Large Scale Record Linkage in the Presence of Missing Data

Thilina Ranbaduge
The Australian National University
Canberra, Australia
thilina.ranbaduge@anu.edu.au

Peter Christen
The Australian National University
Canberra, Australia
peter.christen@anu.edu.au

Rainer Schnell
University Duisburg-Essen
Duisburg, Germany
rainer.schnell@uni-due.de

ABSTRACT

Record linkage is aimed at the accurate and efficient identification of records that represent the same entity within or across disparate databases. It is a fundamental task in data integration and increasingly required for accurate decision making in application domains ranging from health analytics to national security. Traditional record linkage techniques calculate string similarities between quasi-identifying (QID) values, such as the names and addresses of people. Errors, variations, and missing QID values can however lead to low linkage quality because the similarities between records cannot be calculated accurately. To overcome this challenge, we propose a novel technique that can accurately link records even when QID values contain errors or variations, or are missing. We first generate attribute signatures (concatenated QID values) using an Apriori based selection of suitable QID attributes, and then relational signatures that encapsulate relationship information between records. Combined, these signatures can uniquely identify individual records and facilitate fast and high quality linking of very large databases through accurate similarity calculations between records. We evaluate the linkage quality and scalability of our approach using large real-world databases, showing that it can achieve high linkage quality even when the databases being linked contain substantial amounts of missing values and errors.

1 INTRODUCTION

Organisations such as financial institutions, statistical agencies, and government departments, increasingly require records about entities from multiple databases to be integrated to allow efficient and accurate decision making [12], where such databases can contain millions of records with detailed information about people, such as customers or patients [6, 18]. Record linkage (RL) [15] is one major task required when databases are to be integrated. RL aims to identify and match records that refer to the same entities across different databases [6]. Linked databases allow improvement of data quality, enrichment of the information known about entities, and facilitate the discovery of novel patterns and relationships between entities that cannot be identified from individual databases [7, 12, 32].

Because there is often a lack of unique entity identifiers (such as social security numbers) across the databases to be linked, RL is commonly based on partially identifying attributes, known as quasi-identifiers (QIDs) [8], such as names, addresses, dates of birth, and so on. Data quality aspects such as typographical errors, variations, and changes of values over time (for example when people move or change their names due to marriage) are common in many of the QID attributes used for RL [6]. Due to errors and variations in QIDs, exact matching of attribute values can lead to poor linkage quality [6, 8].

One major data quality aspect that so far has only seen limited attention in RL is missing data [4, 16, 19, 28]. There are various reasons why missing values can occur, ranging from equipment malfunction or data items not considered to be important, to deletion of values due to inconsistencies, or even the refusal of individuals to provide information for example when answering surveys. Missing data can be categorised into different types [26].

Data missing completely at random (MCAR) are missing values that occur without any patterns or correlations at all with any other values in the same record or database. For example, if a first name is missing for an individual, then neither last name, address, age, nor gender, can help predict the missing first name value (assuming no external database is accessible where a complete record of that person is available). With data missing at random (MAR) one can assume that a missing value can be predicted by other values in the same record and/or database. As an example, for a record of a surgeon in an employment database, her salary could be predicted by averaging the salaries of all other (female) surgeons in that database. Data missing not at random (MNAR) do occur for some specific reasons, for example if a patient in a medical study suffered from a stroke and therefore did not return to re-examinations then there will be missing values for this patient in the study’s database. Finally, structurally missing data are values that are missing because they should not exist, and missing is their correct value. For example, young children should not have an occupation. Structurally missing data are different to MNAR data because for the former the correct actual value is an empty value, while for MNAR data there does exist a correct value, but not recorded.

Missing data can often occur in the QID attributes used to link databases. While data imputation can be applied with the aim to fill such missing values before the databases are linked [22, 26], in our work we assume that not all missing values have been imputed. Specifically, imputation is not possible for missing values of types MCAR and structurally missing. For example, as shown in Table 1, if the street address is missing for an individual (like for \( r_1 \)), then no other QID value of this record can help to predict this missing last name value. Missing values can lead to lower similarities between records and thereby affect linkage quality. If alternatively those records or QIDs with missing values are not used for a linkage at all, then linkage quality will also likely suffer.

As an example, given the five records of three entities in the two databases \( D_A \) and \( D_B \) in Table 1, a linkage between \( D_A \) and \( D_B \) would potentially classify the record pairs \( (r_1, r_4) \) and \( (r_2, r_4) \) as matches because they have similar QID values, and it would potentially classify records \( r_3 \) and \( r_5 \) to refer to different entities because they have a low similarity due to name variations and missing values. Therefore, this linkage will be of poor quality due to the wrongly matched record pair \( (r_1, r_4) \) and the non-matched true matching record pair \( (r_3, r_5) \).
Table 1: Two small example databases, $D_A$ and $D_B$, with missing values and variations, and where RecordID and EntityID represent record and entity identifiers, respectively.

| Database | RecordID | EntityID | FirstName | LastName | BirthDate | StreetAddress | City | PhoneNumber |
|----------|----------|----------|-----------|----------|-----------|---------------|------|-------------|
| $D_A$    | $r_1$    | $e_1$    | Peter     | Smith    | 1981-11-25 |             |      |             |
|          | $r_2$    | $e_2$    | Peter     | Smith    | 1981-11-25 | 43 Skye Pl   | Dublin | +353 456 785 |
|          | $r_3$    | $e_3$    | Anne      | Miller   | 1991-09-11 | 43 Skye Pl   | Dublin | +353 456 785 |
| $D_B$    | $r_4$    | $e_2$    | Peter     | Smith    | 1981-11-25 | 43 Skye Pl   |      |             |
|          | $r_5$    | $e_3$    | Ann       | Myller   |           | 43 Skye Place| Dublin | +353 456 785 |

**Contribution:** We propose a novel RL technique that is applicable in situations where QID values contain errors and variations, and importantly that can be missing. For each record in a database to be linked, our approach first generates several distinct attribute signatures by concatenating values from a set of QID attributes [34]. We propose an Apriori [5] based technique to select suitable QID attributes for signature generation. As we detail in Section 4, the aim of attribute signatures is to uniquely describe records such that record pairs can be matched based on the number of common attribute signatures they share.

We then utilise the relationships between entities to identify matching records assuming they contain missing or dirty values in their QID attributes. We first generate a graph of records based on the relationships between them, for example the roles of individuals in a census household (such as father of or spouse of), or shared attribute values such as addresses or phone numbers. We then generate a relational signature for each record based on its neighbourhood in this graph, and calculate the similarities between relational signatures of pairs of records.

We analyse our approach in terms of its computational complexity, and evaluate linkage quality using large real-world data sets, including simulated German census databases containing in total over 130 million records. As the experimental results in Section 5 show, our approach scales to large databases and incorporating relational signatures can help to substantially improve linkage quality compared to several baseline approaches [13, 15, 28, 34].

### 2 RELATED WORK

Missing data has always been a challenge for linking records across databases because missing QID values can result in lower linkage quality. Ong et al. [28] introduced three methods to improve the accuracy of probabilistic RL [15] when records have missing values: redistribute matching weights of attributes that have missing values to non-missing attributes, estimate the similarity between attributes when values are missing in a record, or use a set of additional attributes to calculate similarities if a primary QID value is missing.

Enamorado et al. [13] proposed an approach based on the probabilistic RL model [15] that allows for missing data and the inclusion of auxiliary information when linking records. This approach uses the Expectation-Maximisation (EM) algorithm [9] to estimate matching weights in an unsupervised manner [33]. An approach similar to [13] was proposed by Zhang et al. [35] for adjusting match weights of a record pair when missing data occurred using the EM algorithm, but does not scale to large databases due to its computationally expensive weight estimations.

Goldstein and Harron [19] developed an approach to link attributes of interest for a statistical model between a primary database and one or more secondary databases that contain the attributes of interest. The approach exploits relationships between attributes that are shared across the databases, and treats the linkage of these databases as a missing data problem. The approach uses imputation to combine information from records in the different databases that belong to the same individual, and calculates match weights to correct selection bias.

Ferguson et al. [16] proposed an approach to improve RL when the databases to be linked contain missing values by using a modification of the EM algorithm [9] that considers both the imputation of missing values as well as correlations between QID attribute values. Aninya et al. [4] analysed how different blocking techniques are affected by missing values. They showed that techniques that insert each record into multiple blocks, such as canopy clustering and suffix array indexing [6], performed best when the attributes used for blocking contained missing values.

In contrast to these existing methods [4, 16, 19, 28], our approach does not consider imputation or estimation of similarities when QID values are missing. Instead, we exploit relational information between records to increase the overall similarities between record pairs even if their attribute similarities are low due to missing values, errors, or variations. To the best of our knowledge this work is the first to consider relational information for similarity calculations in the linkage process when records contain missing values.

The use of combinations of QID values (called linkage keys) is commonly used for deterministic linkage [6]. A single attribute combination (such as SLK-581 [23]) or multiple attribute combinations (such as p-signatures [34]), which can improve the likelihood of identifying matches [29], can be used to generate linkage keys to identify matches. However, linkage keys cannot tolerate differences in QID values, nor can they handle missing values or use additional information such as relationships between records [23, 29, 34].

### 3 PROBLEM FORMULATION

Without loss of generality, we assume two deduplicated databases [6], $D_A$ and $D_B$, such that each entity is represented by only one record in a database. We define two disjoint sets, $M$ and $U$, from the cross-product $D_A \times D_B$. A record pair $(r_i, r_j)$, with $r_i \in D_A$ and $r_j \in D_B$, is a member $M$ (true matches) if $(r_i, r_j)$ represents the same entity;
otherwise \((r_i, r_j)\) is a member of \(U\) (true non-matches) and \(r_i\) and \(r_j\) represent two different entities. With the true class (\(M\) or \(U\)) unknown, the record linkage process attempts to accurately classify each record pair as belonging to either \(M\) or \(U\) [6, 15].

As we detail in Section 4, the aim of our approach is to link records between databases based on their values in QID attributes, as well as relationship information between records. We first generate a set of attribute signatures for each record, where each signature is formed by concatenating one or more tokens (substrings) extracted from QID values [34]. These tokens are generated by applying various string manipulation functions. Any pair of records with the same values for a given set of QID attributes will have the same attribute signature, thus leading to the identification of matching records. We define an attribute signature as:

\textbf{Definition 3.1 (Attribute Signature).} Let \(D\) be a database where each record \(r \in D\) contains values \(a\) in a set of QID attributes \(A\). Let \(S = \{a \in A : C(a)\}\) be a list of attributes where each \(a \in S\) is selected according to a certain criteria \(C\). The attribute signature of \(r\) using \(S\) is defined as \(\mathcal{A}(r, S) = \text{concat}((g_a(r.a) : a \in S))\), where \(\text{concat}()\) is the string concatenation function and \(g_a()\) is a manipulation function applied on the value \(r.a\) of attribute \(a\).

For example, let us assume the attributes selected for attribute signature generation are based on a criteria \(C\) of an attribute having a maximum of 20% of records in a database with missing values. Thus, assuming an attribute combination \(S_1 = \{\text{FirstName}, \text{LastName}, \text{yearOf(BirthDate)}\}\) is selected, the attribute signature generated for record \(r_1\) in Table 1 is PeterSmith1981, where the values 1981 is a token and the string manipulation function \(\text{yearOf()}\) returns the year of a date of birth value.

No signature can be generated for \(r\) if a QID value used in \(S\) is missing for \(r\) [34]. Furthermore, errors and variations in QID values can result in different signatures, which can lead to record pairs to be classified as false matches or false non-matches. For example, assuming the same attribute combination as \(S_1\), the records \(r_1\) and \(r_4\) in Table 1 will be classified as a match because they have the same signature \(\mathcal{A}(r_1, S_1) = \mathcal{A}(r_4, S_1) = \text{PeterSmith1981}\), while \(r_3\) and \(r_5\) will be classified as non-match since no attribute signature can be generate for \(r_5\) due to its missing date of birth value.

To improve similarities when records contain missing values, or errors and variations, we use the relationships between records in a database, as identified through some attributes such as family relationship, address, or phone number. For example, the records \(r_2\) and \(r_3\) in Table 1 can be considered as related because they share the same phone number. We represent records and their relationships in a record graph, defined as:

\textbf{Definition 3.2 (Record Graph).} Let \(G = (V, E)\) be an undirected graph where \(V\) is the set of vertices, and each \(v \in V\) represents a record \(r \in D\). The set of edges of \(G\) is defined as \(E = \{(v_i, v_j) : v_i, v_j \in V \land v_i \xrightarrow{a} v_j\}\) where \(v_i \xrightarrow{a} v_j\) represents a relationship over an attribute \(a \in A\) between records \(r_i\) and \(r_j\).

We then generate a \textit{relational signature} for each \(v \in G\) based on its graph neighbourhood [2], such as the degree of \(v\), where we generate \(m \geq 1\) features for the relational signature of a record. We define a relational signature as:

\textbf{Definition 3.3 (Relational Signature).} The relational signature of a record \(r \in D\) based on its corresponding vertex \(v \in G\), using its neighbourhood \(N(v) = \{v_j : (v, v_j) \in E\}\) is defined as \(\mathcal{R}(r) = (f_1(N(v)), \cdots, f_m(N(v)))\), with \(f_i\) being a certain graph feature generated from the neighbourhood \(N(v)\).

As we describe next, the features \(f_i\) that can be used in relational signatures include degree and density using the egonet of a vertex [2], or we can use the QID values of neighbouring vertices (records) as features for a given vertex. For example, records \(r_3\) and \(r_4\) in Table 1 can be matched based on their respective neighbouring records \(r_2\) and \(r_4\), given they share a highly similar street address, and generate the same attribute signature \(\mathcal{A}(r_3, r_4) = \mathcal{A}(r_2, r_4) = \text{Peter1991Skye}\) for \(S_2 = \{\text{FirstName}, \text{yearOf(BirthDate)}, \text{streetName(StreetAddress)}\}\).

\section{Signature Based Record Linkage in the Presence of Missing Data}

Our approach consists of three main steps. We first provide an adaptive method to select attribute combinations (from the set of QID attributes \(A\)) that are suitable to generate attribute signatures. We then generate several attribute signatures per record, as well as one relational signature per record based on the record graph we build for each database to be linked. Finally, we use the generated attribute and relational signatures to identify matching records.

\subsection{Attribute Selection}

The choice of QID attributes plays an important role for attribute signature generation. The aim of each attribute signature is to distinctively describe each record, such that if two records share the same attribute signature it is highly likely that they belong to the same entity. Due to errors, variations, and missing values in QIDs, however, a certain attribute combination might not be suitable as an attribute signature. For example, \(S_3 = \{\text{FirstName}, \text{BirthDate}\}\) in Table 1 would generate the same attribute signature \(\text{Peter1981-11-25}\) for records \(r_1, r_2, r_4\), and result in the false matching of record pair \((r_1, r_4)\).

One way to overcome this issue is to select a set \(S\) of attributes based on domain knowledge [34]. However, such knowledge is not always available, or it might be inadequate for a given linkage project, leaving a user to randomly select combinations of (potentially not suitable) QIDs for attribute signature generation. We therefore propose a method to select suitable QID attributes for signature generation based on their data characteristics. We consider two aspects in the selection process, (1) completeness, which measures the amount of missing values in each attribute, and (2) Gini impurity [20], which measures the homogeneity of an attribute with respect to the number of its distinct values.

As we outline in Algorithm 1, we follow an Apriori based approach [3, 5] where we use an iterative search over attribute combinations of length \(k\) generated from suitable attribute combinations of length \(k-1\). First, in lines 1 and 2, we initialise an inverted index \(C\) to store the combinations we need to process. In lines 3 to 13 we then loop over each attribute combination of size \(k\), with \(2 \leq k \leq |A|\). In line 4, using the function \text{genCombinations()} we generate the set \(C[k]\) of attribute combinations of size \(k\) based on the previously generated combinations \(C[k-1]\) of size \(k-1\).
Algorithm 1: Attribute Selection

Input:
- D: Database to be linked
- A: List of QID attributes
- n_a: Number of combinations required
- α: Score weight, with 0 ≤ α ≤ 1
- ε_t: Attribute selection threshold, with 0 ≤ ε_t ≤ 1

Output:
- C_S: List of candidate attribute combinations

1: C = (); T = []; k = 2 // Initialise variables
2: C[1] = genCombinations(A) // Set initial combinations
3: while k ≤ |A| do: // Loop over all sizes of combinations
4: C[k] = genCombinations(C[k − 1])
5: foreach S ∈ C[k] do: // Loop over each combination S
6: s_c = getCompletenessScore(S, D) // Completeness of S
7: s_g = getGiniScore(S, D) // Gini impurity of S
8: s = α · s_c + (1 − α) · s_g // Calculate overall score of S
9: if s ≥ ε_t do: // Check if score s is at least ε_t
10: T = add(S, s) // Add the combination and its score
11: T = removeSubCombinations(S, T) // Remove subsets
12: else: // Score s is less than ε_t
13: C[k].remove(S) // Remove the combination S
14: k = k + 1 // Increment k
15: C_S = getTopCombinations(T, n_a) // Get best combinations
16: return C_S

Algorithm 2: Signature Generation

Input:
- D: Database to be linked
- A: List of QID attributes
- C_S: List of candidate attribute combinations
- F: List of graph feature functions
- p_t: Probability threshold, with 0 ≤ p_t ≤ 1

Output:
- S: Signature database

1: S = []; A = []; L = ∅ // Initialise variables
2: foreach r ∈ D do: // Loop over each record in the database
3: A[r.id] = ∅ // Initialise to an empty set
4: foreach S ∈ C_S do: // Loop over each combination
5: Ss = genAttrSignature(r, S) // Attr. signature (Def. 3.1)
6: A[r.id].add(Ss) // Add the generated signature to A
7: L.add(Ss) // Add the generated signature to the set L
8: foreach Ss ∈ L do: // Loop over attribute signatures
9: p = getSigProbability(Ss, A) // Calculate the probability
10: if p < p_t do: // Check if the probability is less than p_t
11: A = removeSignature(Ss, A) // Remove the signature
12: G = genRecordGraph(D, A) // Generate the graph (Def. 3.2)
13: foreach r ∈ G do: // Loop over each record in G
14: Ss = genRelSignature(r, G, F) // Rel. Signature (Def. 3.3)
15: S[r.id] = (A[r.id], Ss) // Add signatures of r to S
16: return S

Following the Apriori principle [3], to generate an attribute combination \( S \) of size \( k \) requires that all its attribute combinations of size \( k − 1 \) are in \( \mathcal{C}[k − 1] \), which means all its subsets must satisfy the selection criteria we detail below. For example, for the attribute combination \( \{a_1, a_2, a_3\} \) of size \( k = 3 \), where \( a_i \in A \), all three combinations \( \{a_1, a_2\}, \{a_2, a_3\}, \) and \( \{a_1, a_3\} \) must be in \( \mathcal{C}[2] \).

In lines 5 to 7, the algorithm iterates over each combination \( S \in \mathcal{C}[k] \) and calculates the completeness and Gini impurity scores \( s_c \) and \( s_g \), respectively. We calculate \( s_c = (|D| - m_S)/|D| \), where \( |D| \) is the number of records in \( D \) and \( m_S \) is the number of records with missing values for any attribute in \( S \). We calculate the Gini impurity of \( S \) as \( s_g = \sum_{v \in V} P(v) \cdot (1 – P(v)) \), where \( V \) is the list of unique values in \( S \) and the probability \( P(v) = f_v/|D| \) with \( f_v \) being the frequency of value \( v \) in \( D \). In lines 8 and 9, a combination \( S \) is selected as a candidate attribute signature if the weighted score \( s = α \cdot s_c + (1 − α) \cdot s_g \) is at least the threshold \( ε_t \), where \( α \) determines the importance of completeness over Gini impurity.

If the score \( s \) is at least \( ε_t \), in lines 10 and 11 we add \( S \) along with its score \( s \) to the list \( T \), and remove any subsets of \( S \) from \( T \) that were added in previous iterations. This subset pruning prevents redundant attribute combinations and reduces the costs of generating not required attribute signatures. For instance, if the attribute combination \( \{\text{FirstName}, \text{LastName}\} \) is selected, then all its subsets \( \{\text{FirstName}\}, \{\text{LastName}\}, \) and \( \{\text{LastName}, \text{BirthDate}\} \) are pruned because they cannot provide more distinctive attribute signatures.

In line 13, we remove the combination \( S \) from the set of combinations \( \mathcal{C}[k] \) if its score \( s \) is less than \( ε_t \). This ensures the supersets of \( S \) will not be processed in subsequent iterations. For instance, if the score of the attribute combination \( \{\text{FirstName}, \text{LastName}\} \) is less than the threshold \( ε_t \), then it is unlikely that its superset, such as \( \{\text{FirstName}, \text{LastName}, \text{BirthDate}\} \), can provide more distinctive attribute signatures.

In line 14 we increment the value of \( k \) by 1 allowing the algorithm to continue processing attribute combinations until \( k = |A| \). Finally, in line 15 we select the \( n_a \) attribute combinations with the highest scores in the list \( T \) to create the final list of combinations \( \mathcal{C}_S \). As we show in Section 5, increasing the number of attribute combinations, \( n_a \), can lead to an increase of the overall runtime of our approach as more signatures are generated per record, but potentially can also increase the linkage quality as more attribute signatures will be considered when comparing a pair of records.

The complexity of Algorithm 1 is \( O(|D| \cdot 2^{|A|}) \). The attribute selection threshold, \( ε_t \), can be used to increase or decrease the number of candidate attribute combinations that are pruned in each iteration, with lower values for \( ε_t \) generating more attribute combinations.

4.2 Signature Generation

As shown in Algorithm 2, in the second step we generate attribute and relational signatures for each record \( r \) in the database \( D \). In line 2 we loop over each \( r \in D \), and initialise an inverted index list in \( A \) by adding the corresponding record identifier \( r.id \) as a key and with an empty set as values (line 3). Next, for each attribute combination \( S \) in the list of attribute combinations \( \mathcal{C}_S \) from Algorithm 1, we generate the corresponding attribute signature \( \mathcal{A}_S \) (as per Definition 3.1) and add it to the sets \( A[r.id] \) and \( L \) (lines 5 to 7).
Attribute signatures are generated only if all attributes in \( S \) have a value for a given record. As we discussed in Section 3, we require signatures to be unique to a record because otherwise they can lead to incorrectly linked records. The probability for a given attribute signature \( A_S \) to occur repeatedly in \( n \) records is governed by a Binomial distribution [26].

The probability of an attribute value combination in a record to become an attribute signature decreases if the value combination occurs in multiple records. We followed the same probability calculation described by Zhang et al. [34] to calculate the probability \( p \) of an attribute signature \( A_S \in L \) to be considered as a signature, which can be calculated as \( p = P(A_S | n = \{r.id : \forall r.id \in A \in \Lambda \}) = 1/(1 + \lambda^n \mu) \), with \( 0 < \mu < 1 < \lambda \). The two parameters \( \lambda \) and \( \mu \) control how fast the maximum of \( p \) decreases as the number of records \( n \) that have signature \( A_S \) increases [34]. We refer the reader to [34] for more details on this probability calculation.

We keep \( A_S \) if its probability \( p \) is at least the threshold \( p_t \) (line 10), otherwise we remove \( A_S \) from all records in \( A \) in line 11. In line 12 we then generate the record graph \( G \) following Definition 3.2. In line 13 we loop over each record \( r \in G \) and in line 14 we generate the relational signature \( R_S \) for \( r \) based on its local neighbourhood structure in \( G \). We provide a list \( F \) of graph feature functions to the function \textit{genRelationalSignature()} which generates a \( R_S \).

To generate a relational signature we use different features that describe the local graph neighbourhood of a vertex in \( G \). Features include degree and egoenit density of a vertex [2], as well as the attribute signatures of its neighbouring vertices for a given vertex. Finally, in line 15, we add the set of generated attribute signatures \( A[r.id] \) and \( R_S \) of each record \( r \in D \) into the signature database \( S \) using the corresponding record identifier \( r.id \) as the key.

Generating the graph \( G \) is of \( O(|D| + |D| \cdot |F|) \), assuming the average number of neighbours of a record in \( G \) (its degree) is \( d \). If we assume \( |C_S| \) attribute combinations have been generated by Algorithm 1, and each record in \( D \) is on average represented by \( l \) attribute signatures, and \( |F| \) is the number of features considered to generate a relational signature, then the complexity of the signature generation process in Algorithm 2 is \( O(|D| \cdot ((|C_S| + l \cdot d) \cdot |F|)) \).

### 4.3 Signature based Record Matching

In the last step, as outlined in Algorithm 3, we compare the attribute and relational signatures generated for each record to find matching record pairs that correspond to the same entity. We first calculate the similarities between attribute signatures, and if these are low due to missing QID values, or errors and variations in QID values, we calculate the similarities between relational signatures.

Our signature based matching process uses the two signature databases \( S_A \) and \( S_R \) of databases \( D_A \) and \( D_B \), respectively, as generated by Algorithm 2. We use the function \textit{simA()} in Algorithm 3 to calculate a similarity between records based on the number of attribute signatures that they have in common, while \textit{simR()} calculates similarities between features in relational signatures. For example, \textit{simR()} can be a set based similarity function such as Jaccard or Dice similarity [6] if we use the QID values of neighbouring records as relationship features.

In line 2, the function \textit{genRecordPairs()} returns the set of all record pairs \( R = \{(r_A, r_B) : A_S \in S_A[r_A.id], A_S \in S_B[r_B.id] \} \) that have at least one attribute signature in common. In line 3, we loop over each \( (r_A, r_B) \in R \) and get its respective set of attribute and relational signatures, \( \Lambda_A, \Lambda_B, \) \( \Gamma_A \), and \( \Gamma_B \) in line 4. We calculate the similarity \( s_A \) between the sets of attribute signatures \( \Lambda_A \) and \( \Lambda_B \), and if \( s_A \) is at least a user specified threshold \( s_t \) then we add \((r_A, r_B)\) into the set \( M \) of matching record pairs (lines 5 to 7).

For non-matching record pairs, in line 9 we calculate the similarity \( s_R \) between their relational signatures \( \Gamma_A \) and \( \Gamma_B \), and then calculate the weighted average similarity \( s \) using both \( s_A \) and \( s_R \). If \( s \) is at least \( s_t \) then in line 12 the record pair \((r_A, r_B)\) is classified as a match and added to \( M \), which is returned in line 13.

The complexity of Algorithm 3 is \( O(n) \) if we assume \( n = |D_A| = |D_B| \) and each record in \( D_A \) and \( D_B \) has generated a unique attribute signature in the signature generation step in Algorithm 2.

### 5 EXPERIMENTAL EVALUATION

We use six real-world data sets to empirically evaluate our proposed approach, as summarised in Table 2, where each data set contains a pair of databases. Two are bibliographic data sets [24], DBLP-Scholar and DBLP-ACM, where their entities are academic publications, and each record contains title, authors, venue, and year of publication. We added missing values randomly, following the missing completely at random (MCAR) missing data category, to authors, venue, and year of publication, ensuring each record contains at most two missing values. The relationships between publications are identified based on their common authors.

The UKCD data set consists of census records of 12,044 households collected from 1851 to 1901 in 10 year intervals for the town of Rawtenstall and surrounds in the United Kingdom [17]. We use the role of individuals in a household to identify the relationships
between records. We used first name, middle name, surname, address, occupation, gender, age, and birth parish as QIDs, where 24% of records contain missing values in at most four of these attributes.

We assume the missing data in the UKCD data set represents the MCAR, MAR, and MNAR categories. This is because the missing values in attributes such as first or middle name cannot be imputed using other QID values, which makes them MCAR data. The missing values in address could be imputed based on the other available information of the household as we assume all members lived at the same address when the census was collected, hence they follow the MAR category. Finally, some missing values in the occupation attribute follow MNAR as records about children do not contain an occupation.

The NCVR data sets contain records from an October 2019 snapshot of the North Carolina voter registration database (available from: http://dl.ncsbe.gov/). We extracted 309,877 household units from this snapshot and created two subsets, NCVR-20 and NCVR-50, where we randomly created (assuming MCAR) at most five missing values in the QID attributes first, middle, and last names, street address, city, and zip code in 20% and 50% of records, respectively. To evaluate our approach with data of different quality, we then applied various corruption functions using the GeCo data corruptor [8] on between 1 to 3 randomly selected QID values of 20% of records. For relationship information we considered if two records shared the same last name and address.

Finally, we use two full NCVR snapshots from October 2017 and October 2019, named as NCVR-2017 and NCVR-2019, respectively, as two databases to be linked. We use the same QID attributes first name, middle name, last name, street address, city, and zip code as the other NCVR data sets for linkage. The last name and address QIDs did not contain any missing values, and we therefore consider two voters as related if they share the same address and last name. Among the 89% voters who appear in both snapshots, 1%, 3%, 1.3%, 17%, 10%, and 12.5% of voters have changed their first name, middle name, last name, address, city, and zip code, respectively.

We compare our approach (RA-Sig) with four baseline linkage techniques. We use traditional probabilistic record linkage (ProbLink) as proposed by Fellegi and Sunter [15] as a baseline given this approach is widely used in practical record linkage applications [16, 19]. We also use the method by Ong et al. [28] (ReDistLink) that redistributes weights of QID attributes that have missing values to non-missing QID attributes, where these attribute weights are calculated based on the probabilistic RL method [15].

The third baseline is the probabilistic signature approach (P-Sig) proposed by Zhang et al. [34], which identifies attribute signatures that distinctly describe records, without however considering errors, variations, nor missing values. Finally, we use the recently proposed probabilistic linkage approach by Enamorado et al. [13], named FastLink. This approach also utilises the Expectation Maximisation algorithm based probabilistic RL model [9, 15] which estimates matching weights considering missing values and auxiliary information when linking records.

Based on a set of parameter sensitivity experiments, in Algorithm 1 we set \( n_q = [1, 5, 10], \alpha = 0.5, \) and \( e_I = [0.5, 0.7, 0.9]. \) Following [34], we set \( \lambda = 1.2, \mu = 0.2, \) and \( p_I = [0.5, 0.7, 0.9] \) in Algorithm 2. We use the attribute signatures of neighbouring vertices as features in Algorithm 3. The Jaccard coefficient [6] is used for both \( \text{sim}_A() \) and \( \text{sim}_I() \), and in Algorithm 3 we set \( \beta = 0.5. \) Following [28] we set the similarity threshold \( s_I \) in Algorithm 3 to range from 0.5 to 1.0 (in 0.1 steps) for all techniques.

We evaluated scalability using runtime, and linkage quality using precision and recall [6]. Precision measures the number of true matched record pairs against the total number of record pairs generated by a particular approach; and recall measures the number of true matched record pairs against the total number of record pairs in the linked ground truth data [21]. We do not use the F-measure for evaluation because recent research has shown that F-measure is not suitable for measuring linkage quality in record linkage due to the relative importance given to precision and recall which depends upon the number of predicted matches [21].

We ran experiments on a server with 64-bit Intel Xeon (2.1 GHz) CPUs, 512 GBytes of memory, and running Ubuntu 18.04. We implemented all techniques in Python (version 3) except FastLink for

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### Table 2: A summary of the number of records, percentage of records containing missing values, and the number of ground truth record pairs for each data set pair used in the experimental evaluation.

| Data Set Pair                  | DBLP - Scholar | DBLP - ACM | UKCD | NCVR-20 | NCVR-50 | NCVR-2017 - NCVR-2019 |
|-------------------------------|----------------|-----------|------|---------|---------|-----------------------|
| Records                       | 2,616          | 64,263    | 2,616| 2,294   | 877,012 | 877,012               |
| Missing %                     | 17%            | 54%       | 20%  | 20%     | 50%     | 12%                   |
| Ground truth pairs            | 2,386          | 2,220     | 18,354| 877,012 | 877,012 | 6,948,248             |

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### Table 3: Average runtime results (in seconds) for linking the different data set pairs.

| Data Set Pair                  | DBLP - Scholar | DBLP - ACM | UKCD | NCVR-20 | NCVR-50 | NCVR-2017 - NCVR-2019 |
|-------------------------------|----------------|-----------|------|---------|---------|-----------------------|
| ProbLink [15]                 | 143            | 12        | 164  | 1,155   | 1,143   | 38,468               |
| ReDistLink [28]               | 141            | 11        | 148  | 1,090   | 1,125   | 34,766               |
| P-Sig [34]                    | 9              | 6         | 8    | 45      | 47      | 892                  |
| FastLink [13]                 | 15             | 26        | 38   | 267     | 279     | 6,482                |
| RA-Sig (steps 1 / 2 / 3)      | 5 / 1 / 5      | 5 / 1 / 2 | 10 / 2 / 3 | 112 / 43 / 17 | 123 / 39 / 19 | 861 / 363 / 198 |
Large Scale Record Linkage in the Presence of Missing Data

which we used an Apache Spark based Python implementation developed by the Ministry of Justice in the United Kingdom [27]. Though their original implementation takes the advantage of parallelisation, we ran all experiments on a single-core to allow a fair evaluation. We followed [1, 10] to measure the statistical significance of linkage results. To facilitate repeatability, the programs and data sets are available from: https://dmm.anu.edu.au/ra-sig.

Table 3 shows the runtime of all approaches on the different data sets. As can be seen, the attribute selection step of our approach has the longest runtime due to the complexity of the Apriori based iterative selection method. This runtime can however be decreased by increasing \( c_i \) to reduce the number of candidate attribute combinations to be processed in each iteration. As shown in Table 3, the linkage between two full NCVR snapshots took less than 30 minutes to complete all three steps of our approach. This shows our approach scales to large database sizes, making it applicable for large-scale linkages of databases that contain errors and missing values. Overall, P-Sig was the fastest approach (however it cannot handle errors nor missing values), while ProbLink, ReDistLink, and FastLink required substantially longer runtime due to the weight calculations and attribute string comparison they employ [6].

The top row of Figure 1 shows the linkage quality of our approach for different values of \( c_i \) used in the adaptive attribute selection method. A low value of \( c_i \) resulted in lower linkage quality because attribute combinations that are selected can include QID attributes with more missing or less distinct values. However, irrespective of the value of \( c_i \), the Apriori based attribute selection method results in substantially increased linkage quality compared to randomly selecting QID attribute combinations for attribute signatures.

The middle row in Figure 1 shows the linkage quality of our approach with different numbers of attribute combinations \( n_a \) in Algorithm 1. As can be seen, an increase in the number of combinations, \( n_a \), improves both overall precision and recall. This is because more attribute signatures can be generated for each record which can potentially identify matching record pairs even their QID values are missing or contains errors and variations.

We measured the linkage quality of our approach with different probability thresholds \( p_t \) for the attribute signature generation in Algorithm 2. As shown in the bottom row of Figure 1, a lower \( p_t \) value reduces the precision of our approach because the generated attribute signatures are not distinct enough (they are shared by many records), which can potentially lead to false positives. On the other hand, a higher \( p_t \) value tends to increase precision with
Table 4: Average precision and recall results (P / R) with $s_t = 0.8$. The best results are shown in bold.

|                       | DBLP - Scholar | DBLP - ACM | UKCD   | NCVR-20 | NCVR-50 | NCVR-2017 - NCVR-2019 |
|-----------------------|----------------|------------|--------|---------|---------|-----------------------|
| ProbLink [15]         | 0.53 / 0.31    | 0.94 / 0.53 | 0.83 / 0.64 | 0.72 / 0.83 | 0.67 / 0.41 | 0.82 / 0.81 |
| ReDistLink [28]       | 0.67 / 0.32    | 0.96 / 0.57 | 0.84 / 0.65 | 0.73 / 0.84 | 0.67 / 0.66 | 0.82 / 0.84 |
| P-Sig [34]            | 0.87 / 0.61    | 0.97 / 0.65 | 0.95 / 0.71 | **0.97 / 0.82** | 0.91 / 0.70 | 0.95 / 0.85 |
| FastLink [13]         | 0.73 / 0.58    | 0.96 / 0.69 | 0.91 / 0.71 | 0.93 / 0.77 | 0.68 / 0.63 | 0.85 / 0.88 |
| RA-Sig                | 0.86 / 0.73    | **0.99 / 0.83** | 0.92 / 0.86 | **0.97 / 0.91** | **0.96 / 0.84** | **0.98 / 0.93** |

Table 5: Average runtime (in seconds) and linkage quality results with $s_t = 0.8$ for German census data sets.

|                         | Attribute selection step (Algorithm 1) | Signature generation step (Algorithm 2) | Record matching step (Algorithm 3) |
|-------------------------|---------------------------------------|----------------------------------------|-----------------------------------|
| Runtime                 | 7,903                                 | 4,573                                  | 3,438                             |
| Linkage quality         | Precision                              | Recall                                 | 0.999                             |
|                         | 0.962                                  |                                        |                                   |

a drop of recall because only a few signatures are compared in the matching process. We also noted that a lower $p_t$ value can increase the runtime of our approach by 5% to 10% due to many attribute signatures being generated in Algorithm 2.

The average linkage quality achieved by the different approaches for similarity threshold $s_t = 0.8$ in Algorithm 3 is shown in Table 4. As can be seen, RA-Sig resulted in high precision and recall values with all data sets which illustrates that the use of relationship information between records can correctly match records even when their QID attributes contain missing values, or variations and errors. The linkage quality results remain qualitatively similar if we change the threshold $s_t$ from 0.5 to 1.0.

The probabilistic linkage approaches performed poorly due to missing values that resulted in low similarities (even with weight redistribution [28] or estimation of weights considering missing values [13]), and many record pairs were classified as non-matches. P-Sig achieved similar precision as our approach because we are using the same set of candidate signatures generated in Algorithm 1 for P-Sig. However, RA-Sig achieved, based on Tukey’s honestly significant difference (HSD) post hoc test [1], statistically significant improvement in recall (10% to 20%) even if the QID attributes contain large numbers of missing values.

### 6 LARGE SCALE REAL DATA LINKAGE

In this section, we describe how we apply our approach in a real-world record linkage setting. We use our approach to link two simulated Census data sets containing information of all households in Germany.

**Problem Description:** Due to the number of changes required on population censuses and increasing demands for faster and more frequent census statistics, European countries transition from traditional census operations to register-based censuses [31]. In Germany, the next census will be similar to the Census 2001 a combination of a register-based and a traditional census. After the Census 2022, Germany will use a register-based census to decrease respondent burden, cost and time needed for processing [25]. A major challenge for any register-based census is linking various available administrative registers if no unique personal identification number is available.

**German Census Simulation Data:** Since no unique personal identification number is currently available in Germany, QID attributes such as names, date of birth, and place of birth have to be used for linking. Data protection regulations, such as GDPR [14], do not permit the permanent storage of QID attribute values in official statistics. Therefore, data sets used for the development of linkage applications have to use artificially simulated data [30]. Such data have to consider regional variations in household size, compositions of households, number and kind of institutional populations, name variations according to date of birth and many more restrictions usually not considered when generating artificial data for simulations. Furthermore, the amounts of errors and the frequency of incomplete QID attributes have to be considered.

Destatis [11], the Federal Statistical Office of Germany, therefore, commissioned a research group at the University of Duisburg-Essen to develop suitable data sets which fulfill the given constraints. These data sets are based on real-world samples of first names and last names, the actual distribution of households at given addresses and marginal distributions of population characteristics [30]. Two of these data sets, with 81,194,354 and 55,321,209 with an overlap of 55,126,620 records, are used in the experiments presented here. We use first and last names, date of birth, gender, and street address as QIDs for linkage and household identifiers to get relationships between entities. The two data sets contain 1% missing values, with 4%, 3.3%, 2.6%, and 1.3% of individuals having changes in their first name, last name, date of birth, and street address, respectively.

**Results and Discussion:** Table 5 shows the runtime and linkage quality results our approach achieved linking these two census data sets. As can be seen, our approach completed the linkage in less than 5 hours. Our approach generated approximately 400 million unique attribute signatures in Algorithm 2 when we selected the five best attribute combinations in Algorithm 1, and set the score weight as $c_t = 0.5$ and attribute selection threshold as $c_r = 0.6$, respectively. As shown in Table 5, our approach achieved an overall precision and recall of 0.999 and 0.962, respectively, which involves the comparison of approximately 54 million candidate record pairs.

The initially used combination of algorithms (including exact matching [6], phonetic matching [6], and FastLink [13]) needed more than 300 hours on average to link the two data sets achieving similar linkage quality which shows the superiority of our approach when linking large databases containing millions of records.
7 CONCLUSION
We have presented an efficient approach to link records even when they contain errors or missing values. Our approach generates suitable attribute signatures using an unsupervised selection method, and relational signatures from relationship information between records. Combined these signatures can uniquely identify individual records and facilitate very fast and accurate linking of large databases compared to other state-of-the-art linkage techniques. As future work, we plan to evaluate our approach under different missing data scenarios, and to use graph embeddings to generate improved relational signatures. We also aim to extend our approach to facilitate efficient and accurate private record linkage [7].

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