Ontology Mapping Discovery with Uncertainty

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Abstract. Resolving semantic heterogeneity among information sources is a central problem in information interoperation, information integration, and information sharing among websites. Ontologies express the semantics of the terminology used in these websites. Semantic heterogeneity can be resolved by mapping ontologies from diverse sources. Mapping large ontologies manually is almost impossible and results in a number of errors of omission and commission. Therefore, automated ontology mapping algorithms are a must. However, most existing ontology mapping tools do not provide exact mappings. Rather, there is usually some degree of uncertainty. We describe a framework to improve existing ontology mappings using a Bayesian Network. Omen, an Ontology Mapping ENhancer uses a set of meta-rules that capture the influence of the ontology structure and the semantics of ontology relations and matches nodes that are neighbors of already matched nodes in the two ontologies. We have implemented a protype ontology matcher using probabilistic methods that can enhance existing matches between ontology concepts. Experiments demonstrate that Omen successfully identifies and enhances ontology mappings significantly.

1 Introduction

Information sources, even those from the same domain, are heterogeneous in nature. Semantic heterogeneity of information sources occurs because the semantics of the information in one source differs from that in another. Resolving semantic heterogeneity among information sources is a central problem in information interoperation, information integration, and information sharing. Ontologies express the semantics of the terminology used in these information sources.

In order to enable interoperation among heterogeneous information sources or to compose information from multiple sources, we often need to establish mappings between ontologies or database schemas. These mappings capture the semantic correspondence between concepts in schemas or ontologies. Such ontology mappings are also useful when information sources are being integrated. For example, when two banks are being merged, the schema of their corresponding databases, and the metadata of their information sources, might need to be mapped before these information sources can be integrated. Mapping large ontologies manually is almost impossible and results in a number of errors of omission and commission. Therefore, automated ontology mapping algorithms are essential.

In recent years, researchers have developed a number of tools for finding these mappings in a semi-automated fashion (see Section 6 for a brief overview). Interactive tools enable experts to specify the mappings. In most cases, the mappings produced are imprecise. For instance, automatic ontology-mapping tools can rank possible matches, with the ones that are more likely to be correct getting higher rankings. Most automatic ontology-mapping tools use heuristics or machine-learning techniques, which are imprecise by their very nature. Even experts sometimes could be unsure about the exact match between concepts and typically assign some certainty rating to a match.

This work is based on the following premise: if we know a mapping between two concepts from the source ontologies (i.e., they *match*), we can use the mapping to derive mappings between related concepts. Once a particular set of mappings is established (by an expert or a tool), we can analyze the structure of ontologies in the neighborhood of these mappings to derive additional mappings. For example, if two properties and their domains match, then we can infer (with some certainty) that their ranges may be related as well. To do so, we build a Bayesian Net with the concept mappings. The Bayesian Net uses a set of *meta-rules* based on the semantics of the ontology relations that expresses how each mapping affects other related mappings. We can use existing automatic and semi-automatic tools to come up with initial probability distributions for mappings. Next, we use this probability distribution to infer probability distributions for other mappings.

We have implemented a tool called Omen (Ontology Mapping ENhancer). Omen uses a Bayesian Net and enhances existing ontology mappings by deriving missed matches and invalidating existing false matches. Our preliminary results show that by using Omen we can enhance the quality of existing mappings between concepts across ontologies.

The primary contributions of this paper are as follows:

1. We introduce a probabilistic method of enhancing existing ontology mappings by using a Bayesian Net to represent the influences between potential concept mappings across ontologies.
2. In Omen, we provide an implemented framework where domain knowledge of mapping influences can be input easily using simple meta-rules.
3. We demonstrate the effectiveness of Omen in our preliminary experiments.

To the best of our knowledge, no existing work has extensively used a probabilistic representation of ontology mapping rules and probabilistic inference to improve the quality of existing ontology mappings.

The rest of the paper is organized as follows. Section 2 contains a description of the knowledge model used to represent the ontologies and the mapping expressions, and, we discuss the use of meta-rules to generate new probability distributions based on existing ones. Section 4 contains a description of how the Bayesian Net that Omen uses is constructed. In Section 5, we briefly outline our prototype implementation and provide the results of our experiments. Section 6 describes some scope for future work. In Section 7, we discuss the related work and conclude the paper in Section 8.

2 OMEN and its Bayesian Network

In this section, we define some preliminary concepts and then describe the OMEN algorithm.

2.1 Knowledge Model

We assume a simple ontology model (similar to RDF Schema). We use the following components to express ontologies:

Classes Classes are concepts in a domain, organized in a subclass–superclass hierarchy with multiple inheritance.

Properties Properties describe attributes of classes and relationships between classes. Properties have one or more **domains**, which are classes to which the property can be applied; and one or more **ranges**, which restrict the classes for the values of property.

We use the following notation conventions through the rest of this paper:

- all concepts from O have no prime ('); all concepts from O' have a prime (');
- upper-case C with or without a subscript is a class;
- lower-case q with or without a subscript is a property;
- $P(C_1\ \theta\ C_2, x)$ indicates that the probability of the match $(C_1\ \theta\ C_2)$ is x.

2.2 The BN-Graph: Nodes and Edges

Each node in the Bayesian Net graph represents a unique match between two concepts in the source ontologies. Consider Figure 1. This figure represents some classes in ontology O in the left-hand tree and some classes in ontology O' in the right-hand tree. The thin arrows in the figure are relationships between classes in the ontology, such as subclass–superclass relationships. The gray nodes and arrows represent the BN graph superimposed on the graphs representing ontologies. Nodes in the BN graph are matches between pairs of classes or properties from different ontologies. Arrows in the BN graph (the solid gray arrows in Figure 1) represent the influences between the nodes in the BN graph. For example, in Figure 1, the mapping between concepts C_1 and C'_1 affects the mapping between concepts C_2 and C'_2, which in turn affects the mapping between C_3 and C'_3 Conditional Probability Tables (CPTs) represent how a probability distribution in one node in the BN graphs affects the probability distribution in another node downstream from it.

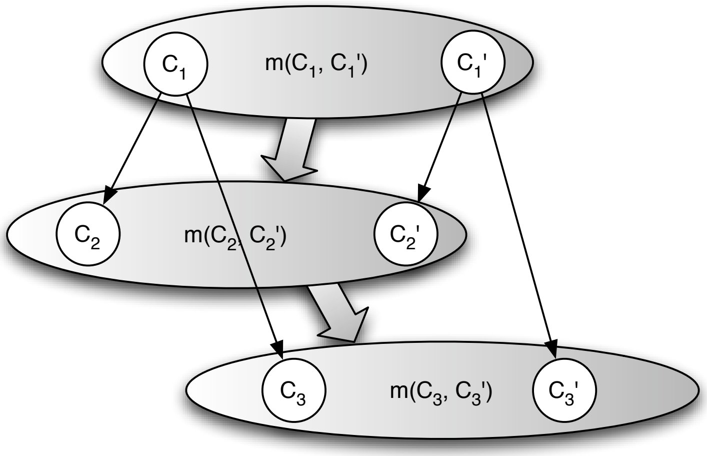


Fig. 1. Subgraphs representing some concepts in ontologies O and O' (small circles) and relations between them (thin arrows). The large gray ovals and solid arrows represent a snippet of the BN graph with nodes corresponding to matches and arrows corresponding to influences in the BN graph.

2.3 *a priori* Probabilities, Evidence and CPTs

We refer to the matcher whose output is input to Omen as the *prior matcher*. The input to the Omen algorithm consists not only of the two source ontologies to be matched, but also, of the initial probability distributions on the "root" nodes (nodes with no parents) in the BN graph as generated by a prior matcher. We refer to this probability value as the *a priori probability* of the node. Note that our definition of mapping allows for inputs that are themselves imprecise and contain some probability values. For instance, if there is an ontology matcher that produces a set of pairs of matches ordered according to the algorithm's certainty about the match we can translate that into specific values for each $m(C_n, C'_k)$ where the probability value for "=" is less than 1 and diminishes as we go further down in the ranked list of the external matcher's result.

In order to run a Bayesian Net we need to provide it with two types of information: (1) evidence (obtained from the *a priori* probabilities) describing what we already know with high confidence, and (2) Conditional Probability Tables, describing how the parent nodes influence the children or how the children influence the parent nodes in the Bayesian Network.

We refer to a node as an *evidence node* if and only if the prior matcher identified the pair of ontology concepts that the node represents to be matched with very high certainty (e.g., the probability of match computed by the prior matcher exceeds a high threshold).

The final missing piece are the CPTs. The CPTs describe how a match between two classes affects other matches (these are the solid gray arrows in Figure 1). For example, a match between two classes from the source ontologies affects the match between their superclasses. Or a match between properties affects the match between their domains. These rules depend on the knowledge model and semantics of the relationships (such as subclass or domain) defined in the knowledge model. Therefore, we have developed a set of generic *meta-rules* that enable us to generate CPTs for each particular pair of ontologies automatically. In fact, our implementation is parameterized with respect to the meta-rules, and we can add or remove meta-rules to evaluate which ones work best for a particular knowledge model.

We present some of the meta-rules that we used in the next Section.

2.4 A Scalable Selection of Nodes

We assume that the influence of a matching node traverses to nodes that are at a distance of k from an evidence node, where the distance is measured as the minimum number of edges traversed from the evidence node to reach the node. If the node is too far from the evidence node, the influence of the evidence node is negligible. Therefore, to improve the performance of the Bayesian Network, it makes sense to prune the BN-graph and retain only those nodes within a distance of k from an evidence node. Therefore, OMEN generates only nodes in the BN-graph that are at a maximum distance of k from an evidence node. The value of k is tuneable by the expert running the system, but empirically, we found a small value like $k = 1$ or $k = 2$ suffices. That is, larger values of k make very little difference to the result but increase the size of the Bayesian Net significantly. For small values of k, the graph may be disconnected. In such a case, the algorithm is run separately on each graph.

Anther factor that effects the size of the BN-graph is the number of parents (i.e., nodes that influence the match) that each node has. For example, if a concept C has 5 parents, and C' has 8 parents, the node representing a match between C and C' would have 40 parent nodes in the BN-graph. As we discuss in the next section, the size of a CPT is exponential with respect to the number of parents of a node. Therefore, generating the CPT would cost 2^40 units of computation. Even if the computation is very small, this number is exceedingly large and very soon makes the Bayesian Net unweildy. Thus, we restrict the maximum number of parent nodes for a single node to 10. We choose these 10 parents by selecting the top 5 parents with the maximum *a priori* probability and the top 5 parents with the minimum *a priori* probability. The logic behind such a choice is that if the strong influences of these nodes do not alter the decision whether the two concepts match or not, then the weaker influences of the parents that were not chosen will also not alter the above-mentioned decision.

If the Bayesian Net is constructed by adding edges such that matching ancestor nodes in an ontology influence the children nodes, we refer to this method as the "top-down" method since the influence flows down from the top. A method where OMEN constructs the Bayesian Net edges such that matching descendant nodes influence their ancestors, we call the method a "bottom-up" method. In case the ontologies contain cycles and this introduces cycles in the BN-graph, the algorithm breaks cycles in the BN-graph by rejecting the edges from the parents whose matching information is minimum (*a priori* probability near 0.5).

2.5 The Omen Algorithm

The following summarizes the Omen algorithm:

- Input: source ontologies O and O', initial probability distribution for matches, positive and negative evidence thresholds.
- Steps:
  1. If initial probability of a match is above a given threshold, create a node representing the match and mark it as evidence node.
  2. For each pair of concept pair of concepts (C, C') , where $C \in O$ and $C' \in O'$, create a node in the BayesNet graph.
  3. Create edges between the added nodes using the rules for top-down or bottom-up iterations.
  4. Prune out nodes that are at a distance greater than k from an evidence node (a node with a priori probability above the positive threshold or below the negative threshold).
  5. Use the meta-rules to generate CPTs for the BayesNet.
  6. Run the BayesNet to generate the *a posteriori* probabilities of each node.
  7. Select those nodes with *a posteriori* probabilities over a given threshold as matches.
- Output: a new set of matches

The output of Omen overrides the input matches and is accepted as the new set of matches. The new set of matches may override an initial match or generate a new match that the input did not contain.

3 Meta-rules for Generating New Probability Distributions

In this section, we show examples of meta-rules that are used to match the ontologies and discuss how Omen generates new probability distributions depending upon existing ones.

3.1 Examples of Meta-rules

The following is one of the basic meta-rules we used in our implementation: if two concepts C_1 and C_1' match, and there is a relationship q between C_1 and C_2 in O and a matching relationship q' between C_1' and C_2' in O', then we can increase the probability of match between C_2 and C_2'. Informally, if two nodes in an ontology graph match and so do two arrows coming out of these nodes, then the probability that nodes at the other end of the arrows match is increased. In the formal rule below we generalize this meta-rule to any relationship θ between C_1 and C'_1, not just match.

$$P(C_1\ \theta\ C'_1, x) \wedge P(q = q', 1) \wedge q(C_1, C_2) \wedge q'(C'_1, C'_2) \Rightarrow P(C_2\ \theta\ C'_2, min(1, x + \delta))$$

where δ is an expert-provided constant less than 1. We use a similar meta-rule for the case where relationships q and q' do not match (i.e., for arbitrary pair of outgoing edges), but subtract *delta* from x in the consequent. Other meta-rules rely more heavily on the semantics of the ontology language.

The following is an example of a meta-rule to generate a mapping between classes in the range of a property based on the mapping of the properties themselves and their domains. Not included explicitly in the rule (for brevity) is an assumption that both properties, q and q', have a single domain and range.

$$\begin{aligned}&P(C_d = C'_d, x) \wedge P(q = q', 1) \wedge domainOf(q, C_d) \wedge domainOf(q', C'_d) \wedge\\ &rangeOf(q, C_r) \wedge rangeOf(q', C'_r)\\ &\Rightarrow P(C_r = C'_r, x)\end{aligned}$$

Below are some (informal) examples of other metarules:

Mappings between properties and ranges of properties: If two properties match, and each of them has a single range, we can increase the probability of match between the classes representing the range. Similarly, if two properties q and q' match and the range of q is a union of classes C_1 and C_2, and the range of q' is a class C', then the tool can increase the probability that C_1 is a specialization of C' and C_2 is a specialization of C'.

Mapping between properties: If the ranges between two classes are ranges for matching properties, then they may match (but probabilities are reduced somewhat in comparison to the case when the domains match as well).

Mappings between superclasses and all but one sibling: In this case, we say that the existing matches between the superclasses and the matched siblings result in the remaining siblings matching with high probability.

We experimented with three different ways of generating the CPTs for the nodes in a BN graph:

1. Fixed Influence Method (FI): The meta-rules state that the probability of the children matching depends upon whether the parents match and is given by a set of constants. An example of such a rule is:

$$P[C_p = C'_p, x] \wedge x > t_{max} \wedge q(C_p, C_c) \wedge q(C'_p, C'_c) \Rightarrow P[C_c = C'_c, 0.9]$$

where t_{max} is an expert-defined threshold value. There are similar rules for the other cases.

2. Initial Probability Method (AP): The meta-rules state that the probability distribution of a child node is affected depending upon the probability distribution of the parent node by a set of constants. An example of this class of meta-rules is:

   $$P(C_1 \,\theta\, C_1', x) \wedge P(q = q', 1) \wedge q(C_2, C_1) \wedge q'(C_2', C_1') \wedge P[C_2 \,\theta C_2', y] \wedge (y > t_{max}) \Rightarrow P(C_1 \,\theta\, C_1', min(1, (x + \delta))$$

   where t_{max} and δ are expert-provided constants less than 1.
3. Parent Probability Method (PP): The meta-rules state that the probability distribution of the child node is derived from the probability distribution of the parent node using a set of constants.

The algorithm must combine probabilitic influences of different rules and determine the probability distribution of a mappings. For example, consider a pair of classes, C and C' (Figure 2). In the example in the figure, the following mappings can affect the probability that they match (depending on a specific set of meta-rules used):

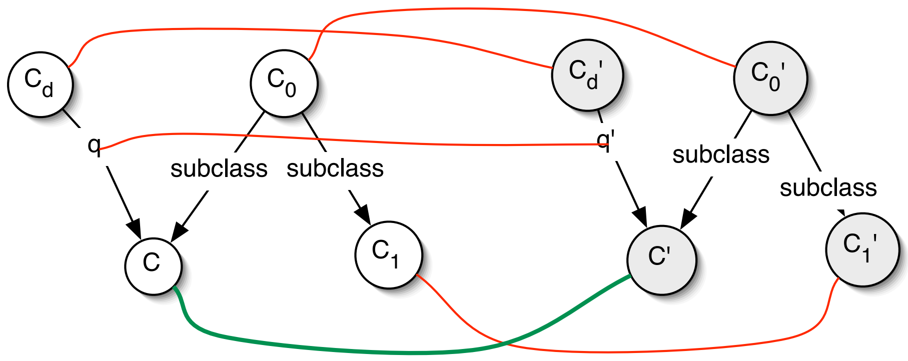


Fig. 2. The probability distribution for the mapping between C and C' is affected by the mappings between their superclasses, siblings, and domains of the properties q and q' for which C and C' are ranges.

– A mapping between superclasses of C and C'
– Mappings between the siblings of C and C'
– A mapping between properties q and q' $(P(q = q', 1))$ for which C and C' are ranges respectively, and mappings between domains of q and q' $(P(C_d = C_d', z))$.

4 Experimentation and Results

Omen uses BNJ, Version 3.0 pre-Alpha 3 [1] as its probabilistic inference engine. We used two ontologies obtained from the Knowledge Representation and

Reasoning group at the Vrije University.[3] The ontologies are expressed in RDF using RDF-Schema. They contain concepts related to university departments and students, staff and faculty of the departments.

Metrics: We used the metrics of precision and recall as defined in the standard information retrieval literature. Precision identifies the ratio of correct matches among the matches identified by the tool and recall identifies the number of matches the tool was able to detect among the "ideal" set of correct matches.

The parameters of the experiment were as follows. The size of the ontologies were 134 nodes and 198 nodes respectively.

a priori Probabilities: We obtained the *a priori* probabilities by running the Lexical Matcher obtained from the ONION project [10]. We considered an evidence threshold of 0.99 for the *a priori* probability. Note, that these figures implies that 10% of the evidence supplied to OMEN was wrong. From the results, we see that OMEN is robust enough to overcome these wrong evidence inputs to a reasonable extent.

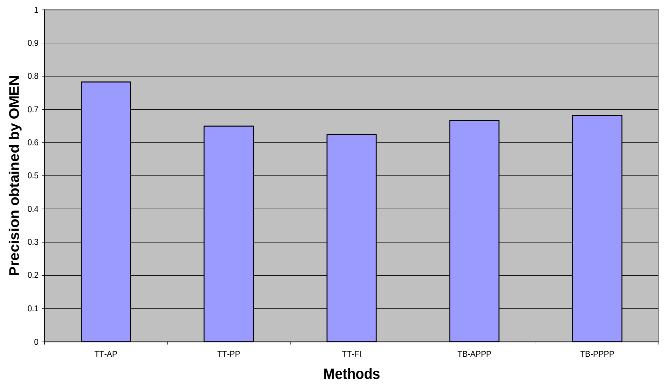
We set $k = 2$, where k is the maximum distance of a node from the evidence node in the Bayesian Network. The thresholds used for the *a posteriori* probabilities to be considered matches were 0.75 for true matches and 0.25 for false matches. We ran OMEN for two passes to generate the results reported below. The input of the first pass was the output obtained from the Lexical Matcher. The input of the second pass was the output generated by the first pass of OMEN. The second pass considered the matches generated by the first pass with high probabilities as evidence and tried to generate even more matches. We also continued the experiments beyond the second pass, however, additional passes did not produce significant changes in the precision and recall for our datasets. Hence we do not report those results.

We show the results of the experiments in Figure 3. The sizes of the Bayesian Networks generated by the different methods varied from 100 to 1300 in the first pass and from 1400 to 1450 nodes in the second pass for all the methods shown. That is, OMEN considered 1400 matches and selected the final results from among them.

In generating the results, we tallied only the new results that OMEN generated. That is, we did not attribute to OMEN any result that was already correctly generated by the Lexical Matcher. The results show that OMEN can successfully generate good quality results even when the easier results have been generated by the prior matcher. This indicates that OMEN can be a good value-add to ontology matching tools and enhance and refine existing ontology matches.

Because of the large sizes of the ontologies, we could not manually match the entire ontologies and therefore do not have the recall values of the entire ontologies. We resorted to sampling to bring the sizes down to get an idea of the recall of our algorithms. Nevertheless, for the large ontologies, whereas the Lexical Matcher generated at most 12 correct matches (with a threshold of 0.85), OMEN generated 74 correct matches (using its best method). These numbers

[3] `http://wbkr.cs.vu.nl/`



TT-AP: Pass1 = Top Down MethodType = AP, Pass2 = Top Down MethodType = AP
TT-PP: Pass1 = Top Down MethodType = PP, Pass2= Top Down MethodType = PP
TT-FI: Pass1 = Top Down MethodType = FI, Pass2= Top Down MethodType = FI
TB-APPP: Pass1 = Top Down MethodType = AP, Pass2= Bottom Up MethodType = PP
TB-PPPP: Pass1 = Top Down MethodType = AP, Pass2= Bottom Up MethodType = PP

Fig. 3. Results for the ontologies of size 134 x 198 nodes

indicate that Omen identifies a significant number of matches that were missed by the Lexical Matcher, has a higher recall than the Lexical Matcher, and can reduce the amount of human intervention required in ontology mapping.

To study the recall of Omen, we sampled the ontologies and computed the ideal results on the small set of ontology selections manually. For the next experiments, we extracted portions of the ontologies manually to make sure that they have at least some overlap. Matching predicates is beyond the scope of this tool. If we want to match predicates, a work-around is to *reify* them, that is represent the predicates as nodes lying between the nodes whose relationships they represent. We obtained matched predicates across the ontologies using the Lexical Matcher using a threshold. When we decided that two predicates represented the same relationship, the names of one predicate was replaced by the names of the matching predicate in the other. As indicated earlier, we limited experiments to small portions of ontologies because we wanted to generate the benchmark correct mappings manually and we did not have resources to create this benchmark manually for large ontologies. Note that the algorithm itself is scalable and does not require such extraction.

Threshold values of 0.85 and 0.15 (for positive and negative matches respectively) are used to determine a match from the posterier probability generated by Omen. In some cases, the threshold was taken to be too stringent and resulted in lower recall. As future work, we intend to look into dynamically selecting proper thresholds by clustering.

We experimented with two sets of ontology graphs. In the first set, both graphs had 11 nodes each and in the second case both had 19 nodes. The preliminary results that we obtained are given in the two tables below:

Table 1 lists the results for the case where the source ontologies were of size 11 nodes each. In this case, we specified three matching nodes as positive evidence

Table 1. Summary of results for the smaller ontologies

Case No.	CPT-Method	Precision	Recall	F-measure
1	FI	0.75	0.375	0.5
	AP	1.0	0.5	0.67
2	FI	1.0	0.5	0.67
	AP	1.0	0.875	0.933
3	AP	1.0	0.75	0.85
4	AP	1.0	0.125	0.22

and four pairs of nodes that do not match as negative evidence. The precision, recall and f-measure are calculated in the usual Information Retrieval (IR) sense using both the positive match and the negative match results together. In case 1, the evidence was introduced at random points. In case 2, the evidence was introduced at or very near the leaf nodes. The results show that introducing the evidence at or near the leaf nodes increased the performance of the algorithm. Case 3 is very similar to Case 2, but with false evidence introduced. Case 4 shows the effect of introducing drastic errors in the initial probabilities. Since the CPTs in the AP method depend directly on the quality of the initial probabilities, when we assigned the initial probabilities at random intentionally, the quality of the results deteroriate.

Overall, we see that the AP method outperforms the FI method in both cases. We also see that by giving only 3 matches out of 11, we could generate upto 7 of the missing matches. This implies that the method can be very useful even when the results of the previous matcher is not very good as not as it is totally random.

We show the results for the case where the source ontologies contained 19 nodes each in Figure 4. The figure shows 7 different test cases for the three different CPT-generating methods. The FI method is shown first, followed by the AP method, followed by the PP method for each test case.

The evidence provided in the cases above were as follows: For case 1, we provided positive evidence of 4 matches at or near the leaf nodes. For cases 2, 3, and 4, we provided positive evidence of 5 matches and negative evidence of 4 matches. For cases 5, 6, and 7 we provided positive evidence of 6 matches and negative evidence of 4 matches. In cases 2, and 3 the evidence was also provided at or near the leaf nodes. In cases 4, and 5, the evidence was provided at or near the root nodes. In cases 6 and 7, the evidence was provided at randomly selected nodes. In cases 3, 5, and 7, wrong evidence was introduced.

Not surprisingly, we see that both the AP and the PP methods outperforms the FI method of constructing CPTs and provide good precision and recall values. The AP method slightly outperforms the PP method in general. However, the PP method is more stable, that is, it recovers from a few wrong evidences better than the AP method. In this case, the place where the evidence was introduced did not matter much for the AP and PP methods.

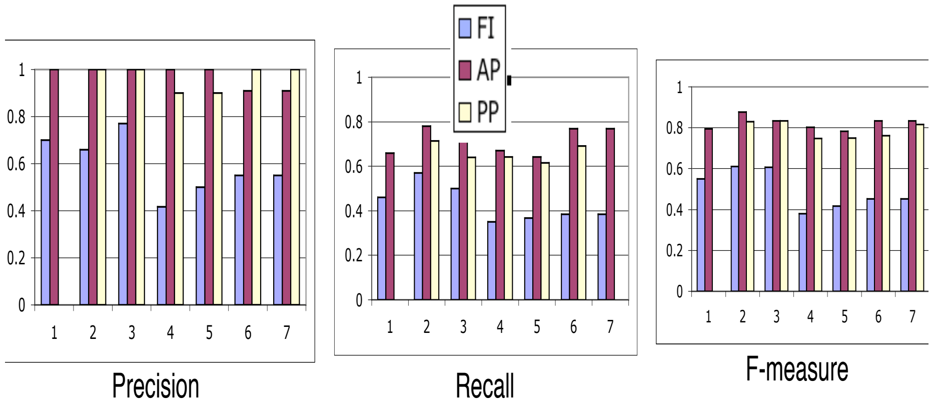


Fig. 4. Results for the ontologies of size 19 nodes

4.1 I3CON Ontologies

We also experimented with the "Computer Science", "Network", "Animal", and "Hotel" ontologies obtained from I^3CON. [4]. Due to lack of space, we show in Figure 5, a comparison of the f-measures of OMEN using the Lexical Matcher from ONION as the initial matcher with other known ontology matchers .

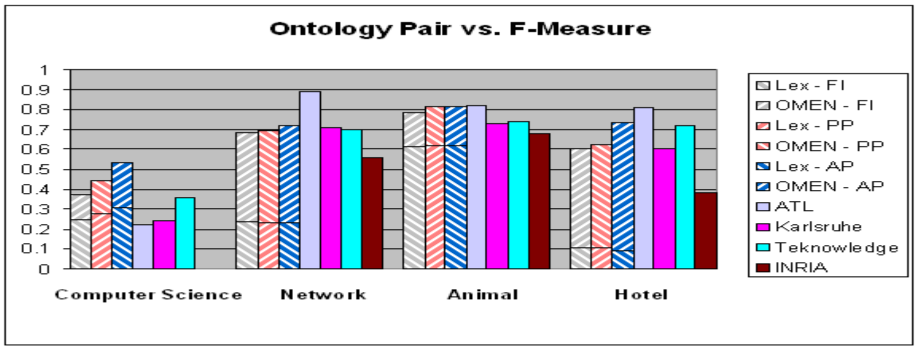


Fig. 5. Results for the I3CON ontologies.

This set of ontologies were proposed by ATL. Most of the other methods whose results were reported did extremely poorly for the "Computer Science" ontology. We observed that the three OMEN algorithms outperform the existing algorithms although the initial results provided by ONION's Lexical Matcher did

[4] http://www.atl.external.lmco.com/projects/ontology/i3con.html

not. For the “Network” ontology, the performance of the OMEN methods were at par with the other methods except for ATL’s methods. Unfortunately, ATL does not publish their exact algorithms. OMEN performs at par with the known and published ontology matching algorithms for this ontology. For the “Animal” ontology, OMEN outperforms other published ontology matching algorithms and matches the performance of ATL’s matcher. OMEN does slightly poorer than Teknowledge’s and ATL’s tool, but provides reasonable performance.

The above-mentioned results indicate that OMEN can be used to complement a set of heuristic ontology mapping tools and enhance the results of ontology matchers. Not surprisingly, it performs reasonably well and is the most valuable when the results of the ontology matchers are not very good in the first place and OMEN has ample scope to enhance the results.

5 Future Work

Designing better CPTs using more of the semantics of the ontology relationships, and emperically evaluating them and experimenting with large ontologies and coupling our matcher with various external matchers are charted for as future work.

We also intend to experiment with OMEN to run it over various other sets of ontologies and also with ontologies with carefully crafted semantics to validate our findings further. One impediment is obtaining such ontologies, but with the adoption of semantic web technologies, we expect to obtain more ontologies to experiment with.

6 Related Work

We reported our initial work in a workshop (without widely disseminated paper proceedings)[9]. Apart from that, we outline works that are most related to ours below. Two research directions are related to our work: automatic or semi-automatic discovery of ontology mappings and the use of uncertainty in knowledge-based systems.

6.1 Automatic ontology mapping

Over the past decade, researchers have actively worked on developing methods for discovering mappings between ontologies or database schemas. For example, Similarity Flooding [8] and AnchorPrompt [12] algorithms *compare graphs* representing the ontologies or schemas, looking for similarities in the graph structure. GLUE [3] is an example of a system that employs *machine-learning techniques* to find mappings. GLUE uses multiple learners exploiting information in concept instances and taxonomic structure of ontologies. GLUE uses a probabilistic model to combine results of different learners. Hovy [5] describes a set of heuristics that researchersat ISI/USC used for semi-automatic alignment of domain ontologiesto a large central ontology. Their techniques are based mainly on*linguistic analysis* of concept names and natural-languagedefinitions of concepts. A number of researchers propose *similarity metrics* between concepts in different ontologies based on their relations to other concepts. For example, a similarity metric between concepts in OWL ontologies developed by Euzenat and Volchev [4] is a weighted combination of similarities of various features in OWL concept definitions: their labels, domains and ranges of properties, restrictions on properties (such as cardinality restrictions), types of concepts, subclasses and superclasses, and so on. Finally, approaches such as ONION [11] and Prompt [13] use a combination of *interactive specifications* of mappings and *heuristics* to propose potential mappings.

The approach that we describe in this paper is complementary to the techniques for automatic or semi-automatic ontology mapping. Many of the methods above produced pairs of matching terms with some degree of certainty. We can use these results as input to our network and run our algorithm to improve the matches produced by others or to suggest additional matches. In other words, our work complements and extends the work by other researchers in this area.

6.2 Probabilistic knowledge-base systems

Several researchers have explored the benefits of bringing together Bayes Nets and knowledge-based systems and ontologies. For instance, Koller and Pfeffer [7] developed a “probabilistic frame-based system,” that allows annotation of frames in a knowledge base with a probability model. This probability model is a Bayesian Net representing a distribution over the possible values of slots in a frame. In another example, Koller and colleagues [6] have proposed probabilistic extensions to description logics based on Bayesean Networks.

In the context of the Semantic Web, Ding and Peng [2] have proposed probabilistic extensions for OWL. In this model, the OWL language is extended to allow probabilistic specification of class descriptions. The authors then build a Bayesean Network based on this specification, which models whether or not an individual matches a class description and hence belongs to a particular class in the ontology.

Researchers in machine learning have employed probabilistic techniques to find ontology mappings. For example, the GLUE system mentioned earlier [3], uses a Bayes classifier as part of its integrated approach. Similarly, Prasad and colleagues [14] use a Bayesean approach to find mappings between classes based on text documents classified as exemplars of these classes. These approaches, however, consider instances of classes in their analysis and not relations between classes, as we do. As with other approaches to ontology mapping, our work can be viewed as complementary to the work done by others.

7 Conclusion

We have outlined the design and implementation of Omen, an ontology match enhancer tool, that improves existing ontology matches based on a probabilistic inference. This tool is dependent upon a set of meta-rules that express the influences of matching nodes on the existence of other matches across concepts in source ontologies that are located in the proximity of the matching nodes. We described how we implemented a simple first version of the matching tool and discussed our preliminary results to show that OMEN usefully complement existing ontologing matching tools.

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