

XMap : Results for OAEI 2018

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Abstract. We describe in this paper the XMap system and the results achieved during the 2018 edition of the Ontology Alignment Evaluation Initiative. XMap aims to tackle the issue of matching large scale ontologies by involving particular parallel matching on multiple cores or machines. Our strategies aim to provide a set of requirements that foster the using of a domain-specific thesaurus for the alignment of specialized ontologies.

1 Presentation of the system

The eXtended Mapping (XMap) algorithm relies on the context notion to deal with lexical ambiguity as well as a parallel comparison between concepts to efficiently handle the matching of large ontologies. Our approach to matching ontologies employs different components and steps in the ontology alignment process such as preprocessing, matching, filtering and combining matching results, and oracle validation of mapping suggestions. The contributions are the following:

- Defining a semantic similarity measure using UMLS¹ [1] and WordNet [2] to provide a synonymy degree between two entities from different ontologies, by exploring both of their lexical and structural contexts. In *XMap*, the measurement of lexical similarity in ontology matching is performed using a synset, defined in WordNet and UMLS. In our approach, the similarity between two entities of different ontologies is evaluated not only by investigating the semantics of the entity names, but also taking into account the context, through which the effective meaning is described. It is worth mentioning that the context is the set of information (partly) characterizing the situation of some entities [3]. The context notion is not universal but it is relative to some situations, tasks or applications [4, 5];
- Limiting the number of mapping suggestions to be validated by an oracle. Indeed, our approach employs a double threshold to produce matching candidates and use a small set of constraints [6, 7] (e.g., consistency, locality, and conservativity or quality checks), acting as a filter to select the final alignments. The first threshold is used at the interactive selection algorithm, which will ask the oracle for feedback about mappings when they are below a given similarity threshold, until a given number of negative answers is reached. The second threshold is used at the final

¹ <http://www.nlm.nih.gov/research/umls/>

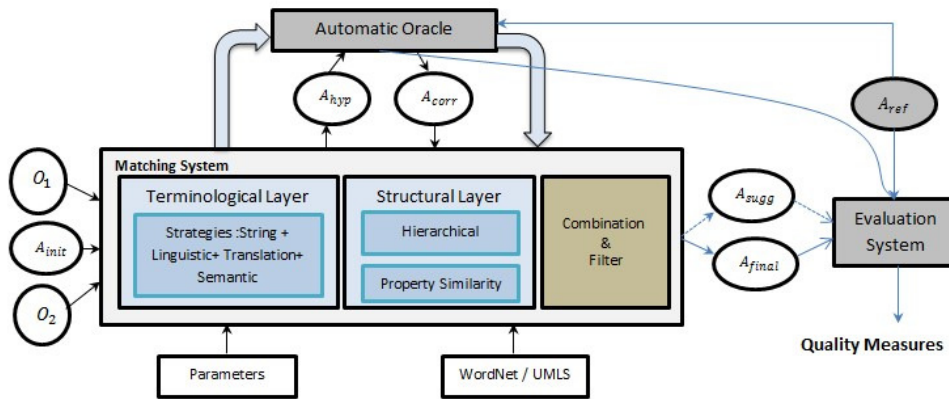


Fig. 1. The different steps for scoring a multiple network alignment.

stage to filter out the set of correspondences having a similarity value below a given threshold. This strategy skips over the problem of the growing size and the complexity of the user participation in the process alignment of large ontologies.

- Applying repair techniques from Applying Logical Constraints on Matching Ontologies (ALCOMO) [8] to make reference alignments coherent, by removing less unsatisfiable classes (discovering disjointness relationships) without having an impact on the F-measure score. Our strategy in the repair mode takes into account the confidence values during the selection of mappings to be removed in order to improve the quality of the repaired alignments in terms of computation time and mapping coherence.
- Finally, is the ability of XMap to deal with large scale ontology matching, by producing good experimental results in terms of quality of the alignments, time performance and scalability.

2 State, purpose, general statement

Our prototype leans on the architecture of a sequential/parallel composition. XMap uses various similarity measures of different categories such as string, linguistic, and structural based similarity measures, each contributing to some extent to the alignment results. At a glance, the mapping process of XMap is depicted in Figure 1. *XMap* receives as an input two source ontologies. The mappings discovered by the terminological level matcher are transferred to the structural level matcher in order to find new correspondences by analyzing the context of the entities in the taxonomy of ontologies. Afterwards, the combined result of the two basic matchers are aggregated by a weighted sum aggregation operator. For the final alignment method, the system uses the threshold method. Moreover, we manually define the filters threshold value to produce the final mappings. A fast repair method is applied so as to detect and remove the inconsistent ones.

3 Results

In this section, we present the evaluation results obtained by running XMap under the SEALS client with *Anatomy*, *Conference*, *Multifarm*, *Interactive matching evaluation*, *Large Biomedical Ontologies*, *Disease and Phenotype* and *Biodiversity and Ecology* tracks.

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 (37 sec.) (cf., Table 1).

Table 1. Results for Anatomy track.

System	Precision	F-Measure	Recall	Time(s)
XMap	0.929	0.896	0.865	37
StringEquiv	0.997	0.766	0.622	946

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. For each reference alignment, three evaluation modalities are applied : a) crisp reference alignments, b) the uncertain version of the reference alignment, c) logical reasoning.

Table 2. Results based on the crisp reference alignments.

	Precision	F-Measure 1	Recall
Original reference alignment (ra1)			
ra1-M1	0.81	0.70	0.61
ra1-M2	0.69	0.31	0.20
ra1-M3	0.81	0.65	0.54
Entailed reference alignment (ra2)			
ra2-M1	0.79	0.65	0.55
ra2-M2	0.77	0.34	0.22
ra2-M3	0.77	0.61	0.5
Violation reference alignment (rar2)			
rar2-M1	0.78	0.66	0.57
rar2-M2	0.77	0.34	0.22
rar2-M3	0.76	0.62	0.52

As depicted in Table 2 and 3, XMap produces fairly consistent alignments when matching the conference ontologies. Finally, XMap generated only one incoherent alignment for the evaluation based on logical reasoning.

Table 3. Results based on the uncertain version of the reference alignment.

Precision	F-Measure 1	Recall
Uncertain reference alignments (Sharp)		
0.81	0.65	0.54
Uncertain reference alignments (Discrete)		
0.66	0.74	0.83
Uncertain reference alignments (Continuous)		
0.74	0.70	0.66

Multifarm This track is based on the translation of the OntoFarm collection of ontologies into 9 different languages. XMap have low performance due to many internal exceptions. The results are showed in Table 4.

Table 4. Results for Multifarm track.

System	Different ontologies			Same ontologies		
	P	F	R	P	F	R
XMap	0.2	0.3	0.07	0.13	0.14	0.19

Interactive matching evaluation The goal of this evaluation is to imitate interactive alignment [9, 10], where a oracle user is involved to validate the correspondences found by the alignment approach by checking the reference alignment, and changing error values in order to assess their influence on the performance of alignment systems. For the 2018 edition, participating systems are evaluated on the *Conference* and *Anatomy* datasets using an oracle based on the reference alignment.

XMap uses various similarity measures to generate candidate mappings. It applies two thresholds to filter the candidate mappings: one for the mappings that are directly added to the final alignment and another for those that are presented to the user for validation. The latter threshold is selected to be high in order to minimize the number of requests and the rejected candidate mappings from the oracle; the requests are mainly about incorrect mappings. The mappings accepted by the user are moved to the final alignment. For the three years 2016, 2017 and 2018, XMap preserved roughly the same F-Measure value, and it benefits the least from the interaction with the oracle. Whereas, for the conference track, XMap has increases in precision, recall and F-measure. XMap's measures differ with less than 0.2% from the non-interactive runs, and performance does not change at all with the increasing error rates.

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). The results obtained by XMap (Evaluated without UMLS) are depicted by Table 5.

Table 5. Results for the Large BioMedical track.

Test set	Precision	Recall	F-Measure	Time(s)
Small FMA-NCI	0.977	0.783	0.869	7356
Whole FMA-NCI	0.877	0.741	0.803	66499
Small FMA-SNOMED	0.962	0.647	0.774	25544
Whole FMA- Large SNOMED	0.723	0.608	0.661	299027
Small SNOMED-NCI	0.835	0.588	0.69	123597
Whole SNOMED-NCI	0.64	0.582	0.61	426584

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.

Disease and Phenotype This track based on a real use case where it is required to find alignments between disease and phenotype ontologies. Specifically, the selected ontologies are the Human Phenotype Ontology (HPO), the Mammalian Phenotype Ontology (MP), the Human Disease Ontology (DOID), and the Orphanet and Rare Diseases Ontology (ORDO).

XMap achieved fair results according to the three evaluation (Silver standard, Manually generated mappings and Manual assessment of unique mappings).

Biodiversity and Ecology This track aims finding the alignments between the Environment Ontology (ENVO) and the Semantic Web for Earth and Environment Technology Ontology (SWEET), and between the Flora Phenotype Ontology (FLOPO) and the Plant Trait Ontology (PTO). The results are showed in Table .

Table 6. Results for the Biodiversity and Ecology track.

Test set	Precision	Recall	F-Measure	Time(s)
Small flopo-pto	0.987	0.761	0.619	153
Whole envs-sweet	0.868	0.785	0.716	547

4 General comments

4.1 Comments on the results

This is the 6th time that we participate in the OAEI campaign. The official results of OAEI 2018 show that XMap is competitive with other well-known ontology matching systems in all OAEI tracks.

4.2 Comments on the OAEI 2018 procedure

As a sixth 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.

5 Conclusion

Generally, according to our results obtained during the compaign OAEI 2018, our system delivered good results comparatively to other well-known ontology matching systems. The used benchmark greatly helped to identify the power and weaknesses of the algorithm. used benchmark helped greatly identify the power and weaknesses of the algorithm. In addition, XMap showed the feasibility of our approach especially on large-scale biomedical ontologies which was a thriving challenge in ontology matching domain.

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