

OAEI 2020 results for AML and AMLC

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Abstract. AgreementMakerLight (AML) is a scalable and extensible ontology matching system with an alignment repair functionality and a strong focus on the use external knowledge. In OAEI 2020, AML's development focused mainly on expanding its range of complex matching algorithms, but there were also improvements on its instance matching pipeline and ontology parsing algorithm. AML remains the system with the broadest coverage of OAEI tracks, and among the top performing systems overall.

1 Presentation of the System

1.1 State, Purpose, General Statement

AgreementMakerLight (AML) is an ontology matching system inspired on AgreementMaker [1, 2] but designed anew to tackle the matching of very large ontologies efficiently [7]. It is a general purpose system that is able to successfully tackle problems across the whole spectrum of ontology matching, irrespective of domain.

AML is primarily based on lexical matching algorithms [8], but also includes structural algorithms for both matching and filtering, as well as its own logical repair algorithm [9]. It is capable of using external background knowledge, and even automatically selecting background knowledge sources for any given ontologies to match [6].

AMLC is a new version of AML developed to tackle complex ontology matching. At this time, it remains separate from the main AML code-base and OAEI submission, but we aim to merge the two versions in the near future.

This year, our development focused mainly on the implementation of pattern mining ontology matching algorithms on AMLC, based on association rules and inspired by the work of Zhou et al. [10]. As of our OAEI submission, AMLC included only variants of these algorithms for detecting simple class and property mappings, but we are in the process of implementing variants for complex mappings.

As has been the case in recent years, we also participated in the SPIMBENCH and Link Discovery tracks via the HOBBIT platform. In the case of SPIMBENCH, we participated with the HOBBIT adaptation of the main AML code-base. In the case of Link Discovery, we participated with two specialized versions of AML (AML-Spatial and

AML-Linking for the Spatial and Linking tasks respectively), due to the unique characteristics of these matching tasks and to the unavailability of the TBox assertions in the HOBBIT datasets.

1.2 Specific Techniques Used

This section describes only the features of AML that are new for the OAEI 2020. It also describes AMLC, a variant of AML tailored to complex matching. For further information on AML’s simple matching strategy, please consult AML’s original paper [7] as well as the AML OAEI results publications of 2016-2018 [4, 3, 5].

Our main development this year was a modular association rule mining framework for ontology matching, inspired by the work of Zhou et al. [10]. This strategy resembles the common market basket analysis, where we take into account how frequently two entities of different ontologies are related to common instances, given a populated dataset. Our framework features a central association rule mining algorithm implementation that selects patterns (i.e., mappings) based on their confidence and support, and a suite of algorithms devoted to finding individual types of patterns and computing their confidence and support from among the set of instances. As of the OAEI submission we had implemented only algorithms for detecting simple class and property mappings, but we are in the process of implementing algorithms for each type of complex mapping.

1.3 Adaptations made for the evaluation

As has been the case in recent OAEI editions, the Link Discovery submission of AML is adapted to these particular tasks and datasets, as their specificities (namely the absence of a Tbox) demand a dedicated submission. The same is also true to some extent of AML’s Complex Matching submission.

As usual, our submission included precomputed dictionaries with translations, to circumvent Microsoft® Translator’s query limit.

1.4 Link to the system and parameters file

AML is an open source ontology matching system and is available through GitHub: <https://github.com/AgreementMakerLight>.

2 Results

AML’s OAEI 2020 results are summarized in Table 1 and discussed in the following subsections.

Table 1: Summary of OAEI 2020 results for AML and AMLC.

Task	Precision	Recall/ Coverage	F-measure	Run time (s)	Rank ¹
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	— Anatomy —				
Mouse-Human	0.956	0.927	0.941	29	1
	— Biodiversity & Ecology —				
FLOPO-PTO	0.766	0.820	0.792	53.7	3
ENVO-SWEET	0.810	0.927	0.865	38.8	1
ANAEETHES-GEMET	0.976	0.764	0.857	4.2	3
AGROVOC-NALT	0.955	0.835	0.890	139.5	1 ^a
	— Complex —				
Conference	0.31	0.37	0.34	-	1 ^a
Populated Conference	0.23-0.51	0.26-0.31	N/A	-	N/A
Hydrography	0.45	0.05	0.10	-	1 ^b
Geolink	0.50	0.23	0.32	-	2
Populated Geolink	0.50	0.23	0.32	-	4
Populated Enslaved	0.73	0.28	0.40	-	1
Taxon	0.19-0.40	0	N/A	-	N/A
	— Conference —				
OntoFarm (ra1-M3)	0.84	0.66	0.74	-	1
OntoFarm (ra2-M3)	0.82	0.61	0.70	-	1
OntoFarm (rar2-M3)	0.78	0.62	0.69	-	2
OntoFarm (Discrete)	0.79	0.77	0.78	-	1
OntoFarm (Continuous)	0.80	0.74	0.77	-	1
DBpedia-OntoFarm	0.48	0.67	0.56	-	1
	— Disease & Phenotype —				
HP-MP	0.910	0.79	0.816	102	3
DOID-ORDO	0.682	0.834	0.750	200	2
	— Interactive Matching —				
Anatomy (error 0.0)	0.972	0.933	0.952	37.3	1
Anatomy (error 0.1)	0.962	0.929	0.945	37.5	1
Anatomy (error 0.2)	0.951	0.928	0.939	37.4	1
Anatomy (error 0.3)	0.942	0.924	0.933	37.2	1
Conference (error 0.0)	0.91	0.698	0.79	30.1	2
Conference (error 0.1)	0.843	0.682	0.754	30	1
Conference (error 0.2)	0.777	0.677	0.723	30.3	1
Conference (error 0.3)	0.721	0.65	0.684	30.5	1
	— Knowledge Graph —				
Aggregate (class)	0.98	0.81	0.89	-	1
Aggregate (property)	0.92	0.57	0.70	-	6
Aggregate (instance)	0.90	0.80	0.85	-	3 ^b
Aggregate (all)	0.90	0.80	0.85	3055	3 ^b
	— Large Biomedical Ontologies —				
FMA-NCI small	0.958	0.91	0.933	38	1
FMA-NCI whole	0.806	0.881	0.842	82	1
FMA-SNOMED small	0.923	0.762	0.835	101	1
FMA-SNOMED whole	0.685	0.710	0.697	181	3
SNOMED-NCI small	0.906	0.746	0.818	629	1

SNOMED-NCI whole	0.862	0.687	0.765	381	1
—— Link Discovery ——					
Spatial (mainbox)	1.0	1.0	1.0	11172	1 ^b
—— Multifarm ——					
Different Ontologies	0.72	0.35	0.47	170	1
Same Ontologies	0.94	0.28	0.17	–	2
—— SPIMBENCH ——					
SPIMBENCH (mainbox)	0.839	0.884	0.860	38772	4

¹according to F-measure; ^a only system with results; ^b tied with other systems

2.1 Anatomy

AML had a 0.7% increase in precision and a 0.9% decrease in recall, resulting in a 0.2% decrease in F-measure, in comparison with its performance in recent years. These differences are an unexpected consequence of minor changes in AML's general configuration.

2.2 Biodiversity and Ecology

AML improved its results on both the FLOPO-PTO and the ENVO-SWEET tasks in comparison with last year. It was surpassed by two versions of LogMap on the FLOPO-PTO task, but remained the best performing system in the ENVO-SWEET task. With respect to the new tasks, AML ranked third on the ANAEETHES-GEMET task, and was the only system able to produce results on the AGROVOC-NALT task.

2.3 Complex Matching

AMLC was one of three tools able to generate complex correspondences, and the only tool able to produce results in the (non-populated) Conference task, that uses the simple reference alignment as input. While its performance was among the best in most tasks, it remains mediocre in comparison with its performance in simple matching tasks, underpinning the fact that there is much room for improvement in complex ontology matching.

We unfortunately were unable to finish implementing the suite of pattern mining algorithms for complex ontology matching in time for this OAEI edition, which likely would have improved AML's performance substantially in populated complex tasks.

2.4 Conference

AML had the exact same results were exactly the same performance as in recent years, with F1-measures of 74% according to the full reference alignment (ra1), 70% according to the extended reference alignment (ra2), 78% according to the discrete uncertain reference alignment, and 77% according to the continuous one, ranking first in all four evaluation variants. It ranked second in the evaluation with the violation free version of

the extended reference alignment (rar2), likely because AML's repair algorithm deliberately does not address conservativity violations, as we do not subscribe to conservativity as a guiding principle in ontology matching.

AML was one of only five systems able to participate in a new unannounced task consisting in matching the DBpedia to the OntoFarm ontologies, and had the highest F-measure among those five.

2.5 Disease and Phenotype

AML ranked third and second in F-measure on the HP-MP and DOID-ORDO tasks, respectively. However, as has been the trend, AML was one of the systems with the highest number of unique mappings (i.e., mappings not proposed by any other system). Since the evaluation on this track is based on a 3-vote consensus alignment, rather than a true reference alignment, and unique mappings are not otherwise assessed, this severely affects AML's evaluation, making its results below-average in comparison with other biomedical matching tasks.

2.6 Interactive Matching

AML had a lower performance than last year on the Anatomy task, undoubtedly tied to its change in performance in the non-interactive version of the task. Its results on the Conference task remained the same. Overall it remains the interactive system that is the least impacted by the oracle errors.

2.7 Large Biomedical Ontologies

AML's performance on this track was similar to last year's, but with decimal increases in F-measure across all tasks, likely due to the same changes that affected its performance on the Anatomy track. It remains the best performing system in five out of the six tasks.

2.8 Knowledge Graph

Contrarily to last year, AML was able to complete all of the five tasks in a timely manner, having a global F-measure of 0.85 which ranked it third overall. It had the best performance in matching classes.

2.9 Link Discovery

As in previous years, AML and all other participants produced a perfect result (100% F-measure) in the Spatial task. AML had the highest run time among participating systems, though this was not true in all tasks.

2.10 Multifarm

AML's results were slightly better than last years, with a 2% increase in F-measure in the different ontologies modality and a 1% increase in the same ontologies modality. These differences are due to correcting a minor configuration problem on the use of AML's word-matching algorithm in a multilingual setting.

2.11 SPIMBENCH

AML obtained the same results as last year, with an F-measure of 86% which ranked it fourth.

3 General comments

3.1 Comments on the results

In 2020, AML was once again the system that tackled the most OAEI tracks and datasets, and maintained its status as one of best performing and broadest matching systems competing in the OAEI.

Nonetheless, there is still some work to be done in terms of complex matching, in order to be able to provide more robust results. We will strive to refine and improve AML's complex matching pipeline, particularly by upgrading our association rule based approach.

4 Conclusion

Like in recent years, AML was the matching system that participated in the most OAEI tracks and datasets, and it was among the top performing systems in most of them. AML's performance was very similar to those of recent years in any of the long-standing OAEI tracks, as most of our development effort went into tackling new challenges, such as pattern mining approaches for complex matching.

Complex matching remains one of the biggest challenges in ontology matching, and will remain the main focus of AML's development in the near future.

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References

1. I. F. Cruz, F. Palandri Antonelli, and C. Stroe. AgreementMaker: Efficient Matching for Large Real-World Schemas and Ontologies. *PVLDB*, 2(2):1586–1589, 2009.
2. I. F. Cruz, C. Stroe, F. Caimi, A. Fabiani, C. Pesquita, F. M. Couto, and M. Palmonari. Using AgreementMaker to Align Ontologies for OAEI 2011. In *ISWC International Workshop on Ontology Matching (OM)*, volume 814 of *CEUR Workshop Proceedings*, pages 114–121, 2011.
3. D. Faria, B. S. Balasubramani, V. R. Shivaprabhu, I. Mott, C. Pesquita, F. M. Couto, and I. F. Cruz. Results of AML in OAEI 2017. In *OM-2017: Proceedings of the Twelfth International Workshop on Ontology Matching*, page 122, 2017.
4. D. Faria, C. Pesquita, B. S. Balasubramani, C. Martins, J. Cardoso, H. Curado, F. M. Couto, and I. F. Cruz. OAEI 2016 results of AML. In *Ontology Matching Workshop*. CEUR, 2016.
5. D. Faria, C. Pesquita, B. S. Balasubramani, T. Tervo, D. Carrigo, R. Garrilha, F. M. Couto, and I. F. Cruz. Results of aml participation in oaei 2018. In *OM-2018: Proceedings of the Thirteenth International Workshop on Ontology Matching*, pages 125–131, 2018.
6. D. Faria, C. Pesquita, E. Santos, I. F. Cruz, and F. M. Couto. Automatic Background Knowledge Selection for Matching Biomedical Ontologies. *PLoS One*, 9(11):e111226, 2014.
7. D. Faria, C. Pesquita, E. Santos, M. Palmonari, I. F. Cruz, and F. M. Couto. The Agreement-MakerLight Ontology Matching System. In *OTM Conferences - ODBASE*, pages 527–541, 2013.
8. C. Pesquita, D. Faria, C. Stroe, E. Santos, I. F. Cruz, and F. M. Couto. What’s in a “nym”? Synonyms in Biomedical Ontology Matching. In *International Semantic Web Conference (ISWC)*, pages 526–541, 2013.
9. E. Santos, D. Faria, C. Pesquita, and F. M. Couto. Ontology alignment repair through modularization and confidence-based heuristics. *PLoS ONE*, 10(12):e0144807, 2015.
10. L. Zhou, M. Cheatham, and P. Hitzler. Towards association rule-based complex ontology alignment. In X. Wang, F. A. Lisi, G. Xiao, and E. Botoeva, editors, *Semantic Technology*, pages 287–303, Cham, 2020. Springer International Publishing.