

POMap results for OAEI 2017

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Abstract. Ontology matching is an effective strategy to find the correspondences among different ontologies in a scalable and heterogeneous semantic web. In order to find these correspondences, a matching system should be built aiming to ensure the interoperability between the aligned entities. POMap (Pairwise Ontology Mapping) is an automated ontology matching system dealing with the three main types of heterogeneity: syntactic, semantic and structural. During our first participation in the OAEI campaign, POMap succeeded to be one of the top three performing systems in the Anatomy track. In the remaining of this paper, we briefly introduce POMap and discuss its OAEI 2017 results according to four tracks: Anatomy, Conference, Large Biomedical Ontologies, Disease and Phenotype.

Keywords: Semantic web, ontology matching, semantic matching, syntactic matching, structural matching

1 Presentation of the system

1.1 State, purpose, general statement

An ontology can model a particular domain as well as the relationships between its entities in order to ensure its reuse by different stakeholders. Several ontologies describing the similar domain are generated and used by various parties and terminologies. Despite the standardization of the ontology language representation, the heterogeneity problem emerges. Therefore, it is important to overcome this heterogeneity to ensure the reusability of various ontologies. Indeed, many researchers has been proposing and developing many automated ontology matching systems. Ontology matching is the process of finding a set of semantic correspondences between the entities of two or more ontologies representing a similar domain. Therefore, these systems are using a variety of strategies relying on the combination of several techniques such as: Syntactic, semantic and structural based matching. As depicted in the figure 1, POMap is pursuing a sequential composition during these three matching techniques. POMap is exploring all these three techniques in order to ensure a high quality matching. Dealing with

the anatomy track, we employ a semantic matcher. Then, for all the other OAEI tracks, we used a syntactic matcher, which follows an all-against-all strategy. Next, our structural matcher takes as an input the generated mappings from the semantic matcher and the syntactic matcher in order to find new alignments. The adopted sequential composition aims to prune the search space used by the structural matcher. This structural matcher is composed of two structural sub-matchers: siblings and subclasses. A broader explanation of POMap could be found in [1]. In the next subsection we will describe briefly each component of our system as well as the used techniques.

1.2 Specific techniques used

The POMap workflow for our first participation on the OAEI comprises three main steps, as flagged by the figure 1: Ontology indexing and loading, ontology matching and output alignment generation.

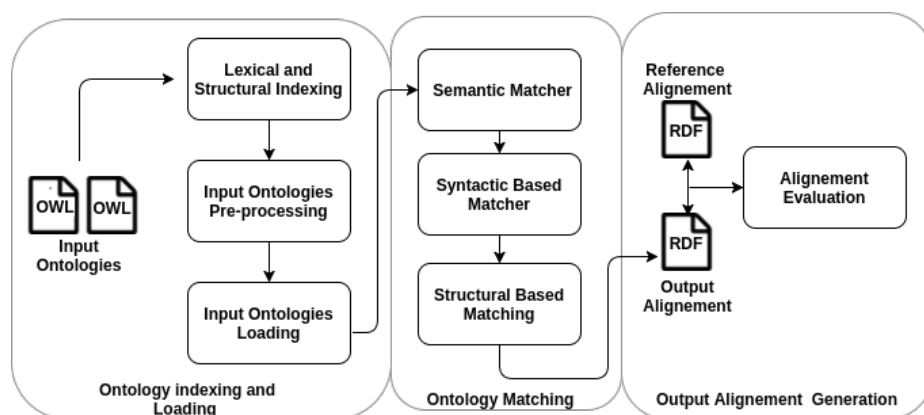


Fig. 1. The architecture of POMap.

Step 1: Ontology indexing and loading

The initial step of POMap is the extraction of all the annotations within the two compared ontologies. In terms of lexical indexing, POMap builds a multimap data structure that contains the triplet: the set of entities, their names as well as the property type of each name. For the structural indexing, all relationships between the extracted entities are stored in a multimap data structure. Every record of this multimap contains two entities and the relationship property between them. After accomplishing the lexical and the structural indexing, we perform several preprocessing strategies, such as: the removal of non-alphanumeric characters, the removal of stopwords, the stemming process and the lowercasing.

Step 2: Ontology matching

Step 2.1: The semantic Matcher

The first step in the matching process is the performing of the semantic matcher. We argue this choice by the high precision of the adopted semantic matcher. Therefore, we will be based on it to enrich the resulted mappings by new ones through the use of syntactic and structural strategies. During our first participation in the OAEI campaign, we adopted the semantic matching only for the Anatomy track. We plan to expand the use of this matcher in our future participation. In order to ensure the semantic matching, we employed Uberon [3] as an external biomedical knowledge source for the alignment of the Anatomy track. Uberon is an integrated cross-species ontology covering anatomical structures and includes relationships to taxon-specific anatomical ontologies. Indeed, we explored the annotation property "hasDbXref", which is mentioned in almost every class of Uberon. This property references the classes' URI of external ontologies such as the human and mouse of the Anatomy track. Consequently, we align every two entities of the Anatomy track in case they are both referenced in a single class of Uberon.

Step 2.2: The syntactic Matcher

After performing the semantic matching process, we are able to apply the syntactic matcher. This syntactic matcher compute the similarity score between every two names of the two input ontologies using a string similarity measure. The variety of the existing state of the art similarity measure arises the problematic of choosing the right one associated with its optimal threshold. Therefore, we tested the available syntactic similarity measure (<https://goo.gl/1kUgkH>) while varying the associated threshold value. Hence, we select ISUB combined with a threshold of 0.9. Only the couple of entities having a similarity score above 0.9 are considered as new mappings candidates. As we are performing a pairwise (1:1) matching process, for every single entity from the first ontology, we select only one entity with the maximum similarity score. In case of two candidate mappings have the same similarity score, we consider randomly one of them as the final alignment.

Step 2.3: The structural Matcher

For the set of available alignments derive from the semantic and the syntactic matcher, we are able to enrich them by a set of new alignments through the use of a structural matcher. This structural matcher is composed of two sub-matchers: siblings and subclasses.

Step 2.3.1: The structural Matcher based on siblings

For the structural matcher based on siblings, we follow the intuition of: if two entities match, then their sibling should somehow similar [2]. Therefore, if two entities are aligned using the syntactic matcher, we compute the similarity score between their siblings. Then, following an alignment multiplicity of 1:1, we match the siblings having a similarity score between ISUB 0.9 (syntactic threshold) and ISUB 0.8. The resulted mappings from the structural matcher based on siblings are added to the already discovered alignments by the two earlier matchers.

Step 2.3.2: The structural Matcher based on subclasses

Concerning the structural matcher based on subclasses, we pursue the intuition that if two classes are similar, then their subclasses should be similar. This intuition should be straightforward applied if two classes are having a very small number of subclasses. Nonetheless, this will be complicated in case if there are many descendants. Therefore, as a first step, we remove all the common tokens between an already aligned entity and its descendants. We argue that there is a syntactic inheritance between an entity and their descendants. Therefore, the removal of the similar tokens, will permit to better capture the similarity between two entities. Then, we compute the similarity score among all the descendants of two already aligned entities while applying the similarity measure of Monge Elkan 0.85 [4]. Unlike to ISUB, we argue the use of Monge Elkan due to his particularity in capturing the dissimilarity between two textual sequences containing numerical values. However, this similarity measure is not recommended for a heavy matching process, due to its time consuming.

Step 3: output alignment generation

As a final step, we generate an RDF file, which contains the final alignments based on the resulted mappings resulted by all the matchers.

1.3 Link to the system and parameters file

The SEALS wrapped version of POMap for the OAEI 2017 is available at: <https://goo.gl/mZ4PzR>

1.4 Link to the set of provided alignments

The resulted alignments by POMap as well as the results for each track during our first participation of OAEI 2017 are available at: <https://goo.gl/mZ4PzR>

2 Results

2.1 Anatomy

The Anatomy track consists of finding the alignments between the Adult Mouse Anatomy and the NCI Thesaurus describing the human anatomy. The evaluation

was run on a server coupled with 3.46 GHz (6 cores) and 8GB of RAM. Table 1 draws the performance of POMap compared to the five top matching systems. Our system achieved the third best result for this data set with an F-measure of 0.933, which is very close to the top results. We argue the importance of the obtained results by the effectiveness of the overall employed matchers, the use of all the names of the input ontologies and applying an efficient preprocessing process. The remaining challenge is to speed up the execution time by applying more optimizations. We also target the improvement of precision value for our next participation in OAEI.

Table 1. POMap results in the anatomy track compared to the OAEI 2017 systems.

System	Precision	Recall	F-Measure	Runtime
AML	0.95	0.936	.943	47
YAM-BIO	0.948	0.922	0.935	70
POMap	0.94	0.925	0.933	808
LogMapBio	0.889	0.899	0.894	820
XMap	0.926	.836	.893	37

2.2 Conference

The purpose of the conference track is to find the alignments within a collection of ontologies describing the domain of organizing conferences. Matching systems are evaluated according to the combination of three reference alignments along with three evaluation modalities (M1, M2 and M3). These evaluation modularities are containing respectively: only classes, properties as well as classes and properties. Since we did not focused on the matching of properties, the table 2 draws the obtained results by POMap results only for the modularities: M1 and M3. Therefore, we plan for our next participation in the OAEI to include the property matching in order to make a more comprehensive evaluation for this track.

Table 2. POMap results for the conference track

	Precision	Recall	F1-Measure
Ra1-M1	0.88	0.47	.61
Ra1-M3	0.73	0.4	0.52
Ra2-M1	0.83	0.43	0.57
Ra2-M3	0.67	.37	.48
Ra2-M1	0.889	0.899	0.894
Ra2-M3	0.69	0.38	0.49

2.3 Large biomedical ontologies

We are waiting for the results

2.4 Disease and Phenotype

We are waiting for the results

3 Conclusion

The first version of POMap ontology matching system as well as its obtained results in the OAEI campaign were presented in this paper. We proposed three matchers: semantic, syntactic and structural. We performed the structural matching without any syntactic similarity score propagation or computation of a structural similarity score. We are guided only by the syntactic treatment of both subclasses and siblings. The obtained results are promising especially on the anatomy track in which we ranked as the third top performing matching system. However, we did not opt to match larger ontologies in the given runtime threshold. Consequently, we are planning to optimize our matching system for larger biomedical tasks while taking into consideration the automatic tuning of the matching configuration.

References

1. A. Laadhar, F. Ghazzi, I. Megdiche, F. Ravat, O. Teste, F. Gargouri POMap: An Effective Pairwise Ontology Matching System 9th International Joint Conference on Knowledge Discovery, Knowledge Engineering and Knowledge Management (KEOD'17), Funchal (Madeira, Portugal) 2017
2. Shvaiko, P., Euzenat, J. (2013). Ontology matching: state of the art and future challenges. IEEE Transactions on knowledge and data engineering, 25(1),
3. Mungall, Christopher J., et al. "Uberon, an integrative multi-species anatomy ontology." Genome biology 13.1 (2012): R5.
4. Monge, Alvaro E., and Charles Elkan. "The Field Matching Problem: Algorithms and Applications." KDD. 1996.