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## LogMap Family Participation in the OAEI 2024

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#### Abstract

We present the participation of LogMap and its variants in the OAEI 2024 campaign. The LogMap project started in January 2011 with the objective of developing a scalable and logic-based ontology matching system.

#### 1. Presentation of the system

LogMap [1, 2] is an ontology matching system that *(i)* can efficiently match semantically rich ontologies containing tens (and even hundreds) of thousands of classes, *(ii)* incorporates sophisticated reasoning and repair techniques to minimise the number of logical inconsistencies [3], and *(iii)* provides support for user intervention during the matching process [4]. LogMap ISWC 2011 paper [1] was awarded the SWSA Ten-Year Award.<sup>1</sup>

#### 1.1. LogMap variants in the 2024 campaign

As in previous campaigns, in the OAEI 2023 we have participated with two additional variants:

- **LogMapLt** is a "lightweight" variant of LogMap, which essentially only applies (efficient) string matching techniques.
- **LogMapBio** includes an extension to use BioPortal [5] as a (dynamic) provider of mediating ontologies instead of relying on a few preselected ontologies [6].

The OAEI results also report about LogMap-KG, which is the same as LogMap but with the flag to output instance mappings activated.

#### 1.2. Link to the system and parameters file

LogMap is open-source and released under the Apache-2.0 License.<sup>2</sup> LogMap components and source code are available from the LogMap's GitHub page: https://github.com/ernestojimenezruiz/logmap-matcher/.



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<sup>&</sup>lt;sup>1</sup>http://swsa.semanticweb.org/content/swsa-ten-year-award

<sup>&</sup>lt;sup>2</sup>http://www.apache.org/licenses/

LogMap distributions can be easily customized through a configuration file containing the matching parameters.

#### 1.3. Results

Please refer to http://oaei.ontologymatching.org/2024/results/ for the results of the LogMap family in the OAEI 2024 campaign. It is worth mentioning that LogMap-Bio was one of the top systems in the Bio-ML track [7, 8], surpassing more sophisticated systems relying on machine learning and large language model techniques.

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