MDMapper Results for OAEI 2025

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Abstract

This paper reports on the participation of MDMapper in the Ontology Alignment Evaluation Initiative (OAEI) 2025. MDMapper is an ontology matching system tailored for Product Master Data Model (PMDM) contexts, integrating hierarchical reasoning and property-based similarity to support both equivalence and non-equivalence correspondences. Following its initial participation in OAEI 2024 (Anatomy and Conference tracks), MDMapper also compete in these two tracks in 2025 and additionally participated in the new Beyond Equivalence track, which evaluates alignment relations beyond equivalence. Although no significant architectural changes were made to the system, MDMapper achieved outstanding performance in Beyond Equivalence track, particularly on PMDM tasks.

Keywords

Ontology Matching, Ontology Alignment Evaluation, Product Master Data Models

1. Introduction

MDMapper [1] is an ontology matching system developed to support consistent data exchange across digital information supply chain as described in [2], with a particular focus on aligning product classification hierarchies enriched with attributes. It leverages hierarchical reasoning and property compatibility analysis to detect not only equivalence but also containment and overlap correspondences between ontology entities.

MDMapper first participated in OAEI 2024 [3], where it was evaluated in the Anatomy and Conference tracks. Building on this foundation, the 2025 edition extended the participation to include the newly introduced Beyond Equivalence [4] track, which focuses on finding correspondences beyond equivalence.

2. Results

MDMapper was evaluated in three OAEI 2025 tracks: *Anatomy, Conference*, and *Beyond Equivalence*. Compared to the 2024 results, the system maintained stable performance on the Anatomy and Conference tracks, showing only minor variations due to (1) the inclusion of explicit correspondences beyond equivalence, and (2) adjustment on default configuration parameters in terms of similarity thresholds.

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Table 1Results of MDMapper in OAEI 2024 and 2025.

Track	Year	Prec.	Rec.	F1
Anatomy	2024 2025	0.926 0.899		0.903 0.889
Conference	2024 2025	0.660 0.690	0.530 0.500	0.590 0.580
Beyond Equiv.	2025	0.479	0.105	0.164

Furthermore, the newly introduced Beyond Equivalence track provided the matching context involving PMDM and STROMA/TaSeR tasks. Here, MDMapper achieved the highest scores in the PMDM tasks, such as TIM–ECLASS, ECLASS–UNSPSC, ECLASS-GPC, GPC–UNSPSC, and GPC–UNSPSC+. The results demonstrate its outperforming capability in matching classification ontologies with hierarchical structure and attribute-rich context.

2.1. Anatomy

Table 1 shows that MDMapper achieved stable results on the Anatomy track compared with 2024. This year, MDMapper achieved slightly lower scores on the Anatomy track due to the inclusion of explicit correspondences beyond equivalence, which were excluded in the last year. The precision decreased slightly from 0.926 to 0.899, and recall remained nearly unchanged, yielding an F1-score of 0.889 in 2025 versus 0.903 in 2024. In terms of F1-measure, MDMapper (0.889) ranked 6th of 12 compared matchers, following Matcha [5, 6] (0.941), Agent-OM [7] (0.920), ALIN [8] (0.912), LogMapLLM [9] (0.899), and LogMapBio [10] (0.898).

However, it is important to note that this alignment includes non-equivalence correspondences, which are evaluated against a reference alignment that considers only equivalences. This mismatch can lead to an underestimation of performance, as some correct non-equivalence correspondences are are incorrectly penalized, contributing to the observed decrease in scores compared to last year.

2.2. Conference

Table 1 shows that MDMapper achieved stable results on the Conference track compared with 2024. It achieved a precision of 0.69, recall of 0.50, and an F1 score of 0.58, which are close to its 2024 performance (0.66 / 0.53 / 0.59). The slight increase in precision, accompanied by a decrease in recall, is likely due to the stricter similarity thresholds introduced this year. In terms of F1-measure, MDMapper ranked 5th out of 9 participating matchers, following ALIN (0.65), LogMap (0.64), Matcha (0.63), and Agent-OM (0.61).

Once again, the inclusion of non-equivalence correspondences may have led to an underestimation of MDMapper's true performance.

Table 2Results of MDMapper in the Beyond Equivalence track (OAEI 2025). Metrics marked with * indicate isAmong evaluation.

Task	Prec.	Rec.	F1	Prec.*	Rec.*	F1*
ECLASS-GPC	0.1283	0.0190	0.0370	0.1081	0.0609	0.0629
ECLASS-UNSPSC	0.1156	0.0011	0.0021	0.1186	0.0504	0.0556
ETIM-ECLASS	0.9677	0.2855	0.4409	0.4217	0.3873	0.3950
GPC-UNSPSC	0.1373	0.0029	0.0056	0.1635	0.0875	0.0907
GPC-UNSPSC+	0.1379	0.0022	0.0044	0.0423	0.0293	0.0288
g1-web	0.8824	0.3636	0.5150	0.4596	0.3920	0.4069
g2-disease	0.5745	0.0763	0.1347	0.1103	0.0764	0.0807
g3-text	0.3853	0.0551	0.0964	0.1497	0.0649	0.0837
g5-groceries	0.4651	0.1282	0.2010	0.2884	0.2481	0.2461
g7-literature	1.0000	0.1341	0.2366	0.2707	0.2147	0.2292
Average	0.4794	0.1051	0.1640	0.2133	0.1612	0.1680

2.3. Beyond Equivalence

The Beyond Equivalence track was newly introduced in OAEI 2025 to evaluate ontology matching systems on their ability to detect relations beyond equivalence. The datasets used in this track are derived from Product Master Data Models (PMDMs) as well as from the STROMA [11] and TaSeR [12] test cases.

In addition to traditional metrics, the Beyond Equivalence track employed the *isAmong* evaluation [4], enabling fairer assessment of non-equivalence correspondences.

MDMapper achieved the best results on all PMDM tasks under both traditional and isAmong evaluation methods, while its performance on the STROMA/TaSeR datasets was moderate compared to other systems. Nevertheless, as shown in Tables 1 and 2, the overall scores remain low, highlighting the challenges of the Beyond Equivalence track and the methodological gaps in current ontology matching systems.

3. Discussion

MDMapper demonstrated robust and adaptable performance across both classical equivalenceonly and beyond-equivalence matching tasks. Its consistent results on the Anatomy and Conference tracks confirm the stability of the framework, while its performance on the Beyond Equivalence track highlights its strength in handling hierarchical and attribute-rich ontologies, particularly for PMDMs. However, the overall low scores observed across beyond-equivalence tasks underscore the persistent difficulty of identifying non-equivalence correspondences.

Future work will focus on integrating Large Language Models (LLMs) to address the challenge of relation typing [12] in the matching process. The goal is to enable the prediction of relations between candidate entity pairs based on their contextual information, thereby supporting more reliable navigation and resulting in improved alignment that beyond equivalence.

Declaration on Generative Al

During the preparation of this work, the authors used Grammarly in order to grammar and spell check, and improve the text readability. After using the tool, the authors reviewed and edited the content as needed to take full responsibility for the publication's content.

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