Extending the *MaCSim* approach using similarity weight matrix to assess the accuracy of record linkage

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Abstract

Record linkage is the process of bringing together the same entity from overlapping data sources, both administrative and substantive while removing duplicates. Statistical, health, government and business organisations often link administrative, survey, population census and other files to create a new file with complete information for comprehensive analysis. It is also crucial to assess the accuracy of the linked file in order to make valid inferences based on the combined data. Interestingly, there has been limited work on this issue of record linkage accuracy to date. In our first paper, we proposed a Markov Chain based Monte Carlo simulation approach (*MaCSim*) for assessing linkage accuracy and illustrated the utility of the approach using a synthetic dataset provided by the Australian Bureau of Statistics (ABS) based on realistic data settings. *MaCSim* utilizes two linked files with known true match status to create an agreement matrix and then simulates the matrix using a proposed algorithm developed to generate re-sampled versions of the agreement matrix. In this paper, we aim to improve this method by calculating a similarity weight to create the agreement matrix. This weight allows partial agreement of the linking variable values for record pairs in the form of a similarity weight. To assess the average accuracy of linking, correctly linked proportions are investigated for each record. Test results on this extension of the
MaCSim approach using the similarity weight concept show higher accuracy of the assessment of linkages.

**Keywords:** Record linkage, linkage accuracy, Markov Chain Monte Carlo, simulation, similarity weight, agreement threshold, agreement tolerance.

1. **Introduction**

In the absence of a unique identifier, records that belong to the same entity are identified and brought together by a record linkage method (Fellegi and Sunter 1969). The advancement of modern record linkage methods came from three disciplines: statistics, computer science, and operations research. The foundation of record linkage is from statistics where the basic ideas of record linkage were first introduced by the geneticist Howard Newcombe and his collaborators (Newcombe et al., 1959, 1962). In their work, they described odds ratios of frequencies and decision rules that identified matches and non-matches. Many algorithms have been developed to handle the record linkage problem using software systems that incorporate ideas from these three disciplines. Despite this, record linkage practice is very limited. The implementation of these software systems is time consuming, costly and induces security concerns over sharing information. Moreover, it is not easy to estimate matching parameters and error rates automatically, as highlighted by the work of Larsen and Rubin (1999). Newcombe’s ideas have been implemented in software for epidemiological applications. This software often relies on previously estimated odds-ratios using large national health files.
Fellegi and Sunter (1969) provided a theoretical foundation of record linkage based on the ideas of Newcombe. According to the Fellegi-Sunter model, a record pair is compared on linking variable values, such as name, address, age, sex, etc that are typically not considered as unique identifiers of entities. The variables used for connecting records are generally called linking variables or linking fields. After the comparison, each record pair is given a weight by assessing each linking field for agreement or disagreement. The assumption of conditional independence of agreement on linking variables within matches and non-matches allows a composite weight to be calculated for each record pair as a simple sum of the individual linking field weights. A decision rule, typically based on a cut-off value, finally determines whether the record pair is asserted to be linked, non-linked or should be considered further as a possible link.

To improve matching efficacy, Newcombe et al. (1959, 1962) introduced the idea of relative frequency of strings. However, Winkler (1989c) and Yancey (2000) noted that in a number of situations the use of relative frequency will not improve matching. The problem of using the relative frequency of strings rigorously is that in some cases the two files may not overlap, and then agreement on a rare value for a field has more discriminatory power in matching than agreement on a frequently occurring value. Also, higher typographical error rates for rare names can result in misleading relative frequency tables.

The computer science literature proposes some advanced methods for record linkage based on textual information, such as, name and address. Some methods focus on parsing and standardising names and addresses into components so that they can be
easily compared (e.g., Winkler 1995, Borkar et al. 2001, Christen et al. 2002, Churches et al. 2002). Parsing is the process of separating a sentence into grammatical parts and standardization involves replacing various spelling of words with a single spelling. Name standardization means identifying components such as first names, titles, surnames or last names etc. and address standardization determines components, for example, house numbers, street numbers, post office boxes etc. Linking records for the variants of names and addresses is not easy, especially for business lists (Winkler 1995).

Winkler (1990a) and Cohen et al. (2003a,b) proposed methods for string comparison based on typographical error. For many typographical errors, it is not always possible to compare two string fields character-by-character. String comparison aims to compare pairs of strings, for example, ‘Smith’ and ‘Snith’. Approximate string comparison has been an important research area for many authors in the computer science literature (e.g., Hall and Dowling, 1980, Navarro 2001). The function for the approximate agreement takes values between 0 and 1 by allowing degrees of partial transpositions. The complete agreement of values is represented by 1 and the total disagreement by 0.

Jaro (1976, see also 1989) proposed a string comparator that takes a value of 1 for exact agreement and takes values less than 1 for partial agreement. The basic algorithm uses the string lengths, the number of common characters in the two strings and the number of transpositions. The transpositions represent the number of characters in one string that are not in the correct sequence of the corresponding common character from the
other string. The distance of the common characters (agreeing character) between strings is half the length of the shorter string.

Winkler (1990a) modelled the effect of different values of string comparators on the likelihood in the Fellegi-Sunter decision rule using truth data sets. Winkler also showed that the alternative to the Jaro string comparator improves matching compared to no string comparator. Winkler's method employs some ideas of Pollock and Zamora (1984) where they provided empirical evidence of the increasing probability of keypunch errors with the character changing position (move to the right) in a string.

The methods mentioned above may not perform well in case of large numbers of typographical errors or non-standardization of records. The inconsistencies of name and address information, non-homogeneous identifying characteristics of record pairs, lack of easy comparable variables for matching, missing matching variables and so on may make automatic matching infeasible or impossible.

Huge amounts of data are now being collected by public or private organizations as well as by researchers and individuals. Linking and analysing relevant information from this massive data reservoir can provide new insights into society. However, this is also associated with challenges such as missing values, typographical or spelling errors and non-standardized formats of data. Consequently, sometimes it is hard to identify a correct link even after clerical review. Besides, linking data involves issues of privacy and confidentiality. Statistical, health, government and business organisations often link administrative, survey, population census and other files to create a new file with complete information for comprehensive analysis. Due to the increasing number of
applications, it is crucial to assess the accuracy of the linked file in order to make valid inferences based on the combined data. There is also a need to develop techniques to improve the linking process to achieve higher accuracy.

In our first paper (Haque et. al., submitted), we proposed a Markov Chain based Monte Carlo simulation approach (MaCSim) for assessing linkage accuracy and illustrated the utility of the approach using synthetic data provided by the Australian Bureau of Statistics (ABS) designed to represent a realistic data setting. MaCSim utilizes two linked files with known true match status to create an agreement matrix and then simulates the matrix using a defined algorithm developed to generate re-sampled versions of the agreement matrix. The defined linking process is simulated using these comparison outcomes and the linkage accuracy is estimated for every record in each simulation. These estimates are collated and summarized to provide an overall linkage accuracy.

In this paper, we aim to improve this method by calculating a similarity weight for every linking variable value for each record pair. These weights are then used to create the agreement matrix. The similarity weight allows partial agreement of the linking variable values for record pairs. A threshold is calculated for every linking variable based on a pre-defined tolerance for that variable. Note that, there may be different thresholds for different linking variables. In the linking process, a record pair will be considered to agree on a linking variable if its similarity weight exceeds the corresponding threshold.

To assess the average accuracy of linking, correctly linked proportions are investigated for each record in all simulations and also for all records in each simulation. The
accuracy of linkages is observed using different blocking strategies. When we block a data file based on a variable i.e. blocking variable, it splits the file into groups that have same value for the blocking variable. Blocking reduces the number of comparisons of record pairs by only comparing record pairs within a block in both files.

The rest of the paper is organized as follows. In Section 2 we introduce the similarity weight concept in the MaCSim algorithm. We present results of data analyses using the new concept in Section 3. We conclude in Section 4 with a summary and discussion about potential applications of the proposed method.

2. **MaCSim with similarity weight**

The MaCSim method utilizes synthetically generated two linked files, $X$ and $Y$, having $R_X$ and $R_Y$ entries, respectively. Both files have same number of $L$ linking fields. Matching parameters $m_l$ and $u_l$ are estimated from these files as true matches are known of these two linked files. Here, $m_l$ is the probability that the $l$th linking field values in both files is the same for a matched pair of records and $u_l$ is the probability that the $l$th linking field values in both files are the same for a non-matched pair of records. We also define $g_l$ to be the probability that either or both of the $l$th linking field values in any record pair are missing regardless of whether the record pair is matched or non-matched.

The MaCSim algorithm assesses the linking process using a Markov Chain based Monte Carlo simulation approach. Several steps are employed: create an agreement matrix; generate re-sampled versions of the agreement matrix; employ a defined linking process to link records using the simulated agreement matrices; and estimate the linkage accuracy for every record in each simulation.
These steps are briefly described in the following sections.
2.1 Create agreement matrix, $A$

An agreement matrix, $A$, is created with a similarity weight for each record pair for every linking variable from the two linked files, $X$ and $Y$, where

$$A = (A_{ijl}); \quad i = 1, \ldots, R_X, \quad j = 1, \ldots, R_Y, \quad l = 1, \ldots, L,$$

is a three-dimensional array consisting of similarity weights of all linking fields across all records in the two files. Here, $A_{ijl}$ takes real values in the range 0 to 1 according to the partial agreement of linking field $l$ for record pair $(i,j)$. The partial agreement values are given using a defined similarity weight formula (Section 2.2). Values of 0 and 1 indicate complete disagreement and agreement, respectively. When either or both of the values in the $l$th linking fields of file $X$ and file $Y$ are missing, a value of '-1' is given.

For simplicity of notation, $A_{iil}$ represents the agreement value of the $l$th linking field for the true matched record pair in both files.

2.2 Similarity weight calculation

The similarity weight of any record pair $(i, j)$ for every linking variable $l$ is calculated by the formula,

$$V_{ijl} = \left(1 - \frac{d_{ijl}}{T_l}\right),$$

where, for any record pair $(i,j)$, $d_{ijl}$ is calculated by the difference between the values for the variable $l$. $T_l$ is the difference between the maximum and minimum values of variable $l$. We set a tolerance for each variable $l$, i.e. $\delta_l$ which is the maximum difference of values of linking variable $l$ that can be accepted as an agreement. We calculate an individual agreement threshold for each linking variable $l$ by

$$\theta_l = \left(1 - \frac{\delta_l}{T_l}\right)$$
For any record pair \((i,j)\) and linking variable \(l\), if the similarity weight \(V_{ijl}\) is greater than or equal to the value of agreement threshold \(\theta_l\), then the variable value is accepted as an agreement.

2.3 Simulating the agreement matrix \(A\)

To generate re-sampled versions of the agreement matrix \(A\), the MaCSim algorithm develops a Markov Chain \(\{A^{(n)}\}_{n=0,1,2,...}\) on \(A=\{\text{set of possible agreement pattern arrays}\}\), with \(A^{(0)} = A\), the observed agreement pattern array for the files \(X\) and \(Y\).

The observed agreement matrix \(A\) is simulated using a defined algorithm to create \(A^*\), where \(A^*\) contains all the simulated agreement matrices. The original MaCSim algorithm described in our first paper (Haque et. al. 2018) is modified here to reflect the changes of agreement matrix with partial agreement values.

A defined linking method (Section 2.5) is applied to link records using the simulated agreement matrices (from \(A^*\)) in each simulation. We estimate the linkage accuracy for each record in every simulation.

The structure of the transition probabilities for the MCMC algorithm employed by extended MaCSim is now outlined. Given the current state of the chain, \(A^{(n)}\), the next state, \(A^{(n+1)}\), will be constructed as follows:
The extended MaCSim considers the initial agreement matrix as the current state, and follows the algorithm to determine the next state that is the next simulated agreement matrix. In the next iteration, the new simulated agreement matrix becomes current state, and in the same way following the algorithm it determines the next state that is another instance of agreement matrix and so on.

Similar to our original MaCSim algorithm, the structure of the transition probabilities for the proposed Markov chain is outlined to replicate circumstances whereby a random element of file $X$ is selected and then its value for the $lth$ linking variable is changed with probability based on its current agreement status with its corresponding partner in the opposite file. On this basis, the internal consistency patterns of agreement are
maintained. If a change has made, this has the consequent effect of changing the agreement patterns in the associated non-matching record pairs. The algorithm describes all possible cases for which a change in one variable value of match and non-match records has impact of other record pairs and changes values accordingly. In the algorithm, the agreement and disagreement values for matched and non-matched records (whether a record pair agrees or disagrees on a variable) are compared to individual threshold of the variable. Note that, in the original MaCSim algorithm, it was compared to 1 (for agree) or -1 (for disagree). Based on this comparison, agree or disagree decision is reached. The current state of the algorithm determines whether the agreement or disagreement value will be changed with probability in the next state. Previously, the changes are made by ‘1 to -1’, and ‘-1 to 1’. In the extended MaCSim, if we decided to change the value in the next state, we change it to (1-value in current state).

In the original MaCSim algorithm, the appropriate selection of the transition probability parameter $p = (p_1, p_2)$ and $q = (q_1, q_2, q_3)$ values ensure that the stationary distribution of the chain maintains the required probabilities of agreement for both matched and non-matched records across the two files. Once values for $p$ and $q$ are determined to ensure the stationary distribution of the chain has the desired structure, this Markov chain is used to generate an appropriate set of re-sampled agreement matrices (Haque et al., 2018). Note that the extended MaCSim algorithm also maintains internal agreement consistency and the selection of the transition probability parameters $p = (p_1, p_2)$ and $q = (q_1, q_2, q_3)$ remains the same as before to ensure the stationary distribution of the chain has the desired structure, and this Markov chain can be used to generate an appropriate set of re-sampled agreement matrices.
2.4 Calculating $m$, $u$ and $g$ probabilities

These probabilities can be estimated using a linked file or they may be known from previous linkages of similar types of data. To recap, $m$ is the probability that the variable values agree when the record pair represents the same entity; $u$ is the probability that the variable values agree when the record pair represents two different entities, and $g$ is the probability when the variable values are missing from either or both records in the pair. From the agreement matrix with similarity weights, it is determined whether the variable values of a record pair agrees or not, based on the agreement threshold of that variable. That is, if the value $V_{ijl}$ in the agreement matrix is greater than or equal to the threshold $\theta_l$, the record pair are determined as agree. For each linking field $m$, $u$, and $g$ are estimated in the following way:

- $m = \frac{\text{number of values that agree for matched record pairs}}{\text{total number of matched record pairs}}.$
- $u = \frac{\text{number of values that agree for non-matched record pairs}}{\text{total number of non-matched record pairs}}.$
- $g = \frac{\text{total number of record pairs of which one or both values are missing}}{\text{total number of possible record pairs}}.$

2.5 Creating an observed link

To create the observed links, the weight of each record pairs is calculated from the agreement matrix $A$ using the probabilities $m$, $u$ and $g$. For any record pair $(i, j)$ and any linking variable, the weight is calculated by

$$w_{ijl} = \log \left( \frac{m_{ijl}}{u_{ijl}} \right)$$
when the values agree (i.e. $A_{ij} \geq \theta_{ij}$); if the values disagree (i.e. $A_{ij} < \theta_{ij}$), the weight is calculated using

$$w_{ij} = \log \frac{1 - m_t - g_t}{1 - u_t - g_t}$$

and for a missing value (i.e. $A_{ij} = -1$), the weight formula is

$$w_{ij} = \log \frac{g_t}{g_t} = \log (1).$$

After all the weights $W_{ij}$ of all record pairs are calculated, the observed links are created following the steps below:

a. First, all record pairs are sorted by their weight, from largest to smallest.
b. The first record pair in the ordered list is linked if it has a weight greater than the chosen cut-off value.
c. All the other record pairs containing either of the records that have been linked in step b are removed from the list. Thus, possible duplicate links are discarded.
d. Go to step b for the second record and so on until no more records can be linked.

The possible number of links that can be declared by the linking process described above will be less than or equal to the number of records in the smaller file since it contains the maximum number of possible matches.

3. Analysis

3.1 Analysis setup

For the analysis, a synthetic dataset is used which consists of information regarding hypothetical individuals. The dataset has been generated by the Australian Bureau of Statistics (ABS). A large file $Y$ is created with 400,000 records. Then, a random
A subsample of 50,000 records is taken from file Y to form file X. Every record has eight data fields or linking variables. These fields are: RECID (Record Identifier), SA1 (Statistical Area 1), MB (Meshblock), BDAY (Birth day), BYEAR (Birth year), SEX (Male/Female), EYE (Eye colour) and COB (Country of birth). The value of each linking field (or linking variable) is generated independently except the value of COB. For COB, 300,000 records are coded by ‘1101’ indicating ‘Born in Australia’ and the remaining 100,000 records are randomly assigned one of about 300 country codes according to the corresponding proportion of people in the 2006 Australian Census.

Some values in file X are changed by replacing them either with a randomly chosen value from the records in file Y or setting the value to ‘missing’ to simulate errors in linking fields. In both files, the RECID (Record Identifier) stays the same (Haque, et al. submitted).

MaCSim creates an agreement matrix using two linked files with known true match status. The agreement matrix is simulated many times using a developed algorithm to generate samples of the agreement matrix. A linking method is defined and followed to link records of the two files using simulated agreement matrices and estimate the accuracy of the link for every record in each simulation.

3.2 Analyses results

Two different blocking variables, namely SA1 (Statistical Area 1), and combined variable SA1 & SEX, are used for the analyses. Blocking takes into account those record pairs in a block to compare that have the same value for a blocking variable, thus reducing the number of comparisons of record pairs.
The agreement matrix $A$ is simulated to obtain $S = 1,000$ replicates $A^*$ of $A$. The value of the thinning parameter $d$ is set to 1,000. Therefore, 1,000,000 MCMC simulations are run and $s$ samples $A^{(s)}$, where, $s = 1, \ldots, 1000$, are retained. Thus, in $A^*$, we have 1000 instances of the agreement matrix $A$.

3.2.1 Distances

The distances between the entries of each $A^*$ ($A^{(2)}, A^{(3)}, \ldots, A^{(S)}$) and the initial agreement matrix $A^{(1)}$ are calculated. In every simulation, the distance is calculated by the total number of agreement values that are changed from the initial values divided by the total number of agreement values. The distance plot in Figure 2 shows the proportion of agreement values that are changing in each simulation.

Figure 2 shows the distances in 1000 simulations using two blocking strategies: (i) blocking variable SA1, (ii) combined variable SA1 & SEX.
The distance plot also ensures that the retained simulated matrices are less correlated
by admitting a thinning parameter $d$. From the distance plot on blocking variable ‘SA1’
in Fig. 2 (i), approximately 28% of the values in the elements of $A^*$ are changed. The
chain converged after 10 iterations. The chain stays stable in 1000 simulations. For the
combined blocking variable SA1 & SEX, the plot (Fig. 2 (ii)) shows that the chain
converges after 5 iterations to around 0.35. Note that convergence occurs at two
different points for these two blocking variables, SA1 and SA1 & SEX. For both variables,
the proportions of agree, disagree, and missing values are different and in each
simulation the chances of agreement and disagreement in the next state depend on the
respective values in the current state.

3.2.2 Correct re-link proportion per X record
In every simulation, the records are linked using the simulated agreement matrices in $A^*$, following the defined linking process in Section 2.6. The total number of times each record is re-linked to the record to which it was originally linked.

When blocking the data with SA1, the first block contains 59 records in File X. Figure 3 (i) shows the correct re-link proportion of each X record in 1000 simulations. The plot shows that the proportion of correct re-links for each of the 59 records lies between 97% and 100% and the average accuracy is 99.75%, indicated with the red line. The
error for each individual record is low with a maximum error of 3% for record number 23.

With the combined variable SA1 & SEX (Fig. 3 (ii)), there are 26 records in the first block in file X. The correct re-link proportion of each X record exceeds 98% in the 1000 simulations. In the plot, the red line shows that the average accuracy is 99.7%. The maximum error is only 1.8%, for record number 17.

3.2.3 Correct re-link proportion per simulation

(i) Correct re-link proportion in every simulation with SA1

(ii) Correct re-link proportion in every simulation with SA1 & SEX

Figure 4: Correct re-link proportion in every simulation when blocking with variable (i) SA1 and (ii) Combined variable SA1 & SEX
In this analysis, the accuracy for all records in File X is estimated in every simulation. The plot (Fig. 4 (i)) shows the correct re-link proportion of all 59 records in each of 1000 simulations when blocking with variable SA1. We obtained 100% accuracy in most of the simulations. In some simulations 98.3% accuracy is obtained where only one record is incorrectly re-linked out of 59 records. The smallest accuracy 96.6% (=57/59) is obtained in only eight simulations where two records are incorrectly linked. It is noticeable that the average accuracy in Fig. 4 (i) for all records in every simulation is 99.75%, which is exactly the same as the average accuracy for each record in all simulations in Fig. 3 (i), as it is expected.

When blocking with SA1 & SEX in Figure 4 (ii), we obtained 100% accuracy in most of the simulations. In some simulations 96.1% accuracy is obtained when 25 records (out of 26) are correctly linked to their original records. The smallest accuracy, 92.3% (=24/26), is obtained in only one simulation. Again, the average accuracy for all records in every simulation is 99.7%, which is the same as the average accuracy that is obtained previously for each record in all simulations in Fig. 3 (ii), as expected.

4. Conclusion

MaCSim assesses linkage accuracy using a Markov chain based Monte Carlo simulation method. In this paper, the use of partial agreement of the linking variable values in the form of a similarity weight in the agreement matrix allows us to reduce the risk of missing potential matches. Since it is not practical to set the same tolerance limit for agreement or disagreement of values for different linking variables, a different agreement threshold is applied for each linking variable which is used to determine the
values for agreement and disagreement for each record pair. Adding this feature to MaCSim is not expensive with respect to computation time but provides greater accuracy than obtained using the original algorithm (Haque et al., submitted for publications).

The similarity weight formula is applied to numeric data fields in the synthetic dataset analysed in this paper. However, for text data fields a different formula is required. As discussed here, this may be achieved by exploiting the processes of parsing and standardisation. Moreover, different similarity weight formulae may be chosen even for numeric values, depending on the context. In addition to using a similarity weight, this paper also demonstrates the use of different agreement thresholds for different variables based on the corresponding tolerance. An alternative approach may be to avoid the use of a tolerance altogether and combine the similarity weights directly. This is an avenue for further investigation. In any event, the extended MaCSim approach described here is shown to be effective in estimating agreement accuracy of two linked files, thereby filling a gap in the existing literature and meeting a practical need in a wide range of applications where linked records are employed.

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