MELT

Matching EvaLuation Toolkit





Sven Hertling; **Jan Portisch**; Heiko Paulheim SEMANTiCS 2019 – Karlsruhe – 2019/09/11

Joint Work

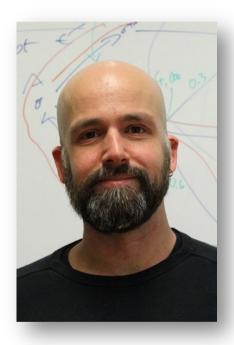




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Agenda



- Motivation
- What is MELT?
- Usage Example
- Q&A



MOTIVATION

Ontology Alignment Evaluation Initiative (OAEI)





Ontology Alignment Evaluation Initiative

- running campaigns since 2005
- structured in tracks (similar to task sets)
- researchers submit their implementation
 - centrally evaluated by track organizers
 - results published

Tooling







Semantic Evaluation at Large Scale

- (among others) packaging and evaluation
- OAEI support since 2010

Holistic Benchmarking of Big Linked Data

- (among others) packaging and evaluation
- OAEI support since 2017
- OAEI 2018: 6/19 matchers support HOBBIT

Pain Points



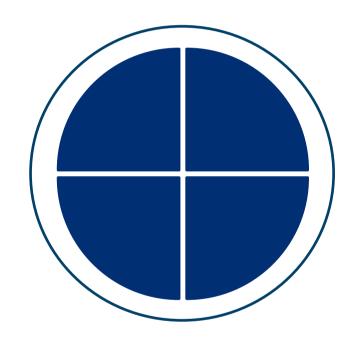
- Limited evaluation capabilities in SEALS, HOBBIT, and the Alignment API
- No easy-to-use parameter tuning
- Packaging process might be complicated for new entrants to the community
- Tooling Java-focused (no Python)
- Implementation of the Alignment API not maven-based
- Tool breaks





- **Easy** matcher development
- Non-Java matcher development
- Maven support

- Facilitate matcher packaging
- Facilitate matcher submission



 Allow for parameter optimization

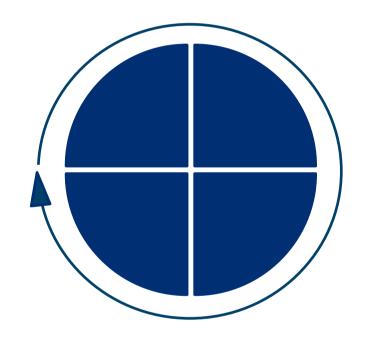
- Advanced evaluation capabilities
- Evaluation before packaging
- Allow for interactive visualization
- Streamlined development process
- Integration with existing tooling
- OAEI support
- **Extensibility**



Matcher

Development

Matcher **Submission**



Matcher

Fine-Tuning

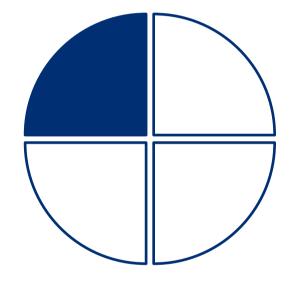
Matcher **Evaluation**



Matcher

Development

Matcher **Submission**



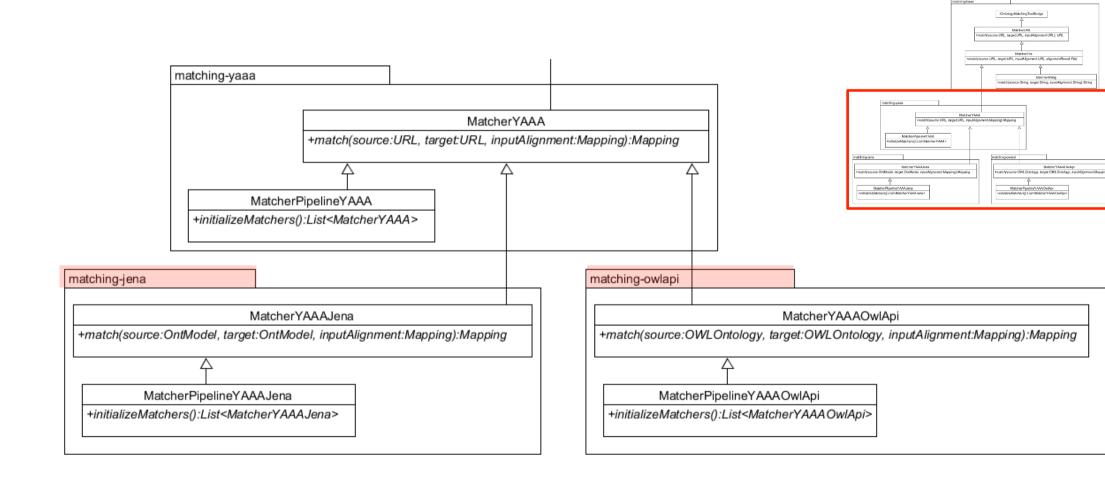
Matcher

Fine-Tuning

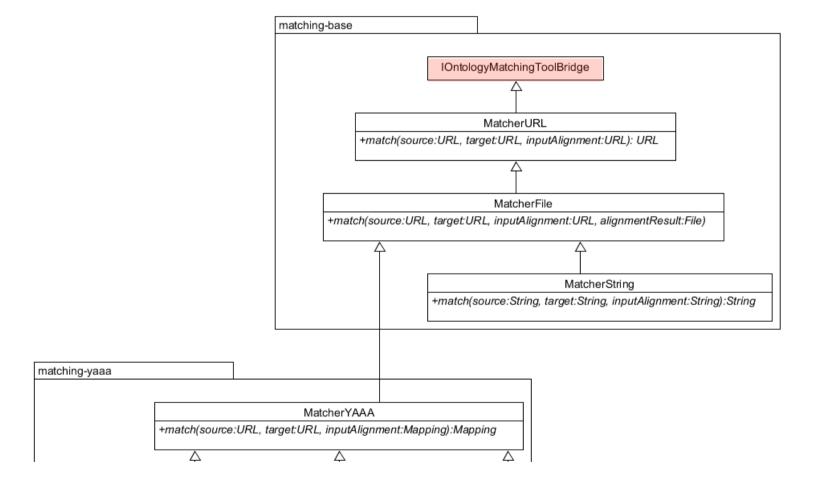
Matcher **Evaluation**

Yet Another Alignment API (YAAA)

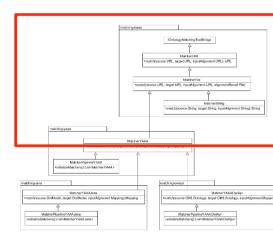




Full SEALS/HOBBIT Support

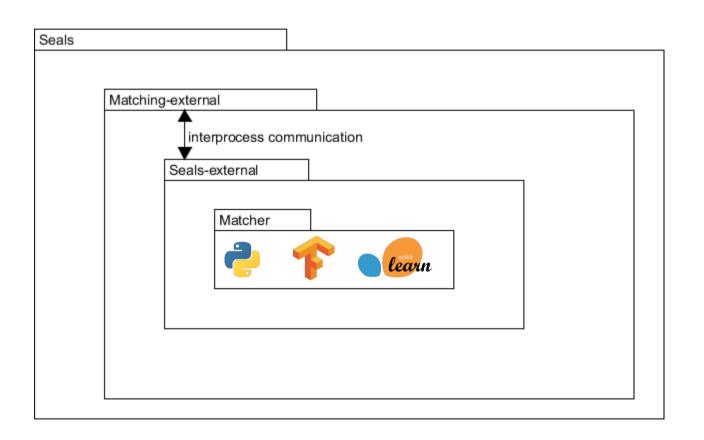






External Matching





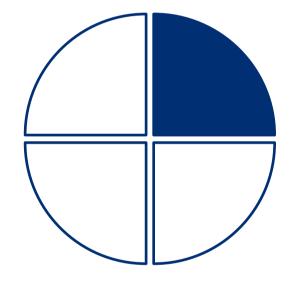
- Simple wrapping
- Packageable for HOBBIT and SEALS
- Matcher can still be evaluated in MELT
- Documentation and demo project available on GitHul



Matcher

Development

Matcher **Submission**



Matcher

Fine-Tuning

Matcher **Evaluation**

Parameter Tuning



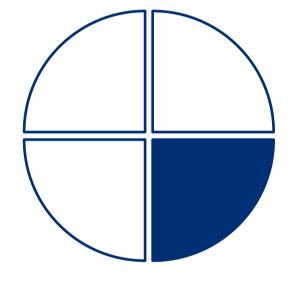
- Run matcher configurations in parallel (i.e., multi-threaded)
- Hand over ExecutionResultSet to Evaluator and pick best value according to what you want to optimize
- Out-of-the-box classes that assist you



Matcher

Development

Matcher **Submission**



Matcher

Fine-Tuning

Matcher **Evaluation**

Evaluation



Full OAEI support: All tracks available (one-time automated download)

```
Track track = TrackRepository.Multifarm.getSpecificMultifarmTrack("ar", "cn");

ExecutionResultSet ers = new ExecutionResultSet();
ers.addAll(Executor.run(track.getTestCases(), new Matcher(), "Matcher"));

EvaluatorCSV evaluatorCSV = new EvaluatorCSV(ers);
evaluatorCSV.write();

Multiple evaluators available, extensible.
```

Exemplary Evaluation



"Show me the false positive class-class mappings for *Multifarm* on track ende for matcher WiktionaryMatcher."

🛃 de-en_de-en-v2	14.08.2019 13:07	File folder	
alignmentCube.csv	14.08.2019 13:07	OpenOffice.org 1	237 KB
testCasePerformanceCube.csv	14.08.2019 13:07	OpenOffice.org 1	10 KB
trackPerformanceCube.csv	14.08.2019 13:07	OpenOffice.org 1	1 KB

Exemplary Evaluation



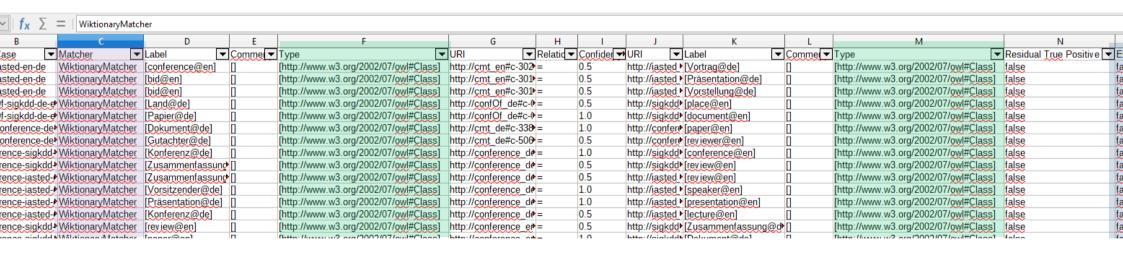
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trackPerformanceCube.csv	14.08.2019 13:07	OpenOffice.org 1	1 KB

Exemplary Evaluation



"Show me the false positive class-class mappings for *Multifarm* on track ende for matcher WiktionaryMatcher." → Just filter the correspondences!



More Evaluation



Filter for Scores or Correspondences

- Micro Average Precision and Macro Average Precision over track Conference
- All residual true positives for track Anatomy
- Macro Average Class-F₁ for all tracks

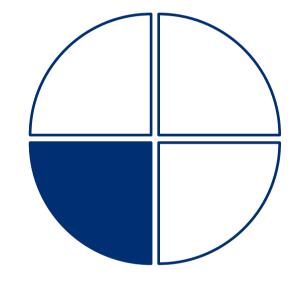
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Matcher

Development

Matcher **Submission**



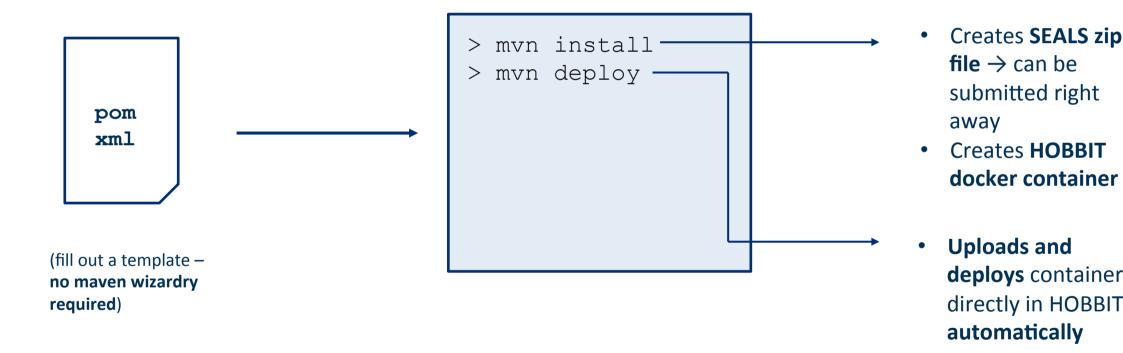
Matcher

Fine-Tuning

Matcher **Evaluation**

Matcher Submission







Usage Example

Usage Example



Motivation

"Which matchers are interesting candidates for combination?"

 \rightarrow Matchers with a high F₁ score and high "diversity".

Quantitative Analysis I



Analysis OAEI 2018 results for Conference and Anatomy: **Jaccard overlap of Alignments** rendered as heatmap in LaTex.

$$J(a_1, a_2) = \frac{|corr(a_1) \cap corr(a_2)|}{|corr(a_1) \cup corr(a_2)|}$$

Executor.loadFromAnatomyResultsFolder("myPath");
// few lines of other code (available on GitHub
as // example)

Results for Anatomy



Table 1. OAEI Anatomy 2018 Alignment Similarity

	 &	4COD3	20° 20	Š		松	0.79	Q.	78	g. 29	Loethe Colle		SANON X	N 92
	ACL	ACC.	AM	00	\$	100	TEN STATE	E. E.	2000	2000	2000	200	8	4 Pic
ALIN	1	0.93	0.62	0.97	0.72	0.47	0.79	0.63	0.66	0.6	0.81	0.63	0.62	0.65
ALOD2Vec	0.93	1	0.65	0.94	0.77	0.45	0.81	0.67	0.7	0.63	0.84	0.66	0.64	0.68
AML	0.62	0.65	1		0.76	0.3	0.74	0.72	0.8	0.82	0.72	0.83	0.79	0.83
DOME	0.97	0.94	0.62	1	0.73	0.47	0.79	0.64	0.66	0.6	0.81	0.63	0.62	0.66
FCAMapX	0.72	0.77	0.76	0.73	1	0.35	0.75	0.69	0.82	0.77	0.89	0.77	0.75	0.78
Holontology	0.47	0.45	0.3	0.47	0.35	1	0.38	0.3	0.32	0.29	0.39	0.31	0.3	0.31
KEPLER	0.79	0.81	0.74	0.79	0.75				0.78	0.72	0.75	0.76	0.71	0.76
Lily	0.63	0.67	0.72	0.64	0.69	0.3	0.69	1		0.68	0.69	0.72	0.72	0.72
LogMap	0.66	0.7	0.8	0.66	0.82	0.32	0.78	0.7	1	0.9	0.81	0.81	0.8	0.81
LogMapBio	0.6	0.63	0.82	0.6	0.77	0.29	0.72	0.68		1	0.74	0.8	0.78	0.78
LogMapLt	0.81	0.84	0.72	0.81	0.89	0.39	0.75	0.69	0.81	0.74	1	0.74	0.74	0.75
POMAP++	0.63	0.66	0.83	0.63	0.77	0.31	0.76	0.72	0.81	0.8	0.74	1	0.79	0.83
SANOM	0.62	0.64	0.79	0.62	0.75	0.3	0.71	0.72	0.8	0.78	0.74	0.79	1	0.78
XMap	0.65	0.68	0.83	0.66	0.78	0.31	0.76	0.72	0.81	0.78	0.75	0.83	0.78	1

Results for Conference



Table 2. OAEI Conference 2018 Alignment Similarity

			No. The			10x 100	1 () () () () () () () () () (A STATE OF THE STA	Se.M.	Q. N.S.	ANO)	Allego Allego
4.7.73	Δ,											
ALIN		0.75	0.65				0.53		0.72			0.6
ALOD2Vec	0.75	1	0.58	0.87	0.67	0.75	0.61	0.37	0.67	0.86	0.5	0.54
AML	0.65	0.58				0.56	0.53	0.45	0.71	0.59	0.63	0.64
DOME	0.84	0.87	0.61	1	0.67	0.81	0.59	0.39	0.7	0.86	0.52	0.56
FCAMapX	0.63	0.67	0.58	0.67			0.55	0.41	0.62	0.66	0.51	0.53
Holontology	0.77	0.75	0.56	0.81	0.6		0.53	0.37	0.64	0.72	0.49	0.52
KEPLER	0.53	0.61	0.53	0.59		0.53	1	0.41	0.57	0.62	0.5	0.54
Lily	0.43	0.37	0.45	0.39	0.41	0.37	0.41	1	0.46	0.39	0.48	0.51
LogMap	0.72	0.67	0.71	0.7	0.62	0.64	0.57	0.46	1	0.7	0.63	0.66
LogMapLt	0.76	0.86	0.59	0.86	0.66	0.72	0.62	0.39	0.7	1	0.51	0.56
SANOM	0.52	0.5	0.63	0.52	0.51	0.49	0.5	0.48	0.63	0.51	1	0.61
XMap	0.6	0.54	0.64	0.56	0.53	0.52	0.54	0.51	0.66	0.56	0.61	1

Quantitative Analysis II



Mean Absolute Deviation (MAD) of Similarities plotted against F₁.

$$MAD = \frac{1}{n} \sum_{i=1}^{n} |x_i - mean(X)|$$

Results for Anatomy



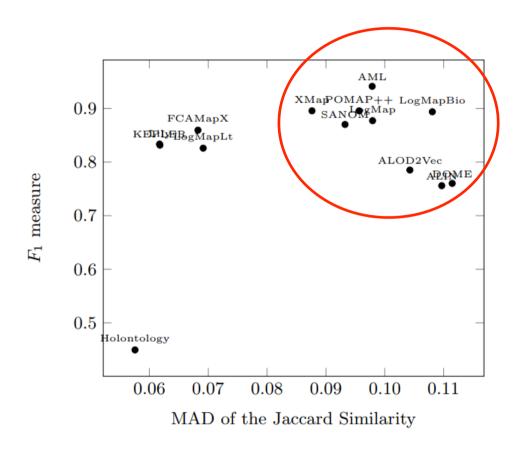


Fig. 2. Matcher comparison using MAD and F_1 on the Anatomy data set

Results for Conference



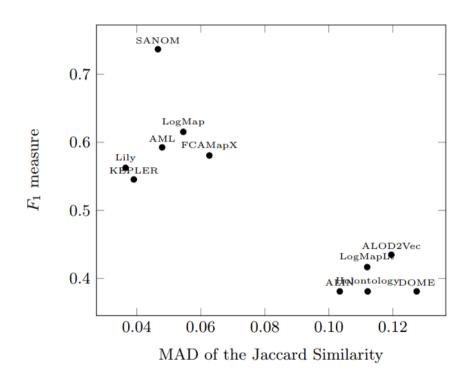


Fig. 3. Matcher comparison using MAD and F_1 on the Conference data set

There is MUCH more to MELT



Ontology **Caching** Services

Multi-Threaded Matcher Execution

Baseline **Matchers**

ecution of SEALS
ckages from within
ELT

TRY IT!



Alignment Refine

Alignment Extension

OAEI-Track Organizer
Tools

ExecutionResult **Indexing**

One-Time **Auto-Download** of OAEI Tracks

Automatic Reading of OAEI Result Alignments

Matcher **Pipelining**

Thank you!



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