

# A Hybrid Genetic-Bootstrapping Approach to Link Resources in the Web of Data

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**Abstract.** In the Web of Data, real-world entities are represented by means of resources, for instance the southern Spanish city “Seville” that is represented by means of the resource that is available at <http://es.dbpedia.org/page/Sevilla> in the DBpedia dataset. Link rules are intended to link resources that are different, but represent the same real-world entities; for instance the resource that is available at <https://www.wikidata.org/wiki/Q8717> represents exactly the same real-world entity as the resource aforementioned. A link rule may establish that two resources that represent cities should be linked as long as the GPS coordinates are the same. Such rules are then paramount to integrating web data, because otherwise programs would deal with every resource independently from the other. Knowing that the previous resources represent the same real-world entity allows them to merge the information that they provide independently (which is commonly known as integrating link data). State-of-the-art link rules are learnt by genetic programming systems and build on comparing the values of the attributes of the resources. Unfortunately, this approach falls short in cases in which resources have similar values for their attributes, but represent different real-world entities. In this paper, we present a proposal that hybridises a genetic programming system that learns link rules and an ad-hoc filtering technique that bootstraps them to decide whether the links that they produce must be selected or not. Our analysis of the literature reveals that our approach is novel and our experimental analysis confirms that it helps improve the  $F_1$  score, which is defined in the literature as the harmonic mean of precision and recall, by increasing precision without a significant penalty on recall.

## 1 Introduction

The Web of Data has made it possible for programs to have access to a variety of data about real-world entities. Furthermore, the Linked-Data principles [4]

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support the idea that resources that are different but represent the same real-world entities must be linked so as to facilitate data integration. Link rules are intended to help link resources automatically.

The literature provides several proposals to machine learn link rules by means of genetic programming systems [2, 11, 12, 19, 20]. Such rules build on transformation and similarity functions that are applied to the values of the attributes of two resources to check if they can be considered similar enough (by attributes we mean their datatype properties); if they are, then the input resources are assumed to represent the same real-world entity and are then linked; if they are not, then the input resources are kept apart. Our experience confirms that such link rules fall short because some resources that represent different real-world entities have attributes with similar values. For instance, think of the many different authors who have the same name or the many different films that have similar titles.

In this paper, we present a hybrid approach to the problem: first, we use a state-of-the-art genetic programming system to learn a set of link rules; we then select a base link rule and apply it in order to obtain a collection of candidate links; the remaining rules are then bootstrapped to analyse the neighbours of the resources involved in each candidate link (the neighbours are the resources that can be reached by means of their object properties); finally, we analyse how similar they are in order to decide which of the candidate links must be selected as true positives and which must be discarded as false positives. Our analysis of the related work unveils that this is a novel approach since current state-of-the-art link rules do not take the neighbours into account. Our experimental analysis confirms that precision can be improved by 68% in average, with an average -10% impact on recall; overall, the average improvement regarding the  $F_1$  score is 47%. We also conducted the Iman-Davenport test to check that these differences are statistically significant regarding precision and the  $F_1$  score, but not regarding recall. Our conclusion is that ours is a very good approach to help programs integrate the data that they fetch from the Web of Data.

The rest of the article is organised as follows: Sect. 2 reports on the related work; Sect. 3 provides the details of our proposal; Sect. 4 presents our evaluation results; finally, Sect. 5 summarises our conclusions.

## 2 Related Work

The earliest techniques to learn link rules were devised in the field of traditional databases, namely: de-duplication [7, 17], collective matching [1, 3, 6, 14, 21], and entity matching [15]. They set a foundation for the researchers who addressed the problem in the context of the Web of Data, where data models are much richer and looser than in traditional databases.

Some of the proposals that are specifically-tailored to web data work on a single dataset [10, 16], which hinders their general applicability; there are a few that attempt to find links between different datasets [5, 8, 9, 13], but they do not take the neighbours of the resources being linked into account, only the values of

the attributes; that is, they cannot make resources with similar values for their attributes apart in cases in which they represent different real-world entities. An additional problem is that they all assume that data are modelled by means of OWL ontologies. Unfortunately, many common datasets in the Web of Data do not rely on OWL ontologies, but on simple RDF vocabularies that consists of classes and properties whose relationships and constraints are not made explicit.

The previous problems motivated several authors to work on techniques that are specifically tailored to work with RDF datasets. Most such proposals rely on genetic programming algorithms [11, 12, 19, 20] in which chromosomes encode the link rules as trees, which facilitates performing cross-overs and mutations. They differ regarding the expressivity of the language used to encode the link rules and the heuristics used to implement the selection, replacement, cross-over, and mutation operators, as well as the performance measure on which the fitness function relies. Isele and Bizer [11, 12] contributed with a supervised proposal called Genlink. It is available with the Silk framework [24], which is gaining impetus thanks to many real-world projects [23]. It uses a tournament selection operator, a generational replacement operator, custom cross-over and mutation operators, and its fitness function relies on the Matthews correlation coefficient. It can use a variety of custom string transformation functions and the Levenshtein, Jaccard, Numeric, Geographic, and Date string similarity measures. An interesting feature is that the size of the link rules must not be pre-established at design time, but it is dynamically adjusted during the learning process. Ngomo and Lyko [19] contributed with a supervised proposal called Eagle, which is available with the LIMES framework [18]. It uses a tournament selection operator, a  $\mu + \beta$  replacement operator, tree cross-over and mutation operators, and its fitness function relies on the  $F_1$  score. It does not use transformation functions, but the Levenshtein, Jaccard, Cosine, Q-Grams, Overlap, and Trigrams string similarity functions. The maximum size of the link rules must be pre-established at design time. Nikolov et al. [20] contributed with an unsupervised proposal. It uses a roulette-wheel selection operator, an elitist replacement operator, a tree cross-over operator, a custom mutation operator, and a pseudo  $F_1$  fitness function. Transformations are not taken into account, but the library of similarity functions includes Jaro, Levenshtein, and I-Sub. The maximum size of the link rules is also set at design time. There is a diverging proposal by Soru and Ngomo [22]. It supports the idea of using common machine-learning techniques on a training set that consists in a vectorisation of the Cartesian product of the resources in terms of the similarity of their attributes. Transformation functions are not taken into account and the only string similarity functions considered are Q-Grams, Cosine, and Levenshtein. Whether the size of the rules must be pre-set or not depends on the underlying machine learning technique. Unfortunately, none of the proposals that work on RDF datasets take the neighbours of the resources into account.

The previous analysis, makes it clear that the state of the art does not account for a proposal to link resources in RDF datasets that takes their neighbours into account. Our proposal is specifically-tailored to work with such datasets and it

is novel in that it is not intended to generate link rules, but leverages the rules that are learnt with other proposals and bootstraps them in order to analyse the neighbours, which our experimental analysis confirms that has a positive impact on precision without degrading recall.

### 3 Our Proposal

Our proposal consists in two components, namely: the first one learns link rules and the second one filters out the links that they produce.

The link rule learner is based on Genlink [12], which is a state-of-the-art genetic programming system that has proven to be able to learn good link rules for many common datasets. It is well-documented in the literature, so we focus on describing the second one, which constitutes our original contribution. The filter is an ad-hoc component that works as follows: it takes a link rule and executes it to produce a set of candidate links; then, it analyses the neighbours of the resources involved in each candidate link by bootstrapping the remaining rules; links in which the corresponding neighbours are similar enough are preserved as true positive links while the others are discarded as false positive links.

Below, we present the details of the filter, plus an ancillary method that helps measure how similar the neighbours of two resources are.

*Example 1.* Figure 1 presents two sample datasets that are based on the DBLP and the NSF datasets. The resources are depicted in greyed boxes whose shapes encode their classes (i.e., the value of property *rdf:type*), the properties are represented as labelled arrows, and the literals are encoded as strings. The genetic programming component learns the following link rules in this scenario, which we represent using a Prolog-like notation for the sake of readability:

$$\begin{aligned}
 r_1: \text{link}(A, R) \text{ if } & \text{rdf:type}(A) = \text{dblp:Author}, \text{rdf:type}(R) = \text{nsf:Researcher}, \\
 & N_A = \text{dblp:name}(A), N_R = \text{nsf:name}(R), \\
 & \text{levenstein}(\text{lfname}(N_A), \text{lfname}(N_R)) > 0.80.
 \end{aligned}$$

$$\begin{aligned}
 r_2: \text{link}(A, P) \text{ if } & \text{rdf:type}(A) = \text{dblp:Article}, \text{rdf:type}(P) = \text{nsf:Paper}, \\
 & T_A = \text{dblp:title}(A), T_P = \text{nsf:title}(P), \\
 & \text{jaccard}(\text{lowercase}(T_A), \text{lowercase}(T_P)) > 0.65.
 \end{aligned}$$

where *levenstein* and *jaccard* denote the well-known string similarity functions (normalised to interval [0.00, 1.00]), *lfname* is a function that normalises people’s names as “last name, first name”, and *lowercase* is a function that changes a string into lowercase.

Intuitively, link rule  $r_1$  is applied to a resource  $A$  of type *dblp:Author* and a resource  $R$  of type *nsf:Researcher*; it computes the normalised Levenshtein similarity between the normalised names of the author and the researcher; if it is greater than 0.80, then the corresponding resources are linked. Link rule  $r_2$

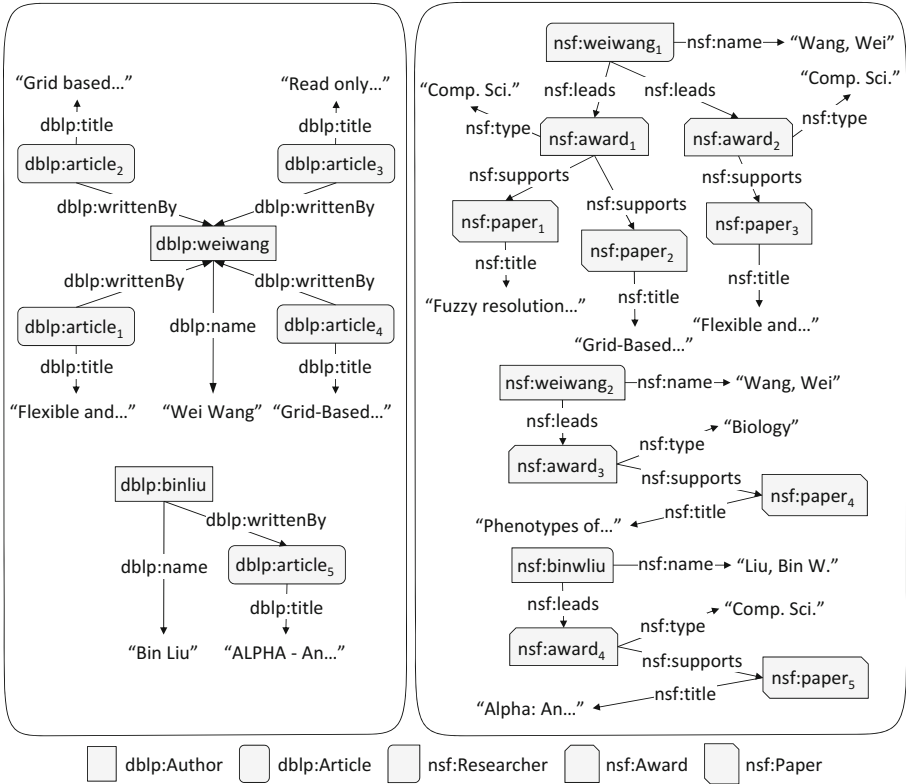


Fig. 1. Running example.

should now be easy to interpret: it is applied to a resource  $A$  of type  $dblp:Article$  and a resource  $P$  of type  $nsf:Paper$  and links them if the normalised Jaccard similarity amongst the lowercase version of the title of article  $A$  and the title of paper  $P$  is greater than 0.65.

It is not difficult to realise that link rule  $r_1$  links resources  $dblp:weiwang$  and  $nsf:weiwang_1$  or  $dblp:binliu$  and  $nsf:binwliu$ , which are true positive links, but also  $dblp:weiwang$  and  $nsf:weiwang_2$ , which is a false positive link. In cases like this, the only way to make a difference between such resources is to analyse their neighbours, be them direct (e.g.,  $dblp:weiwang$  and  $dblp:article_2$ ) or transitive (e.g.,  $nsf:weiwang_1$  and  $nsf:paper_2$ ). ■

### 3.1 Filtering Links

Figure 2 presents the method to filter links. It works on a base link rule  $r$ , a set of supporting link rules  $S$ , a source dataset  $D_1$ , a companion dataset  $D_2$ , and a threshold  $\theta$  that we explain later. It returns  $K$ , which is the subset of links produced by base link rule  $r$  that seem to be true positive links.

```

1: method filterLinks( $r, S, D_1, D_2, \theta$ ) returns  $K$ 
2:    $K := \emptyset$ 
3:    $(C_1, C_2) := (\text{sourceClasses}(r), \text{targetClasses}(r))$ 
4:    $L_1 := \text{apply}(r, D_1, D_2)$ 
5:   for each link rule  $r' \in S$  do
6:      $(C'_1, C'_2) := (\text{sourceClasses}(r'), \text{targetClasses}(r'))$ 
7:      $(P_1, P_2) := (\text{findPath}(C_1, C'_1, D_1), \text{findPath}(C_2, C'_2, D_2))$ 
8:      $L_2 = \text{apply}(r', D_1, D_2)$ 
9:     for each  $(p_1, p_2) \in P_1 \times P_2$  do
10:      for each link  $(a, b) \in L_1$  do
11:         $(A, B) := (\text{findResources}(a, p_1, D_1), \text{findResources}(b, p_2, D_2))$ 
12:         $E := L_2 \cap (A \times B)$ 
13:         $w := \text{computeSimilarity}(A, B, E)$ 
14:        if  $w \geq \theta$  then
15:           $K := K \cup \{(a, b)\}$ 
16:        end
17:      end
18:    end
19:  end
20: end

```

**Fig. 2.** Method to filter links.

The method first initialises  $K$  to an empty set, stores the source and the target classes of the base link rule in sets  $C_1$  and  $C_2$ , respectively, and the links that result from applying it to the source and the companion datasets in set  $L_1$ .

The main loop then iterates over the set of supporting link rules using variable  $r'$ . In each iteration, it first computes the sets of source and target classes involved in link rule  $r'$ , which are stored in variables  $C'_1$  and  $C'_2$ , respectively; next, it finds the set of paths  $P_1$  that connect the source classes in  $C_1$  with the source classes in  $C'_1$  in dataset  $D_1$ ; similarly, it finds the set of paths  $P_2$  that connect the target classes in  $C_2$  with the target classes in  $C'_2$  in dataset  $D_2$ . By path between two sets of classes, we mean a sequence of object properties that connect resources with the first set of classes to resources with the second set of classes, irrespective of their direction. Simply put: the idea is to find the way to connect the resources linked by the base link rule with the resources linked by the supporting link rule, which is done by the intermediate and the inner loops.

The intermediate loop iterates over the set of pairs of paths  $(p_1, p_2)$  from the Cartesian product of  $P_1$  and  $P_2$ . If there is at least a pair of such paths, it then means that the resources involved in the links returned by base link rule  $r$  might have some neighbours that might be linked by supporting link rule  $r'$ .

The inner loop iterates over the collection of links  $(a, b)$  in set  $L_1$ . It first finds the set of resources  $A$  that are reachable from resource  $a$  using path  $p_1$  in source dataset  $D_1$  and the set of resources  $B$  that are reachable from resource  $b$  using path  $p_2$  in the companion dataset  $D_2$ . Next, the method applies supporting link rule  $r'$  to the source and the companion dataset and intersects the resulting links

with  $A \times B$  so as to keep resources that are not reachable from  $a$  or  $b$  apart; the result is stored in set  $E$ . It then computes the similarity of sets  $A$  and  $B$ ; intuitively, the higher the similarity, the more likely that resources  $a$  and  $b$  refer to the same real-world entity. If the similarity is equal or greater than threshold  $\theta$ , then link  $(a, b)$  is added to set  $K$ ; otherwise, it is filtered out. When the main loop finishes, set  $K$  contains the collection of links that involve neighbours that are similar enough according to the supporting rules.

We do not provide any additional details regarding the algorithms to find paths or resources since they can be implemented using Dijkstra’s algorithm to find the shortest paths in a graph. Computing the similarity coefficient is a bit more involved, so we devote a subsection to this ancillary method below.

*Example 2.* In our running example, link rule  $r_1$  is the base link rule, i.e., we are interested in linking authors and researchers, and we use link rule  $r_2$  as the support link rule, i.e., we take their articles and papers into account. Their source classes are  $C_1 = \{dblp:Author\}$  and  $C'_1 = \{dblp:Article\}$ , respectively, and their target classes are  $C_2 = \{nsf:Researcher\}$  and  $C'_2 = \{nsf:Paper\}$ , respectively. Link rule  $r_1$  returns the following links:  $L_1 = \{(dblp:weiwang, nsf:weiwang_1), (dblp:weiwang, nsf:weiwang_2), (dblp:binliu, nsf:binwliu)\}$ ; note that the first and the third links are true positive links, but the second one is a false positive link. Link rule  $r_2$  returns the following links:  $L_2 = \{(dblp:article_1, nsf:paper_3), (dblp:article_2, nsf:paper_2), (dblp:article_4, nsf:paper_2), (dblp:article_5, nsf:paper_5)\}$ , which are true positive links.

The sets of paths between the source and target classes of  $r_1$  and  $r_2$  are  $P_1 = \{\langle dblp:writtenBy \rangle\}$  and  $P_2 = \{\langle nsf:leads, nsf:supports \rangle\}$ . Now, the links in  $L_1$  are scanned and the resources that can be reached from the resources involved in each link using the previous paths are fetched.

Link  $l_1 = (dblp:weiwang, nsf:weiwang_1)$  is analysed first. The method finds  $A = \{dblp:article_1, dblp:article_2, dblp:article_3, dblp:article_4\}$  by following resource  $dblp:weiwang$  through path  $\langle dblp:writtenBy \rangle$ ; similarly, it finds  $B = \{nsf:paper_1, nsf:paper_2, nsf:paper_3\}$  by following resource  $nsf:weiwang_1$  through path  $\langle nsf:leads, nsf:supports \rangle$ . Now supporting link rule  $r_2$  is applied and the results are intersected with  $A \times B$  so as to keep links that are related to  $l_1$  only; the result is  $E = \{(dblp:article_1, nsf:paper_3), (dblp:article_2, nsf:paper_2), (dblp:article_4, nsf:paper_2)\}$ . Then, the similarity of  $A$  and  $B$  in the context of  $E$  is computed, which returns 0.67; intuitively, there are chances that  $l_1$  is a true positive link.

Link  $l_2 = (dblp:weiwang, nsf:weiwang_2)$  is analysed next. The method finds  $A = \{dblp:article_1, dblp:article_2, dblp:article_3, dblp:article_4\}$  by following resource  $dblp:weiwang$  through path  $\langle dblp:writtenBy \rangle$ ; next, it finds  $B = \{nsf:paper_4\}$  by following resource  $nsf:weiwang_2$  through path  $\langle nsf:leads, nsf:supports \rangle$ . Now supporting link rule  $r_2$  is applied and the result is intersected with  $A \times B$ , which results in  $E = \emptyset$ . In such a case the similarity is zero, which intuitively indicates that it is very likely that  $l_2$  is a false positive link.

Link  $l_3 = (dblp:binliu, nsf:binwliu)$  is analysed next. The method finds  $A = \{dblp:article_5\}$  by following resource  $dblp:binliu$  through path  $\langle dblp:writtenBy \rangle$ ;

```

1: method computeSimilarity(A, B, E) returns d
2:   A' := reduce(A, E)
3:   B' := reduce(B, E)
4:   W := intersect(A', B', E)
5:   d := |W| / min{|A'|, |B'|}
6: end

```

**Fig. 3.** Method to compute similarity.

next, it finds  $B = \{nsf:paper_5\}$  by following resource  $nsf:binwliu$  through path  $\langle nsf:leads, nsf:supports \rangle$ . Now supporting link rule  $r_2$  is applied and the result is intersected with  $A \times B$ , which results in  $E = \{(dblp:article_5, nsf:paper_5)\}$ . The similarity is now 1.00, i.e., it is very likely that link  $l_3$  is a true positive link.

Assuming that  $\theta$  is set to, e.g., 0.50, the *filterLinks* method would return  $K = \{(dblp:weiwang, nsf:weiwang_1), (dblp:binliu, nsf:binwliu)\}$ . Note that the previous value of  $\theta$  is intended for illustration purposes only because the running example must necessarily have very little data.

### 3.2 Computing Similarity

Figure 3 shows our method to compute similarities. Its input consists of sets  $A$  and  $B$ , which are two sets of resources, and  $E$ , which is a set of links between them. It returns the Szymkiewicz-Simpson overlapping coefficient, namely:

$$overlap(A, B) = \frac{|A \cap B|}{\min\{|A|, |B|\}}$$

The previous formula assumes that there is an implicit equality relation to compute  $A \cap B$ ,  $|A|$ , or  $|B|$ . In our context, this relation must be inferred from the set of links  $E$  by means of Warshall's algorithm to compute the reflexive, commutative, transitive closure of relation  $E$ , which we denote as  $E^*$ .

The method to compute similarities relies on two ancillary functions, namely: *reduce*, which given a set of resources  $X$  and a set of links  $E$  returns a set whose elements are subsets of  $X$  that are equal according to  $E^*$ , and *intersect*, which given two reduced sets of resources  $X$  and  $Y$  and a set of links  $E$  returns the intersection of  $X$  and  $Y$  according to  $E^*$ . Their definitions are as follows:

$$\begin{aligned}
reduce(X, E) &= \{W \mid W \propto W \subseteq X \wedge W \times W \subseteq E^*\} \\
intersect(X, Y, E) &= \{W \mid W \propto W \subseteq X \wedge \exists W' : W' \subseteq Y \wedge W \times W' \in E^*\}
\end{aligned}$$

where  $X \propto \phi$  denotes the maximal set  $X$  that fulfils predicate  $\phi$ , that is:

$$X \propto \phi \iff \phi(X) \wedge (\nexists X' : X \subseteq X' \wedge \phi(X'))$$

The method to compute similarities then works as follows: it first reduces the input sets of resources  $A$  and  $B$  according to the set of links  $E$ ; it then computes the intersection of both reduced sets; finally, it computes the similarity using Szymkiewicz-Simpson's formula on the reduced sets.



*Example 3.* Analysing link  $l_1 = (dblp:weiwang, nsf:weiwang_1)$  results in sets  $A = \{dblp:article_1, dblp:article_2, dblp:article_3, dblp:article_4\}$ ,  $B = \{nsf:paper_1, nsf:paper_2, nsf:paper_3\}$ , and  $E = \{(dblp:article_1, nsf:paper_3), (dblp:article_2, nsf:paper_2), (dblp:article_4, nsf:paper_2)\}$ . If  $E$  is interpreted as an equality relation by computing its reflexive, symmetric, transitive closure, then it is not difficult to realise that  $dblp:article_2$  and  $dblp:article_4$  can be considered equal, because  $dblp:article_2$  is equal to  $nsf:paper_2$  and  $nsf:paper_2$  is equal to  $dblp:article_4$ . Thus, set  $A$  is reduced to  $A' = \{\{dblp:article_1\}, \{dblp:article_2, dblp:article_4\}, \{dblp:article_3\}\}$  and set  $B$  is reduced to  $B' = \{\{nsf:paper_1\}, \{nsf:paper_2\}, \{nsf:paper_3\}\}$ . As a conclusion,  $|A' \cap B'| = |\{\{dblp:article_1, nsf:paper_3\}, \{dblp:article_2, dblp:article_4, nsf:paper_2\}\}| = 2$ ,  $|A'| = 3$ , and  $|B'| = 3$ ; so the similarity is 0.67.

When link  $l_2 = (dblp:weiwang, nsf:weiwang_2)$  is analysed,  $A = \{dblp:article_1, dblp:article_2, dblp:article_3, dblp:article_4\}$ ,  $B = \{nsf:paper_4\}$ , and  $E = \emptyset$ . Since the equality relation  $E^*$  is then empty, the similarity is zero because the intersection between the reductions of sets  $A$  and  $B$  is empty.

In the case of link  $l_3 = (dblp:binliu, nsf:binliu)$ ,  $A = \{dblp:article_5\}$ ,  $B = \{nsf:paper_5\}$ , and  $E = \{(dblp:article_5, nsf:paper_5)\}$ . As a conclusion,  $|A' \cap B'| = |\{\{dblp:article_5, nsf:paper_5\}\}| = 1$ ,  $|A'| = 1$ , and  $|B'| = 1$ , where  $A'$  and  $B'$  denote, respectively, the reductions of sets  $A$  and  $B$ ; so the similarity is 1.00. ■

## 4 Experimental Analysis

In this section, we first describe our experimental environment and then comment on our results.

**Computing facility:** We run our experiments on a virtual computer that was equipped with four Intel Xeon E5-2690 cores at 2.60 GHz and 4 GiB of RAM. The operating system was CentOS Linux 7.3.

**Prototype:** We implemented our proposal with Java 1.8 and the following components: the Genlink implementation from the Silk Framework 2.6.0 to generate link rules, Jena TDB 3.2.0 to work with RDF data, ARQ 3.2.0 to work with SPARQL queries, and Simmetrics 1.6.2, SecondString 2013-05-02, and JavaStringSimilarity 1.0.1 to compute string similarities.

**Evaluation datasets:**<sup>1</sup> We used the following datasets: DBLP, NSF, BBC, DBpedia, IMDb, RAE, Newcastle, and Rest. We set up the following scenarios: (1) DBLP–NSF, which focuses on the top 100 DBLP authors and 130 principal NSF researchers with the same names; (2) DBLP–DBLP, which focuses on the 9 076 DBLP authors with the same names who are known to be different people; (3) BBC–DBpedia, which focuses on 691 BBC movies and 445 DBpedia films that have similar titles; (4) DBpedia–IMDb, which focuses on 96 DBpedia movies and 101 IMDb films that have similar titles; (5) RAE–Newcastle, which focuses

<sup>1</sup> The datasets are available at <https://goo.gl/asvKQV>.

on 108 RAE publications and 98 Newcastle papers that are similar; and (6) Rest–Rest, which focuses on 113 and 752 restaurants published by OAEI.

**Baseline:** Our baseline was the Genlink implementation from the Silk Framework 2.6.0, which is a state-of-the-art genetic programming system to learn link rules.

**Measures:** We measured the number of links returned by each proposal (*Links*), precision (*P*), recall (*R*), and the  $F_1$  score ( $F_1$ ) using 2-fold cross validation. We also computed the normalised differences in precision ( $\Delta P$ ), recall ( $\Delta R$ ), and  $F_1$  score ( $\Delta F_1$ ), which measure the ratio from the difference found between the baseline and our proposal and the maximum possible difference for each performance measure. We also applied Iman-Davenport’s test and computed the corresponding p-values to check if the differences found are statistically significant or not at the standard confidence level ( $\alpha = 0.05$ ).

**Parameters:** We set  $\theta = 0.01$ . We explored a large portion of the parameter space and our conclusion was that setting  $\theta$  to this small value helps our proposal perform the best. Note that it is very small, which means that it generally suffices to find a single link amongst the neighbours of the resources involved in another link so that it can be considered a true positive link.

Scenario	Genlink				Our proposal				$\Delta P$	$\Delta R$	$\Delta F_1$	
	Links	P	R	$F_1$	Links	P	R	$F_1$				
<b>DBLP - NSF</b>	127	0.25	0.97	0.40	52	0.62	0.97	0.75	-75	0.49	0.00	0.41
<b>DBLP - DBLP</b>	78,348	0.12	1.00	0.21	9210	0.98	1.00	0.99	-69,138	0.98	0.00	0.01
<b>BBC - DBpedia</b>	525	0.85	1.00	0.92	461	0.96	1.00	0.98	-64	0.74	0.00	0.24
<b>DBpedia - IMDB</b>	118	0.27	0.55	0.36	42	0.67	0.48	0.56	-76	0.54	-0.13	0.69
<b>RAE-Newcastle</b>	404	0.22	0.82	0.35	68	0.72	0.45	0.56	-336	0.64	-0.45	0.68
<b>Rest - Rest</b>	103	0.90	0.83	0.87	96	0.97	0.83	0.89	-7	0.68	0.00	0.78
<b>Average <math>\Delta</math></b>									0.68	-0.10	0.47	
<b>Iman-Davenport’s test</b>									0.00	0.25	0.00	

**Fig. 4.** Experimental results.

**Results:** The results are presented in Fig. 4. We analyse them regarding precision, recall, and the  $F_1$  score below.

The results regarding precision clearly show that our technique improves the precision of the rules learnt by GenLink in every scenario. In average, the difference in precision is 68%. The worst improvement is 49% in the DBLP–NSF scenario since these datasets are clearly unbalanced: the top authors in DBLP have about 500 papers in average, but NSF records an average of 7 papers in the projects in which they are involved; this obviously makes it difficult for our proposal to find enough context to make a decision. The best improvement is 98% in the DBLP–DBLP scenario since there are 9 076 authors with very similar names, which makes it almost impossible for GenLink to generate rules with good precision building solely on the attributes of the resources. Note that the p-value

computed by Iman-Davenport’s test is 0.00; since it is clearly smaller than the standard confidence level, we can interpret it as a strong indication that there is enough evidence in our experimental data to confirm the hypothesis that our proposal works better than the baseline regarding precision.

The normalised difference of recall  $\Delta R$  shows that our proposal generally retains the recall of the link rules learnt by GenLink, except in the DBpedia-IMDb and the Rae-Newcastle scenarios. The problem with the previous scenarios was that there are many incomplete resources, that is many resources without neighbours. For instance, there are 43 papers in the Newcastle dataset that are not related to any authors. The incompleteness of data has also a negative impact on the recall of the base link rules. In our prototype, we are planning on implementing a simple check to identify incomplete resources so that the links in which they are involved are not discarded as false positives, but identified as cases on which our proposal cannot make a sensible decision. Note that Iman-Davenport’s test returns 0.25 as the corresponding p-value; since it is larger than the standard confidence level, it may be interpreted as a strong indication that the differences in recall found in our experiments are not statistically significant. In other words, the cases in which data are that incomplete do not seem to be common-enough for them to have an overall impact on our proposal.

We also studied  $\Delta F_1$ , which denotes the normalised difference in  $F_1$  score. Note that it is 47% in average and that the corresponding Iman-davenport’s p-value is 0.00, which can be interpreted as a strong indication that the difference is significant from a statistical point of view. Overall, this result confirms that our proposal helps improve precision without degrading recall.

## 5 Conclusions

Programs need to link the resources that they find on the Web of Data so that they can enrich the data about a real-world entity that is found in a source dataset with data that comes from companion datasets. Current link rules take the values of the attributes of the resources into account, but not their neighbours, which sometimes results in false positives that have a negative impact on their precision. We have presented a hybrid proposal<sup>2</sup> that learns a set of link rules using a genetic programming approach and then bootstraps them. Our proposal may be fed with rules generated by any genetic programming approach from the literature, the afterwards bootstrap that performs has proven to improve the overall  $F_1$  score.

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<sup>2</sup> The prototype is available at <https://github.com/AndreaCimminoArriaga/Teide>.

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