Temporary version

RELAIS

Version 2.0

User's Guide

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Index

Introduction

RELAIS (REcord Linkage At IStat) is a toolkit providing a set of techniques for dealing with record linkage projects.

The purpose of record linkage is to identify the same real world entity that can be differently represented in data sources [3], even if unique identifiers are not available or are affected by errors. In statistics, record linkage is needed for several applications, including: enriching the information stored in different datasets; de-duplicating datasets; improving the data quality of a source; measuring a population amount by capture-recapture method; checking the confidentiality of public-use microdata. Starting from the earliest contributions, dated back to 1959 [13], there has been a proliferation of different approaches based on statistics, databases, machine learning, knowledge representation. However, despite this proliferation, no particular record linkage technique has emerged as the best solution for all cases. We believe that such a solution does not actually exist, and that an alternative strategy should be adopted [5]. In fact, record linkage can be seen as a complex process consisting of several phases involving different knowledge areas; moreover, several different techniques can be adopted for each phase. We believe that the choice of the most appropriate technique not only depends on the practitioner’s skill but, most of all, it is application specific. Moreover, in some applications, there is no evidence to prefer a given method to others or of the fact that different choices, at some linkage stage, could bring to the same results. This is why it could be reasonable to dynamically select the most appropriate technique for each phase and to combine the selected techniques for building a record linkage workflow of a given application. RELAIS is a toolkit relying on these ideas.

The principal features of RELAIS are [5, 9, 11, 12]:

It is designed and developed to allow the combination of different techniques for each of the record linkage phases, so that the resulting workflow is actually built on the basis of application and data specific requirements.

It has been developed as an open source project, so several solutions already available for record linkage in the scientific community can be easily re-used. It is released under the EUPL licence (European Union Public Licence).

It has been implemented by using two languages based on different paradigms: Java, an object-oriented language, and R, a functional language. This choice depends on our belief that a record linkage process is composed of techniques for manipulating data, for which Java is more appropriate, and of calculation-oriented techniques for which R is a preferable choice. The choice of Java and R is also in line with the open source philosophy of the RELAIS project.

It has been implemented using a relational database architecture, in particular it is based on a mySql environment that is also in line with the open source philosophy of the RELAIS project.

The RELAIS project aims to provide record linkage techniques easily accessible to not-expert users. Indeed, the developed system has a GUI (Graphical User Interface) that on the one hand permits to build record linkage workflows with a good flexibility. On the other hand it checks the execution order among the different provided techniques whereas precedence rules must be controlled.

The current version of RELAIS provides a set of techniques to execute record linkage applications according to the decomposition described in Section 2.

Add-ons of RELAIS 2.0

With respect to RELAIS version 1.0, RELAIS 2.0 has the following main new features:

- A relational database architecture in order to optimize the performances with respect to the management of huge amount of data.
- Several distance functions for approximate string comparisons. Specifically, matching variables can be compared not only by means of the equality function but also via several other suitable distances (both for numerical and string variables).
- Exact and deterministic decision models are available, to be used either as alternatives or in conjunction with the probabilistic model.
- A data profiling phase in which a set of quality metadata are calculated starting from real data; these metadata help the user in the critical phases of choosing the best blocking or matching variables.

Record Linkage Processes in RELAIS 2.0

The complexity of the whole linking process relies on several aspects of different nature. If unique identifiers are available in the considered data sources the problem can be quite easily treated because its complexity is reduced only to computational constraints. But, generally, unique identifiers are not available and more sophisticated statistical procedures, relying on “matching variables” chosen for linking data, are requested.

However, data sources are often hard to combine since errors or lacking information in the record identifiers may complicate the integrated use of the information, in order to overcome such obstacles record linkage techniques provide multidisciplinary set of methods and practices whose purpose is to identify the same real world entity, which can be differently represented in one or more data sources.

RELAIS aims to join the statistical and computational essence of the linkage problem.

Phases

The idea of decomposing the record linkage process in its phases is the core of the RELAIS toolkit and makes the whole process easier to manage; each phase has its own windows. Now, a general overview on the main phases is given while more details are added later in the specific paragraph devoted to the considered phase.

The main phases (shown in Figure 1) are:

Data cleaning - preparation of the input files (pre-processing);

Choice of the common identifying attributes (matching variables);

Choice of comparison functions;

Search space creation/reduction;

Choice of a decision model;

Record linkage procedures evaluation.

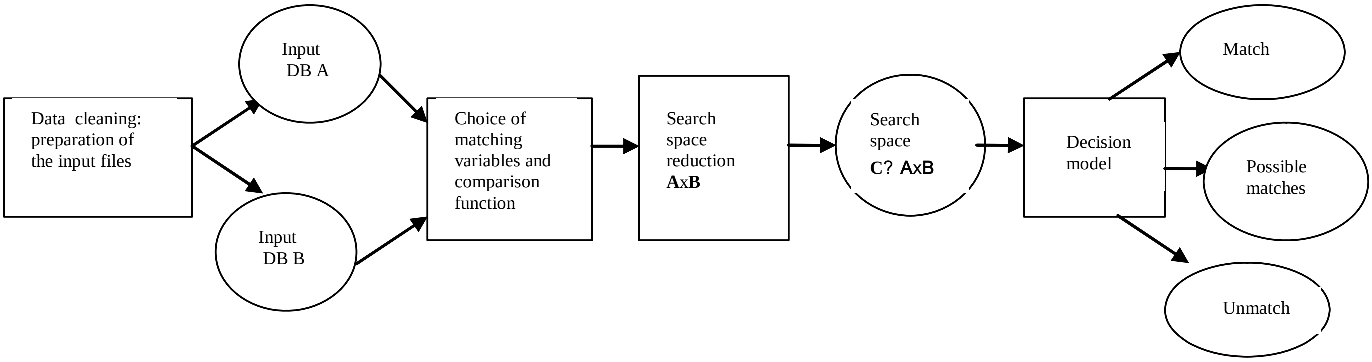


Figure 1: Phases of record linkage

Generally speaking, the *preparation of input files* is the first phase which, according to [14], requires 75% of the whole effort to implement a record linkage procedure, in fact data can be recorded in different formats, some items may be missing or with inconsistencies or errors. The key job of this phase is to convert the input data in a defined format, resolving the inconsistencies in order to reduce errors deriving from an incorrect reported data. In this phase null strings are cancelled, abbreviations, punctuation marks, upper/lower cases, etc. are cleaned and any necessary transformation is carried out to standardize variables. Furthermore the spelling variations are replaced with standard spelling for the common words.

After the previous phase, it is important to *choose matching variables* that are as suitable as possible for the considered linking process. The matching attributes are generally chosen by a domain expert; in Relais 2.0 a set a metadata support the users in the choice of matching attributes. If unique identifiers are available in the linkable data sources, the easiest and most efficient way is to use these ones as link variables; but very strict controls need to be made in case of using numeric identifiers alone. Variables like *name*, *surname*, *address*, *date of birth*, can be used jointly instead of using each of them separately; in such a way, one can overcome problems like the wide variations of the *name* spelling or the changes in *surname* depending on the variability of the marital status. It is evident that the more heterogeneous are the items of a variable, the higher is its identification power; moreover, if missing cases are relevant in a field it is not useful to choose it as a matching variable.

C*omparison functions* are used to compute the distance between records on the values of the chosen matching variables.

In a linking process of two datasets, say *A* and *B*, the pairs needed to be classified as matches, non-matches and possible matches are those in the cross product *A x B*. If a de-duplication problem is considered the space is *A x (A-1)/2*. When dealing with large datasets, comparing all the pairs (*a; b*), *a* belonging to *A* and *b* belonging to *B*, in the cross product is almost impracticable, in fact while the number of possible matches increases linearly, the computational problem raises quadratic, being the complexity $\boldsymbol{O}(n^2)$ [15]. To reduce this complexity it is necessary to reduce the number of pairs ($a; b$) to be compared. There are many different techniques that can be applied to reduce the search space; blocking and sorted neighbourhood are the two main methods. *Blocking* consists of partitioning the two sets into blocks and of considering linkable only records within each block. The partition is made through blocking keys; two records belong to the same block if all the blocking keys are equal or if a hash function applied to the blocking keys of the two records gives the same result. *Sorted neighbourhood* sorts the two input files on a blocking key and searches possible matching records only inside a window of a fixed dimension which slides on the two ordered record sets.

Starting from the reduced search space, we can apply different decision models that define the rules used to determine whether a pair of records ($a; b$) is a match, a non-match or a possible match.

The core of a record linkage process is the *choice of a decision model* that enables to classify pairs into M, the set of matches and U, the set of non-matches. The decision rule can be empirical or probabilistic. In the deterministic approach, a pair is a match if it agrees completely on all the matching variables chosen or satisfies a defined rule-base system, that is if it reaches a score that is beyond a threshold when applying the comparison function.

The probabilistic approach, based on the Fellegi and Sunter model [4], requires an estimation of the model parameters that can be performed via the EM algorithm, Bayesian methods, etc.

A linkage process can be also classified as: (i) one-to-one problem, if one record in the set A links to only one record in B and also the other way around, (ii) one-to-many problem if a record in a set can be matched with more than one of the compared file, (iii) many-to-many problem if more than one record in each file match with more than one record in the other. The latter two problems may imply the existence of duplicate records in the linkable data sources.

Finally, as not every record matched in the linkage process refers to the same identity, in "the record linkage procedure evaluation", it's important to establish whether a match is a "true one" or not. In other words, during a linkage project is necessary to classify records as true link or true non link, minimizing the two types of possible errors: false matches and false non-matches. The first type of error refers to matched records which do not represent the same entity, while the latter indicates unmatched records not correctly classified, that imply truly matched entities were not linked.

RELAIS 2.0 Techniques

Each of the phases described in the previous section can be performed according to different techniques; depending on specific applications and features of the data at hand, it can be suitable to iterate and/or omit some phases, as well as it could be better to choose some techniques rather than others. In the current version, RELAIS provides some of the most widespread methods and techniques for the following phases:

Choice of matching variables

Choice of comparison functions

Creation and reduction of the search space of link candidate pairs

Choice of the decision model

Selection of unique links

In the following, for each of the implemented phase, we briefly detail the available techniques.

1.1.1 Phase 1: Choice of Matching Variables

The choice of identifying attributes (or matching variables) is supported by a set of metadata that can assist RELAIS's users in this task. The set of metadata currently available are:

- Completeness
- Accuracy
- Consistency
- Entropy
- Correlation
- Frequency Distributions

In Section 0 the meaning and usage of each metadata are detailed.

1.1.2 Phase 2: Choice of Comparison Functions

In the current version of RELAIS, several comparison functions are available, namely:

- Equality
- Numeric Comparison
- 3Grams
- Dice
- Jaro
- JaroWinkler
- Levenshtein
- Soundex

In Section 0 the details of such functions are introduced.

1.1.3 Phase 3: Creation and Reduction of the Search Space of Link Candidate Pairs

A first functionality that RELAIS 2.0 makes available is the creation of the search space of the pairs to be linked by means of:

- Cartesian Product

A reduction of the search space can be performed by means of two available techniques, namely:

- Blocking
- Sorted Neighborhood
- Both techniques need the setting of blocking variables. Such a choice is supported by a set of metadata, partially overlapping with those available for the choice of the matching variables. These are:
- Completeness
- Accuracy
- Consistencies
- Categories
- Frequency Distributions
- Blocking Adequacy
- Entropy

In Section 0, a detailed discussion on such metadata is available.

1.1.4 Phase 4: Choice of Decision Model

Two kind of decision models are currently available in RELAIS, namely *deterministic* and *probabilistic*.

The deterministic model, about which details are discussed in section 0, includes:

- Exact matching
- Rule-based matching

The probabilistic model consists of an implementation of the:

- Fellegi-Sunter decision model [4]

The details of this model are in Section 0.

1.1.5 Phase 5: Selection of Unique Links

In this phase a reduction from a matching M:N to a matching 1:1 can be performed. The techniques currently available are:

- Optimal 1:1 linkage on Fellegi-Sunter output
- Greedy 1:1 linkage on Fellegi-Sunter output
- Optimal 1:1 linkage on Rule-based Matching
- Greedy 1:1 linkage on Rule-based Matching

Details on the selection of unique links phase are in Section 0.

Examples of Record Linkage Workflows

RELAIS is based on the consideration that every record linkage process is application dependent. As seen in the previous section, we can consider the whole process decomposed in its constituting different phases; for each phase we can choose between the available techniques or on the basis of a suitable decision model. For instance, choosing the decision model to apply is not immediate: the probabilistic one can be more appropriate for some applications but less appropriate for others, for which an empirical decision model could prove more successful.

Indeed, the available tools do not provide a satisfying answer to the various requirements that different applications can exhibit. So the RELAIS toolkit is composed by a collection of techniques for each of the singled phase that can be dynamically combined in order to build the best record linkage workflow, given the application constraints and data features provided as input (see Figure 2).

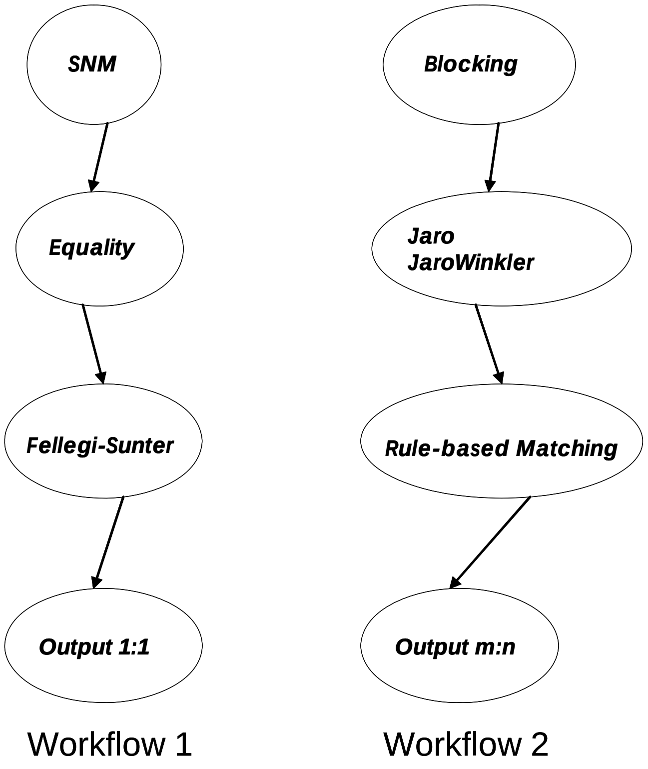


Figure 2: Examples of record linkage workflows

Installation

In this section we present the details to install Relais 2.0 both in Windows environment and in Linux environment.

Windows Environment: Requirements

To run RELAIS 2.0, Java, R and mySql environments must have been installed. More precisely:

Java 2 Runtime Environment (J2SE) 6.0 with at least JDK 6.0.x

mySql server environment (www.mysql.com)

mySql Odbc 5.x Driver or higher

R 2.6 or higher

R package “lpSolve” 5.5 or higher

R package “RODBC”

It is important to verify that the system variable PATH contains the Java.exe, R.exe and mysql.exe paths.

The PATH variable can be found browsing the menu (in the XP Windows Operating System):

Start → Settings → Control Panel → System → Advanced → Environment variables

To modify the system variable PATH it is necessary to be PC administrator.

If different version of Java and/or R are installed on the PC, the new paths of Java and/or R must be written in the PATH variable string before the paths of the previous version; we recommend to insert the new paths at the beginning of the PATH variable.

An example of how to set the PATH variable follows:

```
PATH=C:\Programs\Java\jre1.6.0_03\bin;C:\Programs\R\R-2.5.1\bin;C:\Programs\mysql\MySql Server 5.0\bin
```

Finally, it is important to check that the operating system is updated at least to Service Pack 2. To verify this requirement, click with the right button of the mouse on the Computer Resources icon and select the Properties menu, in the General menu is described the Service Pack version currently installed. If an update is needed, just click on the Windows Update icon (on the Start menu) and follow the instructions.

Windows Environment: Installation and Execution

To install RELAIS 2.0, starting from the setup_RELAIS.exe file, just execute this file and follow the instruction. The directory, in which Relais 2.0 has been installed, will contain the following files:

Relais.bat

Relais.jar

mu_gen_embedded.R

LP.R

and the lib directory which contains the file my-sql-connector-java-5.1.6-bin.jar that is necessary for the connection to the database.

To run the program just double click on the Relais.bat file.

While installing mySql environment it is necessary to create an anonymous account besides the system account.

After the installation it is necessary, for using RODBC package, to create a new data source. After creating relais data base in mySql environment, browse the menu (in the XP Windows Operating System):

Start → Settings → Control Panel → Adminitration Tools → Data Sources (ODBC)

In the window that will be opened the User DSN menu must be chosen; in this menu clicking on the Add button, a new window will be open, in this window the mySql ODBC driver must be chosen. In the new window that will be opened, the following settings must be done:

data source = relais

server = localhost

database = relais

To install R packages, run the R environment and browse the menu:

Packages → Install packages

After choosing a CRAN, a list of packages will be displayed. In this list, click on the lpSolve package and on the RODBC package[1].

---

[1] If there are problems to reach a CRAN, click with the right button of the mouse on the R icon and select the Properties menu, in the Connection menu write `–internet2` at the end of the destination. For example:

C:\Programs\R\R-2.8.1\bin\Rgui.exe –internet2.

Linux Environment: Requirements

To run RELAIS 2.0, Java, R and mySql environments must have been installed. More precisely:

Java 2 Runtime environment (J2SE) 6.0 with at least JDK 6.0.x

mySql server environment (www.mysql.com)

mySql Odbc 5.x Driver or higher

R 2.6 or higher

R package "lpSolve" 5.5 or higher

R package "RODBC"

Linux Environment: Installation and Execution

To install RELAIS2.0 starting from the RELAIS2.0.zip file, it is necessary to unzip this file in a directory, for example C:\RELAIS. This directory will contain the following files:

Relais.bat

Relais.jar

Mu_gen_embedded.R

LP.R

and the lib directory which contains the file my-sql-connecotr-java-5.1.6-bin.jar that is necessary for the connection to the database.

During the installation of mySql environment it is necessary to create the user "root" specifying a password. Moreover, it is necessary to create an anonymous user "" giving him all the grants on the following schemas:

information_schema

mysql

relais

Thus the relais schema must have been created using the instruction:

CREATE DATABASE relais

It is important to notice that the data base name relais **must be** written in lower cases being the Linux operating system case sensitive.

If no specific knowledge about the Linux operating system is held, it could be useful to install the mySql Gui tool that gives a graphical interface to the data base and make easier to perform all the operations described below.

Moreover, it is important to check that the libmyODBC library has been installed, this library contains the header necessary for a correct running of mySql.

Moreover, the libraries:

unixODBC_dev

unixODBC

must have been installed, these are necessary to connect to the data base starting from a R program.

Finally, it is necessary to modify the hidden file .ODBC.ini (that can be found in the own home folder) writing the following instructions:

```
[ODBC Data Sources]

relais =  Connector/ODBC 3.51 Driver DSN

[relais]

Driver = /usr/lib/odbc/libmyodbc.so

Description = Connector/ODBC 3.51 Driver DSN

Server = localhost

DSN = relais

Port = 3306

User =

Password =

Database = relais

ServerType = MySql

Option  =

TraceFile = /var/log/mysql_test_trace.log

Trace = 0
```

To run the program just use the following command:

```
java –jar relais.jar
```

or after changing the Relais.bat file making an executable file (chmod 777 Relais.bat), just double click on the Relais.bat file icon.

To install R packages, run the R environment and write the instruction:

```
install.packages(“name_of_package”, dependencies=TRUE)
```

For example, to install lpSolve package write the following instruction:

```
install.packages(“lpSolve”, dependencies=TRUE)
```

The RELAIS Menu

As shown in Figure 4, the RELAIS menu is composed by the following items:

Project

Dataset

Data Profiling

Search Space Creation

Decision Model

Linkage 1:1

Linkage Result

Save

Utility

In following sections, each of this menu will be detailed.

Project

Connection items are listed in the Project menu as shown in Figure 3.

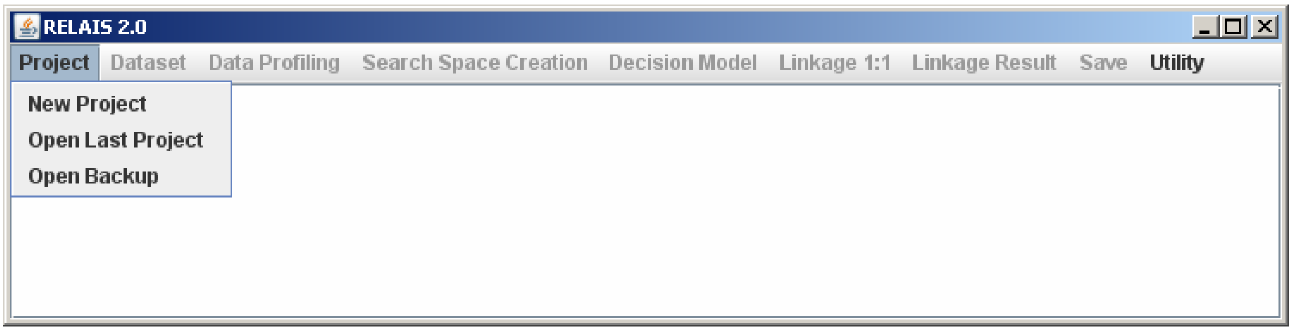


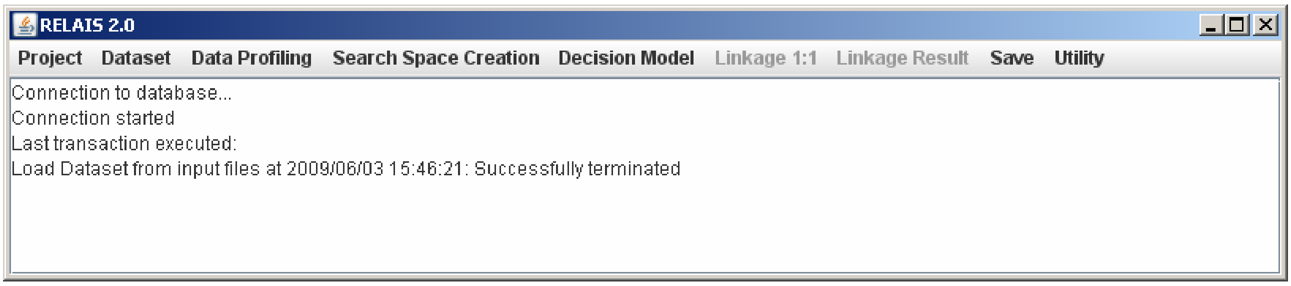
Figure 3: Project menu

Choosing the New Project item the internal database is initialized removing the content of the current repository.

Thus choosing this option, the new connection refers to an empty database.

This operation is required in first run of the software.

Choosing the item Open last project a new connection to the database is performed without removing the content of the repository which is up-to-date to the last run exit and the last transaction is returned on the output window (see Figure 4).



```
Connection to database...
Connection started
Last transaction executed:
Load Dataset from input files at 2009/06/03 15:46:21: Successfully terminated
```

Figure 4: Connection to database

Choosing the item Open backup, the window shown in Figure 5 will be open. This window allows to choose and to restore a process, previously saved as internal backup (see Section 0). By choosing this functionality, the content of the repository is removed and a connection starts to the repository initialized with the content of the chosen process.

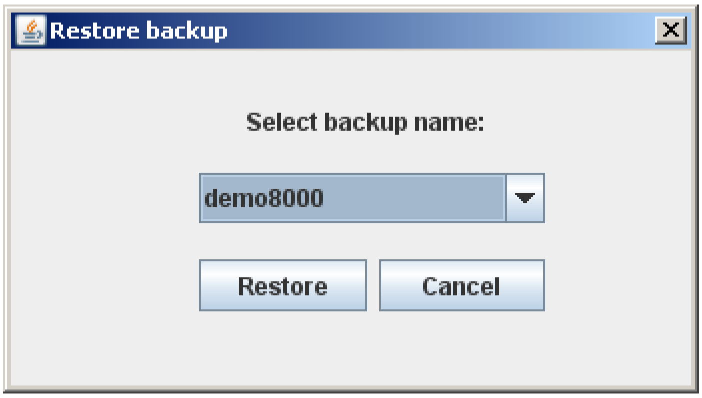


Figure 5: Selection of a backup

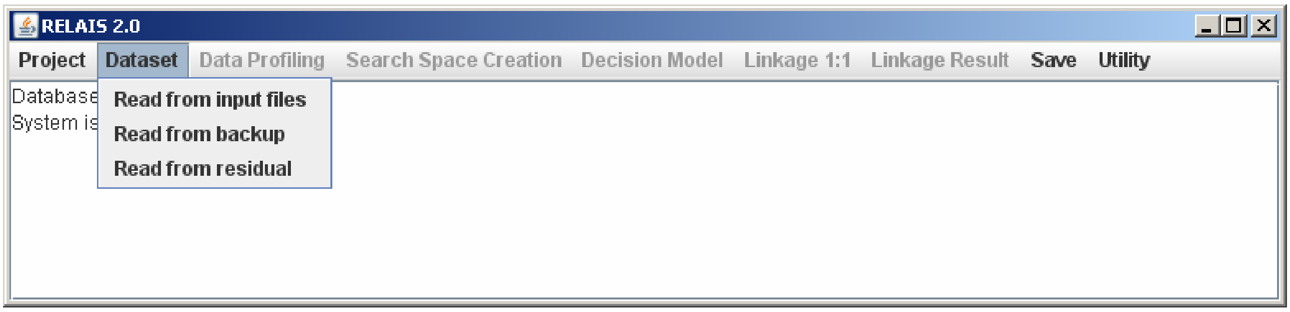
Dataset

The Dataset menu lists the different methods available to load the two input data sets. As shown in Figure 6 these methods are:

Read from input files

Read from backup

Read from residual



Database
System is

Figure 6: Dataset menu

Choosing Read from input file menu, the window shown in Figure 7 will be open. This window allows to insert the input file paths and to specify, for each of them, a field separator character. This character can be specified by the user or selected among those listed.

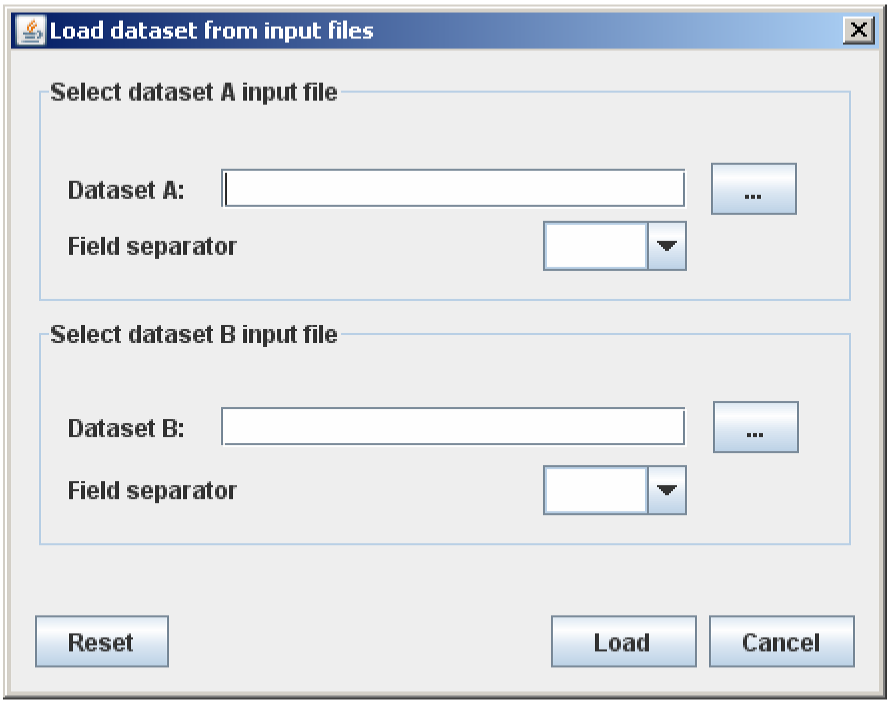


Figure 7: Selection of input datasets

Each data set must be a text file. The new line character defines each single record in the data set, the separator character defines unambiguously the limits of each variable in a record, thus the separator character cannot appear as part of a variable value. Moreover, the separator character has to be unique in all the data set.

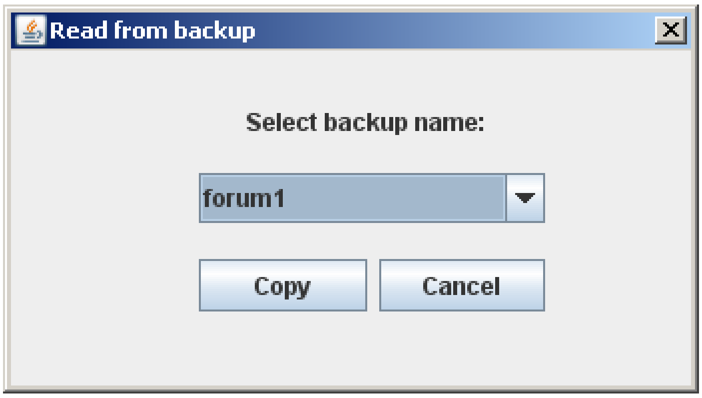
Note: The use of a space as field separator is allowed. It is necessary to insert the space character in the Field separator combo box.

The first record must specify the data set schema. The two data set schemas can be different but must contain a set of common variables that are used in the following phases of a record linkage process. The common variables must have the same name, it is important to notice that the whole data set is case sensitive.

The common variables are detected in a phase called schema reconciliation.

In the reading phase, unique identifier are added for each data set named respectively key_dsa for the data set A and key_dsb for the data set B.

Choosing the Read from backup menu, the window shown in Figure 8 will be open. In this window is possible to choose an internal backup, previously saved (see Section 0), to be used to restore the input data set.



Select backup name: forum1

Figure 8: Selection of internal backup

Choosing the Read from residual menu, a window similar to the one shown in Figure 8 will be open. In this window is possible to choose the residual results of a process previously saved, to be used as current input datasets.

After the Dataset reading phase the following tables are created in the database:

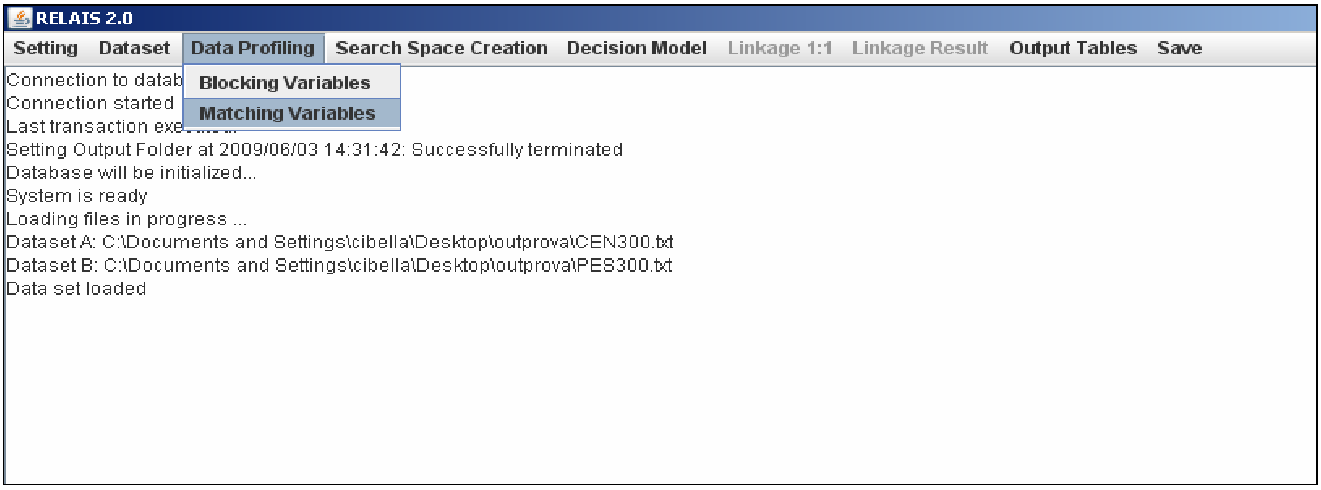
DSA : contains the dataset A with the generated variable key_dsa;

DSB : contains the dataset B with the generated variable key_dsb;

RECONCILED_SCHEMA : contains the list of the common variables between the two data sets.

Data Profiling

To give the opportunity to the user of designing the record linkage workflow more appropriate for the application at hand, RELAIS 2.0 toolkit supplies a data profiling phase in which a set of quality metadata are calculated starting from real data provided as input; these metadata help the user in the critical phase of choosing the best blocking or matching variables among those available and common to the two datasets. Moreover, in order to come towards needs of non-skilled users, RELAIS proposes also a default set of parameters, coming from communities and manuals, to help the decision-making stages.



```
Connection to datab
Connection started
Last transaction exe
Setting Output Folder at 2009/06/03 14:31:42: Successfully terminated
Database will be initialized...
System is ready
Loading files in progress ...
Dataset A: C:\Documents and Settings\cibella\Desktop\outprova\CEN300.txt
Dataset B: C:\Documents and Settings\cibella\Desktop\outprova\PES300.txt
Data set loaded
```

Figure 9: The data profiling menu

Methodological Aspects

The choice of the indicators for helping not expert users in selecting the variables most suitable for the record linkage process is not easy. As stated above, the process is very complex and we identify some essential indicators which could be helpful in the choice.

All the measures vary in the interval between 0, the minimum and the worst values, and 1, the highest and the best for the selected indicator. The indicators are calculated separately for the two data sets considered and for more than one variable, depending on the choices adopted by the user.

For each of the selected variables the toolkit outputs the values of the picked out indicators.

It’s important to underline that we consider a set of indicators both suitable for selecting the blocking and the matching variables but, as the aims of the selection are different, there are also some measures that differ.

In particular, the indicators common in the selection of blocking and matching variable are:

completeness;

accuracy;

consistency;

categories;

frequency distribution;

entropy.

In detail, the *completeness* (1) is the proportion of non-missing records on the overall (N_A or N_B) for the considered variable in dataset A and B, respectively. A completeness equal to 1 means no missing value in the variables (blocking or matching one).

The *accuracy* (2) implies the comparison of the recorded value of a variable with a dictionary or a set of reference values that are known to be correct for the variable; this measure provides the number of correct - not out of range - values on the overall.

The *consistency* (3) gives information on how well each item of the selected variable relates to the items of a selected variable (e.g. province and region). It is necessary to indicate the variable that you want to compare the item with and to give the set of values that the associated variable can assume.

The *categories* (4) report the number of different categories in the selected variable for both datasets, A and B.

The *frequency distribution* (5) returns in output the tables (for A and B) related to the frequency distribution of the variable, sorted by frequency.

The *entropy* (6) calculates the Gini index for the selected variables, both for A and B datasets. An index equal to 0 means that all the frequencies are concentrated in a single item of the variables, instead, a value of the index equal to 1 means a complete heterogeneity in the variable (all the *i* items have the same relative frequencies, $f_{i=}1/K$). The formula adopted is:

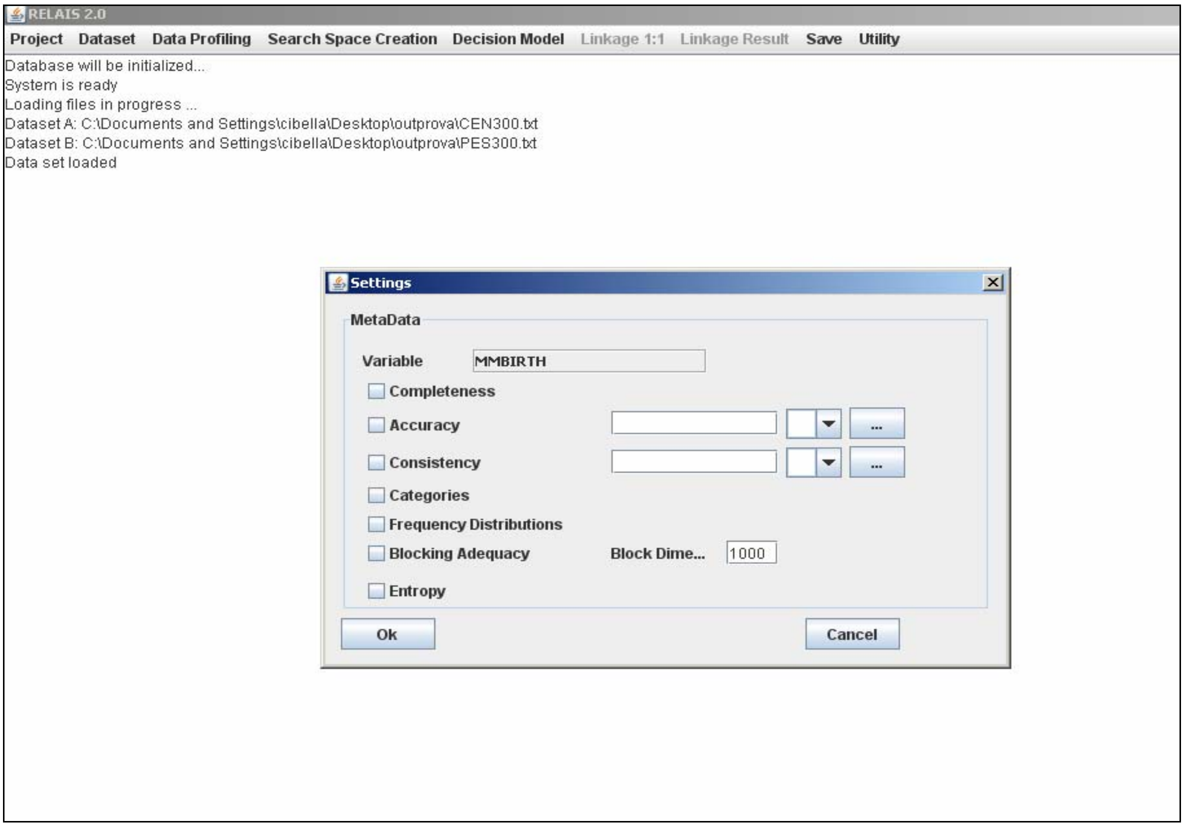
$$G = -\sum_{i=1}^{K} f_i \log_K f_i$$

where i , i = 1,2,..K, are the items of the selected variable.

Diagnostics for Selecting Blocking Variables

In order to reduce the search space of the candidate pairs, the most suitable variables are generally those most discriminating and accurate, i.e., not affected by errors or missing values. Usually, variables as zip code, municipality, geographic area, year of birth can be chosen as blocking variables when dealing with individual records. Then, links are searched only within the blocks, assuming that there are no matches out of them; therefore, if the blocking variable is error affected, some true links could be missed. Furthermore, it is useful to avoid blocking variables which create too small groups (i.e. blocking variable with a large amount of values) in order to reduce risk of errors in the blocking variable; in addition, also blocking variables which create too large groups must be avoided, generally because they do not allow to reduce enough the search space.

Generally speaking, it is suitable to create blocks of the same size, selecting one or more variables, which present a consistent number of values uniformly distributed among the units (for instance, the day and month of birth).



```
Database will be initialized...
System is ready
Loading files in progress ...
Dataset A: C:\Documents and Settings\cibella\Desktop\outprova\CEN300.txt
Dataset B: C:\Documents and Settings\cibella\Desktop\outprova\PES300.txt
Data set loaded
```

Variable MMBIRTH

☐ Completeness

☐ Accuracy

☐ Consistency

☐ Categories

☐ Frequency Distributions

☐ Blocking Adequacy Block Dime... 1000

☐ Entropy

Figure 10: Blocking variable indicators

Beside the above mentioned indicators, in case of the blocking variable selection we can also consider the *blocking adequacy* measure (see Figure 10).

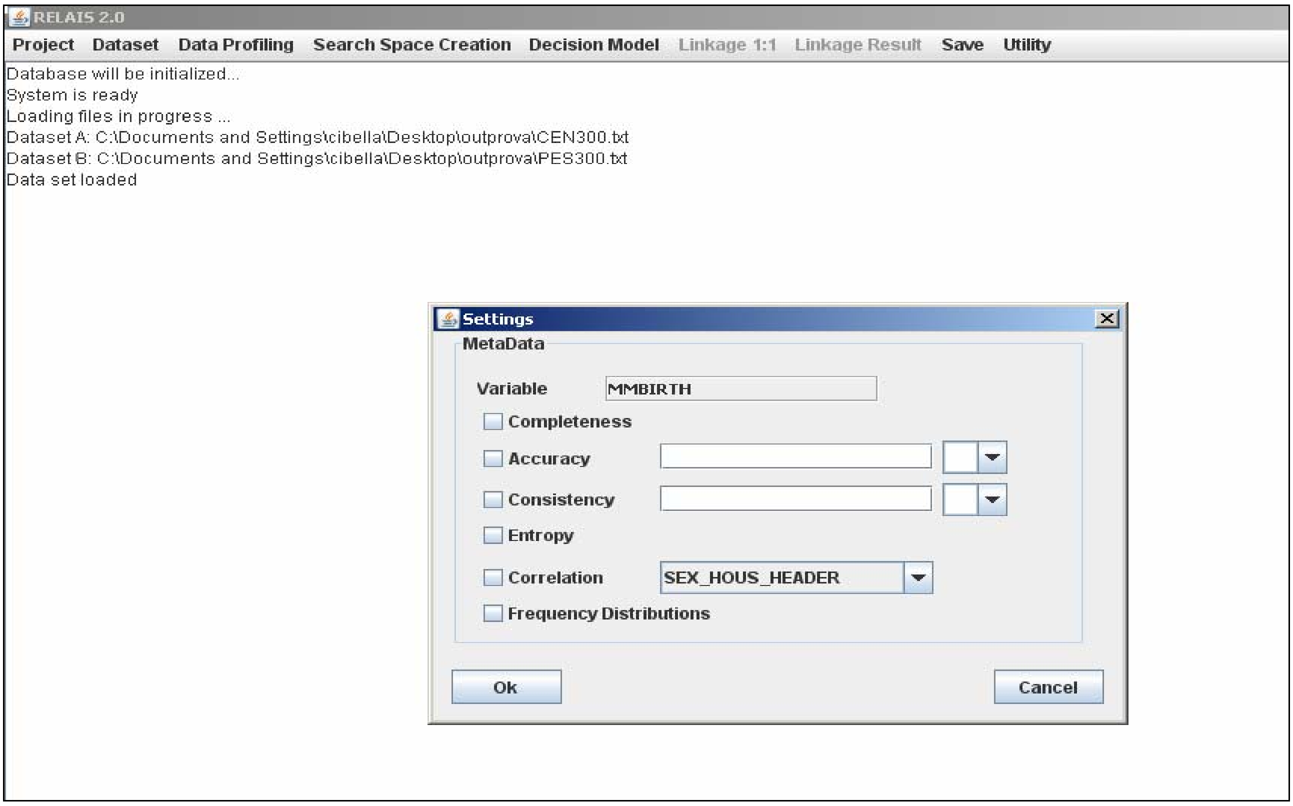
The indicator of the *blocking adequacy* gives, in case of the selection of a certain variable, the proportion of *blocks* under a fixed threshold *(the default one is 1.000)* on the overall. A blocking adequacy indicator equal to 1 means that all the modalities of the selected variable create blocks below the fixed threshold.

Diagnostics for Selecting Matching Variables

Generally speaking, the matching variables determine if a pair of records identifies or not the same unit. As for the blocking variables, also for the matching ones, it is suitable to select those with a high identification power and a low error and missing rates.

The identification power of a variable increases according to its different values and depends on the distribution of these values among the units: when a variable has a large number of categories, but few of these are much more frequent than others, it would be useless to select them as matching variables, e.g. the surname Rossi can be more frequent than some other surnames. The larger the number of categories of a variable is, the higher is its discriminative power.

The indicators that can be calculated in order to have a suggestion useful to the selection are those indicated in Figure 11 and described in Section 0.



```
Database will be initialized...
System is ready
Loading files in progress ...
Dataset A: C:\Documents and Settings\cibella\Desktop\outprova\CEN300.txt
Dataset B: C:\Documents and Settings\cibella\Desktop\outprova\PES300.txt
Data set loaded
```

Variable MMBIRTH

☐ Completeness

☐ Accuracy

☐ Consistency

☐ Entropy

☐ Correlation SEX_HOUS_HEADER

☐ Frequency Distributions

Figure 11: Matching variable indicators

In case of the probabilistic model implemented in the current version of RELAIS, in order to identify the model parameters, at least three matching variables must be selected. Furthermore, the adopted model assumes the conditional independency of the matching variables with respect to the matching status. In general, the correct identification of the links depends on the number of matching variables but, at the same time, if strongly correlated variables or variables with correlated errors are included in the model, the estimates could be not reliable, thus increasing the values of the matching weights without improving the identification of the links. For this reason, also the correlation indicator are calculated.

The *correlation* measures the relationship between the selected variable and another one, picked up by the users among all the remaining variables.

The formula for the index is :

$$C = 1- \sqrt{\frac{\sum_{i=1}^{k}\sum_{j=1}^{h}\frac{n_{ij}^{2}}{n_{i.}n_{.j}}}{\min\{(k-1),(h-1)\}}}$$

where i and j are the items of the first and the second chosen variables, i=1,2…,k and j=1,2,…,h

n_{ij} is the joined observed frequency of the i-th and j-th items and $n_{i.}$ ($n_{.j}$) is the observed marginal frequency of the i-th (j) item.

Creation and Reduction of the Search Space

The search space of the candidate pairs is naturally formed by the cross product of the records stored in each input file. The functionality that implements the cross product is described in Section 0. Section 0 introduces the problem of reducing the search space. In Section 1.1.6 the blocking strategy is described, while Section 1.1.7 introduces the sorted neighbourhood method.

Methodological aspects

In a linking process of two datasets, say *A* and *B*, the pairs needed to be classified as matches, non-matches and possible matches are those in the cross product *A x B*. In case we're considering the de-duplication problem the space is *A x (A-1)/2*. Many problems arise when dealing with large data-sets, connected with both computational and statistical aspects (see Section 0). To reduce this complexity it is necessary to reduce the number of pairs (*a; b*), *a* belonging to *A* and *b* belonging to *B* so as to have a set of pairs of manageable size. Starting from this reduced search space, we can apply different decision models that define the rules used to determine whether a pair of records (*a; b*) is a match, a non-match or a possible match.

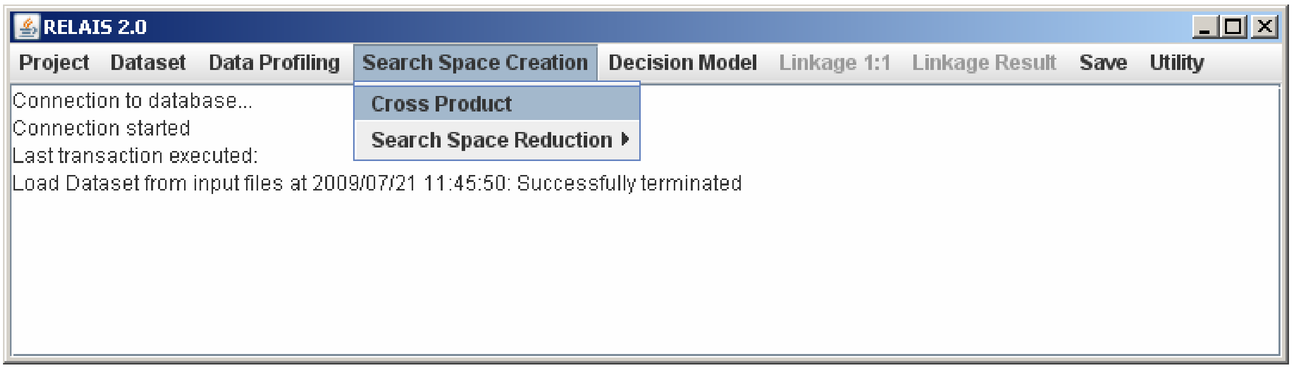
Search Space Creation

The cross product is a functionality that can be selected after reading the input data sets.

It is important to note that, when the search space size is "huge" (e.g., as a general indication formed by more than 25,000 millions of pairs, with original data sets, each of 5,000 records), it is not suitable to create the overall search space via the cross product, while one of the reduction methods described in Sections 1.1.6 and 1.1.7 is suggested.

Figure 12 shows how to select the cross product option browsing the menu:

Search Space Creation -> Cross Product



Connection to database...
Connection started
Last transaction executed:
Load Dataset from input files at 2009/07/21 11:45:50: Successfully terminated

Figure 12: Selection of the cross product

Search Space Reduction

In some linkage applications, the search space reduction can be useful for two different reasons.

First of all, when managing huge amount of data, it can be useful to reduce the execution time and the used memory space by means of a suitable partition of the entire space of pairs coming from the cross product of the input files.

Second, if a probabilistic record linkage approach is used, there can be statistical problems in dealing with huge amount of data. In fact, the probabilistic models, generally used in order to estimate the conditional probabilities of being link or being non-link, do not allow to correctly identify such probabilities when the number of possible links is too small with respect to the whole set of candidate pairs. The statistical problem can be overcome by means of the creation of suitable groups or partitions of the whole cross product set of pairs, so as in each sub-group the number of expected links is not much smaller than the number of candidate pairs. In particular, when the conditional probabilities are estimated via the EM algorithm, as in the current version of the probabilistic decision model implemented by RELAIS, some authors [10] suggest to apply some reduction of the pairs space so that the expected number of links is not below 5% of the overall compared pairs.

Among the several reduction techniques, the current version RELAIS provides the Blocking method and the Sorted Neighbourhood Method. The first step required in RELAIS is the selection of the variables for the reduction. This task can be supported by the data profiling activity (See Section 7).

1.1.6 Blocking

An easy way to reduce the search space is to restrict the comparisons only to the pairs that report the same values for the selected blocking variables.

The blocking step requires the selection of the blocking variables, after which the creation of blocks is automatically performed.

To select the blocking variable, browse the menu:

Search Space Creation → Search Space Reduction → Blocking

Figure 13, shows the window that is opened to select the blocking variable.

After the execution of the blocking step, a Block_Modality table is created that reports information on the number of created blocks and on their sizes, as shown in Figure 14.

The table can be visualized by selecting:

Utility → Table Display

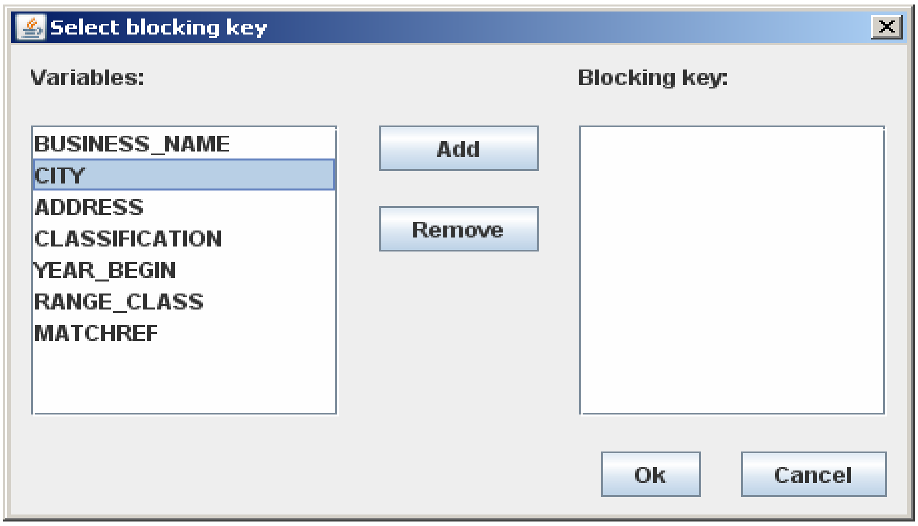
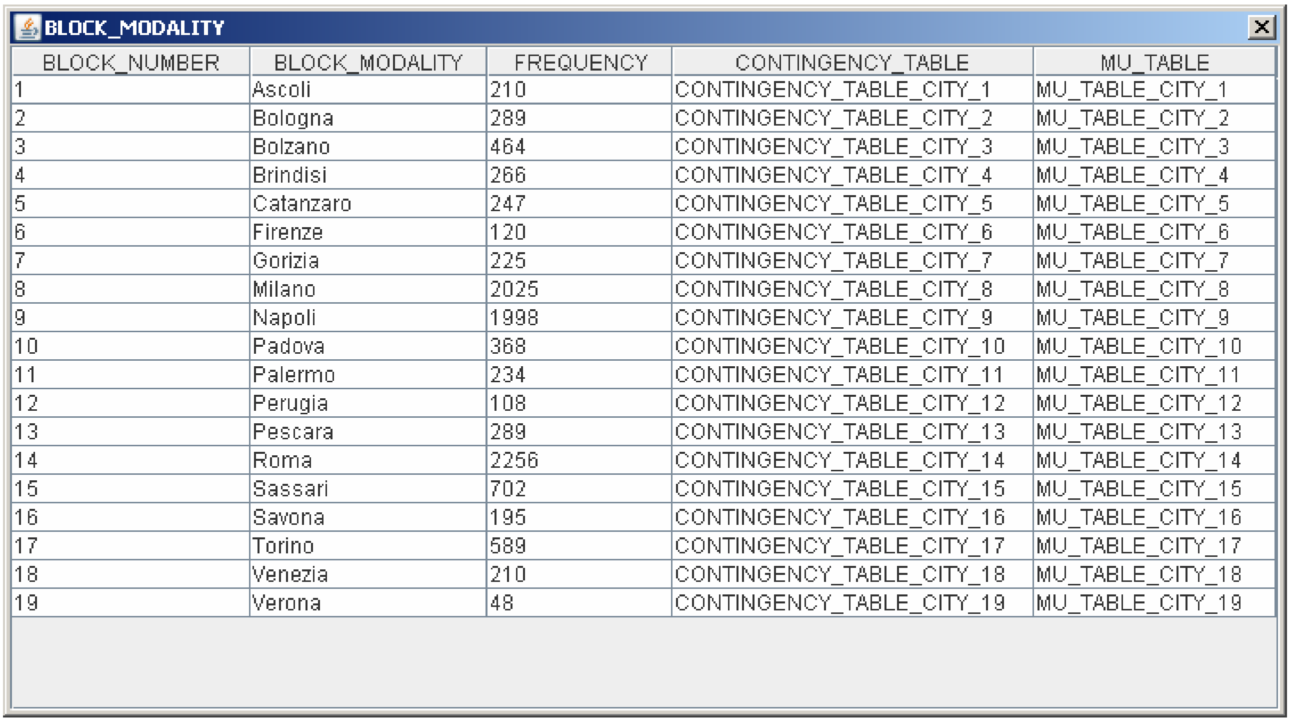


Figure 13: Selection of the blocking variable



BLOCK_NUMBER	BLOCK_MODALITY	FREQUENCY	CONTINGENCY_TABLE	MU_TABLE
1	Ascoli	210	CONTINGENCY_TABLE_CITY_1	MU_TABLE_CITY_1
2	Bologna	289	CONTINGENCY_TABLE_CITY_2	MU_TABLE_CITY_2
3	Bolzano	464	CONTINGENCY_TABLE_CITY_3	MU_TABLE_CITY_3
4	Brindisi	266	CONTINGENCY_TABLE_CITY_4	MU_TABLE_CITY_4
5	Catanzaro	247	CONTINGENCY_TABLE_CITY_5	MU_TABLE_CITY_5
6	Firenze	120	CONTINGENCY_TABLE_CITY_6	MU_TABLE_CITY_6
7	Gorizia	225	CONTINGENCY_TABLE_CITY_7	MU_TABLE_CITY_7
8	Milano	2025	CONTINGENCY_TABLE_CITY_8	MU_TABLE_CITY_8
9	Napoli	1998	CONTINGENCY_TABLE_CITY_9	MU_TABLE_CITY_9
10	Padova	368	CONTINGENCY_TABLE_CITY_10	MU_TABLE_CITY_10
11	Palermo	234	CONTINGENCY_TABLE_CITY_11	MU_TABLE_CITY_11
12	Perugia	108	CONTINGENCY_TABLE_CITY_12	MU_TABLE_CITY_12
13	Pescara	289	CONTINGENCY_TABLE_CITY_13	MU_TABLE_CITY_13
14	Roma	2256	CONTINGENCY_TABLE_CITY_14	MU_TABLE_CITY_14
15	Sassari	702	CONTINGENCY_TABLE_CITY_15	MU_TABLE_CITY_15
16	Savona	195	CONTINGENCY_TABLE_CITY_16	MU_TABLE_CITY_16
17	Torino	589	CONTINGENCY_TABLE_CITY_17	MU_TABLE_CITY_17
18	Venezia	210	CONTINGENCY_TABLE_CITY_18	MU_TABLE_CITY_18
19	Verona	48	CONTINGENCY_TABLE_CITY_19	MU_TABLE_CITY_19

Figure 14: Block_Modality table

1.1.7 Sorted Neighbourhood Method

The Sorted Neighbourhood Method (SNM) consists of ordering the two data sets to link according to a sorting variable. Then a fix size *w* window runs on the unified sorted list and all the pairs falling into the window are considered as candidate pairs.

The sorted neighbourhood also requires the selection of the sorting variable, in the same way as the blocking method. However, it also requires the specification of the size of the comparison window. The size will be selected by taking into account the risk of missing true links, for instance if the number of units with the same value of the sorted variable is larger than the fixed size.

Figure 15 shows the window for the selection of the sorting variable. Figure 16 shows the window where the neighbourhood window size can be specified. This latter is automatically opened after the selection of the sorting variable according to:

Search Space Creation → Search Space Reduction → Sorted Neighborhood

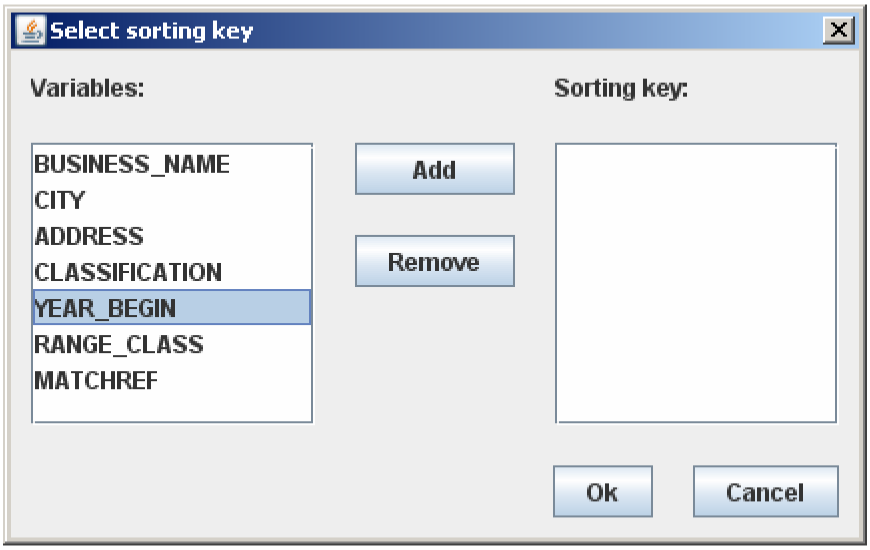


Figure 15: Selection of a sorting variable

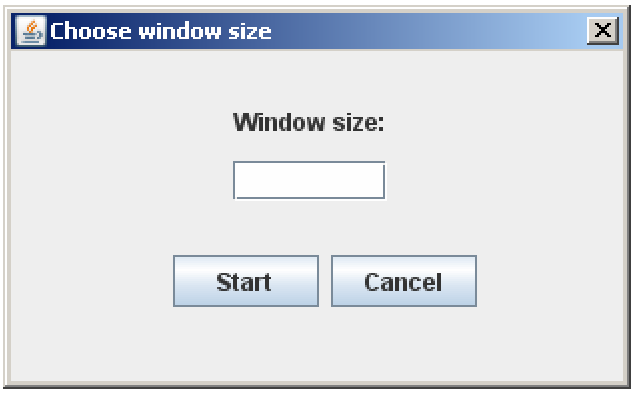


Figure 16: Selection of the window size in the sorted neighbourhood method

Decisional models

As reported in the introduction, RELAIS has the objective to provide different approaches and techniques to deal with the various record linkage problems. The RELAIS 2.0 version implements both a method for probabilistic record linkage, according to the Fellegi and Sunter theory [4] and two methods for deterministic record linkage, based on comparisons of matching variable values. The principal steps to apply the different methods are treated in the next sections, while methodological details on the probabilistic implementation are given in appendix A.

Some general aspects related to the advantages and disadvantages of each method are given in the next section.

Methodological aspects

A distinction between deterministic and probabilistic approaches is often made in research literature, where the former is associated with the use of formal decision rules while the latter makes an explicit use of probabilities for deciding when a given pair of records is actually a match. Actually, it is difficult to make a clear distinction between the two approaches, especially with respect to proposals coming from the computer science area. According to some authors (e.g. Statistic Canada) deterministic record linkage is defined just as the method that individuates links if and only if there is a full agreement of unique identifiers or a set of common identifiers, the matching variables. Other authors backed up that in deterministic record linkage a pair is a link also if it satisfied some specific criteria a priori defined; actually not only the matching variables must be chosen and combined but also a threshold has to be fixed in order to establish whether a pair should be considered a link or not, that is this kind of linkage is almost-exact but not exact in the strict sense [14]. In the deterministic approach, both exact and almost-exact, the uncertainty in the match between two different databases is minimized but the linkage rate could be very low.

Deterministic record linkage can be adopted, instead of probabilistic method, in presence of error-free unique identifiers (such a social security number or fiscal code) or when matching variables with high quality and discriminating power are available and can be combined so as to establish the pairs link status; in this case the deterministic approach is very fast and effective and its adoption is appropriate. From the other side, the rule definition is strictly dependent on the data and on the knowledge of the practitioners. Moreover, due to the strong importance of the matching variable quality, in the deterministic procedure, some links can be missed due to presence of errors or missing values in the matching variables; so the choice between the deterministic and probabilistic methods must take into account "the availability, the stability and the uniqueness of the variables in the files" [14]. It is important also to underline that, in a deterministic context, the linkage quality can be assessed only by means of re-linkage procedures or accurate and expensive clerical reviews. The probabilistic approach is more complex and formal abut can solve problems caused by bad quality data. In particular it can be helpful when differently spelled, swapped or misreported variables are stored in the two data files. In addition the probabilistic procedure allows to evaluate the linkage errors, calculating the likelihood of the correct match.

Generally speaking, the deterministic and the probabilistic approaches can be combined in a two step process: firstly the deterministic method can be performed on the high quality variables then the probabilistic approach can be adopted on the residuals, the units not linked in the first step; however the joint use of the two techniques depends on the aims of the whole linkage project.

Selection of Comparison Functions

Comparison functions measure the “similarity” between two fields. Many of them are proposed in literature and provided in RELAIS 2.0, as described below. Generally speaking, the results of a comparison function can be also composed of categorical or continuous values. In RELAIS 2.0 each comparison function is normalised and its results are in the range [0,1]. Moreover, it is requested to the user to choose a threshold, between 0 and 1, consequently RELAIS 2.0 converts the results in binary elements, treating all the results above the threshold as 1 and all results below the threshold as 0. The higher distance for two strings is, the more similar the strings are.

A part the equality function, hereafter, we list of the comparison function available in RELAIS 2.0 with a short description. The included functions are part of the Java package StringMetrics (http://www.dcs.shef.ac.uk/~sam/stringmetrics.html).

1. Numeric Comparison

This metric compare two strings by their numeric value. Thus named Nx and Ny the numeric value of the two string Sx and Sy the numeric comparison is:

$$\mathrm{NC}(S_x, S_y) = \frac{\min(|N_x|, |N_y|)}{\max(|N_x|, |N_y|)}$$

If the strings are not numeric or the two numbers have different signs the comparison’s result is 0.

2. Levenshtein comparison function

This is the basic edit distance function whereby the distance is given simply as the minimum edit operations which transforms string1 into string2. Edit operations are: copy a character from string1 over to string2 ; delete a character in string1; insert a character in string2; substitute one character for another . Some other comparison functions reported below are extensions of the Levenshtein distance function, and typically they alter the cost of the edit operation, while in the Levenshtein function all the operations have the same cost.

3. Dice comparison function

Dice comparison function is a term based similarity measure and is defined as twice the number of terms common to compared entities divided by the total number of terms in both tested entities.

$$\mathrm{Dice} = \frac{2 * \text{Common Terms}}{\text{Number of terms in String1} + \text{Number of terms in String2}}$$

4. Jaro comparison function [16]

The Jaro comparison function takes into account typical spelling deviations. Briefly, for two strings s and t, let s' be the characters in s that are “common with” t, and let t' be the characters in t that are "common with" s; roughly speaking, a character a in s is "in common" with t if the same character a appears in about the place in t.

Let $T_{s',t'}$ measure the number of transpositions of characters in s' relative to t'. The Jaro similarity metric for s and t is

$$Jaro(s,t)=\frac{1}{3}\left(\frac{|s'|}{|s|}+\frac{|t'|}{|t|}+\frac{|s'|-T_{s',t'}}{2|s'|}\right)$$

5. Jaro-Winkler comparison function [17]

This metric, an extension of the Jaro comparison function (4), tends to modify the weights of the pairs s,t with a common prefix; the Jaro-Winkler distance metric is particularly suitable in case of short strings such as person names.

The Jaro-Winkler function for s and t is

$$Jaro-Winkler(s,t)=Jaro(s,t)+(lp*(1-Jaro(s,t)))$$

where *l* is the length of common prefix at the beginning of the string; p is a constant scaling factor for how much the score is adjusted upwards for having common prefixes. The standard value for this constant in Winkler's work is p = 0.1. This adjustment gives more favourable ratings to strings that match from the beginning for a set prefix length.

6. 3-Grams [18]

Q-grams are generally used in approximate string matching by "sliding" a window of length q over the characters of a string s to create a number of 'q' length grams (in the case of Relais 2.0 we considered q equal to 3) for matching.

A match is then rated as number of q-gram matches within the second string, t, over possible q-grams. When two strings s and t have a small edit distance, they also have a large number of q-grams in common.

7. Soundex comparison function

The Soundex function is a rude phonetic indexing scheme that generally focuses on individuals names; with this metric the errors in phonetic are easily recognized, e.g. the names John, Johne and Jon referred to the same person.

This is a term based evaluation where each term is given a Soundex code, each Soundex code consists of a letter, the first one of the string, and five numbers between 0 and 6. The numbers are based on the consonants as in the following table:

1) B,P,F,V

2) C,S,K,G,J,Q,X,Z

3) D,T

4) L

5) M,N

6) R

The vowels are not used. If two or more adjacent (not separated by a vowel) letters have the same numeric value, only one is used. This also applies if the first letter and the second one have the same value; the second letter would not be used to generate a digit. If there are less then six consonants in the string, the code is filled out with zeros. This approach is very promising for disambiguation of transliterated/misspell names.

Deterministic Decision Models

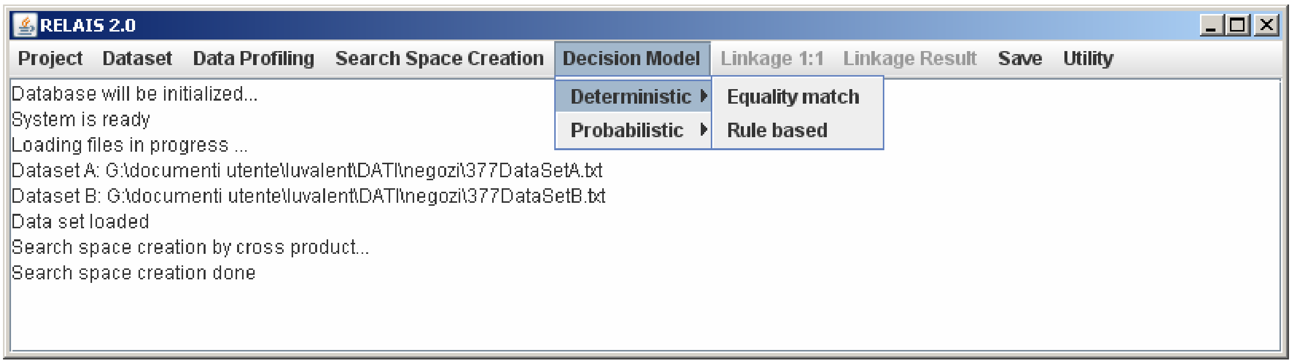
The deterministic record linkage is associated with the use of formal decision rules and it can be adopted, instead of probabilistic method, in presence of error-free unique identifiers (such a fiscal code) or when suitable matching variables with high quality and discriminating power are available and can be combined so as to establish the pairs link status; in this case the deterministic approach is very fast and effective and its adoption is appropriate.

The Decision Model menu, lists the available models to solve a record linkage problem. It contains two menus:

Deterministic

Probabilistic

In particular the Deterministic menu contains two empirical models, based on deterministic rules, to classify pairs of record as match or non-match. Deterministic models, in this implementation, do not admit the state of “possiblematch”.



```
Database will be initialized...
System is ready
Loading files in progress ...
Dataset A: G:\documenti utente\luvalent\DATI\negozi\377DataSetA.txt
Dataset B: G:\documenti utente\luvalent\DATI\negozi\377DataSetB.txt
Data set loaded
Search space creation by cross product...
Search space creation done
```

Figure 17: Deterministic model menu

RELAIS 2.0 (as shown in Figure 17) implements two deterministic model:

Equality match

Rule based

Choosing the Equality match menu the window shown in Figure 18 will be open. This window allows to select variables that will compose the matching key.

Applying the Equality match, a pair of record is classified as a match if all the selected matching keys are equals, otherwise the pair is classified as a non-match.

To evaluate an exact match it is not required the creation of a search space. Moreover, in this model it is not possible to choose a comparison function different from equality.

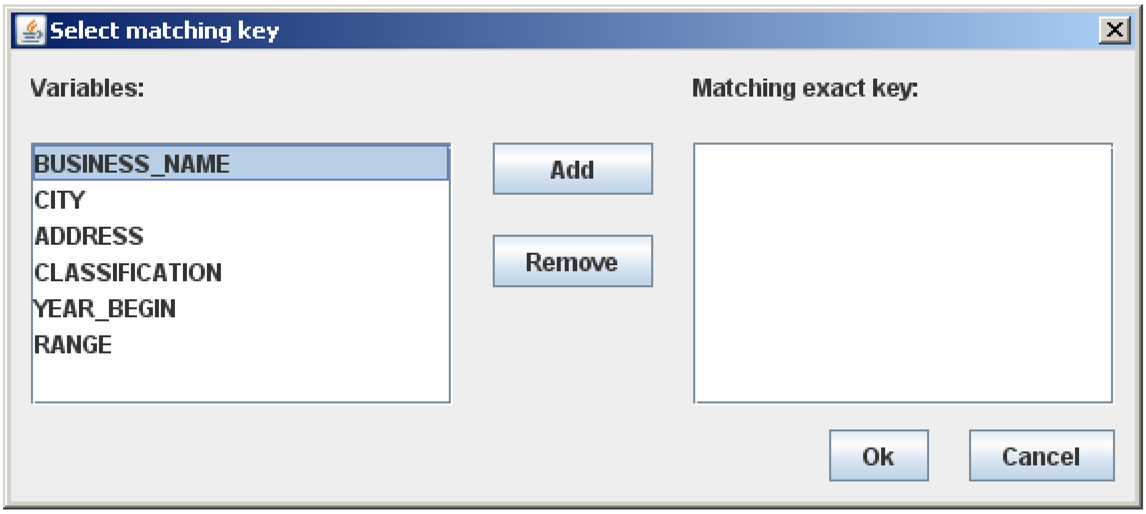


Figure 18: Selection of matching key

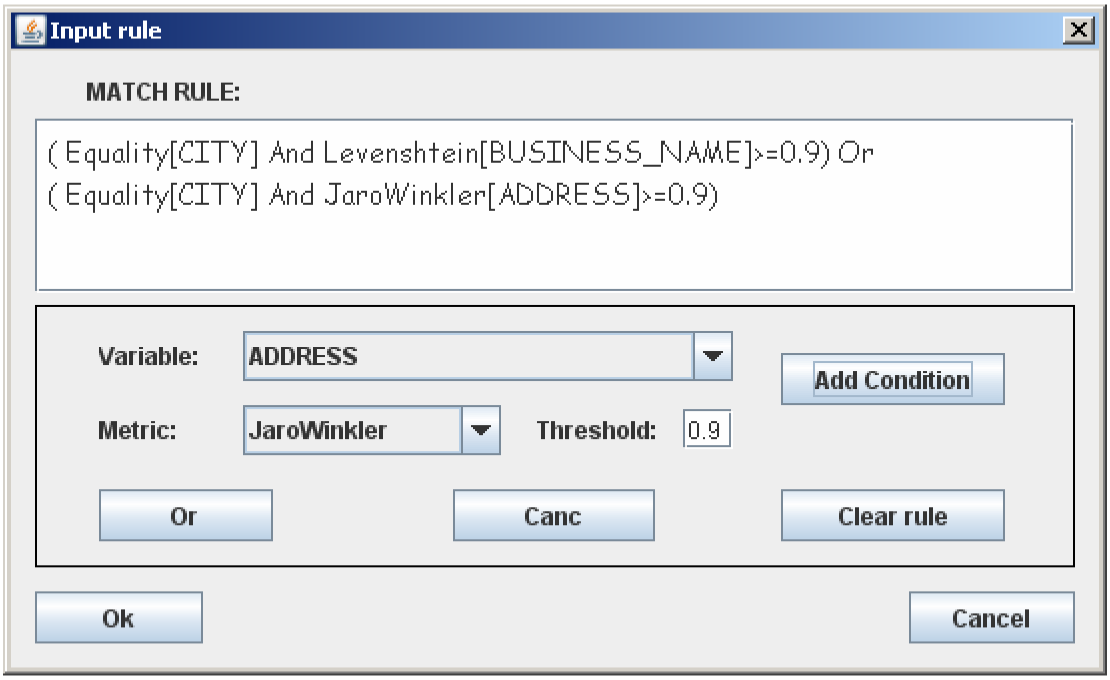
The outputs of the Deterministic Exact model are contained in the tables:

MATCHTABLE : table of match pairs with all the common variables of the two datasets and the generated variables key_dsa and key_dsb;

RESIDUAL_DSA : table containing record of data set A that are not classified as match;

RESIDUAL_DSB : table containing record of data set B that are not classified as match.

Choosing the Rule based menu, the window shown in Figure 19 will be open. This window allows to define a complex rule for classify pairs as match.



MATCH RULE:

(Equality[CITY] And Levenshtein[BUSINESS_NAME]>=0.9) Or
(Equality[CITY] And JaroWinkler[ADDRESS]>=0.9)

Variable: ADDRESS

Metric: JaroWinkler

Threshold: 0.9

Figure 19: Input deterministic match rule

This complex rule is named 'match rule' and is organised in sub-rules. Each sub-rule may consist of conditions that must be checked at once, these conditions are separated by an "AND" operator. The different sub-rules are separated by an "OR" operator, that can be inserted in the rule using the "Or" button.

A single condition can be added using the "Add Condition" button: the variable, the metric and the threshold to be used must be defined in advance.

As shown in Figure 19, the variable "ADDRESS", the metric "JaroWinkler" and the Threshold "0.9" are chosen. Using the "Add Condition" button, the condition "JaroWinkler[ADDRESS]>=0.9" is added to the rule. This condition is separated by the operator "And" from the "Equality[CITY]" condition already existing. Therefore, the sub-rule "Equality[CITY] And JaroWinkler[ADDRESS]>=0.9" is defined. A pair of records verifies this sub-rule if and only if the two records have the same attribute CITY and the attribute ADDRESS similar in the sense that applying the JaroWinkler metric the result is greater than 0.9.

Moreover, in the example shown in Figure 19, an other sub-rule "Equality[CITY] And Levenshtein[BUSINESS_NAME]>=0.9" is defined; the two sub rules are separated by the operator "Or". A pair of records verifies the rule if and only if at least one of the two sub-rules is satisfied.

The outputs of the Deterministic Rule based model are contained in the following tables:

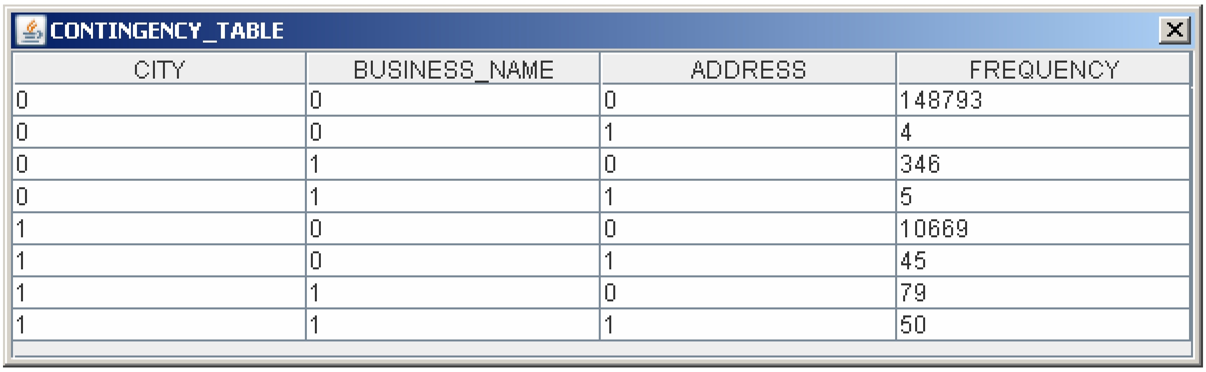
CONTINGENCY_TABLE

DETERMINISTIC_TRUE_TABLE

Each condition is applied to pairs in the search space. The result of the condition applied to a pair is 1 if the condition is verified, 0 otherwise. The concatenation of all the results of the conditions is named "comparison pattern". The frequency of each comparison pattern in the search space is saved in the CONTINGENCY_TABLE.

The patterns verifying the match rule are saved in the DETERMINISTIC_TRUE_TABLE.

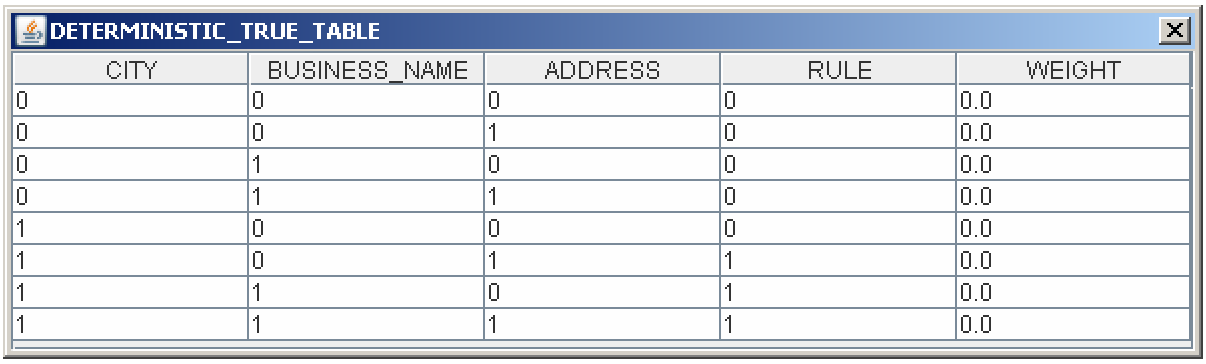
Referring to the rule defined in Figure 19, the output tables are shown in Figure 20 and in Figure 21[2]. Note that each condition is identified by the variable name.



CONTINGENCY_TABLE

CITY	BUSINESS_NAME	ADDRESS	FREQUENCY
0	0	0	148793
0	0	1	4
0	1	0	346
0	1	1	5
1	0	0	10669
1	0	1	45
1	1	0	79
1	1	1	50

Figure 20: Contingency_Table



DETERMINISTIC_TRUE_TABLE

CITY	BUSINESS_NAME	ADDRESS	RULE	WEIGHT
0	0	0	0	0.0
0	0	1	0	0.0
0	1	0	0	0.0
0	1	1	0	0.0
1	0	0	0	0.0
1	0	1	1	0.0
1	1	0	1	0.0
1	1	1	1	0.0

Figure 21:Deterministic_true_table

---

[2] For the definition of the weights see paragraph 10.

Probabilistic Model

The probabilistic decision model available in RELAIS 2.0 follows the Fellegi and Sunter approach. Below we report the main aspects of this approach, with the only aim of introducing and formalizing the problem. In Appendix A, more methodological aspects are provided.

Let A and B be two lists of size nA and nB. The goal of record linkage is to find all the pairs of units (a,b), $a \in A$, $b \in B$, such that a and b refer to the same unit (a=b). Starting from the set $\Omega = \{(a,b); a \in A, b \in B\}$ containing all possible pairs of records from the lists A and B, with size $|\Omega| = \mathrm{N} = \mathrm{n_A} \times \mathrm{n_B}$, a record linkage procedure is a decision rule based on the comparison of k matching variables that, for each single pair of records, can take one of the following decisions: link, possible link and non-link. The comparison between the matching variables of the two units (a,b) is made by means of a suitable comparison function, depending on the kind of variables and their accuracy. For each pair of the set Ω, the result of the comparison of the matching variables is summarized in the vector γ, called comparison vector or comparison pattern. For instance, when the comparison function applied to the k matching variables is the equality, the resulting comparison pattern is a k-dimensional vector composed by 1 or 0, depending on the agreement or disagreement of the variables:

$$\gamma = (\gamma_1, \ldots, \gamma_j, \ldots, \gamma_k) \longrightarrow \gamma = (1, \ldots, 0, \ldots, 1).$$

The probability models for linkage assume that the probability distribution of the comparison pattern comes from a mixture of two probability distributions: the first one comes from the pairs (a,b) that actually are the same unit, called distribution m; the other one comes from the pairs (a,b) that actually represent different units, called distribution u. Starting from the estimations of the two distribution $m(\gamma)$ and $u(\gamma)$, it is possible to define the composite matching weight, given by the likelihood ratio:

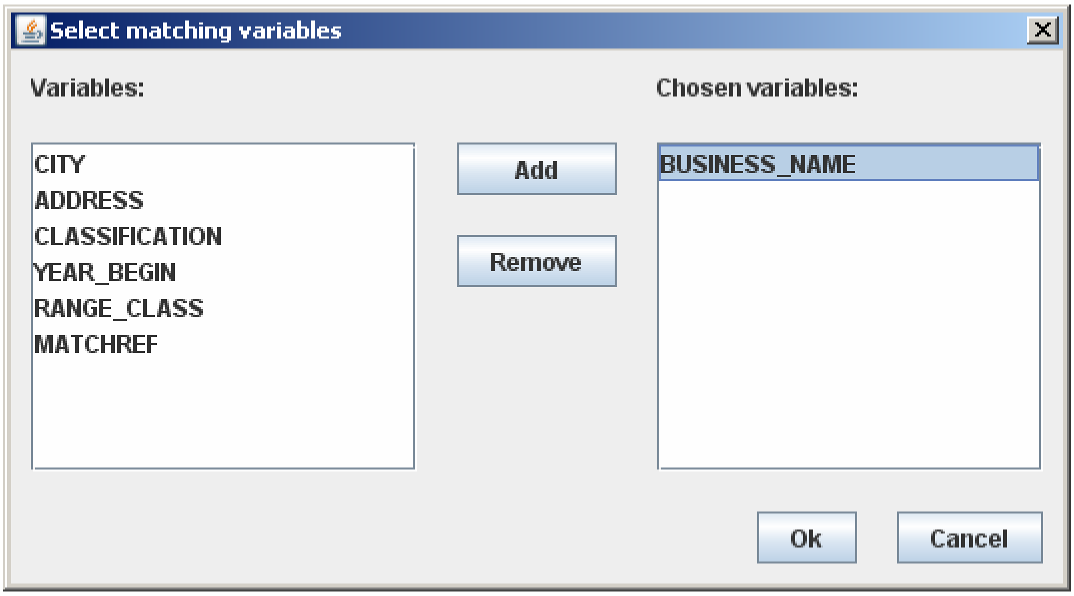
$$r = \frac{m(\gamma)}{u(\gamma)} = \frac{\Pr(\gamma \mid M)}{\Pr(\gamma \mid U)}$$

where M is the set of the pairs that actually are links and U is the set of the pairs corresponding to non-links, with $M \cup U = \Omega$ and $M \cap U = \varnothing$.

Fellegi and Sunter proposed an equation system to achieve the explicit formulas for the estimates of $m(\gamma)$ and $u(\gamma)$ when the matching variables are at most three. In more general situations, the conditional distribution estimates can be obtained via the EM algorithm [19], assuming a latent class model, in which the latent variable is just the link status.

According to the Fellegi and Sunter theory, once the composite weight r is estimated, it is possible to classify a pair as a link if the corresponding weight r is above a certain threshold Tm, and as a non-link if the weight lays below the threshold T_u; finally, for the pairs corresponding to weights falling into the range $I=(T_u, T_m)$, no-decision is made and the pair is assigned to a clerical review analysis. According to the Fellegi and Sunter theory, a decision on the threshold levels has to be made in order to properly manage the trade off between the need of a small number of expected no-decisions and small misclassification error rates for the pairs.

In the following sections the main steps of the probabilistic procedure are shown, the details on methodologies are given in Appendix A. When blocking method is performed to reduce the search space of pairs, RELAIS 2.0 allows to the users two different ways of applying the probabilistic model: it can be applied in a one-shot way to all the blocks or a specific block can be selected. Anyway, the common preliminary operation to do for executing the linkage procedure is the selection of the matching variables and the choice of the related comparison functions and thresholds, as shown in the following figures.



Select matching variables

Variables:

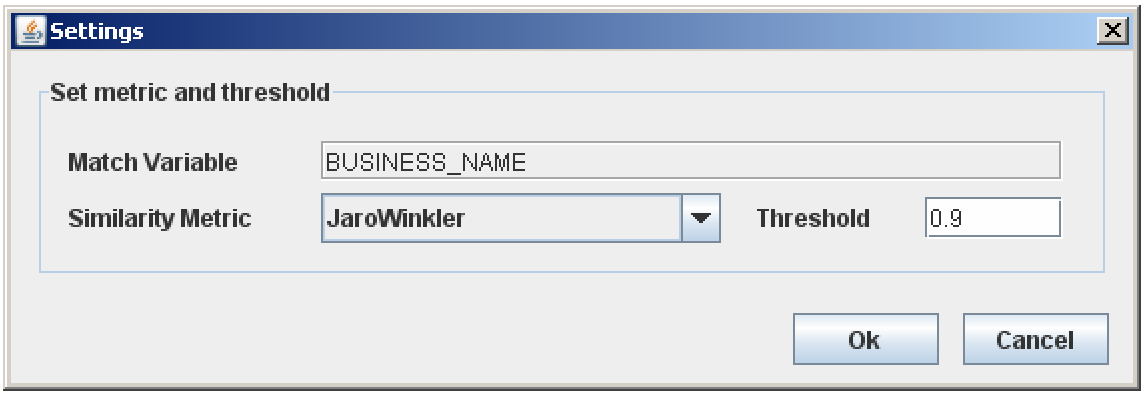
CITY
ADDRESS
CLASSIFICATION
YEAR_BEGIN
RANGE_CLASS
MATCHREF

Chosen variables:

BUSINESS_NAME

Figure 22: Variables selection

It is important to underline that at least 3 matching variables need to be chosen in the current implementation of RELAIS.

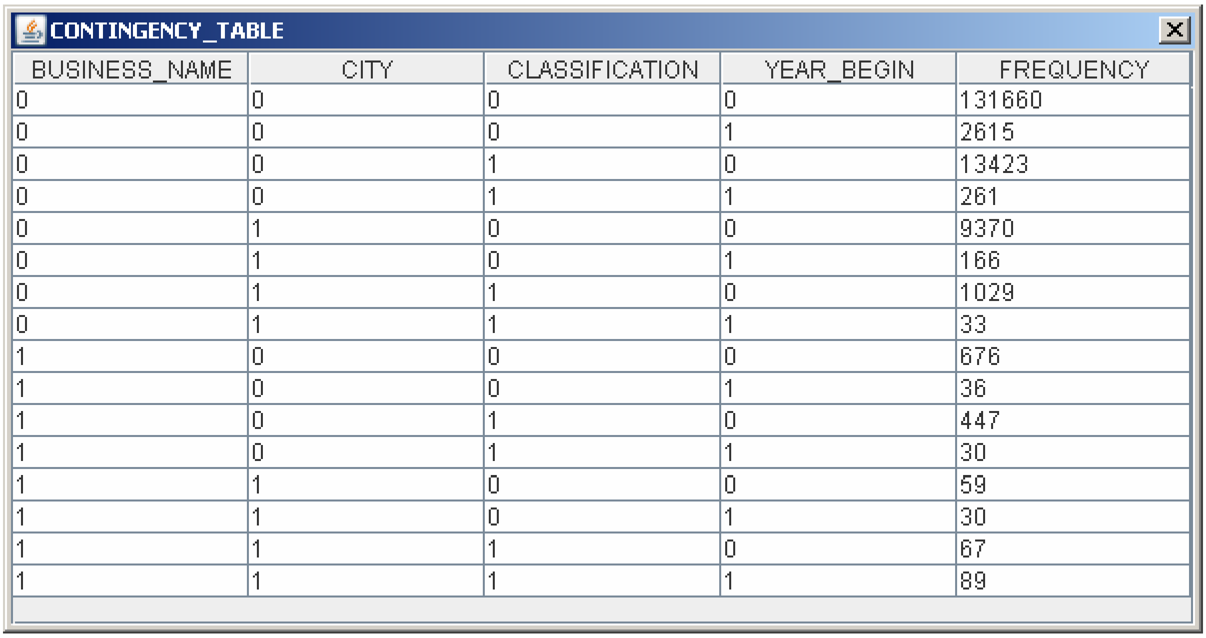


Settings

Set metric and threshold

Match Variable: BUSINESS_NAME
Similarity Metric: JaroWinkler
Threshold: 0.9

Figure 23: Metrics and thresholds setting



BUSINESS_NAME	CITY	CLASSIFICATION	YEAR_BEGIN	FREQUENCY
0	0	0	0	131660
0	0	0	1	2615
0	0	1	0	13423
0	0	1	1	261
0	1	0	0	9370
0	1	0	1	166
0	1	1	0	1029
0	1	1	1	33
1	0	0	0	676
1	0	0	1	36
1	0	1	0	447
1	0	1	1	30
1	1	0	0	59
1	1	0	1	30
1	1	1	0	67
1	1	1	1	89

Figure 24: Contingency table

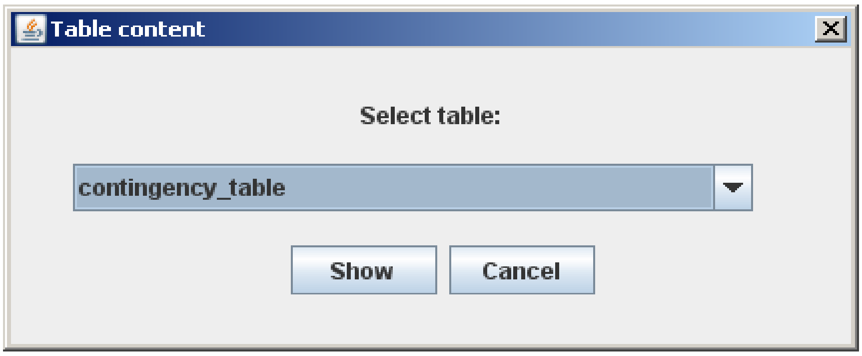
1.1.8 Contingency Table

The first step of the probabilistic procedure consists of computing the comparison vector $\gamma = (\gamma_1,\ldots,\gamma_j,\ldots,\gamma_k)$, given by the result of the function on the k matching variables, for all the pairs in the space Ω. In fact, starting from the vector distribution among the pairs (reported in the contingency table) the goal is the estimation of the probability distribution of the unknown random variable “link status”, which assigns each pair to the set M or to the set U.

The comparison vector considered in RELAIS 2.0 is a binary one, i.e. for each matching variable it reports the equality (corresponding to value 1) or the inequality (corresponding to value 0) between the units. As already reported in Section 0, the comparison vector is binary even if a continuous comparison function has been applied: actually, based on the selected threshold, RELAIS 2.0 converts the results in binary elements, treating all the results above the threshold as 1 and all results below the threshold as 0. This choice is a very common simplification, in order to design the latent class model as simple as possible.

The evaluation of the contingency table is available by browsing the menu:

Utility → Table Display



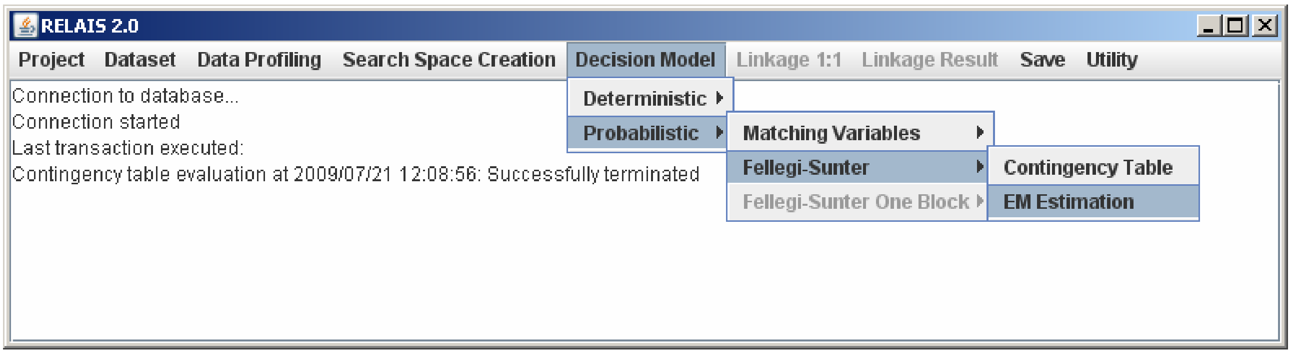
Select table: contingency_table

Figure 25: Contingency table selection

1.1.9 Parameter Estimation of the Probabilistic Model and the Table MU

In the probabilistic approach, the distribution of the comparison vector is supposed to come from two different (unobserved) distributions, according to fact that the pair is a match or not. The estimation of these two distributions can be obtained by means of the maximization of the likelihood function. Such operation, involving a latent variable, requires the use of iterative methods, generally the EM algorithm or its generalizations. Details on the method applied in RELAIS 2.0 to estimate the parameters of the probabilistic model are given in Appendix A, including the initial values of the parameters, the maximum number of iteration allowed and the stop criterion.

The estimation of the model parameters is achieved by browsing the menu (see also Figure 26):



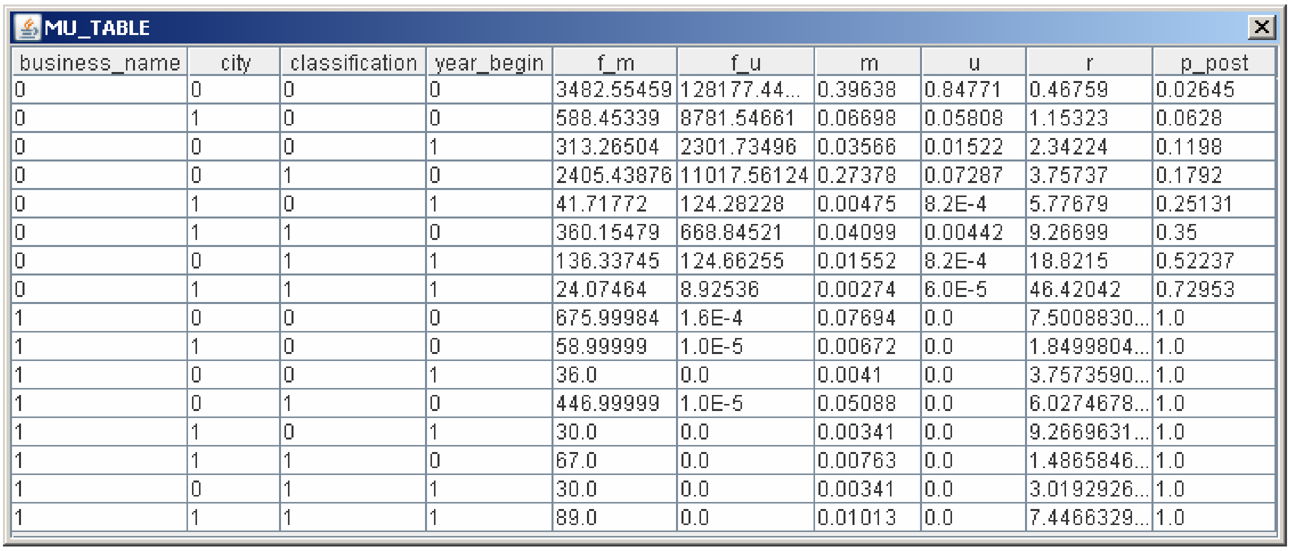
Connection to database...
Connection started
Last transaction executed:
Contingency table evaluation at 2009/07/21 12:08:56: Successfully terminated

Figure 26: EM estimation menu

After the execution of the parameter estimates, the result must be visualised, by means of loading the table containing the computation. The table is loaded by browsing the menu:

Utility → Table Display

Figure 27 shows the loaded table.



business_name	city	classification	year_begin	f_m	f_u	m	u	r	p_post
0	0	0	0	3482.55459	128177.44...	0.39638	0.84771	0.46759	0.02645
0	1	0	0	588.45339	8781.54661	0.06698	0.05808	1.15323	0.0628
0	0	0	1	313.26504	2301.73496	0.03566	0.01522	2.34224	0.1198
0	0	1	0	2405.43876	11017.56124	0.27378	0.07287	3.75737	0.1792
0	1	0	1	41.71772	124.28228	0.00475	8.2E-4	5.77679	0.25131
0	1	1	0	360.15479	668.84521	0.04099	0.00442	9.26699	0.35
0	0	1	1	136.33745	124.66255	0.01552	8.2E-4	18.8215	0.52237
0	1	1	1	24.07464	8.92536	0.00274	6.0E-5	46.42042	0.72953
1	0	0	0	675.99984	1.6E-4	0.07694	0.0	7.5008830...	1.0
1	1	0	0	58.99999	1.0E-5	0.00672	0.0	1.8499804...	1.0
1	0	0	1	36.0	0.0	0.0041	0.0	3.7573590...	1.0
1	0	1	0	446.99999	1.0E-5	0.05088	0.0	6.0274678...	1.0
1	1	0	1	30.0	0.0	0.00341	0.0	9.2669631...	1.0
1	1	1	0	67.0	0.0	0.00763	0.0	1.4865846...	1.0
1	0	1	1	30.0	0.0	0.00341	0.0	3.0192926...	1.0
1	1	1	1	89.0	0.0	0.01013	0.0	7.4466329...	1.0

Figure 27: table MU

The meaning of the table columns is described below:

columns f_m e f_u report the estimates of the frequency distributions respectively for links and non-links, for each pattern of the comparison vector resulting from the selected matching variables; for instance, the table shown in Figure 27 reports no links for the first pattern (the first row of the table), while all the pairs of this pattern are estimated as non-links;

columns m e u visualize, approx. to the third decimal, estimate values of the link and non-link probabilities respectively; as shown in the table of Figure 27, usually non-link distribution is concentrated in the upper-side of the table, that is corresponding to comparison pattern coming from inequality in the matching variables;

column r visualizes, approx. to the third decimal, the values of the ratio between the link and non-link probabilities, that is the matching composite weight. It is crucial, as explained in Section 0, in assigning each pair to the set M or U;

column p_post visualizes, approx. to the third decimal, the values of the posterior probabilities that a pair is a link and it is given by p_post=f_m/(f_m+f_u).

The model estimates are considered not reliable when the conditional probabilities of at most one of the matching variables result $m(\gamma)=0$ or $u(\gamma)=1$; in such conditions, the system stops and the following message is shown:

“Estimation of parameters failed for this model”.

The same error appears when the number of units in the model is smaller than the number of parameters to estimate.

At this point the user can change the decision model with the purpose of modifying the performed choices that have conducted to a not reliable estimation of the model parameters.

Reduction to matching 1:1

As reported in Section 0 the output of a record linkage procedure could be different depending on the aim of the matching process. We can distinguish between (i) a one-to-one linkage, (ii) a one-to-many linkage, and (iii) a many-to-many linkage. In the first case (i) we consider a problem in which a record in A can be matched to only one record in B and also the way around; in (ii) a record in A set can be matched with more than one record of the compared file; (iii) allows more than one record in each file to be matched with more than one record in the other. The latter two problems may imply the existence of duplicate records in the linkable data sources.

In Sections 0 and 0 the solutions adopted in Relais 2.0 to the one-to-one problem are described.

Methodological Aspects

Both in the deterministic and in the probabilistic approach adopted in Relais 2.0, it is allowed the situation in which more than a record of A (B) is matched with more than one record in B

(A). That is, the match composite weight is higher than the fixed match thresholds for more than one record in A (B) or, in the deterministic approach, more than one record satisfies the adopted rules.

However, in several applications, the record linkage target is to recognize exactly and univocally the same units and establish only 1:1 links, that is each record of A with at most one of B and viceversa. This kind of application requires several constraints and it is a difficult problem of optimization, for which different algorithms have been proposed. In the current version of the toolkit we consider two possible solutions to the problem of reduction from N:M linkage to one-to-one: the optimized solution and the greedy solution.

Optimized Solution

In this first alternative we consider an optimal solution for the reduction 1 to 1. Once the matching weight, r, is assigned to each pair, the identification of 1 to 1 links can be solved as a linear programming problem, where the objective function to maximize is the sum of weights for the linked pairs, under the constraints given by the fact that each unit of A must be linked with only one unit in B. In the current version of RELAIS, the solution of such a problem is obtained by means of the simplex algorithm, available in the R package "lpSolve". The original algorithm is modified in order to maximize the log-transformation of the weights; in such a way the number of constraints is reduced (as well as the complexity of the problem) when the number of units belonging to pairs with weight less than 1 is large.

If such a condition is not verified, huge amount of data can required large data structure that can reach the maximum allocation of memory permitted by R. Experiments show that the algorithm can solve problems with input data of some thousands of records.

In the deterministic context the weights can be assigned by the user giving the maximum positive weight for the most important rule and the subsequent ones in descending order according to the relevance of the rule. Nevertheless the system gives its own default weights: the maximum is given to the first rule defined by the user.

Greedy Solution

If the optimal solution is not able to reach a result due to computational limitations, we can apply a "greedy solution" in order to select, from the N : M cluster, the one-to-one linkage. Also in this context, we consider firstly the r weight (for deterministic approach see par. 10.2) and we sort all the record pairs by r. Then we consider as one-to-one pairs those that have the higher r. With this strategy, it is not guaranteed that we reach an optimal solution because we perform local choices.

Linkage Result

The last phase of the record linkage process is the selection of the desired output data. In the following paragraphs the choices to be adopted are described and also all the available outputs in order not only to better end the whole process but also to have the residual to begin the new process with.

Choice of the Thresholds

At this point the unmatch threshold (T_u) and the match threshold (T_m) are selected. If the weight value p_post is higher than T_u and lower than T_m, the pair is assigned to the set of the Possible Match, if the value p_post is higher than T_m, the pair is assigned to the set of Match.

When the same value is chosen for T_u and T_m, the resulting set of Possible Match is empty.

If the value assigned to T_u is higher than T_m an error message is given and new threshold values are requested.

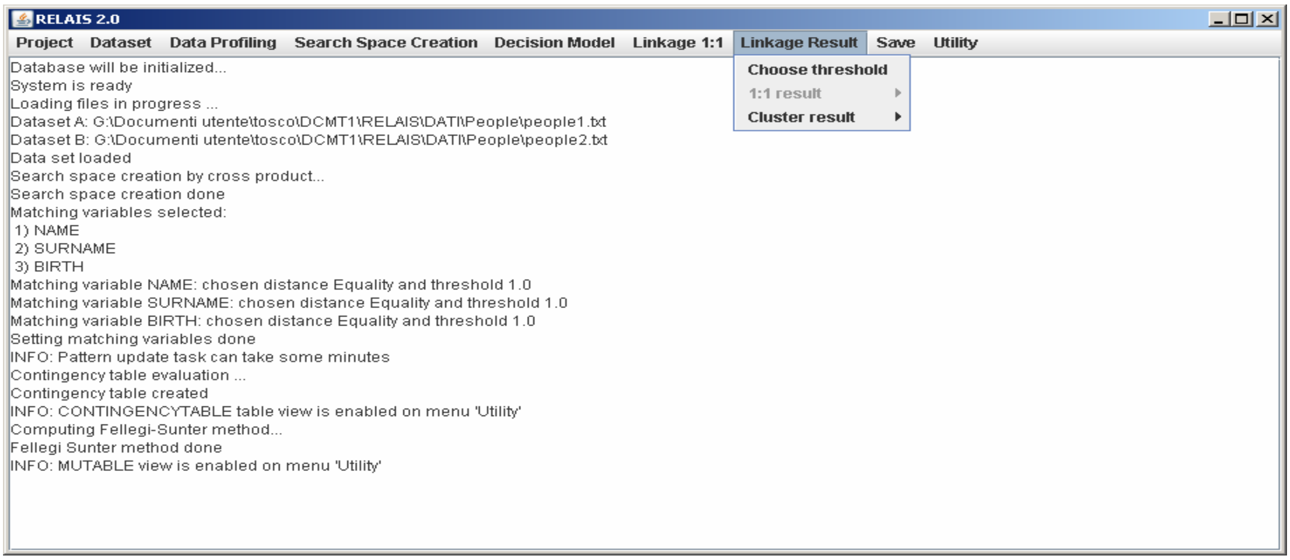
The Linkage Result menu

As shown in Figure 28, the Linkage Result menu contains three menus:

Choose Threshold

1:1 Result

Cluster Result



```
Database will be initialized...
System is ready
Loading files in progress ...
Dataset A: G:\Documenti utente\tosco\DCMT1\RELAIS\DATI\People\people1.txt
Dataset B: G:\Documenti utente\tosco\DCMT1\RELAIS\DATI\People\people2.txt
Data set loaded
Search space creation by cross product...
Search space creation done
Matching variables selected:
 1) NAME
 2) SURNAME
 3) BIRTH
Matching variable NAME: chosen distance Equality and threshold 1.0
Matching variable SURNAME: chosen distance Equality and threshold 1.0
Matching variable BIRTH: chosen distance Equality and threshold 1.0
Setting matching variables done
INFO: Pattern update task can take some minutes
Contingency table evaluation ...
Contingency table created
INFO: CONTINGENCYTABLE table view is enabled on menu 'Utility'
Computing Fellegi-Sunter method...
Fellegi Sunter method done
INFO: MUTABLE view is enabled on menu 'Utility'
```

Figure 28: Linkage Result menu

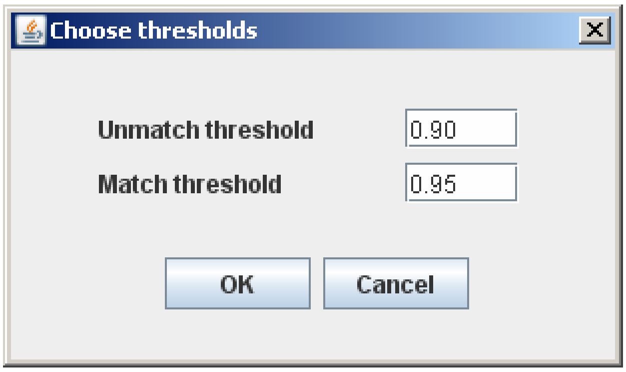
The 1:1 Result menu is disabled if no Linkage 1:1 phase has been executed.

The Choose Threshold menu, as shown in Figure 29, allows to insert the two thresholds: Unmatch threshold and Match Threshold. The two thresholds take two default values:

Unmatch threshold = 0.90

Match threshold = 0.95

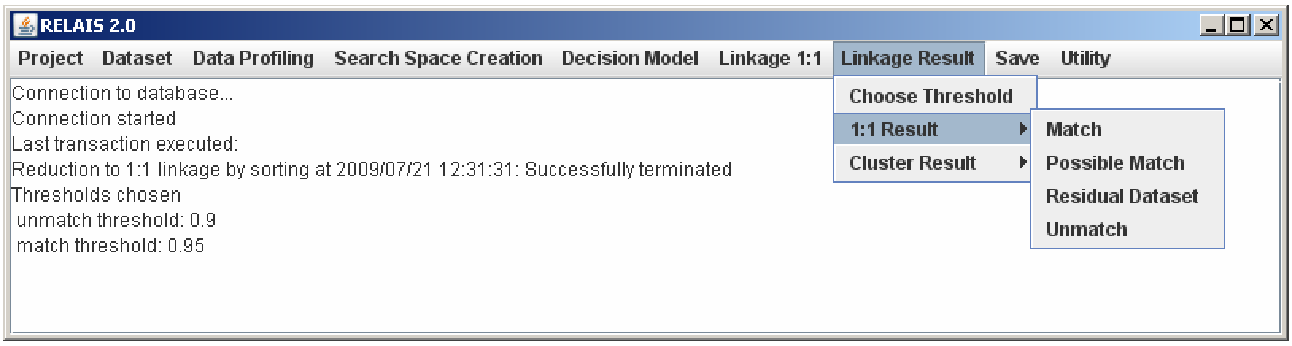
It is possible to change these values with the most appropriate depending on the data.



Unmatch threshold 0.90

Match threshold 0.95

Figure 29: Choose Thresholds window



```
Connection to database...
Connection started
Last transaction executed:
Reduction to 1:1 linkage by sorting at 2009/07/21 12:31:31: Successfully terminated
Thresholds chosen
 unmatch threshold: 0.9
 match threshold: 0.95
```

Figure 30: 1:1 Result menu

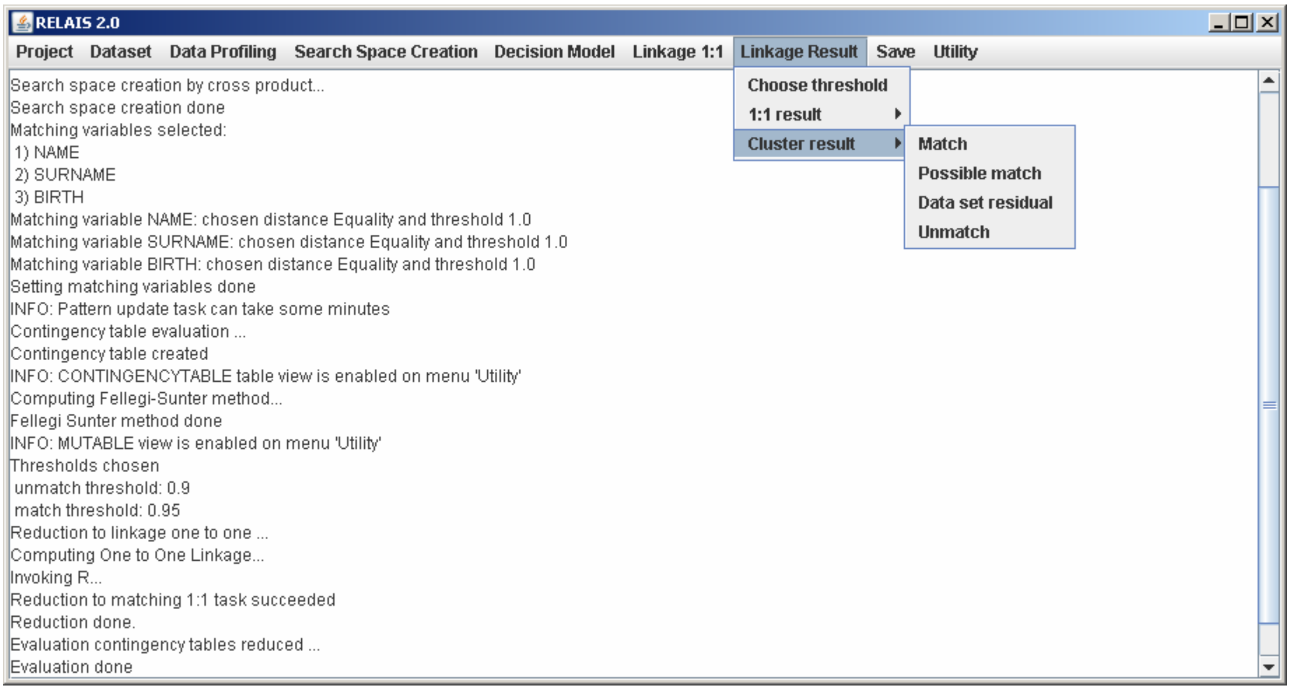
As shown in Figure 30, the 1:1 result menu allows to create four different results:

Match: creates a table named Matchtable containing the pairs of record, one of dataset A and the other of dataset B, that are considered as match. Being a 1:1 result, to one record of dataset A corresponds only one record of dataset B;

Possible Match: creates a table named Possiblematchtable containing the pairs of record that could be a match or a non match and that need a clerical review;

Data set residual: creates two tables named Residual_dsa and Residual_dsb that contain respectively the non-matched, including the possible match, records of dataset A (first data set) and the non-matched, including the possible match, records of data set B (second data set);

Unmatch: creates a table named Unmatchtable that contains the pairs of records that do not correspond to a match.



```
Search space creation by cross product...
Search space creation done
Matching variables selected:
 1) NAME
 2) SURNAME
 3) BIRTH
Matching variable NAME: chosen distance Equality and threshold 1.0
Matching variable SURNAME: chosen distance Equality and threshold 1.0
Matching variable BIRTH: chosen distance Equality and threshold 1.0
Setting matching variables done
INFO: Pattern update task can take some minutes
Contingency table evaluation ...
Contingency table created
INFO: CONTINGENCYTABLE table view is enabled on menu 'Utility'
Computing Fellegi-Sunter method...
Fellegi Sunter method done
INFO: MUTABLE view is enabled on menu 'Utility'
Thresholds chosen
 unmatch threshold: 0.9
 match threshold: 0.95
Reduction to linkage one to one ...
Computing One to One Linkage...
Invoking R...
Reduction to matching 1:1 task succeeded
Reduction done.
Evaluation contingency tables reduced ...
Evaluation done
```

Figure 31: Cluster Result menu

As shown in Figure 31, the Cluster result menu allows to create four different results:

Match: creates a table named Matchtable containing the pairs of record, one of dataset A and the other of dataset B, that are considered as match. Being a N:M result, to one record of dataset A could correspond one or more records of dataset B and to one record of dataset B could correspond one or more records of dataset A;

Possible Match: creates a table named Possiblematchtable containing the pairs of record that could be a match or a non match therefore need a clerical review;

Data set residual: creates two tables named Residual_dsa and Residual_dsb thatcontain respectively the non-matched records of dataset A (first data set) and the non-matched records of data set B (second data set);

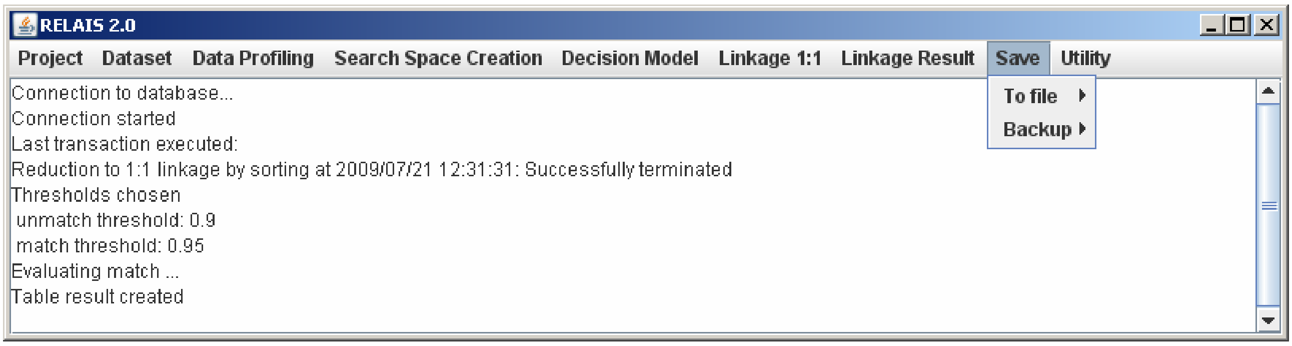
Unmatch: creates a table named Unmatchtable that contains the pairs of records that do not correspond to a match.

Save

As shown in Figure 32, starting from the Save menu, it is possible to choose one of the following menu:

To file: allows to save final and partial results to file;

Backup: allows to produce an internal backup from which restarting the execution.



```
Connection to database...
Connection started
Last transaction executed:
Reduction to 1:1 linkage by sorting at 2009/07/21 12:31:31: Successfully terminated
Thresholds chosen
 unmatch threshold: 0.9
 match threshold: 0.95
Evaluating match ...
Table result created
```

Figure 32: Save menu

The To File menu consists of the following menu:

Choose output folder: this menu allows to choose the folder in which the result files will be written;

Change field separator: allows to change the default value of the field separator that will be used in the write output phase;

Match File: allows to write the content of the Matchtable (already created) to a file named Match.txt. The records of a pair are written one below the other and only the common variables are reported;

Possible match file: allows to write the content of the Possiblematchtable (already created) to a file named PossibleMatch.txt. The records of a pair are written one below the other and only the common variables are reported;

Residual dataset A: allows to write the content of the Residual_dsa table (already created) to a file named ResidualDSA.txt. This file contains records of the first dataset, named dsA, that are not match that is are possible match or non match;

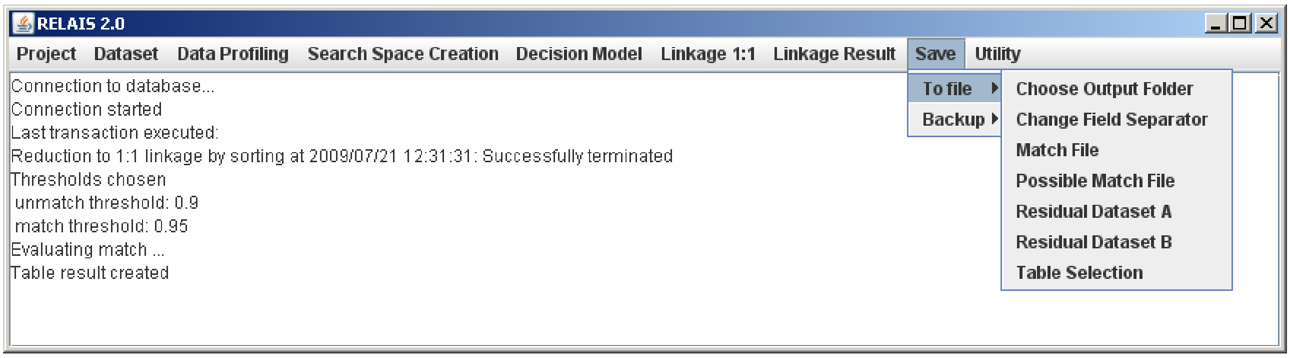
Residual dataset B: allows to write the content of the Residual_dsb table (already created) to a file named ResidualDSB.txt. This file contains records of the second dataset, named dsB, that are not match that is are possible match or non match;

Table selection: this menu open a window from which it is possible to choose one of the table created and write it in a file having the same name of the table and extension .txt.

In Figure 33 the menu:

Save → To file

is shown.



```
Connection to database...
Connection started
Last transaction executed:
Reduction to 1:1 linkage by sorting at 2009/07/21 12:31:31: Successfully terminated
Thresholds chosen
 unmatch threshold: 0.9
 match threshold: 0.95
Evaluating match ...
Table result created
```

Figure 33: To File menu

In Figure 34 the menu:

Save → To file → Choose Output Folder

is shown.

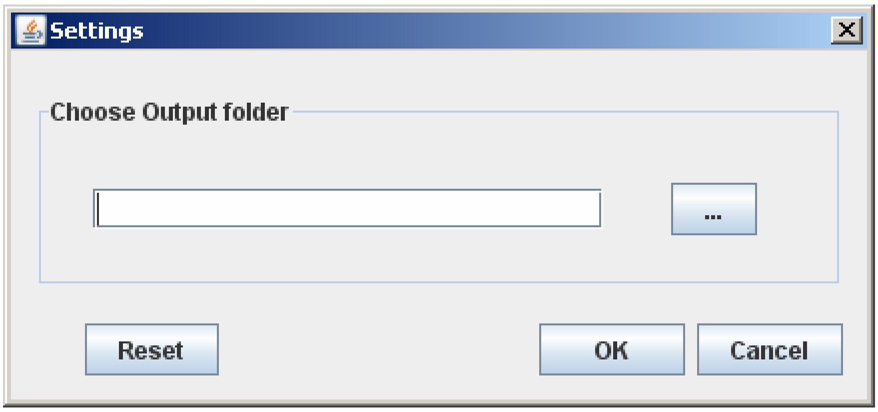
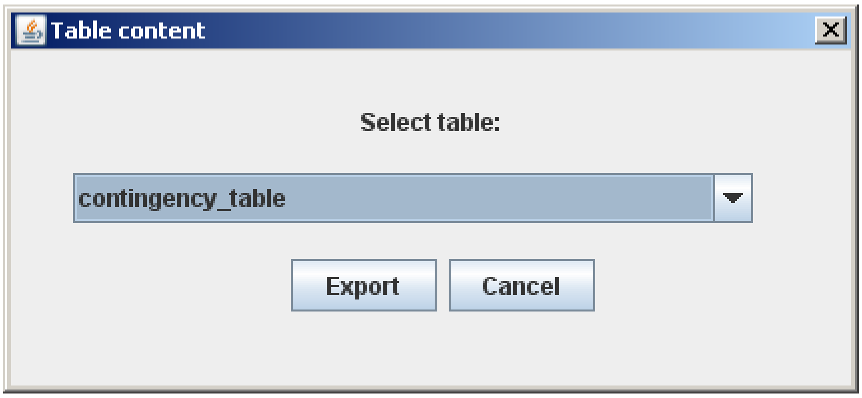


Figure 34: Choose Output Folder menu

In Figure 35 the menu:

Save → To file → Table Selection

is shown.



Select table: contingency_table

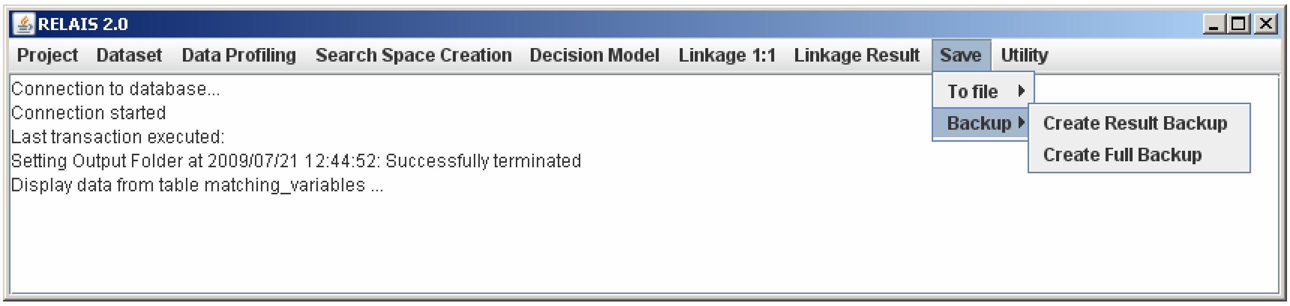
Figure 35: Table Selection menu

The Internal backup menu consists of the following menu:

Create result backup: this menu allows creating a database backup, with a user chosen name, with only the tables containing the final results, that is the Matchtable, the Possiblemachtable, the Unmatchtable, the Residual_dsa table and the Residual_dsb table. Thus, it will be possible to consult the result tables only.

Create full backup: this menu allows to create a backup, with a user chosen name, of the entire database, that is all the created tables are copied into the new database. After restoring from this internal backup all the results, output and intermediate results, will be available to the user.

In Figure 36 the Backup menu is shown.



```
Connection to database...
Connection started
Last transaction executed:
Setting Output Folder at 2009/07/21 12:44:52: Successfully terminated
Display data from table matching_variables ...
```

Figure 36: Backup menu

In Figure 37 the menu:

Save → Internal backup → Create result backup

is shown.

Figure 37: Create result backup menu

In Figure 38 the menu:

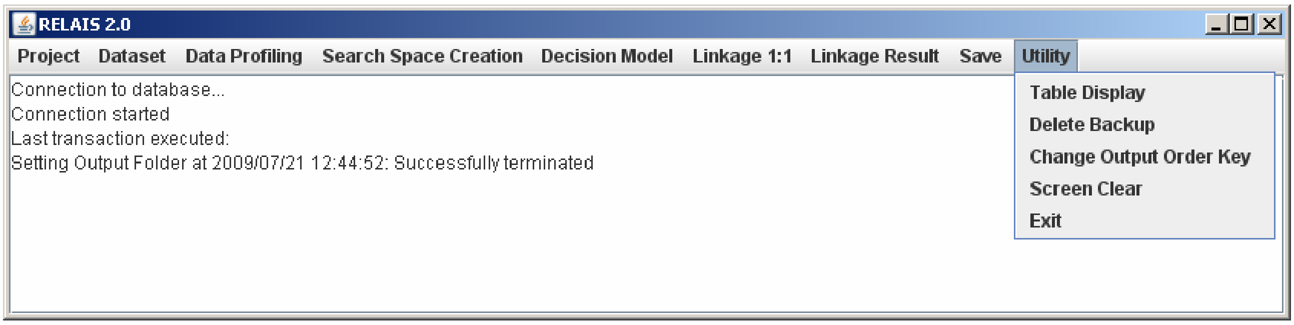
Save → Internal backup → Create full backup

is shown.

Figure 38: Create full backup menu

Utility

The Utility menu, lists some available menus of general utility.



```
Connection to database...
Connection started
Last transaction executed:
Setting Output Folder at 2009/07/21 12:44:52: Successfully terminated
```

Figure 39: Utility menu

As shown in Figure 39 the utility function are:

Table Display: this functionality allows to display the content of a chosen table.

In Figure 40 the window to select the table that will be displayed is shown. In Figure 41 the content of the selected (Contingencytable) table is shown.

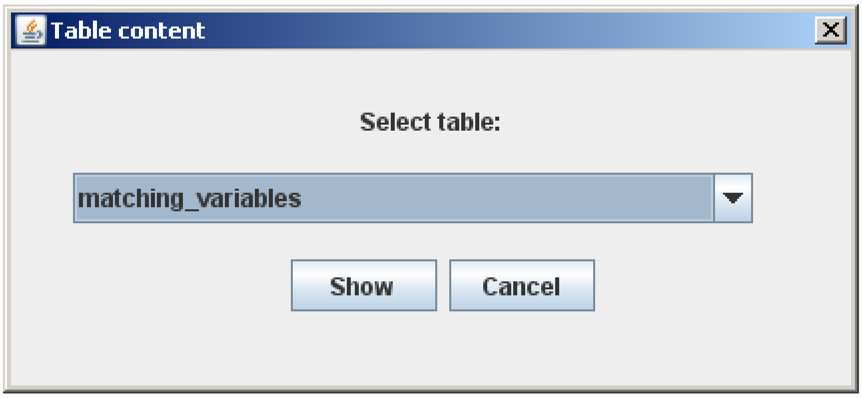
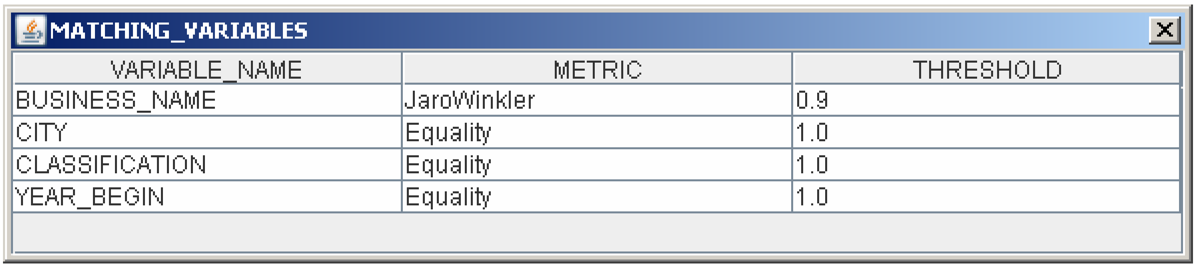


Figure 40: Select table window



VARIABLE_NAME	METRIC	THRESHOLD
BUSINESS_NAME	JaroWinkler	0.9
CITY	Equality	1.0
CLASSIFICATION	Equality	1.0
YEAR_BEGIN	Equality	1.0

Figure 41: Example of a table displayed

Delete Backup: this menu allows to delete a database containing a copy of the tables created in a previous execution of RELAIS;

Change Output Order Key: allows to change the order of the dataset A and dataset B used in the results. By default the first dataset is the dataset A;

Screen Clear: this functionality allows to clear the output window;

Exit: this menu allows to close the application and freeze the current repository.

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Appendix: Parameter Estimation of the Probabilistic Model via the EM Algorithm

To estimate m(γ) and u(γ) Jaro [9] defines a latent vector **g**:

$$\mathbf{g}_{(a,b)} = \begin{cases} \langle 1,0 \rangle & \text{if } (\mathrm{a},\mathrm{b}) \in M \\ \langle 0,1 \rangle & \text{if } (\mathrm{a},\mathrm{b}) \in U \end{cases}$$

and the augmented log-likelihood for the observed vector x of the k matching variables and the vector **g**

$$\ln\left[f\left(\mathbf{x},\mathbf{g} \middle| \mathbf{m},\mathbf{u},p\right)\right] = \sum_{(a,b)\in\Omega} \mathbf{g}_{(a,b)} \begin{pmatrix} \ln\left(\prod_k (m_k^{ab})^{\gamma_k^{ab}} \left(1-m_k^{ab}\right)^{\left(1-\gamma_k^{ab}\right)}\right) \\ \ln\left(\prod_k (u_k^{ab})^{\gamma_k^{ab}} \left(1-u_k^{ab}\right)^{\left(1-\gamma_k^{ab}\right)}\right) \end{pmatrix} + \sum_{(a,b)\in\Omega} \mathbf{g}_{(a,b)} \begin{pmatrix} \ln(p) \\ \ln(1-p) \end{pmatrix}$$

where *p* represents the probability that a randomly chosen pair (a,b) belong to the subset M.

Moreover, a conditional independence assumption is often made, so that

$$m^{a,b} = \prod_{k=1}^{K} m_k^{a,b} \; ; \qquad\qquad u^{a,b} = \prod_{k=1}^{K} u_k^{a,b} \; .$$

where

$$m_k^{ab} = \Pr\left(\gamma_k^{ab} = 1 \middle| (a,b) \in M\right); \qquad\qquad u_k^{ab} = \Pr\left(\gamma_k^{ab} = 1 \middle| (a,b) \in U\right);$$

Since the vector **g** and the subsets M and U cannot be directly observed, the probabilities $m(\gamma)$ and $u(\gamma)$ are estimated via the EM procedure [2], providing initial values for $m(\gamma)$, $u(\gamma)$ and p and estimating expected values for the vector **g**=<g_m, g_u> (STEP E)

$$\hat{g}_m\left(\gamma^{ab}\right) = \frac{\hat{p}\prod_{k=1}^{K}\left(m_k^{ab}\right)^{\gamma_k^{ab}}\left(1-m_k^{ab}\right)^{\left(1-\gamma_k^{ab}\right)}}{\hat{p}\prod_{k=1}^{K}\left(m_k^{ab}\right)^{\gamma_k^{ab}}\left(1-m_k^{ab}\right)^{\left(1-\gamma_k^{ab}\right)} + (1-\hat{p})\prod_{k=1}^{K}\left(u_k^{ab}\right)^{\gamma_k^{ab}}\left(1-u_k^{ab}\right)^{\left(1-\gamma_k^{ab}\right)}}$$

$$\hat{g}_u\left(\gamma^{ab}\right) = 1 - \hat{g}_m\left(\gamma^{ab}\right)$$

After this step, the **g** values can be placed into the log-likelihood [2] and a maximum likelihood estimate for $m(\gamma)$, $u(\gamma)$ and p (STEP M) can be obtained from:

$$\hat{m}_k = \frac{\sum_{(a,b)\in\Omega}\hat{g}_m\left(\gamma^{ab}\right)\gamma_k^{ab}}{\sum_{(a,b)\in\Omega}\hat{g}_m\left(\gamma^{ab}\right)} \qquad \hat{u}_k = \frac{\sum_{(a,b)\in\Omega}\hat{g}_u\left(\gamma^{ab}\right)\gamma_k^{ab}}{\sum_{(a,b)\in\Omega}\hat{g}_u\left(\gamma^{ab}\right)} \qquad \hat{p} = \frac{\sum_{(a,b)\in\Omega}\hat{g}_m\left(\gamma_k^{ab}\right)}{N} \; .$$

The Expectation and the Maximization steps are then iterated until the convergence of the parameters of interest is achieved.

In the current version of RELAIS the initial values of the parameters are $m(\gamma)=0.4$, $u(\gamma)=0.6$ and $p=0.1$; the maximum number of iteration is 150 and the stop criterion is achieved when the difference between the estimates of two iteration is 0.01.

The model estimates are considered not reliable when the conditional probabilities of at most one of the matching variables result $m(\gamma)=0$ or $u(\gamma)=1$; in such conditions, the system stops and the following message is shown:

“Estimation of parameters failed for this model”.

The same error appears when the number of units in the model is smaller than the number of parameters to estimate.