

XMap : Results for OAEI 2015

Warith Eddine DJEDDI^{a,b}, Mohamed Tarek KHADIR^a and Sadok BEN YAHIA^b

^aLabGED, Computer Science Department, University Badji Mokhtar, Annaba, Algeria

^bFaculty of Sciences of Tunis, University of Tunis El-Manar, LIPAH-LR 11ES14, 2092, Tunisia

{djeddi, khadir}@labged.net

sadok.benyahia@fst.rnu.tn

Abstract. This paper describes the configuration of XMap for the OAEI 2015 competition and discusses its results. XMap is able to automatically adapt to the matching task, choosing the best configuration for the given pair of ontologies. This is our third participation in the OAEI and we can see an overall improvement on nearly every task.

1 State, purpose, general statement

XMap [1] [2] is a highly scalable ontology matching system, which is able to deal with hundreds of thousands of entities with an efficient computation time [3]. It is a fast and effective high precision system able to perform matching large ontologies. A semantic similarity measure has been defined using UMLS and WordNet [4] to provide a synonymy degree between two entities from different ontologies, by exploring both their lexical and structural context. XMap relies on the Microsoft Translate API to translate ontologies into many languages.

1.1 Specific techniques used

A high-level view of mapping process is depicted in Figure 1. It is a multi-layer system which uses three different layers to perform the ontology alignment process: a terminological layer, a structural layer and an alignment layer. The output values of each layer serves as input to the upper one and each layer provides an improvement in the computation of the similarity between concepts. Figure 1 shows the architecture of the XMap system.

Matchers in XMap are the algorithms that compare two ontologies and return an alignment between them. The matchers employed various strategies (entity label, structural description of concepts, range for relations, instantiated attributes or extensional descriptions) in each layer which are listed below:

a) Terminological Layer

The terminological layer is responsible for carrying out the process of computing the similarity between the entity names within the ontologies, combining linguistic similarity with the semantic elements of the context of the entities. This layer receives as inputs the values of the string similarity, the linguistic similarity, the semantic similarity and translation-based similarity computed within the lexical-semantic module. The output variable represents the terminological similarity:

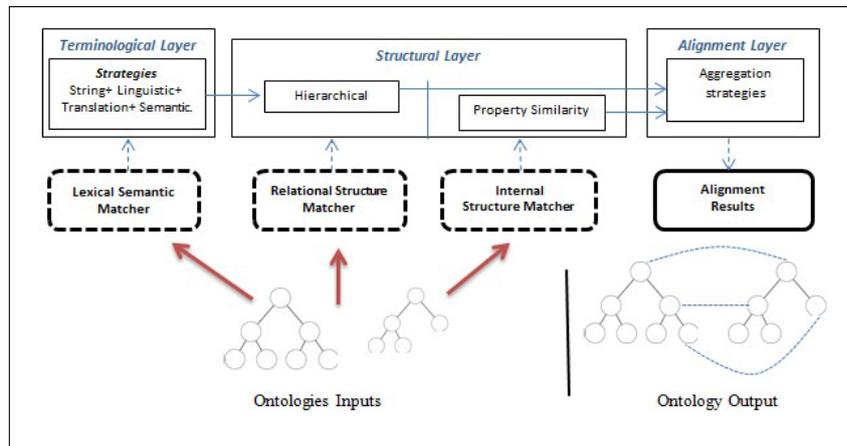


Fig. 1. Architecture for XMAP.

1. The string strategies usually can be applied to the name, the label or the comments concerning entities to discover those which are similar. In general, it can be used for comparing class names and/or URIs. The scaled range is $[0, 1]$ for comparing strings. Our system applies many terminological approaches for computing the similarity measures between two terms: the Levenshtein distance, the Jaro Winkler distance, the n-grams, the Jaccard distance, the Cosine, etc. Note that XMap does not currently store or use comments, definitions, nor instances;
2. The linguistic strategies explore the semantic similarity of the concepts and relations labels. The linguistic based matchers use the external resources WordNet and UMLS to find the semantic similarity between two entities;
3. The translation-based strategies use an automatic translation for obtaining correct matching pairs in multilingual ontology matching. The translation is done locally by querying Microsoft Translator for the full name;
4. The semantic strategies based on auxiliary sources use a domain knowledge available from external sources, such as WordNet, to find additional information for the concepts (synonyms) and the relationships between them. The semantic similarity is incorporated with the aim of adding context information of the concepts during the mapping process.

b) Structural Layer

The structural layer performs two key tasks related to the structure of ontologies. One is the computation of the similarity between the concepts taking into account the taxonomic hierarchy, as well as the computation of the similarity using the information of the internal structure of concepts, i.e., their properties, types and cardinality restrictions:

1. Structural strategies are usually based on the internal structure of an entity or its relations to other entities as a source of detecting correspondences. The first using the relational structure of concepts in the ontology, specifically the taxonomic hierarchy, and the second using the information of the internal structure of concepts, including their properties, types and cardinality restrictions;

2. Constraint strategies consider the concepts and properties data types and cardinalities. They are usually used to provide supplementary information, not as primary matchers (i.e., sting matcher or linguistic matcher); these techniques consider criteria regarding the internal structure of the entities, such as the domain and range of the properties or the types of the attributes, to calculate the similarity between them.

c) Alignment Layer

The alignment layer is the final layer and its aim is to provide the final similarity matrix between the concepts taking into account the influence of the number of properties and the value of similarity that properties bring to the final similarity between them. Once the similarity between ontology entities are available based on different strategies (e.g., string similarity, semantic similarity, structural similarity), aggregating similarities algorithms are needed to combine matchers. Combining and filtering the similarity values obtained from the different matchers, comes most often, to combine similarity values using three types of aggregation operator; these strategies are aggregation, selection and combination [2]. Furthermore, those pairs of concepts with similarity values equal to or greater than a particular threshold are retained in order to obtain the mapping suggestions.

For the requirements of different ontology matching tasks, the selected alignment in XMap can be one to one, one to many, or many to many alignments. Whereas in our case, the desired cardinality in ontology matching is typically one-to-one. The matching rules are created via the Java API Alignment Format, allowing the generation of outputs in different formats.

2 Results

In this section, we present the evaluation results obtained by running XMap under the SEALS client with *Benchmark*, *Anatomy*, *Conference*, *Multifarm* and *Large Biomedical Ontologies* tracks. Adding to that, we present the results of the test *Ontology Alignment for Query Answering* which not follow the classical ontology alignment evaluation on the SEALS platform.

Benchmark XMap performs very well in terms of Precision (1.0) while flagging out a low recall (0.4) in the Benchmark track. Those low values are explained by the fact that ontological entities with scrambled labels and lexical similarity become ineffective. Whereas for the others two test suites our algorithm performed worse in terms of F-Measure because our system does not handle ontology instances. Table 1 summarises the average results obtained by XMap.

Table 1. Results for Benchmark track.

Test	Precision	Recall	F-Measure
biblio	1.0	0.40	0.57
energy	1.0	0.22	0.51

Anatomy The Anatomy track consists of finding an alignment between the Adult Mouse Anatomy (2744 classes) and a part of the NCI Thesaurus (3304 classes) describing the human anatomy. XMap achieves a good F-Measure value of $\approx 89\%$ in a reasonable amount of time (50 sec.) (see Table 2). In terms of F-Measure/runtime, XMap is ranked 2nd among the 15 tools participated in this track.

Table 2. Results for Anatomy track.

System	Precision	F-Measure	Recall	Time(s)
XMap	0.928	0.896	0.865	50

Conference The Conference track uses a collection of 16 ontologies from the domain of academic conferences. Most ontologies were equipped with OWL DL axioms of various types; this opens a useful way to test our semantic matchers. The match quality was evaluated against the original (ra1) as well as entailed reference alignment (ra2) and violation free version of reference alignment (rar2). As Table 3 shows, for the three evaluations, we achieved a good F-Measure values.

For each reference alignment, three evaluation modalities are applied : a) M1 only contains classes, b) M2 only contains properties, c) M3 contains classes and properties.

Table 3. Results for Conference track.

	Precision	F-Measure 1	Recall
Original reference alignment (ra1)			
ra1-M1	0.86	0.73	0.63
ra1-M2	0.67	0.22	0.13
ra1-M3	0.85	0.68	0.56
Entailed reference alignment (ra2)			
ra2-M1	0.81	0.68	0.58
ra2-M2	0.78	0.25	0.15
ra2-M3	0.81	0.63	0.51
Violation reference alignment (rar2)			
rar2-M1	0.8	0.69	0.62
rar2-M2	0.78	0.27	0.16
rar2-M3	0.8	0.64	0.54

Multifarm This track is based on the translation of the OntoFarm collection of ontologies into 9 different languages. XMap's results are showed in Table 4.

Table 4. Results for Multifarm track.

System	Different ontologies			Same ontologies		
	P	F	R	P	F	R
XMap	0.22	0.24	0.27	0.66	0.37	0.27

Large biomedical ontologies This track consists of finding alignments between the Foundational Model of Anatomy (FMA), SNOMED CT, and the National Cancer Institute Thesaurus (NCI). There are 5 sub-tasks corresponding to different sizes of input ontologies (small fragments and whole ontology for FMA and NCI and small and large fragments for SNOMED CT). XMAP has been evaluated with two variants: XMAP-BK and XMAP. XMAP-BK uses synonyms provided by the UMLS Metathesaurus, while XMAP has this feature deactivated. The results obtained by XMAP-BK are depicted by Table 6. XMAP-BK provided the best results

Table 5. Results for the Large BioMed track.

Test set	Precision	Recall	F-Measure	Time(s)
Small FMA-NCI	0.971	0.902	0.935	31
Whole FMA-NCI	0.872	0.849	0.860	337
Small FMA-SNOMED	0.968	0.847	0.903	49
Whole FMA- Large SNOMED	0.769	0.844	0.805	782
Small SNOMED-NCI	0.928	0.606	0.733	396
Whole NCI- Large SNOMED	0.913	0.536	0.675	925

(ranked 1st) among the 12 participating systems in terms of F-measure in FMA-NCI and FMA-SNOMED matching sub-tasks. In general, we can conclude that XMap achieved a good precision/recall values. The high recall value can be explained by the fact that UMLS thesaurus contains definitions of highly technical medical terms.

Ontology Alignment for Query Answering The objective of this test is to check the ability of the generated alignments to answer a set of queries in an ontology-based data access scenario where several ontologies exist. Table 6 shows the F-measure results for the whole set of queries. XMap was one of the 5 matchers whose alignments allowed to answer all the queries of the evaluation.

Table 6. Results for Ontology Alignment for Query Answering.

System	RA1 Reference			RAR1 Reference		
	P	R	F	P	R	F
XMap	0.778	0.675	0.702	0.720	0.654	0.671

3 General comments

3.1 Comments on the results

This is the third time that we participate in the OAEI campaign. We foresee an improvement in the performance of our system which consists of expanding the supported domain of matching problems, such that large-scale biomedical or multi-lingual ontologies can be matched as well. The official results of OAEI 2015 show that XMap is competitive with other well-known ontology matching systems in all OAEI tracks. The current version of XMap has shown a significant improvement both in terms of matching quality and runtime. Additionally, to improve our f-measure for large biomedical ontologies we made use of the UMLS Metathesaurus. Finally, we pre-compiled a local dictionary in order to avoid multiple accesses to the Microsoft Translator during the matching process.

3.2 Comments on the OAEI 2015 procedure

As a third participation, we found the OAEI procedure very convenient and the organizers very supportive. The OAEI test cases are various, and this leads to a comparison on different levels of difficulty, which is very interesting. We found that SEALS platform is a precious tool to compare the performance of our system with the others.

4 Conclusion

In this paper, we presented the results achieved during the 2015 edition of the OAEI campaign. The system managed to improve its performance significantly compared to the previous year, which is reflected in the performance of the different tracks. We have used the UMLS resource for better discarding incorrect mappings for life sciences related ontologies. Moreover, we implemented a cross-lingual ontology matching approach in order to align ontologies in different languages.

References

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