonMeasure>
  <Parameters>
    <MinimumNumberOfClusters threshold="3" />
  </Parameters>
  <AccuracyFunction>
     <Separation partQuant="Min" clusterQuant="Min" objQuant="Min"/>
  </AccuracyFunction>
</D2IClusteringInput>
```

Figure 22: An example XML document for clustering input.

```
<?xml version="1.0" ?>
<!DOCTYPE D2IClusteringOutput PUBLIC "D2IClusteringOutput 1.0" "D2Ico.dtd" >
<D2IClusteringOutput version="1.0">
 <Header copyright="The D2I Project. (http://www.dis.uniroma1.it/~lembo/D2I)"/>
 <DataDictionary numberOfFields="5"> ... </DataDictionary>
 <ClusteringModel modelClass="distributionBased" numberOfClusters="4">
   <MiningSchema> ... </MiningSchema>
   <ModelStats> ... </ModelStats>
   <ComparisonMeasure> ... </ComparisonMeasure>
   <Cluster name="1">
     <AccuracyFeedback>
       <Separation value="5.39" clusterQuant="Min" objQuant="Min"/>
       <Homogeneity value="1.41" clusterQuant="Max" objQuant="Max"/>
     </AccuracyFeedback>
   </Cluster>
   <Cluster name="2">
     <AccuracyFeedback>
       <Separation value="5.0" clusterQuant="Min" objQuant="Min"/>
       <Homogeneity value="2.0" clusterQuant="Max" objQuant="Max"/>
     </AccuracyFeedback>
   </Cluster>
   <Cluster name="3">
     <AccuracyFeedback>
       <Separation value="3.61" clusterQuant="Min" objQuant="Min"/>
       <Homogeneity value="1.41" clusterQuant="Max" objQuant="Max"/>
     </AccuracyFeedback>
   </Cluster>
   <Cluster name="4">
     <AccuracyFeedback>
       <Separation value="3.61" clusterQuant="Min" objQuant="Min"/>
       <Homogeneity value="0.0" clusterQuant="Max" objQuant="Max"/>
     </AccuracyFeedback>
   </Cluster>
   <ClusteringArray>
     <Array> 1 1 2 2 2 3 3 4</Array>
   </ClusteringArray>
 </ClusteringModel>
</D2IClusteringOutput>
```

Figure 23: An example XML document for clustering output.

```
<?xml version="1.0"?>
<?xml-stylesheet href="chrome://global/skin/" type="text/css"?>
<window id="apprsimq-window" title="Approximate Similarity Queries
Input"
    orient="vertical"
<vbox>
  <hbox>
    <label value="Reference point coordinates:"
control="query-point"/>
   <textbox id="query-point"/>
  </hbox>
  <hbox>
    <radiogroup orient="vertical">
      <radio id="kNN" checked="false" label="k best matches"
        -moz-binding: url('chrome://PAC/content/PAC.xbl#kNN')/>
      <radio id="range" checked="true" label="max distance"
        -moz-binding: url('chrome://PAC/content/PAC.xbl#range')/>
    </radiogroup>
    <vbox>
      <hbox>
        <label value="n. of results:" control="k-value"
disabled="true/>
        <textbox id="k-value" disabled="true/>
      </hbox>
      <hbox>
        <label value="threshold value:" control="r-value"/>
        <textbox id="r-value"/>
      </hbox>
    </vbox>
  </hbox>
<label value="accuracy:" control="eps-value"/>
<scrollbar id="eps-value" align="horizontal" curpos="0" maxpos="100"</pre>
    increment="1" pageincrement="10"/>
<label value="reliability:" control="del-value"/>
<scrollbar id="del-value" align="horizontal" curpos="0" maxpos="100"</pre>
    increment="1" pageincrement="10"/>
</vbox>
<button id="start" class="dialog" image="torch.gif" default="true"
 -moz-binding: url('chrome://PAC/content/PAC.xbl#go'/>
/>
</window>
```



```
<?xml version="1.0"?>
<bindings xmlns="http://www.mozilla.org/xbl">
  <binding id="kNN">
    <handlers>
      <handler event="click"
       action="this.checked=true;
document.getElementById('range').checked=false;
          document.getElementById('k-value').disabled=false;
          document.getElementById('r-value').disabled=true;"/>
    </handlers>
  </binding>
  <binding id="range">
    <handlers>
      <handler event="click"
        action="this.checked=true;
document.getElementById('kNN').checked=false;
          document.getElementById('k-value').disabled=true;
          document.getElementById('r-value').disabled=false;"/>
    </handlers>
  </binding>
  <binding id="go">
    <handlers>
      <handler event="click"
       action="var q=document.getElementById('query-point').value;
          var eps=document.getElementById('eps-value').value;
          var del=document.getElementById('del-value').value;
          var k=document.getElementById('k-value').value;
          var r=document.getElementById('r-value').value;
          if(document.getElementById('kNN').checked) PAC_kNN(q, k,
eps, del);
          else PAC_range(q, r, eps, del);"/>
    </handlers>
  </binding>
</bindings>
```

Figure 25: The chrome://PAC/content/PAC.xbl file containing the code for message handlers in XBL.