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Results of the Ontology Alignment Evaluation Initiative 2009*

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Abstract. Ontology matching consists of finding correspondences between ontology entities. OAEI campaigns aim at comparing ontology matching systems on precisely defined test cases. Test cases can use ontologies of different nature (from expressive OWL ontologies to simple directories) and use different modalities, e.g., blind evaluation, open evaluation, consensus. OAEI-2009 builds over previous campaigns by having 5 tracks with 11 test cases followed by 16 participants. This paper is an overall presentation of the OAEI 2009 campaign.

1 Introduction

The Ontology Alignment Evaluation Initiative[1] (OAEI) is a coordinated international initiative that organizes the evaluation of the increasing number of ontology matching

* This paper improves on the "Preliminary results" initially published in the on-site proceedings of the ISWC workshop on Ontology Matching (OM-2009). The only official results of the campaign, however, are on the OAEI web site.

[1] http://oaei.ontologymatching.org

systems [10]. The main goal of OAEI is to compare systems and algorithms on the same basis and to allow anyone for drawing conclusions about the best matching strategies. Our ambition is that from such evaluations, tool developers can learn and improve their systems. The OAEI campaign provides the evaluation of matching systems on consensus test cases.

Two first events were organized in 2004: (i) the Information Interpretation and Integration Conference (I3CON) held at the NIST Performance Metrics for Intelligent Systems (PerMIS) workshop and (ii) the Ontology Alignment Contest held at the Evaluation of Ontology-based Tools (EON) workshop of the annual International Semantic Web Conference (ISWC) [23]. Then, unique OAEI campaigns occurred in 2005 at the workshop on Integrating Ontologies held in conjunction with the International Conference on Knowledge Capture (K-Cap) [2], in 2006 at the first Ontology Matching workshop collocated with ISWC [9], in 2007 at the second Ontology Matching workshop collocated with ISWC+ASWC [11], and in 2008, OAEI results were presented at the third Ontology Matching workshop collocated with ISWC [4]. Finally, in 2009, OAEI results were presented at the fourth Ontology Matching workshop collocated with ISWC, in Chantilly, Virginia USA[2].

We have continued previous years' trend by having a large variety of test cases that emphasize different aspects of ontology matching. This year we introduced two new tracks that have been identified in the previous years:

oriented alignments in which the reference alignments are not restricted to equivalence but also comprise subsumption relations;

instance matching dedicated to the delivery of alignment between instances as necessary for producing linked data.

This paper serves as an introduction to the evaluation campaign of 2009 and to the results provided in the following papers. The remainder of the paper is organized as follows. In Section 2 we present the overall testing methodology that has been used. Sections 3-10 discuss in turn the settings and the results of each of the test cases. Section 11 evaluates, across all tracks, the participant results with respect to their capacity to preserve the structure of ontologies. Section 12 overviews lessons learned from the campaign. Finally, Section 13 outlines future plans and Section 14 concludes the paper.

2 General methodology

We first present the test cases proposed this year to OAEI participants. Then, we describe the three steps of the OAEI campaign and report on the general execution of the campaign. In particular, we list participants and the tests they considered.

2.1 Tracks and test cases

This year's campaign has consisted of 5 tracks gathering 11 data sets and different evaluation modalities.

[2] http://om2009.ontologymatching.org

The benchmark track (§3): Like in previous campaigns, a systematic benchmark series has been produced. The goal of this benchmark series is to identify the areas in which each matching algorithm is strong and weak. The test is based on one particular ontology dedicated to the very narrow domain of bibliography and a number of alternative ontologies of the same domain for which alignments are provided.

The expressive ontologies track offers ontologies using OWL modeling capabilities:

- **Anatomy (§4):** The anatomy real world case is about matching the Adult Mouse Anatomy (2744 classes) and the NCI Thesaurus (3304 classes) describing the human anatomy.
- **Conference (§5):** Participants are asked to find all correct correspondences (equivalence and/or subsumption) and/or 'interesting correspondences' within a collection of ontologies describing the domain of organizing conferences (the domain being well understandable for every researcher). Results are evaluated a posteriori in part manually and in part by data-mining techniques and logical reasoning techniques. They are also evaluated against reference alignments based on a subset of the whole collection.

The directories and thesauri track proposes web directories, thesauri and generally less expressive resources:

- **Fishery gears:** This test case features four different classification schemes, expressed in OWL, adopted by different fishery information systems in FIM division of FAO. An alignment performed on this 4 schemes should be able to spot out equivalence, or a degree of similarity between the fishing gear types and the groups of gears, so as to enable a future exercise of data aggregation across systems.
- **Directory (§6):** The directory real world case consists of matching web sites directories (like open directory or Yahoo's). It is more than 4 thousand elementary tests.
- **Library (§7):** Three large SKOS subject heading lists for libraries have to be matched using relations from the SKOS vocabulary. Results are evaluated on the basis of (i) a partial reference alignment (ii) using the alignments to reindex books from one vocabulary to the other.

Oriented alignments (benchmark-subs §8) :

This track focuses on the evaluation of alignments that contain other relations than equivalences.

Instance matching (§9): The instance data matching track aims at evaluating tools able to identify similar instances among different datasets. It features Web datasets, as well as a generated benchmark:

- **Eprints-Rexa-Sweto/DBLP benchmark (ARS)** three datasets containing instances from the domain of scientific publications;
- **TAP-Sweto-Tesped-DBpedia** three datasets covering several topics and structured according to different ontologies;
- **IIMB** A benchmark generated using one dataset and modifying it according to various criteria.
- **Very large crosslingual resources (§10):** The purpose of this task (vlcr) is to match the Thesaurus of the Netherlands Institute for Sound and Vision (called GTAA) to two other resources: the English WordNet from Princeton University and DBpedia.

Table 1 summarizes the variation in the results expected from these tests.

For the first time this year we had to cancel two tracks, namely Fishery and TAP-Sweto-Tesped-DBpedia due to the lack of participants. This is a pity for those who have prepared these tracks, and we will investigate what led to this situation in order to improve next year.

test	formalism	relations	confidence	modalities	language
benchmarks	OWL	=	[0 1]	open	EN
anatomy	OWL	=	[0 1]	blind	EN
conference	OWL-DL	=, <=	[0 1]	blind+open	EN
fishery	OWL	=	1	expert	EN+FR+ES
directory	OWL	=	1	blind+open	EN
library	SKOS +OWL	exact-,narrow-, broadMatch	1	blind	EN+DU+FR
benchmarksubs	OWL	=,<,>	[0 1]	open	EN
ars	RDF	=	[0 1]	open	EN
tap	RDF	=	[0 1]	open	EN
iimb	RDF	=	[0 1]	open	EN
vlcr	SKOS +OWL	exact-, closeMatch	[0 1]	blind expert	DU+EN

Table 1. Characteristics of test cases (open evaluation is made with already published reference alignments, blind evaluation is made by organizers from reference alignments unknown to the participants, consensual evaluation is obtained by reaching consensus over the found results).

2.2 Preparatory phase

Ontologies to be matched and (where applicable) reference alignments have been provided in advance during the period between June 1st and June 22nd, 2009. This gave potential participants the occasion to send observations, bug corrections, remarks and other test cases to the organizers. The goal of this preparatory period is to ensure that the delivered tests make sense to the participants. The final test base was released on July 6th. The data sets did not evolve after this period.

2.3 Execution phase

During the execution phase, participants used their systems to automatically match the ontologies from the test cases. Participants have been asked to use one algorithm and the same set of parameters for all tests in all tracks. It is fair to select the set of parameters that provide the best results (for the tests where results are known). Beside parameters, the input of the algorithms must be the two ontologies to be matched and any general purpose resource available to everyone, i.e., no resource especially designed for the test. In particular, participants should not use the data (ontologies and reference alignments) from other test cases to help their algorithms. In most cases, ontologies are described in OWL-DL and serialized in the RDF/XML format. The expected alignments are provided in the Alignment format expressed in RDF/XML [8]. Participants also provided the papers that are published hereafter and a link to their systems and their configuration parameters.

2.4 Evaluation phase

The organizers have evaluated the alignments provided by the participants and returned comparisons on these results.

In order to ensure that it is possible to process automatically the provided results, the participants have been requested to provide (preliminary) results by September 1st. In the case of blind tests only the organizers did the evaluation with regard to the withheld reference alignments.

The standard evaluation measures are precision and recall computed against the reference alignments. For the matter of aggregation of the measures we use weighted harmonic means (weights being the size of the true positives). This clearly helps in the case of empty alignments. Another technique that has been used is the computation of precision/recall graphs so it was advised that participants provide their results with a weight to each correspondence they found. New measures addressing some limitations of precision and recall have also been used for testing purposes as well as measures compensating for the lack of complete reference alignments.

2.5 Comments on the execution

After a decreased number of participants last year, this year the number increased again: 4 participants in 2004, 7 in 2005, 10 in 2006, 17 in 2007, 13 in 2008, and 16 in 2009.

The number of covered runs has slightly increased: 53 in 2009, 50 in 2008, and 48 in 2007. This may be due to the increasing specialization of tests: some systems are specifically designed for instance matching or for anatomy.

We have had not enough time to systematically validate the results which had been provided by the participants, but we run a few systems and we scrutinized some of the results.

The list of participants is summarized in Table 2. Similar to previous years not all participants provided results for all tests. They usually did those which are easier to run, such as benchmark, anatomy, directory, and conference. The variety of tests and the short time given to provide results have certainly prevented participants from considering more tests.

The sets of participants is divided in two main categories: those who participated in the instance matching track and those who participated in ontology matching tracks. Only a few systems (DSSim and RiMOM) participated in both types of tracks.

The summary of the results track by track is provided in the following sections.

3 Benchmark

The goal of the benchmark tests is to provide a stable and detailed picture of each algorithm. For that purpose, the algorithms are run on systematically generated test cases.

System	aflood	AgrMaker	AMExt	AROMA	ASMOV	DSSim	FBEM	GeRoMe	GG2WW	HMatch	kosimap	Lily	MapPSO	RiMOM	SOBOM	TaxoMap	Total=16
Confidence		√	√	√	√	√	√	√	√	√	√	√		√	√	√	
benchmarks	√	√		√	√	√		√			√	√	√	√	√	√	12
anatomy	√	√		√	√	√					√	√		√	√	√	10
conference	√	√	√	√	√	√					√						7
directory	√				√	√					√	√			√	√	7
library																√	1
benchmarksubs					√									√		√	3
ars					√	√	√			√				√			5
iimb	√				√	√	√			√				√			6
vlcr						√			√								2
Total	5	3	1	3	7	7	2	1	1	2	4	3	1	5	3	5	53

Table 2. Participants and the state of their submissions. Confidence stands for the type of result returned by a system: it is ticked when the confidence has been measured as non boolean value.

3.1 Test data

The domain of this first test is Bibliographic references. It is based on a subjective view of what must be a bibliographic ontology. There may be many different classifications of publications, for example, based on area and quality. The one chosen here is common among scholars and is based on publication categories; as many ontologies (tests #301-304), it is reminiscent to BibTeX.

The systematic benchmark test set is built around one reference ontology and many variations of it. The ontologies are described in OWL-DL and serialized in the RDF/XML format. The reference ontology is that of test #101. It contains 33 named classes, 24 object properties, 40 data properties, 56 named individuals and 20 anonymous individuals. Participants have to match this reference ontology with the variations. Variations are focused on the characterization of the behavior of the tools rather than having them compete on real-life problems. They are organized in three groups:

Simple tests (1xx) such as comparing the reference ontology with itself, with another irrelevant ontology (the wine ontology used in the OWL primer) or the same ontology in its restriction to OWL-Lite;

Systematic tests (2xx) obtained by discarding features from some reference ontology. It aims at evaluating how an algorithm behaves when a particular type of information is lacking. The considered features were:

- *Name of entities* that can be replaced by random strings, synonyms, name with different conventions, strings in another language than English;
- *Comments* that can be suppressed or translated in another language;
- *Specialization hierarchy* that can be suppressed, expanded or flattened;
- *Instances* that can be suppressed;
- *Properties* that can be suppressed or having the restrictions on classes discarded;

– *Classes* that can be expanded, i.e., replaced by several classes or flattened.

Four real-life ontologies of bibliographic references (3xx) found on the web and left mostly untouched (there were added xmlns and xml:base attributes).

Since the goal of these tests is to offer some kind of permanent benchmarks to be used by many, the test is an extension of the 2004 EON Ontology Alignment Contest, whose test numbering it (almost) fully preserves.

The tests are roughly the same as last year. We only suppressed some correspondences that rendered the merged ontologies inconsistent (in 301 and 304) since an increasing number of systems were able to test the consistency of the resulting alignments.

The kind of expected alignments is still limited: they only match named classes and properties, they mostly use the "=" relation with confidence of 1. Full description of these tests can be found on the OAEI web site.

3.2 Results

Twelve systems participated in the benchmark track of this year's campaign (see Table 2). Three systems that had participated last year (CIDER, SAMBO, and SPIDER) did not participate this year.

Table 3 shows the results, by groups of tests. The results of last year are also provided. We display the results of participants as well as those given by some simple edit distance algorithm on labels (edna). The computed values are real precision and recall and not an average of precision and recall. The full results are on the OAEI web site.

As shown in Table 3, two systems are ahead: Lily and ASMOV, with aflood and RiMOM as close followers (with GeRoME, AROMA, DSSim, and AgreementMaker – which is referred as AgrMaker in the tables and figures – having intermediary performance). Last year, ASMOV, Lily and RiMOM had the best performance, followed by AROMA, DSSim, and aflood. No system had strictly lower performance than edna.

Looking for each group of tests, in simple tests (1xx) all systems have similar performance, excluding SOBOM and TaxoMap. Each algorithm has its best score with the 1xx test series. For systematic tests (2xx), which allows to distinguish the strengths of algorithms, Lily and ASMOV are again ahead of the other systems. Finally, for real cases (3xx), AgreementMaker and aflood provide the best results, with Lily, RiMOM, ASMOV, AROMA, and DSSim as followers. There is no a unique best system for all group cases.

Looking for improvements in the systems participating both this year and in the last campaign, GeRoMe and MapPSO have significantly improved their results both in terms of precision and recall, while aflood provides better recall and AROMA improves its results in real cases.

The results have also been compared with the symmetric measure proposed in [7]. It is a generalisation of precision and recall in order to better discriminate systems that slightly miss the target from those which are grossly wrong. This measure slightly improves traditional precision and recall, which are displayed in Table 3 ("Symmetric relaxed measures"). This year, MapPSO has significantly better symmetric precision and recall than classical precision and recall, to the point that it is at the level of the best

system	refalign		edna		aflood		AgrMaker		AROMA		ASMOV		DSSim		GeRoMe		kosimap		Lily		MapPSO		RiMOM		SOBOM		TaxoMap	
test	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.	Prec.	Rec.
2009																												
1xx	1.00	1.00	0.96	1.00	1.00	1.00	0.98	0.98	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	0.99	0.99	1.00	1.00	1.00	1.00	1.00	1.00	0.98	0.97	1.00	0.34
2xx	1.00	1.00	0.41	0.56	0.98	0.74	0.98	0.60	0.98	0.69	0.96	0.85	0.97	0.62	0.92	0.71	0.94	0.57	0.97	0.86	0.73	0.73	0.93	0.81	0.97	0.46	0.90	0.23
3xx	1.00	1.00	0.47	0.82	0.90	0.81	0.92	0.79	0.85	0.78	0.81	0.82	0.94	0.67	0.68	0.60	0.72	0.50	0.84	0.81	0.54	0.29	0.81	0.82	0.92	0.55	0.77	0.31
H-mean	1.00	1.00	0.43	0.59	0.98	0.80	0.99	0.62	0.94	0.69	0.95	0.87	0.97	0.66	0.91	0.73	0.91	0.59	0.97	0.88	0.63	0.61	0.93	0.82	0.98	0.44	0.86	0.26
Symmetric relaxed measures																												
H-mean	1.00	1.00	0.73	1.00	0.99	0.81	0.99	0.62	0.98	0.72	0.99	0.90	1.00	0.67	0.92	0.74	0.99	0.64	0.99	0.89	0.99	0.96	0.99	0.88	1.00	0.44	0.99	0.30
2008																												
1xx	1.00	1.00	0.96	1.00	1.00	1.00			1.00	1.00	1.00	1.00	1.00	1.00	0.96	0.79			1.00	1.00	0.92	1.00	1.00	1.00			1.00	0.34
2xx	1.00	1.00	0.41	0.56	0.96	0.69			0.96	0.70	0.95	0.85	0.97	0.64	0.56	0.52			0.97	0.86	0.48	0.53	0.96	0.82			0.95	0.21
3xx	1.00	1.00	0.47	0.82	0.95	0.66			0.82	0.71	0.81	0.77	0.90	0.71	0.61	0.40			0.87	0.81	0.49	0.25	0.80	0.81			0.92	0.21
H-mean	1.00	1.00	0.43	0.59	0.97	0.71			0.95	0.70	0.95	0.86	0.97	0.67	0.60	0.58			0.97	0.88	0.51	0.54	0.96	0.84			0.91	0.22

Table 3. Means of results obtained by participants on the benchmark test case (corresponding to harmonic means). The symmetric relaxed measure corresponds to the relaxed precision and recall measures of [7].

systems. This may be due the kind of algorithm which is used, that misses the target, but not by far.

Figure 2 shows the precision and recall graphs of this year. These results are only relevant for the results of participants who provide confidence measures different from 1 or 0 (see Table 2). This graph has been drawn with only technical adaptation of the technique used in TREC. Moreover, due to lack of time, these graphs have been computed by averaging the graphs of each of the tests (instead to pure precision and recall).

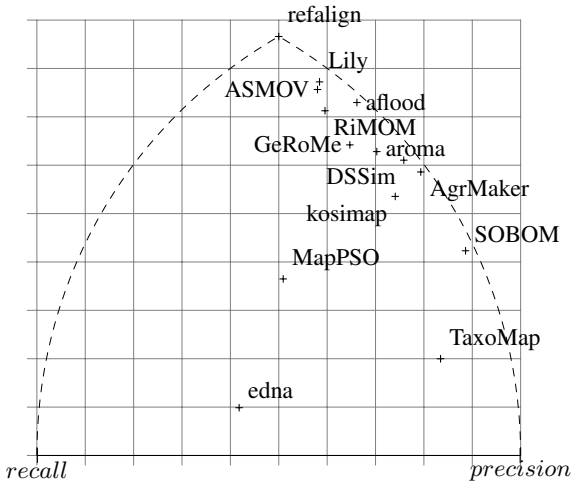

Fig. 1. Each point expresses the position of a system with regard to precision and recall. This shows that most of the systems favor precision over recall.

These results and those displayed in Figure 1 single out the same group of systems, Lily, ASMOV, aflood, and RiMOM which seem to perform these tests at the highest level of quality. Of these, Lily and ASMOV have slightly better results than the two others. So, this confirms the leadership that we observed on raw results.

Like in the three previous campaigns, there is a gap between these systems and their followers (GeRoME, AROMA, DSSim, and AgreementMaker).

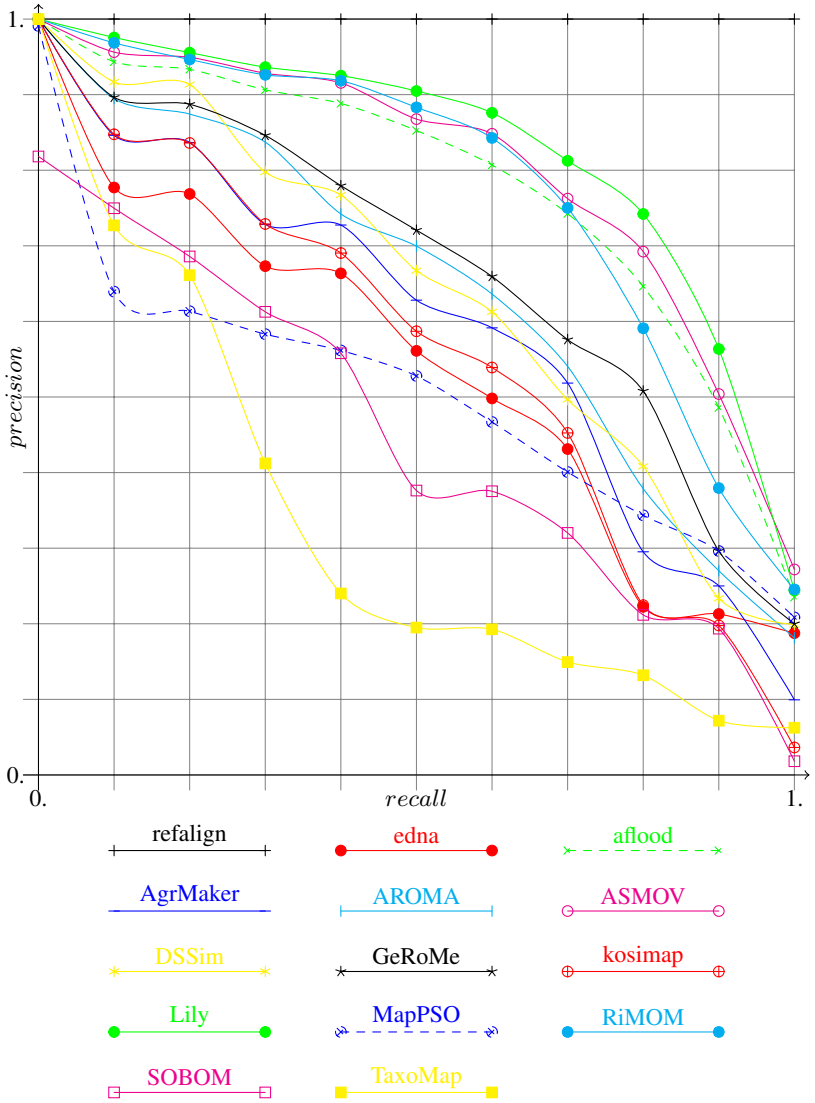

Fig. 2. Precision/recall graphs for benchmarks. The results given by the participants are cut under a threshold necessary for achieving $n\%$ recall and the corresponding precision is computed. Systems for which these graphs are not meaningful (because they did not provide graded confidence values) are drawn in dashed lines.

4 Anatomy

Within the anatomy track we confront existing matching technology with real world ontologies. Currently, we find such real world cases primarily in the biomedical domain, where a significant number of ontologies have been built covering different aspects of medical research. Due to the complexity and the specialized vocabulary of the domain, matching biomedical ontologies is one of the hardest alignment problems.

4.1 Test data and experimental setting

The ontologies of the anatomy track are the NCI Thesaurus describing the human anatomy, published by the National Cancer Institute (NCI)[3], and the Adult Mouse Anatomical Dictionary[4], which has been developed as part of the Mouse Gene Expression Database project. Both resources are part of the Open Biomedical Ontologies (OBO). A detailed description of the data set has been given in the context of OAEI 2007 [11] and 2008 [4].

As proposed in 2008 the task of automatically generating an alignment has been divided into four subtasks. Task #1 is obligatory for participants of the anatomy track, while task #2, #3 and #4 are optional tasks.

- For task #1 the matcher has to be applied with standard settings to obtain a result that is as good as possible with respect to the expected F-measure.
- In task #2 / #3 an alignment has to be generated that favors precision over recall and vice versa. Systems configurable with respect to these requirements will be more useful in particular application scenarios.
- In task #4 we simulate that a group of domain experts created an incomplete reference alignment R_p. Given both ontologies as well as R_p, a matching system should be able to exploit the additional information encoded in R_p.

Due to the harmonization of the ontologies applied in the process of generating a reference alignment (see [3] and [11]), a high number of rather trivial correspondences (61%) can be found by simple string comparison techniques. At the same time, we have a good share of non-trivial correspondences (39%). The partial reference alignment used in subtrack #4 is the union of all trivial correspondences and 54 non-trivial correspondences.

4.2 Results

In total, ten systems participated in the anatomy track (in 2007 there were eleven participants, in 2008 nine systems participated). An overview is given in Table 4. While the number of participants is stable, we find systems participating for the first time (SOBOM, kosimap), systems re-entering the competition after a year of absence (AgreementMaker, which is referred to as AgrMaker in the tables) and systems continuously participating (ASMOV, DSSim, Lily, RiMOM, TaxoMap).

[3] `http://www.cancer.gov/cancerinfo/terminologyresources/`
[4] `http://www.informatics.jax.org/searches/AMA_form.shtml`

System	2007	2008	2009
aflood	-	√	√
AgrMaker	√	-	√+
AROMA	-	√	√
AOAS	√+	-	-
ASMOV	√	√	√
DSSim	√	√	√
Falcon-AO	√	-	-
kosimap	-	-	√
Lily	√	√	√
Prior+	√	-	-
RiMOM	√	√+	√
SAMBO	√+	√+	-
SOBOM	-	-	√+
TaxoMap	√	√	√
X-SOM	√	-	-
avg. F-measure	0.598	0.718	0.764

Table 4. Overview on anatomy participants from 2007 to 2009, a √-symbol indicates that the system participated, + indicates that the system achieved an F-measure ≥ 0.8 in subtrack #1.

In Table 4 we have marked the participants with an F-measure ≥ 0.8 with a + symbol. Unfortunately, the top performers of the last two years do not participate this year (AOAS in 2007, SAMBO in 2008). In the last row of the table the average of the obtained F-measures is shown. We observe significant improvements over time. However, in each of the three years the top systems generated alignments with F-measure of ≈ 0.85. It seems that there is an upper bound which is hard to exceed.

Runtime Due to the evaluation process of the OAEI, the submitted alignments have been generated by the participants, who run the respective systems on their own machines. Nevertheless, the resulting runtime measurements provide an approximate basis for a useful comparison. In 2007, we observed significant differences with respect to the stated runtimes. Lily required several days for completing the matching task and more than half of the systems could not match the ontologies in less than one hour. In 2008 we already observed increased runtimes. This year's evaluation revealed that only one system still requires more than one hour. The fastest system is aflood (15 sec) followed by AROMA, which requires approximately 1 minute. Notice that aflood is run with a configuration optimized for runtime efficiency in task #1, it requires 4 minutes with a configuration which aims at generating an optimal alignment used for #2, #3, and #4. Detailed information about runtimes can be found in the second column of Table 5.

Results for subtracks #1, #2 and #3 Table 5 lists the results of the participants in descending order with respect to the F-measure achieved for subtrack #1. In the first two rows we find SOBOM and AgreementMaker. Both systems have very good results and distance themselves from the remaining systems. SOBOM, although participating for the first time, submitted the best result in 2009. The system seems to be optimized

System	Task #1				Task #2			Task #3			Recall+	
	Runtime	Prec.	Rec.	F	Prec.	Rec.	F	Prec.	Rec.	F	#1	#3
SOBOM	≈ 19 min	0.952	0.777	0.855	-	-	-	-	-	-	0.431	-
AgrMaker	≈ 23 min	0.865	0.798	0.831	0.967	0.682	0.800	0.511	0.815	0.628	0.489	0.553
RiMOM	≈ 10 min	0.940	0.684	0.792	-	-	-	-	-	-	0.183	-
TaxoMap	≈ 12 min	0.870	0.678	0.762	0.953	0.609	0.743	0.458	0.716	0.559	0.222	0.319
DSSim	≈ 12 min	0.853	0.676	0.754	0.973	0.620	0.757	0.041	0.135	0.063	0.185	0.061
ASMOV	≈ 5 min	0.746	0.755	0.751	0.821	0.736	0.776	0.725	0.767	0.745	0.419	0.474
aflood	≈ 15 sec / 4 min	0.873	0.653	0.747	0.892	0.712	0.792	0.827	0.763	0.794	0.197	0.484
Lily	≈ 99 min	0.738	0.739	0.739	0.869	0.559	0.681	0.534	0.774	0.632	0.477	0.548
AROMA	≈ 1 min	0.775	0.678	0.723	-	-	-	-	-	-	0.368	-
kosimap	≈ 5 min	0.866	0.619	0.722	0.907	0.446	0.598	0.866	0.619	0.722	0.154	0.154

Table 5. Participants and results with respect to runtime, precision, recall, recall+ and F-measure.

for generating a precise alignment, however, the submitted alignment contains also a number of non trivial correspondences (see the column Recall+ for subtrack #1).[5]

AgreementMaker generates a less precise alignment, but manages to output a higher number of correct correspondences. None of the other systems detected a higher number of non-trivial correspondences for both subtrack #1 and #3 in 2009. However, it cannot top the SAMBO submission of 2008, which is known for its extensive use of biomedical background knowledge.

The RiMOM system is slightly worse with respect to the achieved F-measure compared to its 2008 submission. The precision has been improved, however, this caused a loss of recall and in particular a significant loss of recall+. Unfortunately, RiMOM did not participate in subtask #3, so we cannot make statements about its strength in detecting non-trivial correspondences based on a different configuration.

The systems listed in the following columns achieve similar results with respect to the overall quality of the generated alignments (F-measures between 0.72 and 0.76). However, significant differences can be found in terms of the trade-off between precision and recall. All systems except ASMOV and Lily favor precision over recall. Notice that a F-measure of 0.755 can easily be achieved by constructing a highly precise alignment without detecting any non-trivial correspondences. At the same time it is relatively hard to generate an alignment with a F-measure of 0.755 that favors recall over precision. Thus, the results of ASMOV and Lily have to be interpreted more positively than indicated by the F-measure.

The observation that it is not hard to construct a highly precise alignment with acceptable recall is supported by the results of subtask #2, where we find relatively similar results for all participants. In particular, it turned out that some systems (ASMOV, DSSim) have their best F-measure in track #2. The evaluation results for aflood require some additional explanations. aflood is run for track #1 with a configuration which results in a significant reduction of the runtime (15 sec), while for track #2 and #3 the

[5] Recall+ is defined as recall restricted to the subset of non trivial correspondences in the reference alignment. A detailed definition can be found in the results paper of 2007 [11].

system required approximately 4 minutes due to different settings. Therefore, aflood creates better alignments as solutions to subtask #2 and #3.

In 2007 we were surprised by the good performance of the naive label comparison approach. Again, we have to emphasize that this is to a large degree based on the harmonization of the ontologies that has been applied in the context of generating the reference alignment. Nevertheless, the majority of participants was able to top the results of the trivial string matching approach this year.

Results for subtrack #4 In the following we refer to an alignment generated for task #1 resp. #4 as A_1 resp. A_4. This year we have chosen an evaluation strategy that differs from the approach of the last year. We compare $A_1 \cup R_p$ resp. $A_4 \cup R_p$ with the reference alignment R. Thus, we compare the situation where the partial reference alignment is added after the matching process has been conducted against the situation where the partial reference alignment is available as additional resource used within the matching process. The results are presented in Table 6.

System	Δ-Precision	Δ-Recall	Δ-F-Measure
SAMBOdtf$_{2008}$	$+0.020_{\ 0.837 \rightarrow 0.856}$	$+0.003_{\ 0.867 \rightarrow 0.870}$	$+0.011_{\ 0.852 \rightarrow 0.863}$
ASMOV	$+0.034_{\ 0.759 \rightarrow 0.792}$	$-0.018_{\ 0.808 \rightarrow 0.790}$	$+0.009_{\ 0.782 \rightarrow 0.791}$
aflood$_{\#3}$	$+0.005_{\ 0.838 \rightarrow 0.843}$	$+0.003_{\ 0.825 \rightarrow 0.827}$	$+0.004_{\ 0.831 \rightarrow 0.835}$
TaxoMap	$+0.019_{\ 0.878 \rightarrow 0.897}$	$-0.026_{\ 0.732 \rightarrow 0.706}$	$-0.008_{\ 0.798 \rightarrow 0.790}$
AgrMaker	$+0.128_{\ 0.870 \rightarrow 0.998}$	$-0.181_{\ 0.831 \rightarrow 0.650}$	$-0.063_{\ 0.850 \rightarrow 0.787}$

Table 6. Changes in precision, recall and F-measure based on comparing $A_1 \cup R_p$, resp. $A_4 \cup R_p$, against reference alignment R.

Four systems participated in task #4. These systems were aflood, AgreementMaker, ASMOV and TaxoMap. In Table 6 we additionally added a row that displays the 2008 submission of SAMBOdtf, which had the best results for subtrack #4 in 2008. For aflood we used A_3 instead of A_1 to allow a fair comparison, due to the fact that A_1 was generated with runtime optimization configuration.

A first look at the results shows that all systems use the partial reference alignment to increase the precision of their systems. Most of them them have slightly better values for precision (between 0.5% and 3.4%), only AgreementMaker uses the additional information in a way which has a stronger impact in terms of a significantly increased precision. However, only three correspondences have been found that have not been in the partial reference alignment previously[6]. Only SAMBOdtf and aflood profit from the partial reference alignment by a slightly increased recall, while the other systems wrongly filter out some correct correspondences. This might be based on two specifics of the dataset. On the one hand the major part of the reference alignment consists of trivial correspondences easily detectable by string matching algorithms, while the unknown parts share a different characteristic. Any approach which applies machine learning techniques to learn from the partial reference alignment is thus bound to fail. On the other hand parts of the matched ontologies are incomplete with respect to

[6] Notice that we only take correspondences between anatomical concepts into account.

subsumption axioms. As pointed out in [16], the completeness of the structure and the correct use of the structural relations within the ontologies has an important influence on the quality of the results. For these reasons it is extremely hard to use the partial reference alignment in an appropriate way in subtask #4.

4.3 Conclusions

Although it is argued that domain related background knowledge is a crucial point in matching biomedical ontologies (see for example [1; 20]), the results of 2009 raise some doubts about this issue. While in 2007 and 2008 the competition was clearly dominated by matching systems heavily exploiting background knowledge (UMLS), this years top performer SOBOM uses none of these techniques. However, the strong F-measure of SOBOM is mainly based on high precision. Comparing the alignments generated by SAMBO in 2008 and SOBOM in 2009 it turns out that SAMBO detected 136 correct correspondences not found by SOBOM, while SOBOM finds 36 correct correspondences not detected by SAMBO. Unfortunately, SOBOM did not participate in subtrack #3. Thus, it is hard to assess its capability for detecting non-trivial correspondences. The results of subtask #4 are disappointing at first sight. Since this kind of task has been introduced in 2008, we expected better results in 2009. However, it turned out again that only minor positive effects can be achieved. But, as already argued, the task of subtrack #4 is hard and systems with acceptable results in subtrack #4 might obtain good results under better conditions.

5 Conference

The conference test set introduces matching several more-or-less expressive ontologies. Within this track the results of participants are evaluated using diverse evaluation methods. First, classical evaluation wrt. the *reference alignment* was made, for the ontology pairs where this alignment is available. Second, posterior manual evaluation was made for all ontology pairs using even sampling across all matchers. Third, the complete results were submitted to a data mining tool for discovery of association hypotheses, taking into account specific mapping patterns. Fourth, alignment incoherence was analysed with the help of a logical reasoner.

5.1 Test data

The collection consists of fifteen ontologies in the domain of organizing conferences. Ontologies have been developed within the OntoFarm project[7]. In contrast to last year's conference track, we alsoconsidered subsumption results in evaluation.

The main features of this test set are:

– *Generally understandable domain.* Most ontology engineers are familiar with organizing conferences. Therefore, they can create their own ontologies as well as evaluate the alignment among their concepts with enough erudition.

[7] `http://nb.vse.cz/~svatek/ontofarm.html`

– *Independence of ontologies.* Ontologies were developed independently and based on different resources, they thus capture the issues in organizing conferences from different points of view and with different terminologies.
– *Relative richness in axioms.* Most ontologies were equipped with DL axioms of various kinds, which opens a way to use semantic matchers.

Ontologies differ in numbers of classes, of properties, in their DL expressivity, but also in underlying resources. Ten ontologies are based *on tools* supporting the task of organizing conferences, two are based on experience of people with *personal participation* in conference organization, and three are based on *web pages* of concrete conferences.

Participants were to provide all correct correspondences (equivalence and/or subsumption) and/or "interesting correspondences" within a collection of ontologies describing the domain of organizing conferences.

This year, results of participants are evaluated by four different methods of evaluation: evaluation based on reference alignment, manual labeling, data mining method, and logical reasoning. In addition, we extended the reference alignment from the previous year. Now we have 21 alignments, which correspond to the complete alignment space between 7 ontologies from the data set. Manual evaluation produced statistics such as precision and will also serve as input into evaluation based on data mining and will help in the process of improving and building a reference alignment. Results of participants are checked with regard to their incoherency. These evaluation methods are concisely described at the track result page.

5.2 Results

We had seven participants: aflood, AgreementMaker (AgrMaker), AMExt (an extended version of AgreementMaker), AROMA, ASMOV, DSSim, and kosimap. Here are some basic data, besides evaluations:

– All participants delivered all 105 alignments, except for aflood, which delivered 103 alignments.
– Two participants (ASMOV and DSSim) delivered not only equivalence correspondences but also subsumptions.
– aflood and DSSim matchers delivered "certain" correspondences; other matchers delivered correspondences with confidence values between 0 and 1.

Evaluation based on reference alignment We evaluated the results of participants against a reference alignment. In the case of ASMOV and DSSim we filtered out subsumptions. It includes all pairwise combinations of different 7 ontologies (21 alignments).

In Table 7, there are traditional precision, recall, and F-measure computed for three different thresholds of certainty factor (0.2, 0.5, and 0.7).

For better comparison we established the confidence threshold which provides the highest average F-measure (Table 8). Precision, Recall, and F-measure are given for this optimal confidence threshold. The dependency of F-measure on confidence threshold

	t=0.2			t=0.5			t=0.7		
	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.
aflood	48%	61%	52%	48%	61%	52%	48%	61%	52%
AgrMaker	45%	61%	50%	45%	61%	50%	6%	55%	56%
AMExt	30%	60%	39%	30%	60%	39%	41%	53%	46%
AROMA	37%	49%	41%	38%	49%	42%	40%	19%	25%
ASMOV	58%	40%	47%	22%	3%	4%	5%	1%	1%
DSSim	15%	51%	22%	15%	51%	22%	15%	51%	22%
kosimap	18%	56%	27%	41%	43%	41%	70%	23%	33%

Table 7. Recall, precision and F-measure for three different confidence thresholds.

matcher	confidence threshold	Prec.	Rec.	FMeas.
aflood	*	48%	61%	52%
AgrMaker	0.75	69%	51%	57%
AMExt	0.75	54%	50%	51%
AROMA	0.53	39%	48%	42%
ASMOV	0.23	68%	38%	47%
DSSim	*	15%	51%	22%
kosimap	0.51	52%	42%	45%

Table 8. Confidence threshold, precision and recall for optimal F-measure for each matcher.

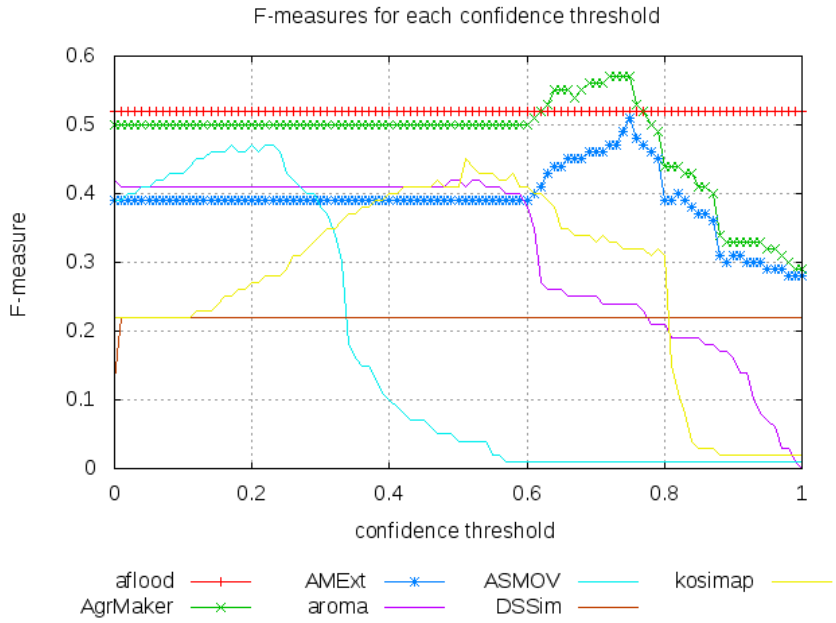

Fig. 3. F-measures depending of confidence.

can be seen from Figure 3. There are two asterisks in the column of confidence threshold for matchers which did not provide graded confidence.

In conclusion, the matcher with the highest average F-measure (.57) is that of AgreementMaker at .75. However we should take into account that this evaluation has been made over small part of all alignments (one fifth).

Comparison with previous year We evaluated the results of participants of OAEI 2008 (ASMOV, DSSim and Lily) against the new reference alignments. For these three matchers from OAEI 2008, we found an optimal confidence threshold in terms of highest average F-measure, see Table 9. In the case of DSSim there is an asterisk because this matcher did not provide graded confidence.

In conclusion, the matcher with the highest average F-measure (0.49) was the DSSim. However we should take into account that this evaluation has been made over small part of all alignments (one fifth). We can also compare performance of participants of both years ASMOV and DSSim. While in terms of highest average F-measure ASMOV improved from 43% to 47%, DSSim declined from 49% to 22%. We can also see that ASMOV matcher from OAEI 2009 delivered more correspondences with lower confidence than in OAEI 2008.

matcher	confidence threshold	Prec.	Rec.	FMeas.
ASMOV	0.22	48%	39%	43%
DSSim	*	48%	56%	49%
Lily	0.25	43%	52%	45%

Table 9. Confidence threshold, precision and recall for optimal F-measure for each matcher.

Restricted semantic precision and recall Furthermore, we computed *restricted semantic precision and recall* using a tool from University of Mannheim [12]. We took into account matchers which delivered correspondences with subsumption relations, i.e., ASMOV and DSSim. In Table 10 there are two different semantics variants (natural and pragmatic) of restricted semantic precision and recall computed for confidence threshold 0.23[8].

	natural		pragmatic	
matcher	Prec.	Rec.	Prec.	Rec.
ASMOV	83%	65%	86%	68%
DSSim	1.7%	94%	2%	95%

Table 10. Restricted semantic precision and recall for a confidence threshold of 0.23.

In conclusion, from Table 10 we can see that considering correspondences with subsumption relations ASMOV has better performance in both precision and recall, whereas DSSim has much better recall at expense of lower precision.

[8] This an optimal confidence threshold in terms of highest F-measure for ASMOV. DSSim does not have graded confidence.

Evaluation based on posterior manual labeling This year we take the most secure, i.e., with highest confidence, correct correspondences as a population for each matcher. It means we evaluate 150 correspondences per matcher randomly chosen from all correspondences of all 105 alignments with confidence 1.0 (sampling). Because AROMA, ASMOV and kosimap do not have enough correspondences with 1.0 confidence we take 150 correspondences with highest confidence. In the case of AROMA it was not possible to distinguish between all 153 correspondences so we sampled over its population.

In table 11 you can see approximated precisions for each matcher over its population of best correspondences. N is a population of all the best correspondences for one matcher. n is a number of randomly chosen correspondences so as to have 150 best correspondences for each matcher. TP is a number of correct correspondences from the sample, and P* is an approximation of precision for the correspondences in each population; additionally there is a margin of error computed as: $\frac{\sqrt{(N/n)-1}}{\sqrt{N}}$ based on [24].

matcher	aflood	AgrMaker	AMExt	AROMA	ASMOV	DSSim	kosimap
N	1779	326	360	153	150	5699	150
n	150	150	150	150	150	150	150
TP	74	120	103	83	127	9	144
P*	49% ±7.8%	80% ±6%	69% ±6.2%	55% ±1.1%	85%	6% ±8.1%	96%

Table 11. Approximated precision for 150 best correspondences for each matcher.

From table 11 we can conclude that kosimap has the best precision (.96) over its 150 more confident correspondences.

Evaluation based on data mining supported with mapping patterns (based on [19]). As opposed to ontology design patterns[9], which usually concern one ontology, mapping patterns deal with (at least) two ontologies. Mapping patterns reflect the internal structure of ontologies as well as correspondences across the ontologies.

We recognise nine mapping patterns:

- MP1 ("Parent-child triangle"): it consists of an equivalence correspondence between classes A and B and an equivalence correspondence between A and a child of B, where A and B are from different ontologies.
- MP2 ("Mapping along taxonomy"): it consists of simultaneous equivalence correspondences between parents and between children.
- MP3 ("Sibling-sibling triangle"): it consists of simultaneous correspondences between class A and two sibling classes C and D where A is from one ontology and C and D are from another ontology.
- MP4: it is inspired by the 'class-by-attribute' correspondence pattern, where the class in one ontology is restricted to only those instances having a particular value for a a given attribute/relation.

[9] See `http://ontologydesignpatterns.org`.

– MP5: it is inspired by the "composite" correspondence pattern. It consists of a class-to-class equivalence correspondence and a property-to-property equivalence correspondence, where classes from the first correspondence are in the domain or in the range of properties from the second correspondence.
– MP6: it is inspired by the "attribute to relation" correspondence pattern where a datatype and an object property are aligned as an equivalence correspondence.
– MP7: it is the variant of the MP5 "composite pattern". It consists of an equivalence correspondence between two classes and an equivalence correspondence between two properties, where one class from the first correspondence is in the domain and the other class from that correspondence is in the range of equivalent properties, except the case where domain and range is the same class.
– MP8: it consists of an equivalence correspondence between A and B and an equivalence correspondence between a child of A and a parent of B where A and B are from different ontologies. It is sometimes referred to as criss-cross pattern.
– MP9: it is the variant of MP3, where the two sibling classes C and D are disjoint.

MP4, MP5, and MP6 are inspired by correspondence patterns from [21]. In principle, it is not possible to tell which mapping pattern is desirable or not desirable. This must be decided on the basis of an application context or possible alternatives. However, we could roughly say that while MP2 and MP5 seems to be desirable, MP7, MP8, and MP9 indicate incorrect correspondences related to inconsistency.

In Table 12 there are numbers of occurrences of mapping patterns in results of participants of OAEI 2009. We already see that some patterns are more typical for some systems than for other. Proper quantification of this relationship as well as its combination with other characteristics of correspondences is however the task for a mining tool.

System	MP1	MP2	MP3	MP4	MP5	MP6	MP7	MP8	MP9
aflood	0	168	0	272	158	108	6	4	0
AgrMaker	0	127	0	272	81	209	22	2	0
amext	0	128	0	346	112	419	25	4	0
AROMA	238	206	6	442	35	61	13	12	0
asmov	0	350	0	393	0	0	0	0	0
dssim	479	74	964	962	47	410	24	47	295
kosimap	38	233	159	815	392	62	10	4	22

Table 12. Occurrences of mapping patterns in OAEI 2009 results.

For the *data-mining analysis* we employed the *4ft-Miner* procedure of the *LISp-Miner* data mining system[10] for mining of *association rules*. We found several interesting *association hypotheses*: $t1$ to $t6$ are related to confidence or underlying resources of ontologies (see Table 13) and $m1$ to $m10$ are related to mapping patterns (see Table 14). In total there were 21117 correspondences in the data matrix. We can interpret some of these hypotheses as follows:

[10] `http://lispminer.vse.cz/`

	Antecedent				Succedent	Values	
	System	Confidence	Resource1	Resource2	Result	Supp	AvgDff
t1	AgrMaker	> 0.9	*	*	+	0.01	2.876
t2	ASMOV	< 0.3	*	*	+	0.01	2.546
t3	kosimap	$< 0.3; 0.6)$	*	*	+	0.01	2.497
t4	DSSim	*	i	w	-	0.01	2.287
t5	kosimap	$< 0.3; 0.6)$	*	t	+	0.01	2.267
t6	kosimap	*	*	i	-	0.02	1.215

Table 13. Hypotheses for tasks 1 and 2.

	Antecedent		Succedent	Values-
	System	ResultMP	Supp	AvgDff
m1	ASMOV	MP2	0.02	3.418
m2	AROMA	MP1	0.01	2.434
m3	DSSim	MP3	0.05	2.164
m4	AMExt	MP6	0.02	1.481
m5	ASMOV	MP4	0.02	0.874
m6	kosimap	MP5	0.02	0.874
m7	DSSim	MP9	0.01	2.448
m8	DSSim	MP8	0.002	1.386
m9	AgrMaker	MP7	0.001	1.266
m10	AMExt	MP7	0.001	0.879

Table 14. Association Hypotheses related to Mapping Patterns.

– Hypothesis t1: Correspondences that are produced by system AgreementMaker and have high confidence values (higher than 0.9) are by 287%, i.e. almost four times, more often correct than correspondences produced by all systems with all confidence values (on average).
– Hypothesis t4: Correspondences that are produced by system DSSim where ontology 1 is based on expert knowledge and ontology 2 is based on web are by 228%, i.e., more than three times, more often incorrect than correspondences produced by all systems for all types of ontologies (on average).
– Hypothesis m1: Correspondences that are produced by matcher ASMOV are by 341%, i.e., more than four times, more often part of MP2 than correspondences produced by all systems (on average).
– Hypothesis m4: Correspondences that are produced by matcher AMExt are by 148%, i.e., more than twice, more often part of MP6 than correspondences produced by all systems (on average).
– Hypothesis m7: Correspondences that are produced by matcher DSSim are by 244%, i.e., more than three times, more often part of MP9 than correspondences produced by all systems (on average).
– Hypothesis m9: Correspondences that are produced by matcher AgreementMaker are by 126%, i.e., more twice, more often part of MP7 than correspondences produced by all systems (on average).

In conclusion, regarding the first three hypotheses we could say that AgreementMaker is more sure about correspondences with high values than other matchers, ASMOV is suprisingly more correct about correspondences with low confidence values than other matchers and kosimap is more correct for correspondences with medium confidence values. According to next three hypotheses we could say that kosimap works better with ontologies based on tool than web. Further DSSim has problems with aligning "expert' ontologies" and "web" ontologies.

Regarding the three first mapping patterns, ASMOV found MP2, AROMA MP1, and DSSim MP3. Furthermore, AMExt found MP6 as simple correspondence, which is discutable. Maybe it could be better to find instead of datatype property to object property "property-chain" which would allow mapping between datatype property to datatype property via object property as an intermediate mapping element. ASMOV found some correspondences where one class is restricted over certain property's value (MP4) and kosimap found composite pattern (MP5). Finally, some occurrences of the last three mapping patterns were found over the results of DSSim, AgreementMaker, and AMExt. However these related hypotheses had low support except for DSSim and MP9. Anyway we can say that these matchers could be improved if they check the consistency of their results.

Evaluation based on alignment coherence In 2008 we evaluated for the first time the coherence of the submitted alignments. Again, we picked up the same evaluation approach using the maximum cardinality measure m^t_{card} proposed in [17]. The m^t_{card} measure compares the number of correspondences that have to be removed to arrive at a coherent subset against the number of all correspondences in the alignment. The resulting number can be considered as the degree of alignment incoherence. A number

of 0% means, for example, that the alignment is coherent. In particular, we use the pragmatic alignment semantic as defined in [18] to interpret the correspondences of an alignment.

In our experiments we focused on equivalence correspondences and removed subsumption correspondences from the submitted alignments prior to our evaluation. We applied our evaluation approach to the subset of those matching tasks where a reference alignment is available. We used the Pellet reasoner to perform our experiments and excluded the Iasted ontology, which caused reasoning problems in combination with some of the other ontologies.

Results are presented in Table 15. For all systems we used the alignments after applying the optimal confidence threshold (see subscript), and the systems marked with * are those systems that did not deliver a graded confidence. Comparing the corresponding results, the ASMOV system clearly distances itself from the remaining participants. All of the generated alignments were coherent and thus we measured 0% degree of incoherence. However, the thresholded ASMOV alignments contain only few correspondences compared to the alignments of the other systems, which makes it more probable to construct coherent alignments. Thus, we also included the untresholded ASMOV alignments (no subscript) in our analysis: We measured a degree of incoherence of 1.8%, a value that is still significantly lower compared to the other systems. These results also concide with the results presented in Table 14 related to the occurrence of the MP7 to MP9 mapping patterns.

While the verification component built into ASMOV detects most incoherences, none of the other systems uses similar strategies. We have to conclude that logical aspects play only a subordinate role within the approaches implemented in the other matching systems. Additionally, we analyzed what happens when the verification component of ASMOV is turned off.[11] The results are presented in the ASMOV^x row. Notice that the measured values are now similar to the coherence characteristics of the other systems.

In conclusion, these observations also offer an explanation for the significant difference between DSSim and ASMOV with respect to restricted semantic precision and recall (see again Table 10). Computing restricted semantic precision and recall of an alignment A requires to compute the closure of A with respect to derivable subsumption correspondences. Suppose now that A is incoherent and a large fraction of concepts $C_1, ..., C_n$ in O_1 and $D_1, ..., D_m$ in O_2 becomes unsatisfiable. It follows that A entails each correspondence of the type ... $\sqsupseteq C_i$ with $i = 1 \ldots n$, respectively $D_j \sqsubseteq$ ... with $j = 1 \ldots m$. A highly incoherent alignment will thus entail a huge amount of incorrect correspondences. This is the explanation for DSSim's low precision of approximately 2%. These considerations also indicate that the degree of incoherence might have a strong effect on any application that requires to exploit an alignment in a reasoning context.

[11] We would like to thank Yves R. Jean-Mary for providing us with the corresponding set of alignments.

System	Correspondences	Incoherent Alignments	m^t_{card}-mean
ASMOV$_{.23}$	140	0	0.0%
ASMOV	233	3	1.8%
kosimap$_{.51}$	189	6	10.6%
ASMOV^x	316	13	14.7%
AgrMaker$_{.75}$	173	12	15.0%
aflood*	288	15	19.8%
AROMA$_{.53}$	264	13	20.1%
AMExt$_{.75}$	236	13	20.3%
DSSim*	789	15	> 42.2%

Table 15. Number of evaluated correspondences, number of coherent alignments (15 alignments have been analyzed), mean of the maximum cardinality measure. Subscripts refer to the application of a confidence threshold, ASMOV^x refers to ASMOV with the semantic verification component turned off.

6 Directory

The directory test case aims at providing a challenging task for ontology matchers in the domain of large directories to show whether ontology matching tools can effectively be applied for the integration of "shallow ontologies". The focus of this task is to evaluate performance of existing matching tools in real world taxonomy integration scenario.

6.1 Test set

As in previous years [9; 11; 4], the data set exploited in the directory matching task was constructed from Google, Yahoo and Looksmart web directories following the methodology described in [13]. The data set is presented as taxonomies where the nodes of the web directories are modeled as classes and classification relation connecting the nodes is modeled as an `rdfs:subClassOf` relation.

The key idea of the data set construction methodology is to significantly reduce the search space for human annotators. Instead of considering the full matching task which is very large (Google and Yahoo directories have up to $3 * 10^5$ nodes each: this means that the human annotators need to consider up to $(3*10^5)^2 = 9*10^{10}$ correspondences), it uses semi automatic pruning techniques in order to significantly reduce the search space. For example, for the data set described in [13], human annotators consider only 2265 correspondences instead of the full matching problem.

The specific characteristics of the data set are:

- More than 4.500 node matching tasks, where each node matching task is composed from the paths to root of the nodes in the web directories.
- Reference alignment for all the matching tasks.
- Simple relationships, in particular, web directories contain only one type of relationships, which is the so-called classification relation.
- Vague terminology and modeling principles, thus, the matching tasks incorporate the typical real world modeling and terminological errors.

6.2 Results

In OAEI 2009, 7 out of 16 matching systems participated on the web directories test case, while in OAEI-2008, 7 out of 13, in OAEI 2007, 9 out of 18, in OAEI 2006, 7 out of 10, and in OAEI 2005, 7 out of 7 did it.

Precision, recall and F-measure results of the systems are shown in Figure 4. These indicators have been computed following the TaxMe2 [13] methodology, with the help of the Alignment API [8], version 3.4.

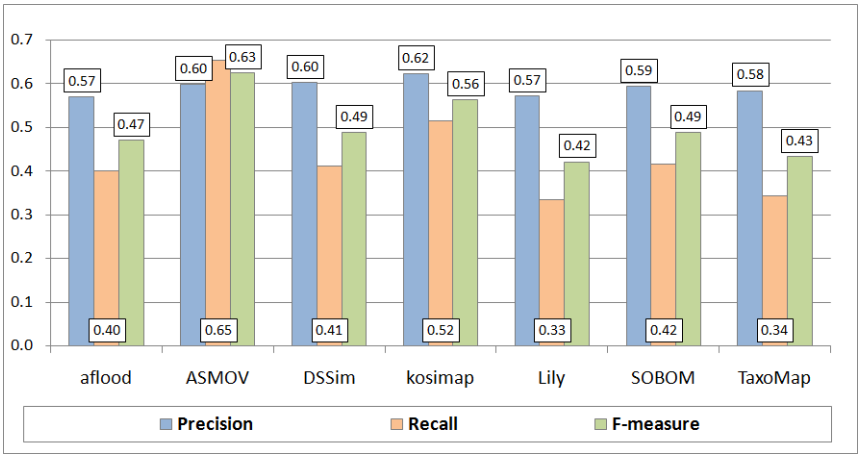

Fig. 4. Matching quality results.

We can observe from Table 16, that in general the systems that participated in the directory track in 2008 (DSSim, Lily and TaxoMap), have either maintained or decreased their precision and recall values. The only system that increased its recall value is ASMOV. In fact, ASMOV is the system with the highest F-measure value in 2009.

Table 16 shows that in total 24 matching systems have participated in the directory track during the 5 years (2005 – 2009) of the OAEI campaigns. No single system has participated in all campaigns involving the web directory dataset (2005 – 2009). A total of 16 systems have participated only one time in the evaluation, only 3 systems have participated 2 times, and 5 systems have participated 3 times.

As can be seen in Figure 5 and Table 16, there is an increase in the average precision for the directory track up to 2008, remaining constant in 2009. The average recall in 2009 increased in comparison to 2008, but the highest average recall remains that of 2007. Considering F-measure, results for 2009 show the highest average in the 4 years (2006 to 2009). Notice that in 2005 the data set allowed only the estimation of recall, therefore Figure 5 and Table 16 do not contain values of precision and F-measure for 2005.

A comparison of the results in 2006, 2007, 2008 and 2009 for the top-3 systems of each year based on the highest values of the F-measure indicator is shown in Figure 6. The key observation here is that even though two of the top-3 systems of 2008 (Lily and DSSim) participated in the directory task this year, they did not manage to get into the top-3, indicating an overall increase of performance by the total set of participating

System	Recall					Precision				F-Measure			
Year →	2005	2006	2007	2008	2009	2006	2007	2008	2009	2006	2007	2008	2009
aflood					0.40				0.57				0.47
ASMOV			0.44	0.12	0.65		0.59	0.64	0.60		0.50	0.20	0.63
automs		0.15				0.31				0.20			
CIDER				0.38				0.60				0.47	
CMS	0.14												
COMA		0.27				0.31				0.29			
ctxMatch2	0.09												
DSSim			0.31	0.41	0.41		0.60	0.60	0.60		0.41	0.49	0.49
Dublin20	0.27												
Falcon	0.31	0.45	0.61			0.41	0.55			0.43	0.58		
FOAM	0.12												
HMatch		0.13				0.32				0.19			
kosimap					0.52				0.62				0.56
Lily			0.54	0.37	0.33		0.57	0.59	0.57		0.55	0.46	0.42
MapPSO				0.31				0.57				0.40	
OCM		0.16				0.33				0.21			
OLA	0.32		0.84				0.62				0.71		
OMAP	0.31												
OntoDNA			0.03				0.55				0.05		
Prior		0.24	0.71			0.34	0.56			0.28	0.63		
RiMOM		0.40	0.71	0.17		0.39	0.44	0.55		0.40	0.55	0.26	
SOBOM					0.42				0.59				0.49
TaxoMap				0.34	0.34			0.59	0.59			0.43	0.43
X-SOM			0.29				0.62				0.39		
Average	0.22	0.26	0.50	0.30	0.44	0.35	0.57	0.59	0.59	0.29	0.49	0.39	0.50
#	7	7	9	7	7	7	9	7	7	7	9	7	7

Table 16. Summary of submissions by year (no precision was computed in 2005). The Prior line covers Prior+ as well and the OLA line covers OLA_2 as well.

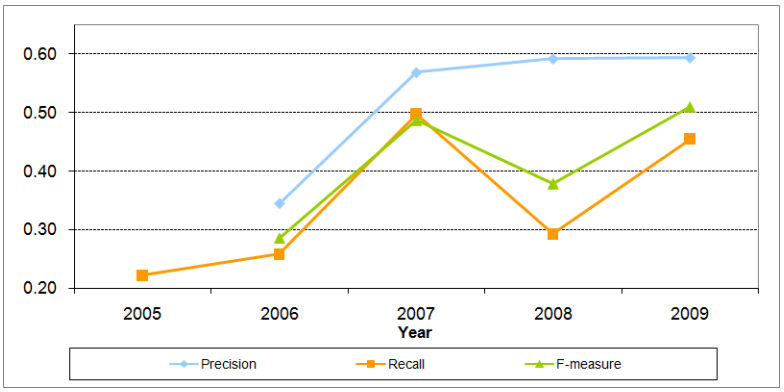

Fig. 5. Average results of the top-3 systems per year.

systems this year. As can be seen in Table 16, DSSim maintained its performance of 2008, having the same F-measure as SOBOM (a newcomer and 3rd place of 2009), only 1% less of recall than SOBOM, but 1% more of precision. ASMOV increased its F-measure, presenting the highest value for this year directory track, and in overall in its 3 years of participation. The second place corresponds to kosimap, also a newcomer.

The quality of the best F-measure result of 2009 (0.63) achieved by ASMOV is higher than the best F-measure of 2008 (0.49) demonstrated by DSSim and higher than that of 2006 by Falcon (0.43), but still lower than the best F-measure of 2007 (0.71) by OLA_2. The best precision result of 2009 (0.62) achieved by kosimap is lower than the best precision value of 2008 (0.64) demonstrated by ASMOV and equal to the results obtained in 2007 by both OLA_2 and X-SOM. Finally, for what concerns recall, the best result of 2009 (0.65) achieved by ASMOV is higher than the best value of 2008 (0.41) demonstrated by DSSim and the best value in 2006 (0.45) by Falcon, but still lower than the best result obtained in 2007 (0.84) obtained by OLA_2.

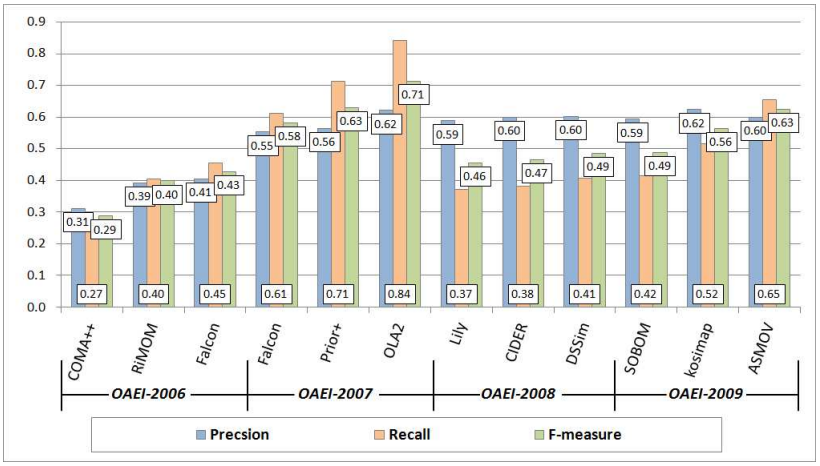

Fig. 6. Comparison of matching quality results in 2006, 2007, 2008 and 2009.

Partitions of positive and negative correspondences according to the system results are presented in Figures 7 and 8, respectively.

Figure 7 shows that the systems managed to discover only 68% of the total number of positive correspondences (Nobody = 32%). Only 26% of positive correspondences were found by all seven participating systems. The percentage of positive correspondences found by the systems this year is higher than the values of 2008, when 54% of the positive correspondences where found. Figure 8 shows that more than half (56%) of the negative correspondences were not found by the systems (correctly) in comparison to 66% not found in 2008. Figure 8 also shows that all participating systems found 17% of the negative correspondences, i.e., mistakenly returned them as positive. The last two observations suggest that the discrimination ability of the dataset remains still high as in previous years.

Let us now compare partitions of the system results in 2006, 2007, 2008 and 2009 on positive and negative correspondences, see Figures 9 and 10, respectively. Figure 9

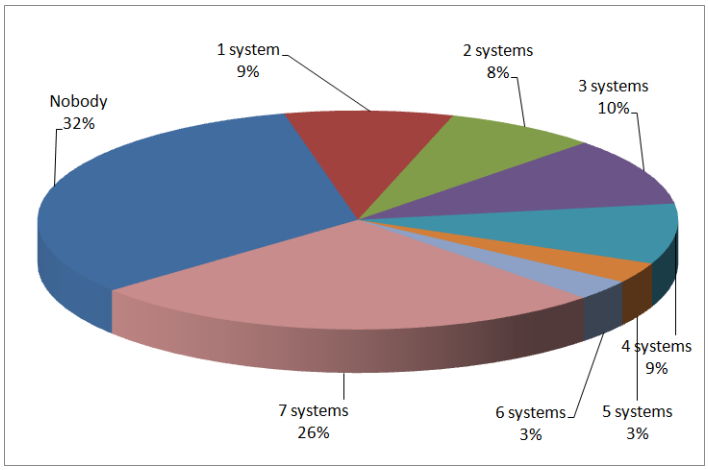

Fig. 7. Partition of the system results on positive correspondences.

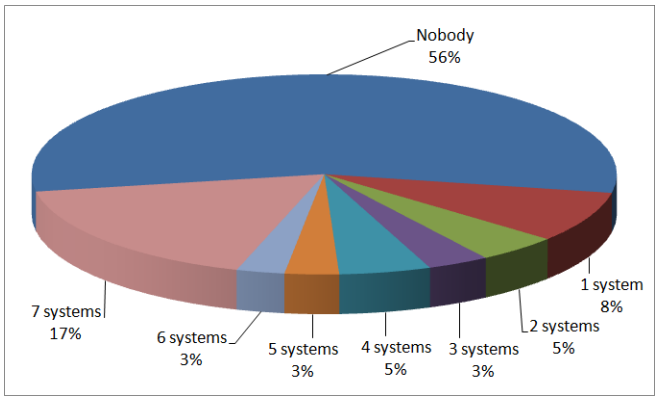

Fig. 8. Partition of the system results on negative correspondences.

shows that 32% of positive correspondences have not been found by any of the matching systems this year. This value is better that the values of 2006 (43%) and 2008 (46%). In 2007 all the positive correspondences have been collectively found; these results (2007) were exceptional because the participating systems all together had a full coverage of the expected results and very high precision and recall. Unfortunately, the best systems of 2007 did not participate this year (nor in 2008) and the other systems do not seem to cope with the results of 2007.

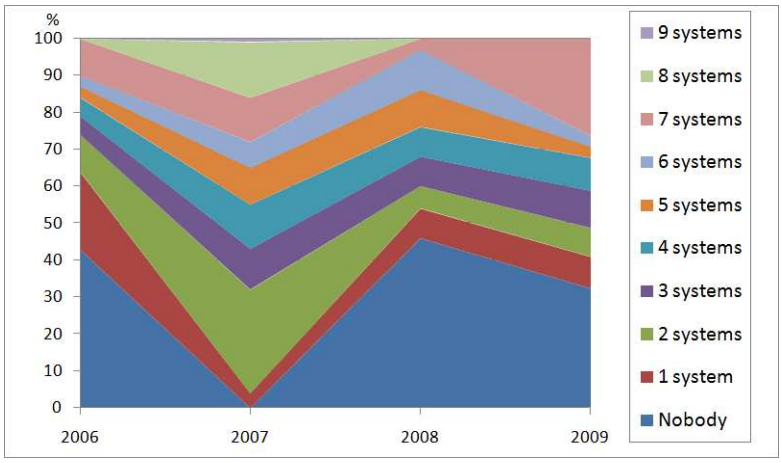

Fig. 9. Comparison of partitions of the system results on positive correspondences in 2006, 2007, 2008 and 2009.

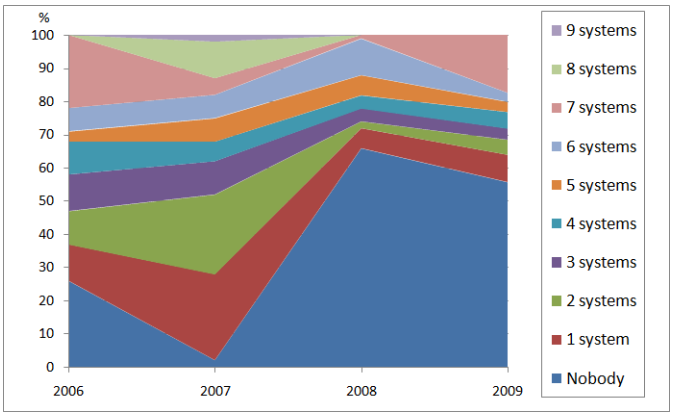

Fig. 10. Comparison of partitions of the system results on negative correspondences in 2006, 2007, 2008 and 2009.

Figure 10 shows that this year 56% of the negatives correspondences were correctly not found. There is a decrease in comparison to the value of 2008, when 66% of the negatives correspondences where not found, being the best value in all years (2006 to 2009). This year 17% of the negative correspondences were mistakenly found by all

the (7) participating systems, being the best value that of last year (1%). An interpretation of these observations could be that the set of participating systems in 2009 have a more cautious strategy than in 2007 and 2006, but still a little bit more brave than in 2008. In 2007, we can observe that the set systems showed the most brave strategy in discovering correspondences of all the yearly evaluation initiatives, when the set of positive correspondences was fully covered, but covering mistakenly also 98% of the negative correspondences. This year the behavior of the overall systems is more similar (but better) to the behavior of the overall set of participating systems in 2008.

6.3 Comments

This year the average performance of the systems (given by F-measure in Figure 5) is the best of all 4 years (2006 to 2009). This suggests that the set of participating systems have found a balance between a brave and cautious behavior for discovering correspondences. However, the value for the F-measure (0.51) indicates that there is still room for further improvements. Finally, as partitions of positive and negative correspondences indicate (see Figure 7 and Figure 8), the dataset still retains a good discrimination ability, i.e., different sets of correspondences are still hard for the different systems.

7 Library

This task, organized in the context of the TELplus[12] project, focuses on a case for which the MACS[13] project established a (partial) manual reference alignment. Participants of this task had to create pairwise alignments between three large subject heading lists in different languages. The required alignments links were SKOS relations. This task is similar, from a methodological perspective, to the OAEI 2008 Library track. It uses however a different dataset.

7.1 Test data

The vocabularies to match are:

- LCSH, the Library of Congress Subject Headings, available as linked data at `http://id.loc.gov`. Contains around 340K concepts, including 250K general subjects.
- RAMEAU, the heading list used at the French National Library, available as linked data at `http://stitch.cs.vu.nl/rameau`. Contains around 150K concepts, including 90K general subjects.
- SWD, the heading list used at the German National Library. Contains 800K concepts, including 160K general subjects.

[12] http://www.theeuropeanlibrary.org/telplus
[13] http://macs.cenl.org

The concepts from the three vocabularies are used as subjects of books. For each concept, the usual SKOS lexical and semantic information is provided: preferred labels, synonyms and notes, broader and related concepts, etc. The three subject heading lists have been represented according to the SKOS model, but an OWL version has also been made available. Note that even though two of these vocabularies are available online as RDF data, we have provided dumps for the convenience of participants.

We have also made available a part of the MACS manual correspondences between these vocabularies, which can be used as a *learning set*. However, none of the participants asked for it.

7.2 Evaluation and results

Only one team handed in final results: TaxoMap, which produced results as listed in Table 17.

Type of relation	LCSH-RAMEAU	RAMEAU-SWD	LCSH-SWD
exactMatch	5,074	1,265	38
broadMatch	116,789	17,220	0
narrowMatch	48,817	6,690	0
relatedMatch	13,205	1,317	0

Table 17. Taxomap results.

We have followed the dual evaluation approach of the previous 2008 Library Track, which featured a "thesaurus merging" evaluation (based on a post-hoc partial reference alignment) and a "re-indexing" one (assessing the use of correspondences for translating subject annotations from one thesaurus to another). The main difference is that the first evaluation method has now been replaced by comparing to an already existing partial reference alignment (the MACS one), avoiding to manually assess the participant's results.

Comparing with partial reference alignment (MACS) As no participant used the training set we provided, we use the complete MACS correspondences as reference alignment. In the version we received (MACS is still currently adding manual correspondences to this reference set), this reference alignment comprised 87,183 LCSH-RAMEAU correspondences, 13,723 RAMEAU-SWD correspondences, and 12,203 LCSH-SWD correspondences.

Table 18 shows the results when taking into account all correspondences that belong to a certain relation selection. For a given relation selection, the token "–" means that no extra relation was provided at that level, hence the results are identical to the ones of the previous selection level. Cov. refers to the coverage, that is, the percentage of MACS correspondences which were found in the evaluated alignment.

Table 19 shows the results obtained when selecting only the "best" available correspondences for one concept (that is, the one with the highest confidence measure), and discarding the others.

TaxoMap links evaluated	LCSH-RAMEAU		RAMEAU-SWD		LCSH-SWD	
	Prec.	Cov.	Prec.	Cov.	Prec.	Cov.
exactMatch	72.1	5.7	27.1	1.4	44.4	0.03
eM + broadMatch	3.6	6.9	2.3	1.9	–	–
eM + bM + narrowMatch	2.8	7.3	1.8	2.0	–	–
all relations	2.7	7.5	1.9	2.2	–	–

Table 18. Results for comparison with MACS (percentage) – using all correspondences.

TaxoMap links evaluated	LCSH-RAMEAU		RAMEAU-SWD		LCSH-SWD	
	Prec.	Cov.	Prec.	Cov.	Prec.	Cov.
exactMatch	78.7	5.7	39.5	1.4	44.4	0.03
eM + broadMatch	22.0	6.0	13.5	1.6	–	–
eM + bM + narrowMatch	14.4	5.9	10.8	1.6	–	–
all relations	13.4	5.8	10.9	1.7	–	–

Table 19. Results for comparison with MACS (percentage) – using only the best correspondences for each concept.

Results for the re-indexing scenario The second usage scenario is based on an *annotation translation* process supporting the re-indexing of books indexed with one vocabulary, using concepts from the mapped vocabulary (see [14]). Here we use book annotations from the British Library (using LCSH), the French National Library (using RAMEAU) and the German National Library (using SWD), see Table 19(a).

For each pair of vocabularies A-B, this scenario interprets the correspondences as rules to translate existing book annotations with A into equivalent annotations with B. In the case at hand, the book collections have a few books in common (cf. Table 19(b)), which are therefore described according to two vocabularies. Based on the quality of the results for those books for which we know the correct annotations, we can assess the quality of the initial correspondences.

(a) Collections and books with subject annotations.

Collection	Books with subject annotation
English	2,448,050
French	1,457,143
German	1,364,287

(b) Common books between different collections.

Collection pair	Common books
French–English	182,460
German–English	83,786
German–French	63,340

Table 20. Data on collections.

Evaluation settings and measures. For each pair of vocabularies A-B, the simple concept-to-concept correspondences sent by participants were transformed into more complex mapping rules that associate one concept from A with a set of concepts from B – as some concepts are involved in several correspondences.

The set of A concepts attached to each book is then used to decide whether these rules are *fired* for this book. If the A concept of one rule is contained by the A annotation of a book, then the rule is fired. As several rules can be fired for a same book, the union of the consequents of these rules forms the translated B annotation of the book.

On a set of books selected for evaluation, the generated concepts for a book are then compared to the ones that are deemed correct for this book. At the annotation level, we measure the precision, the recall, and the Jaccard overlap measure (Jac.) between the produced annotation and the correct one.

In the formulas used, results are counted on a book and annotation basis, and not on a rule basis. This reflects the importance of different thesaurus concepts: a translation rule for a frequently used concept is more important than a rule for a rarely used concept.

Results. Table 21 shows the results when taking into account all correspondences that belong to a certain relation selection.

TaxoMap links evaluated	LCSH-RAMEAU			RAMEAU-SWD			LCSH-SWD		
	Prec.	Rec.	Jac.	Prec.	Rec.	Jac.	Prec.	Rec.	Jac.
exactMatch	22.3	6.1	5.5	14.2	3.1	2.4	1.3	0.003	0.002
eM + broadMatch	2.1	7.8	1.5	2.3	3.6	1.1	–	–	–
eM + bM + narrowMatch	1.2	9.2	1.0	0.8	3.9	0.5	–	–	–
all relations	1.1	9.3	0.9	0.7	4.0	0.5	–	–	–

Table 21. Re-indexing evaluation results (percentage) – using all correspondences.

Table 22 shows the results obtained when selecting only the "best" available mapping for one concept and discarding the others.

TaxoMap links evaluated	LCSH-RAMEAU			RAMEAU-SWD			LCSH-SWD		
	Prec.	Rec.	Jac.	Prec.	Rec.	Jac.	Prec.	Rec.	Jac.
exactMatch	22.8	5.8	5.3	14.2	1.9	1.7	1.2	0.002	0.002
eM + broadMatch	10.2	6.0	4.9	6.9	2.0	1.7	–	–	–
eM + bM + narrowMatch	7.2	4.5	3.3	5.9	1.9	1.5	–	–	–
all relations	6.4	4.0	2.9	5.8	1.9	1.5	–	–	–

Table 22. Re-indexing evaluation results (percentage) – using all Taxomap correspondences.

7.3 Discussion

The setting for this year's library task clearly shows the limits of current matching tools. The case at hand, mostly because of its size and its multilingual aspect, is extremely difficult to handle. The performance of TaxoMap, from this perspective, should be regarded as a significant achievement, as it was the only one to manage to ingest hundreds of concepts and return alignments between them.

The results of TaxoMap, which could not apply its usual partition approach, and uses to a great extent automatic translation, are not very good. More precisely, they

are especially weak when relations other than strict equivalence are considered, highlighting the value of being able to sort mapping results using the type of relation or the strength of the confidence measure granted to correspondences–options which are both offered by TaxoMap. Both precision and coverage/recall are low for the non-equivalence correspondences, even though they bring a huge number of potential matches. The translation could give better results for the equivalent correspondences, at the cost of coverage of course.

It is worth mentioning that as last year, the results for the comparison with a reference mapping and the re-indexing evaluation largely differ, showing that correspondences have a different relevance depending on the application scenario. correspondences based on translation will perform obviously better for scenarios where the intension of concepts matters, rather than for cases where their actual usage in book collections should be carefully taken into account.

8 Oriented alignment

This year we introduced evaluation of alignments containing other relations that the classical equivalence between entities, e.g., subsumption relations.

8.1 Test data

The first dataset (dataset 1) has been derived from the benchmark series of the OAEI 2006 campaign [9] and was created for the evaluation of the "Classification-Based Learning of Subsumption Relations" (CSR) method. As a configuration of CSR exploits the properties of concepts (for the cases where properties are used as features), we do not include the OAEI 2006 ontologies whose concepts have no properties. Furthermore, we have excluded from the dataset the OAEI ontologies with no defined subsumption relations among their concepts. This is done because CSR exploits the subsumption relations in the input ontologies to generate training examples. More specifically, all benchmarks (101-304) except 301 to 304, define the second ontology of each pair as an alteration of the same ontology, i.e., the first one, numbered 101.

The second dataset (dataset 2) is composed of 45 pairs of real-world ontologies coming from the Consensus Workshop track of the OAEI 2006 campaign (all pairwaise combinations). The domain of the ontologies concerns the organization of conferences and they have been developed within the OntoFarm project[7].

The reference alignment for all datasets has been manually created by knowledge engineers. The major guidelines that were followed for the location of subsumption relations are as follows: (a) use existing equivalences in order to find inferred subsumptions, and (b) understand the "intended meaning" of the concepts, e.g., by inspecting specifications and relevant information attached to them. The format of the reference alignment is the Alignment format as used in the benchmark series.

8.2 Participants

Three systems returned results for the first dataset, namely, ASMOV, RiMoM and TaxoMap. We present these results by also presenting the results achieved by CSR (as a comparison basis), presenting also the results of CSR for the second dataset.

8.3 Results

system	CSR			ASMOV			RiMoM			TaxoMap		
test	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.
1xx	0.97	0.97	0.97	1.00	1.00	1.00	1.00	1.00	1.00	NaN	0	NaN
2xx	0.84	0.78	0.80	0.94	0.94	0.94	0.67	0.85	0.69	0.84	0.08	0.25
3xx	0.66	0.72	0.69	0.86	0.60	0.60	0.59	0.81	0.64	0.72	0.11	0.17
Average	0.83	0.79	0.80	0.94	0.90	0.93	0.69	0.86	0.71	0.63	0.07	0.23

Table 23. Results of all systems when applied to data set 1.

Table 23 presents the precision, recall and F-measure values, of each participating system in all tests (average) and separately in each test category, e.g., 1xx. We observe that in terms of F-measure ASMOV achieves the best results, followed by CSR, RiMoM and then by TaxoMap. Also, we observe that although CSR has a higher precision than RiMoM, RiMoM has a higher recall. ASMOV and RiMoM did not make specific changes to their methods for this dataset. TaxoMap exploits the lexicalizations of concepts to compute subsumption relations. Furthermore, CSR does not exploit equivalence relations.

Concerning dataset 2, Table 24 depicts the precision and recall values for each pair of ontologies in the dataset provided by CSR. The other methods did not provide results for this dataset. An observation is that the performance of CSR is worst in this dataset, in comparison to the first dataset.

9 Instance matching

For the first time in OAEI, an instance matching track was proposed to participants. The aim of this track is to evaluate matchers on instance data coming from diverse sources. Both data extracted from published Web datasets, and a testbed presenting various automatically generated values and structure modifications were proposed.

9.1 AKT-Rexa-DBLP

The AKT-Rexa-DBLP (ARS) test case aims at testing the capability of the tools to match individuals. All three datasets were structured using the same schema. The challenges for the matchers included ambiguous labels (person names and paper titles) and noisy data (some sources contained incorrect information).

Ontology pair	Prec.	Rec.	Ontology pair	Prec.	Rec.
Iasted-Cmt	0.6	0.7	Confious-Sigkdd	0.26	0.51
Cmt-confOf	0.76	0.83	crs_dr-Sigkdd	0.09	0.13
Cmt-Confious	0.28	0.31	Iasted-Sigkdd	0.17	0.88
confOf-Confious	0.14	0.47	OpenConf-Sigkdd	0.22	0.39
crs_dr-Confious	0.08	0.11	Pcs-Sigkdd	0.18	0.48
Iasted-Confious	0.08	0.25	Cmt-Conference	0.25	0.11
OpenConf-Confious	0.22	0.45	confOf-Conference	0.43	0.29
Pcs-Confious	0.16	0.43	Confious-Conference	0.15	0.43
Cmt-crs_dr	0.54	0.39	crs_dr-Conference	0.58	0.11
confOf-crs_dr	0.38	0.38	Iasted-Conference	0.2	0.08
confOf-Iasted	0.47	0.38	OpenConf-Conference	0.14	0.15
crs_dr-Iasted	0.18	0.38	Pcs-Conference	0.05	0.05
OpenConf-Iasted	0.15	0.38	Sigkdd-Conference	0.15	0.19
Pcs-Iasted	0.21	0.39	Cmt-ekaw	0.46	0.72
Cmt-OpenConf	0.32	0.41	confOf-ekaw	0.51	0.74
confOf-OpenConf	0.22	0.39	Confious-ekaw	0.22	0.59
crs_dr-OpenConf	0.15	0.32	crs_dr-ekaw	0.21	0.2
Cmt-Pcs	0.47	0.77	Iasted-ekaw	0.32	0.33
confOf-Pcs	0.24	0.47	OpenConf-ekaw	0.28	0.28
crs_dr-Pcs	0.17	0.69	Pcs-ekaw	0.36	0.67
OpenConf-Pcs	0.1	0.26	Sigkdd-ekaw	0.64	0.78
Cmt-Sigkdd	0.54	0.81	Conference-ekaw	0.58	0.65
confOf-Sigkdd	0.29	0.64			
Average				0.29	0.43

Table 24. Results of CSR when applied to dataset 2.

Test set The test case included three datasets from the domain of scientific publications:

- AKT EPrints archive[14]. This dataset contains information about papers produced within the AKT research project.
- Rexa dataset[15]. This dataset was extracted from the Rexa search server, which was constructed at the University of Massachusetts using automatic information extraction algorithms.
- SWETO DBLP dataset[16]. This is a publicly available dataset listing publications from the computer science domain.

The SWETO-DBLP dataset was originally represented in RDF. Two other datasets (AKT EPrints and Rexa) were extracted from the HTML sources using specially constructed wrappers and structured according to the SWETO-DBLP ontology[17]. The ontology describes information about scientific publications and their authors and extends the commonly used FOAF ontology[18]. Authors are represented as individuals of the

[14] http://eprints.aktors.org/
[15] http://www.rexa.info/
[16] http://lsdis.cs.uga.edu/projects/semdis/swetodblp/
[17] http://lsdis.cs.uga.edu/projects/semdis/swetodblp/august2007/opus_august2007.rdf
[18] http://xmlns.com/foaf/spec/

foaf:Person class, and a special class *sweto:Publication* is defined for publications, with two subclasses *sweto:Article* and *sweto:Article_in_Proceedings* for journal and conference publications respectively. The participants were invited to produce alignments for each pair of datasets (AKT/Rexa, AKT/DBLP, and Rexa/DBLP).

Evaluation results Five participants submitted results for the AKT-Rexa-DBLP test case produced by their systems: DSSim, RiMOM, FBEM, HMatch, and ASMOV. The results were evaluated by comparing them with a manually constructed reference alignment and calculating the standard precision, recall, and F-measure. We measured the performance of each system for the classes *sweto:Publication* and *foaf:Person* separately, as well as for the combined set of individuals. These evaluation results are provided in Table 25.

	sweto:Publication			foaf:Person			Overall		
System	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.
AKT/Rexa									
DSSim	0.15	0.16	0.16	0.81	0.30	0.43	0.60	0.28	0.38
RiMOM	1.00	0.72	0.84	0.92	0.70	0.79	0.93	0.70	0.80
FBEM	0.99	0.61	0.76	0.73	0.02	0.03	0.94	0.10	0.18
HMatch	0.97	0.89	0.93	0.94	0.39	0.56	0.95	0.46	0.62
ASMOV	0.32	0.79	0.46	0.76	0.24	0.37	0.52	0.32	0.39
AKT/DBLP									
DSSim	0	0	0	0.15	0.19	0.17	0.11	0.15	0.13
RiMOM	0.96	0.97	0.96	0.93	0.50	0.65	0.94	0.59	0.73
FBEM	0.98	0.80	0.88	0	0	0	0.98	0.16	0.28
HMatch	0.93	0.97	0.95	0.58	0.57	0.57	0.65	0.65	0.65
Rexa/DBLP									
DSSim	0	0	0	0	0	0	0	0	0
RiMOM	0.94	0.95	0.94	0.76	0.66	0.71	0.80	0.72	0.76
FBEM	0.98	0.15	0.26	1.00	0.11	0.20	0.99	0.12	0.21
HMatch	0.45	0.96	0.61	0.40	0.34	0.37	0.42	0.48	0.45

Table 25. Results of AKT-Rexa-DBLP test case.

The AKT/Rexa test scenario was the only one for which the results for ASMOV were available and the only one for which all the systems provided alignments for both *foaf:Person* and *sweto:Publication* classes. FBEM for the AKT/DBLP test case only produced alignments for *Publication* instances, which reduced their overall recall. For the class *Publication* the best F-measure in all three cases was achieved by RiMOM with HMatch being the second. FBEM, which specifically focused on precision, achieved the highest precision in all three cases at the expense of recall. It is interesting to see the difference between systems in the Rexa/DBLP scenario where many distinct individuals had identical titles, e.g., “Editorial.”, or “Minitrack Introduction.”. This primarily affected the precision in the case of HMatch and RiMOM, but reduced recall for FBEM.

The performance of all systems was lower for the class *Person* where ambiguous personal names and different label formats reduced the performance of string similarity

techniques. The highest F-measure was achieved by RiMOM and by HMatch for the three test cases. Again, it is interesting to note the difference between RiMOM, HMatch, and FBEM in the Rexa/DBLP case where the first two systems focused on F-measure and the second one on precision. This distinction of approaches can be an important criterion when a tool has to be selected for a real world use case: in some cases the cost of an erroneous correspondence is much higher than than the cost of a missed one, e.g., the large-scale entity naming service such as FBEM, while in other scenarios this might not be true, e.g., assisting the user who performs manual alignment of datasets. In contrast, in the AKT/Rexa scenario the performance of FBEM was lower than the performance of other systems both in terms of precision and recall. This was caused by different label formats used by AKT and Rexa datasets ("FirstName LastName" vs "LastName, FirstName"), which affected FBEM.

Because in all three scenarios the datasets had more *Person* individuals than *Publication* ones, the overall results were primarily influenced by the performance of the tools on the class *Person*. Again, HMatch and RiMOM had the highest F-measure for all the test cases. We can see a comparison with respect to F-measure in Figure 11.

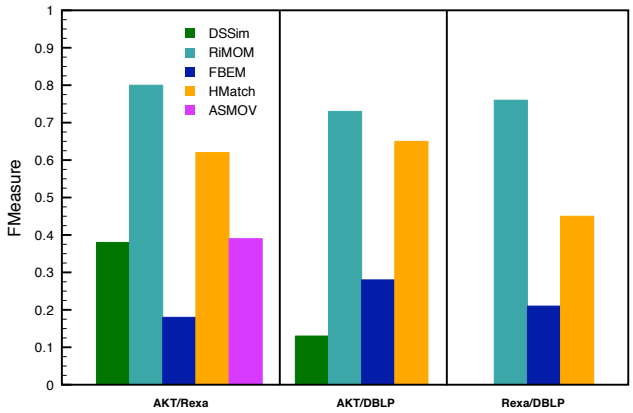

Fig. 11. Comparison on AKT-Rexa-DBLP with respect of FMeasure

9.2 ISLab Instance Matching Benchmark

The ISLab Instance Matching Benchmark (IIMB) is a benchmark automatically generated starting from one data source that is automatically modified according to various criteria. The original data source contains OWL/RDF data about actors, sport persons, and business firms provided by the OKKAM European project[19]. The benchmark is composed by 37 test cases. For each test case we require participants to match the original data source against a new data source. The original data source contains about 200 different instances. Each test case contains a modified version of the original data source and the corresponding reference alignment containing the expected results. Modifications introduced in IIMB are the following:

[19] http://www.okkam.org

– Test case 001: Contains an identical copy of the original data source (instance IDs are randomly changed).
– Test case 002 - Test case 010: Value transformations, i.e., typographical errors simulation, use of different standard for representing the same information. In order to simulate typographical errors, property values of each instance are randomly modified. Modifications are applied on different subsets of the instances property values and with different levels of difficulty, i.e., introducing a different number of errors.
– Test case 011 - Test case 019: Structural transformations, i.e., deletion of one or more values, transformation of datatype properties into object properties, separation of a single property into more properties.
– Test case 020 - Test case 029: Logical transformations, i.e., instantiation of identical individuals into different subclasses of the same class, instantiation of identical individuals into disjoint classes, instantiation of identical individuals into different classes of an explicitly declared class hierarchy.
– Test case 030 - Test case 037: Several combinations of the previous transformations.

Evaluation results. In this first edition of the instance matching track, six systems participated in the IIMB task, namely AFlood, ASMOV, DSSim, HMatch, FBEM, and RiMOM. In Table 26, we provide real precision and recall measures for the participating systems.

System	AFlood			ASMOV			DSSim		
Test	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.
002 - 010	1.00	0.99	0.99	1.00	1.00	1.00	1.00	0.37	0.54
011 - 019	0.90	0.72	0.80	0.99	0.92	0.96	0.99	0.28	0.43
020 - 029	0.85	1.00	0.92	1.00	1.00	1.00	0.85	0.99	0.91
030 - 037	0.94	0.75	0.83	1.00	0.98	0.99	1.00	0.30	0.46
H-means	0.92	0.87	0.89	1.00	0.98	0.99	0.92	0.48	0.63

System	HMatch			FBEM			RiMOM		
Test	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.	Prec.	Rec.	FMeas.
002 - 010	0.97	0.98	0.97	0.95	0.93	0.94	1.00	1.00	1.00
011 - 019	0.88	0.83	0.85	0.78	0.52	0.62	1.00	0.93	0.97
020 - 029	0.78	1.00	0.88	0.08	1.00	0.15	0.85	1.00	0.92
030 - 037	0.94	0.89	0.92	0.10	0.53	0.16	1.00	0.99	0.99
H-means	0.89	0.93	0.91	0.16	0.75	0.27	0.96	0.98	0.97

Table 26. IIMB results: precision and recall.

A first general remark about the results is that three of the participating systems, i.e., AFlood, ASMOV, and DSSim, provide better results in terms of precision rather than in terms of recall, even if AFlood and ASMOV results can be considered very good in both. On the other end, HMatch, FBEM, and RiMOM provide better results in terms of recall, with better performances in case of HMatch and RiMOM. Coming to the four categories of test cases, we can conclude that all the six systems show very good performances on cases 002 - 010, where we just introduced some data errors by

maintaining both the data structure and the logical properties of data. On test cases 011 - 019, where data structures were changed by deleting or modifying property assertions, AFlood, ASMOV, HMatch, and RiMOM still perform over 80% in terms of F-Measure, while both DSSim and FBEM performances are lower, especially with respect to recall. In general, test cases 011 - 019 were more difficult with respect to recall than to precision. Test cases 020 - 029 were focused on logical transformations. In order to achieve good performances here, it is important to take into account logical implications of the schema over the instances. This is achieved by AFlood, ASMOV, DSSim, and RiMOM. HMatch maintains high recall and good precision, while FBEM's precision seems very low. Finally, test cases 030 - 037 as well as the final harmonic mean shown, AFlood, ASMOV, HMatch, and RiMOM provide good results both in terms of precision and in terms of recall. DSSim is more effective on precision, while FBEM is stronger in terms of recall.

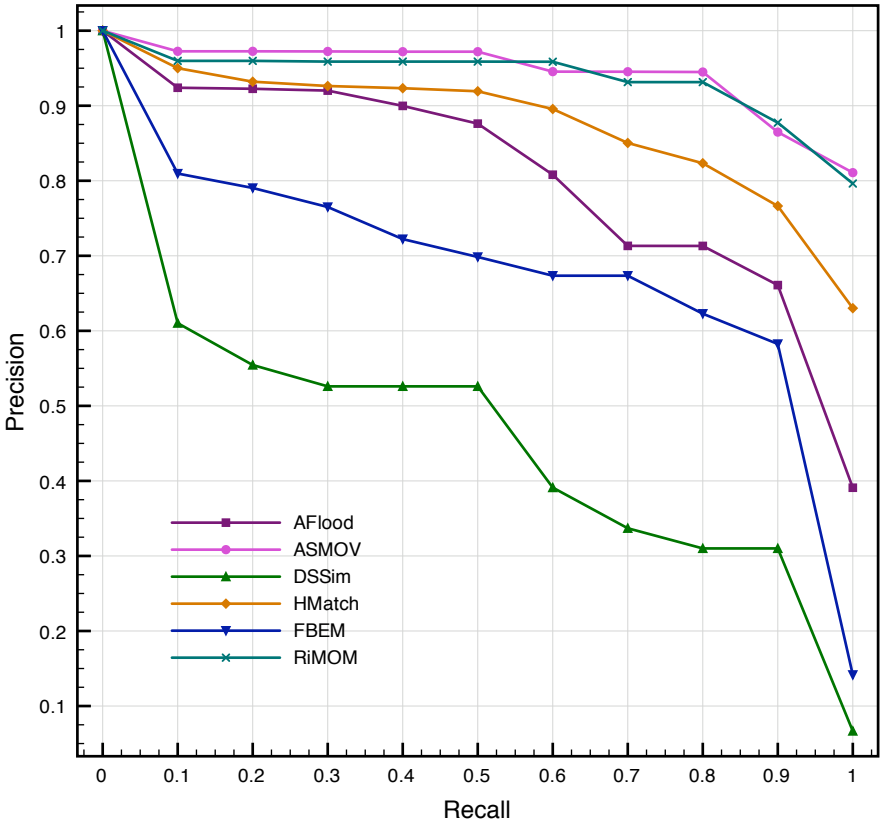

Fig. 12. Precision/recall graphs. They cut the results given by the participants under a threshold necessary for achieving $n\%$ recall and compute the corresponding precision.

All the six systems provided their results with confidence measures. It is thus possible to draw precision/recall graphs in order to compare them (see Figure 12). The graph is computed by averaging the graphs of each of the tests. The precision/recall graph confirms the comparison done over real precision and recall values, especially in case of recall values lower than 50%. After that threshold, ASMOV, RiMOM, and HMatch maintain their performances high, and FBEM performances are stable. Instead, DSSim and AFlood values of precision decrease quite quickly, even if AFlood performances are still better than FBEM and DSSim.

10 Very Large Crosslingual Resources

The goal of the Very Large Crosslingual Resources challenge is twofold. First, we are interested in matching vocabularies in different languages. Many collections throughout Europe are indexed with vocabularies in languages other than English. These collections would benefit from an alignment to resources in other languages to broaden the user group, and possibly enable integrated access to the different collections. Second, we intend to present a realistic use case in the sense that the resources are large, rich in semantics but weak in formal structure, i.e. realistic on the Web. For collections indexed with an in-house vocabulary, the link to a widely-used and rich resource can enhance the structure and increase the scope of the in-house thesaurus. In this task, we aim for skos:exactMatch and skos:closeMatch relations.

10.1 Test data

Three resources are used in this task:

WordNet WordNet is a lexical database of the English language developed at Princeton University[20]. Its main building blocks are synsets: groups of words with a synonymous meaning. In this task, the goal is to match noun-synsets. WordNet contains 7 types of relations between noun-synsets, but the main hierarchy in WordNet is built on hyponym relations, which are similar to subclass relations. W3C has translated WordNet version 2.0 into RDF/OWL.

The original WordNet model is a rich and well-designed model. However, some tools may have problems with the fact that the synsets are instances rather than classes. Therefore, for the purpose of this OAEI task, we have translated the hyponym hierarchy in a skos:broader hierarchy, making the synsets skos:Concepts.

DBpedia DBpedia contains 2.18 million resources or "things", each tied to an article in the English language Wikipedia. The "things" are described by titles and abstracts in English and often also in Dutch. DBpedia "things" have numerous properties, such as categories, properties derived from the wikipedia "infoboxes", links between pages within and outside wikipedia, etc.

GTAA The GTAA is a Dutch thesaurus used by the Netherlands Institute for Sound and Vision to index their collection of TV programs. It is a facetted thesaurus, of which we use the following four facets: (1) **Subject**: the topic of a TV program,

[20] `http://wordnet.princeton.edu/`

≈3800 terms; (2) **People**: the main people mentioned in a TV program, ≈97.000 terms; **Names**: the main "Named Entities" mentioned in a TV program (Corporation names, music bands, etc.), ≈27.000 terms; **Location**: the main locations mentioned in a TV program or the place where it has been created, ≈14.000 terms.

The purpose of this task is to match GTAA concepts to DBpedia "things" and WordNet synsets.

10.2 Evaluation setup

We evaluate the results of the two alignments (GTAA-WordNet, GTAA-DBpedia) in terms of precision and recall. Aside from an overall measure, we also present measures for each GTAA facet separately. We introduce an evaluation on a 3-point scale of 0 - 0.5 - 1. We assign 1 point when the relation between two concepts is correctly identified as a skos:exactMatch or a skos:closeMatch. We assign 0.5 points if the proposed relation is skos:exactMatch while we consider the relation to be skos:closeMatch, or vice versa. Correspondences between concepts that are not related get 0 points. The scores are used to generate generalized precision and recall figures.

Precision For each participant, we take samples of between 71 and 97 correspondences per GTAA facet for both the GTAA-DBpedia and the GTAA-WordNet alignments and evaluate their correctness in terms of exact match, close match, or no match.

Recall Due to time constraints, we only determined recall of the GTAA Subject facet. We use a small reference alignment from a random sample of 100 GTAA concepts, which we manually mapped to WordNet and DBpedia for the VLCR evaluation of 2008. The result of the GTAA-WordNet and GTAA-DBpedia alignments are compared to the reference alignments.

Inter-rater agreement A team of 4 raters rated random samples of DSSim's correspondences. A team of 3 raters rated the GG2WW correspondences, where each alignment was divided over two raters. One rater was a member of both teams.

In order to check the inter-rater agreement, 100 correspondences were rated by two raters. The agreement was high with a Cohen's kappa of 0.87. In addition, we compared this year's evaluation samples with those of 2008. 120 correspondences appeared in both sets, and again the agreement between the scores was high; Cohen's kappa was 0.92.

10.3 Results

Two teams participated to the OAEI VLCR task: DSSim and GG2WW. Table 27 shows the number of concepts in each resource and the number of correspondences returned for each resource pair. Both participants produced only exact matches. After consulting the participants, we have considered using the confidence measures as an indication of

the strenght of the mapping: a mapping with a confidence measure of 1 was seen as an exact match and a mapping with a confidence measure < 1 was seen as a close match. However, this idea lead to lower precision values for both participants and was therefore abandoned. All correspondences in Table 27 are considered to be exact matches.

GTAA facet	#concepts	#corresp. DSSim		#corresp. GG2WW	
		to WN	to DBp	to WN	to DBp
Subject	3800	655	1363	3663	3381
People	97.000	82	2238	0	17516
Names	27.000	681	3989	0	9023
Locations	14.000	987	5566	0	9527
Total	141.800	2405	13156	3663	39447

Table 27. Number of correspondences in each alignment.

Table 28 shows the precision and recall of both systems.

	Precision		Recall	
Alignment	GG2WW	DSSim	GG2WW	DSSIM
name-dbp	0.63	0.64		
location-dbp	0.94	0.80		
person-dbp	0.91	0.79		
subject-dbp	0.86	0.70	0.62	0.30
name-wn	.	0.44		
location-wn	.	0.61		
person-wn	.	0.07		
subject-wn	0.59	0.77	0.59	0.19
total	0.78	0.62		

Table 28. Precision and recall of DSSim and GG2WW for each GTAA facet-resource pair.

Regarding precision, GG2WW scores consistently better than DSSim on the GTAA-DBpedia alignments. Both systems show a similar pattern when comparing the scores of the four GTAA facets: the scores of the Location facet are highest, followed by the Person, Subject and finally the Name facet. DSSim scores best on the GTAA-WordNet alignments, although a comparison is limited since GG2WW only returned correspondences to the GTAA Subject facet.

DSSim has participated in the VLCR task of 2008 as well. However, a direct comparison of the precision scores of 2008 and 2009 is difficult due to differences in the task; in 2008 we considered SKOS exact-, broad-, narrow- and related-matches. The results of 2008 and 2009 do show similarities when comparing the scores of the facets and resources. The GTAA Names facet remains hard to match, which might be due to the many Dutch-specific concepts in this facet, such as Dutch ships named after famous people. WordNet appears again to be less compatible with the GTAA facets, with the exception of the Subject facet.

Recall measures can be compared to last year directly, as we have used the same evaluation measures and reference alignment. DSSim scores exactly the same on the

GTAA-WordNet mapping (0.19) and higher on the GTAA-DBpedia mapping (from 0.22 to 0.30). GG2WW produced 50% more correspondences between GTAA-WordNet and 300% more correspondences between GTAA-DBpedia than DSSIM (Table 27). This translates to a recall score that is 3 and 2 times as high as the DSSim scores.

11 Structural Preservation Measures

This year we performed analyses of the extent to which particular alignments preserved the structure between two ontologies, or more specifically, between two class hierarchies [15; 5]. Here we provide a brief summary of the approach and presentation of the results.

We wish to measure the *smoothness* of such an alignment, while recognizing that being a smooth mapping is neither necessary nor sufficient to be a good mapping. Nonetheless a strong correlation of smoothness with precision, recall or F-measure promises a potentially *automatic* predictor of alignment quality independent of a reference alignment. Additionally, knowledge of the structural properties of alignments is useful for ontology matchers, especially when providing alignments within one domain where structural preservation is desired.

An alignment is modeled as a relation between two semantic hierarchies, modeled as partially ordered sets [6]. Such ordered structures are not, in general, trees, nor even lattices, but can be rich in multiple inheritance and lack unique least common subsumers between nodes.

Let a semantic hierarchy be a bounded partially ordered set (poset) $\mathcal{P} = \langle P, \leq \rangle$, where P is a finite set of ontology nodes, and $\leq \subseteq P^2$ is a reflexive, anti-symmetric, and transitive binary relation such as subsumption ("`is-a`"). For two taxonomies $\mathcal{P} = \langle P, \leq \rangle, \mathcal{P}' = \langle P', \leq' \rangle$, an alignment relation $F \subseteq P \times P'$ is a collection of pairs $\boldsymbol{f} = \langle a, a' \rangle \in F$, indicating that the node $a \in P$ on the "left" side is mapped or aligned to the node $a' \in P'$ on the "right" side. F determines a domain and codomain

$$Q = \{a \in P, \exists a' \in P', \langle a, a' \rangle \in F\} \subseteq P, \quad Q' = \{a' \in P', \exists a \in P, \langle a, a' \rangle \in F\} \subseteq P',$$

We call the $\boldsymbol{f} \in F$ links, the $a \in Q$ the left anchors and the $a' \in Q'$ the right anchors. Let $m = |Q|, m' = |Q'|$, and $N = |F| \leq mm'$.

Our approach is not a *relative* measure of an alignment with respect to a reference alignment, but rather an *inherent* or *independent* measure of the alignment based on the following principles:

Twist, or order discrepancy: a, b should have the same structural relations in $\mathcal{P}$ as a', b' in $\mathcal{P}'$

Stretch, or distance discrepancy: Relative distance between $a, b \in P$ should be the same as $a', b' \in P'$

Let d be a metric on $\mathcal{P}$ and $\mathcal{P}'$. For links $\boldsymbol{f} = \langle a, a' \rangle, \boldsymbol{g} = \langle b, b' \rangle \in F$, we want the metric relations between the $a, b \in Q$ to be the same as their corresponding $a', b' \in Q'$, so that $|\bar{d}(a, b) - \bar{d}'(a', b')|$ is small. In this work, we use the upper and lower cardinality-based distances:

$$d_u(a, b) = |\uparrow a| + |\uparrow b| - 2 \max_{c \in a \vee b} |\uparrow c|, \qquad d_l(a, b) = |\downarrow a| + |\downarrow b| - 2 \max_{c \in a \wedge b} |\downarrow c|,$$

where for a node $a \in P$, its upset $\uparrow a = \{x | x \geq a\}$ and downset $\downarrow a = \{x | x \leq a\}$ are all its ancestors and successors respectively, so that $|\uparrow a|, |\downarrow a|$ are the number of ancestors and successors. The generalized join and meet are

$$a \vee b = \mathrm{Min}(\uparrow a \int \uparrow b) \subseteq P, \qquad a \wedge b = \mathrm{Max}(\downarrow a \int \downarrow b) \subseteq P,$$

where for a set of nodes $R \subseteq P$ the upper bounds and lower bounds are

$$\mathrm{Min}(R) = \{a \in R : \nexists b \in R, b < a\} \subseteq P, \mathrm{Max}(R) = \{a \in R : \nexists b \in R, b > a\} \subseteq P.$$

We need to measure the relative proportion of the overall structure two nodes are apart, so define the normalized upper and lower distances as:

$$\bar{d}_u(a,b) = \frac{d_u(a,b)}{|P|-1} \in [0,1], \quad \bar{d}_l(a,b) = \frac{d_l(a,b)}{|P|-1} \in [0,1].$$

Let d be a metric used in both $\mathcal{P}, \mathcal{P}'$, in our case, the lower distance d_l. Then the link discrepancy is given by: $\delta(\boldsymbol{f}, \boldsymbol{g}) = |\bar{d}(a,b) - \bar{d}(a',b')|$, and the distance discrepancy induced by F between $\mathcal{P}$ and $\mathcal{P}'$ given d is:

$$D(F) = \frac{\sum_{\boldsymbol{f},\boldsymbol{g} \in F} \delta(\boldsymbol{f}, \boldsymbol{g})}{\binom{N}{2}}.$$

$D(F) \in [0,1]$, with $D(F) = 0$ iff F is completely distance preserving, and $D = 1$ if F is maximally distance distorting, e.g. mapping diameters to equality, and neighbors and children to diameters. We also calculate the order discrepancy of each alignment as:

$$\Gamma(F) = \frac{\sum_{\boldsymbol{f},\boldsymbol{g} \in F} \gamma(\boldsymbol{f}, \boldsymbol{g})}{\binom{N}{2}},$$

where for a pair of links $\boldsymbol{f}, \boldsymbol{g} \in F$, and a relation $* \in \{<, >, =, \not\sim\}$ ($\not\sim$ denoting non comparability),

$$\gamma(\boldsymbol{f}, \boldsymbol{g}) = \begin{cases} 0, & \text{if } a * b \text{ and } a' * b' \\ 1, & \text{otherwise} \end{cases}$$

Hence $D(F)$ measures the "stretching" of F, $\Gamma(F)$ measures "twisting", or the number of purely structural violations present.

Figure 13, Figure 14, and Figure 15 show scatter plots of $D(F)$ against precision for all the 1xx, 2xx, and 3xx tests for the benchmark track, respectively. We see a moderate trend of decreasing precision with increasing $D(F)$, with Pearson correlation coefficients of $r = -0.65$ and $r = -0.51$ respectively. Table 29 shows the correlation r for $D(F)$ and $\Gamma(F)$ against precision, recall, and F-measure for all tracks, and all 1xx, 2xx, and 3xx tracks grouped together.

For more details on a particular track, Table 30 shows the results from Test 205 from Benchmark. We can see in this case a particular strong dropoff in precision with increasing discrepancy, with $r = -0.92$.

Table 31 shows the results for the anatomy track. Scatter plots are shown in Figure 16 for all tests. Table 32 summarizes the correlations, combining all tests, and then

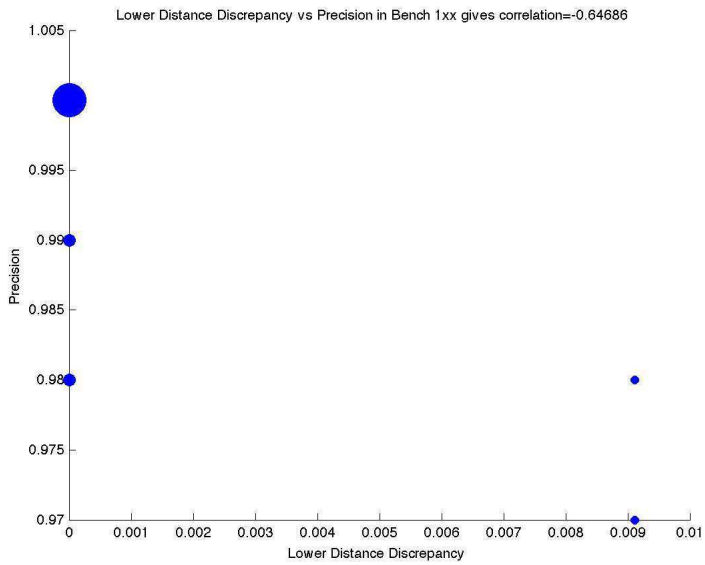

Fig. 13. Precision vs. $D(F)$, Benchmark track: 1xx tests. Marker size is proportional to the number of tests with that combination of values.

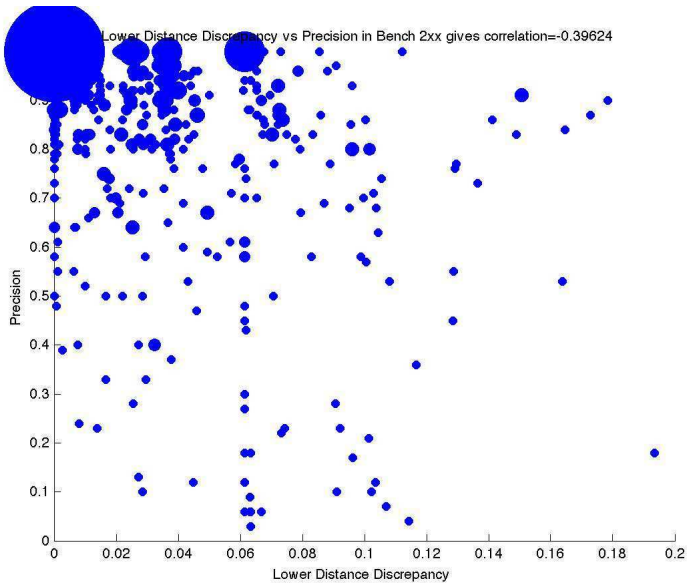

Fig. 14. Precision vs. $D(F)$, Benchmark track: 2xx tests.

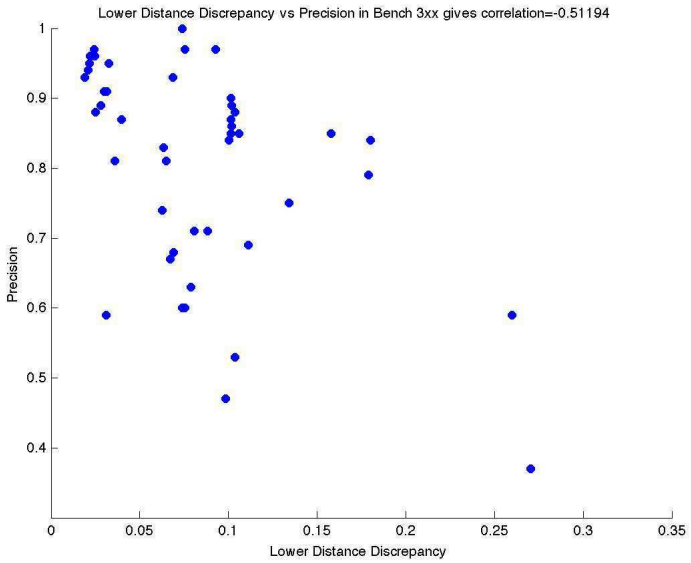

Fig. 15. Precision vs. $D(F)$, Benchmark track: 3xx tests.

r		Prec.	Rec.	FMeas.
Bench 1*	$D(F)$	-0.65	0.03	0.02
	$\Gamma(F)$	-0.65	0.03	0.02
Bench 2*	$D(F)$	-0.41	-0.13	-0.18
	$\Gamma(F)$	-0.48	-0.25	-0.29
Bench 3*	$D(F)$	-0.51	-0.48	-0.53
	$\Gamma(F)$	-0.54	-0.39	-0.46
Bench [1-3]*	$D(F)$	-0.39	-0.02	-0.07
	$\Gamma(F)$			-0.20

Table 29. Pearson correlations for $D(F)$ and $\Gamma(F)$ against precision, recall and F-measure for all tracks, and all 1xx, 2xx, and 3xx tracks grouped together.

Submitter	$D(F)$	Prec.	Rec.	FMeas.
$r(D(F), \cdot)$:		-0.92	-0.73	-0.76
refalign	0.0	1.0	1.0	1.0
MapPSO	0.0	1.0	0.99	0.99
AROMA	0.0	1.0	0.99	0.99
ASMOV	0.0	1.0	0.99	0.99
Lily	0.0	1.0	0.99	0.99
RiMOM	0.0	1.0	0.99	0.99
GeRoMe	0.0	1.0	0.97	0.98
AgrMaker	0.0	1.0	0.97	0.98
DSSim	0.0	0.91	0.81	0.86
aflood	0.008	0.91	0.75	0.82
kosimap	0.083	0.83	0.59	0.69
SOBOM	0.0	1.0	0.29	0.45
TaxoMap	0.108	0.53	0.09	0.15

Table 30. Benchmark 205 results.

broken out by test. Again, we see a strong correlation of increasing $D(F)$ against especially decreasing precision. Note the outlier point, corresponding to Taxomap in test 3 with $D(F) = 0.00145$. If this point is excluded, then among all tests we obtain r values of -0.84 for precision, 0.05 for recall, and -0.61 for F-measure.

These preliminary results are clearly in need of further analysis, which we are now embarking on. Some early comments include:

- These results are consistent with those shown in [5], which showed a moderate correlation of $D(F)$ with F-measure.
- Pearson correlation, the only measure here, is a weak indicator, but suggestive that our lower distance discrepancy may act as a predictor of precision.
- Here only the lower distance $d_l(a, b)$ and distance discrepancy $D(F)$ were used. Further consideration is also required of the role the upper distance $d_u(a, b)$ and the order discrepancy $\Gamma(F)$.

Test	Submitter	$D(F)$	$\Gamma(F)$	Prec.	Rec.	FMeas.
1	aflood	0.00133	0.00155	0.873	0.653	0.747
1	AgrMaker	0.00127	0.00147	0.865	0.798	0.831
1	AROMA	0.00288	0.00298	0.775	0.678	0.723
1	ASMOV	0.00314	0.00368	0.746	0.755	0.751
1	DSSim	0.00156	0.00233	0.853	0.676	0.754
1	kosimap	0.00099	0.00123	0.866	0.619	0.722
1	Lily	0.00259	0.00346	0.738	0.739	0.739
1	Ref_Full	0.00078	0.00066	1.0	1.0	1.0
1	SOBOM	0.00088	0.00091	0.952	0.777	0.855
1	taxomap	0.00149	0.00225	0.87	0.678	0.762
2	aflood	0.00105	0.00098	0.892	0.712	0.792
2	AgrMaker	0.00086	0.00081	0.967	0.682	0.8
2	ASMOV	0.00133	0.00161	0.821	0.736	0.776
2	DSSim	0.00113	0.00123	0.973	0.62	0.757
2	kosimap	0.0023	0.00443	0.907	0.446	0.598
2	Lily	0.00236	0.00341	0.869	0.559	0.681
2	taxomap	0.00075	0.00086	0.953	0.609	0.743
3	aflood	0.00148	0.0016	0.827	0.763	0.794
3	AgrMaker	0.00332	0.00368	0.511	0.815	0.628
3	ASMOV	0.00306	0.00386	0.725	0.767	0.745
3	kosimap	0.00099	0.00123	0.866	0.619	0.722
3	Lily	0.00332	0.00393	0.534	0.774	0.632
3	taxomap	0.01486	0.02115	0.458	0.716	0.559
4	aflood	0.00145	0.00155			
4	AgrMaker	0.00077	0.00066			
4	ASMOV	0.00373	0.0041			
4	taxomap	0.00474	0.00748			

Table 31. Results of anatomy track.

r		Prec.	Rec.	FMeas.
Anatomy 1	$D(F)$	-0.91	-0.25	-0.55
	OD	-0.94	-0.35	-0.64
Anatomy 2	$D(F)$	-0.47	-0.71	-0.85
	OD	-0.36	-0.82	-0.94
Anatomy 3	$D(F)$	-0.68	-0.03	-0.76
	OD	-0.65	-0.07	-0.74
Anatomy [1-3]	$D(F)$	-0.73	0.04	-0.59
	OD	-0.69	-0.03	-0.61

Table 32. Pearson correlation r for $D(F)$ and $\Gamma(F)$ against precision, recall and F-measure for all Anatomy tests.

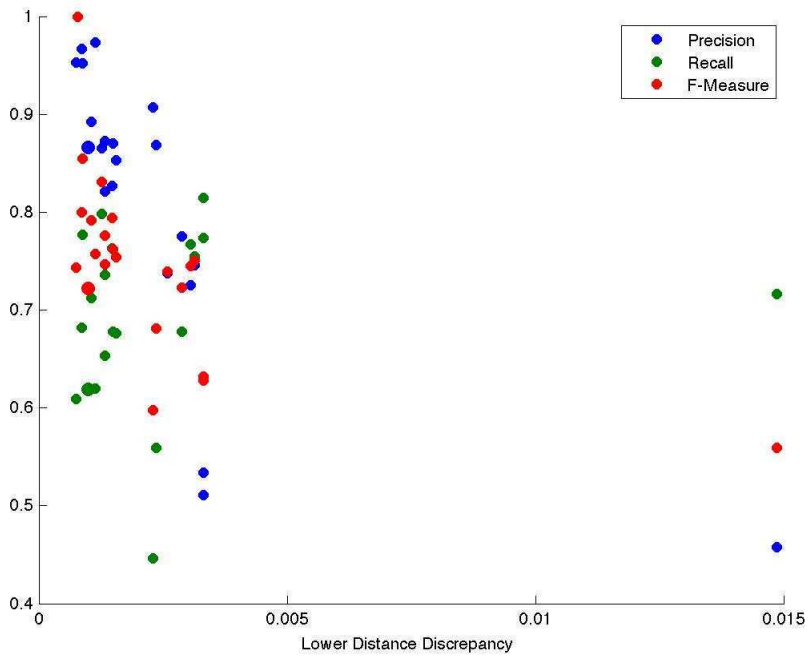

Fig. 16. Anatomy track, all tests, lower distance discrepancy vs. (blue) precision (green) recall (red) F-measure.

12 Lesson learned and suggestions

The lessons learned for this year are relatively similar to those of previous years. There remain one lesson not really taken into account that we identify with an asterisk (*). We reiterate those lessons that still apply with new ones:

A) Unfortunately, we have not been able to maintain the better schedule of two years ago. We hope to be able to improve this through the use of SEALS technology (see §13).
B) The trend that there are more matching systems able to enter such an evaluation seems to slow down. There have been not many new systems this year but on specialised topics. There can be two explanations: the field is shrinking or the entry ticket is too high.
C) We still can confirm that systems that enter the campaign for several times tend to improve over years.
*D) The benchmark test case is not discriminant enough between systems and, as noted last year, automatic test generation could contribute to improve the situation. We plan to introduce this in the SEALS platform.
E) Some tracks provide non conclusive results, we should make effort to improve this situation by knowing, beforehand, what conclusions can be drawn from the evaluations.
F) With the increase in the number of data sets, comes less participants. We will have to set rules for declaring unfruitful, tracks in which there is no minimal independent participation.

Of course, these are only suggestions that will be refined during the coming year, see [22] for a detailed discussion on the ontology matching challenges.

13 Future plans

In order to improve the organization of the Ontology Alignment Evaluation Initiative, plans are made for next year that the evaluation campaign be run on a new open platform for semantic technology evaluation developed by the SEALS project[21]. The SEALS project aims at providing support for the evaluation of semantic technologies, including ontology matching.

The project will provide an automated test infrastructure and will organize integrated evaluation campaigns. This will allow new features in tests cases like test generation on demand and online evaluation. This will lead to a more automated and integrated way to evaluate systems as well as the opportunity for participants to run the evaluation for themselves.

We plan to run the next OAEI campaign within this framework and to have at least three tracks, and if possible more, fully supported by the SEALS platform.

[21] http://www.seals-project.eu

14 Conclusions

Confirming the trend of last year, the number of systems, and tracks they enter in, seems to stabilize. As noticed the previous years, systems which do not enter for the first time are those which perform better. This shows that, as expected, the field of ontology matching is getting stronger (and we hope that evaluation has been contributing to this progress).

Moreover, we had this year more tracks but participants did not enter more tracks than previous years: 3.25 against 3.84 in 2008 and 2.94 in 2007. This figure of around 3 out of 8 may be the result of either the specialization of systems or the short time allowed to the campaign.

All participants have provided a description of their systems and their experience in the evaluation. These OAEI papers, like the present one, have not been peer reviewed. However, they are full contributions to this evaluation exercise and reflect the hard work and clever insight people put in the development of participating systems. Reading the papers of the participants should help people involved in ontology matching to find what makes these algorithms work and what could be improved. Sometimes participants offer alternate evaluation results.

The Ontology Alignment Evaluation Initiative will continue these tests by improving both test cases and testing methodology for being more accurate. Further information can be found at:

`http://oaei.ontologymatching.org`.

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