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SAMOS - A framework for model analytics and management

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A B S T R A C T

The increased popularity and adoption of model-* engineering paradigms, such as model-driven and model-based engineering, leads to an increase in the number of models, metamodels, model transformations and other related artifacts. This calls for automated techniques to analyze large collections of those artifacts to manage model-* ecosystems. SAMOS is a framework to address this challenge: it treats model-* artifacts as data, and applies various techniques—ranging from information retrieval to machine learning—to analyze those artifacts in a holistic, scalable and efficient way. Such analyses can help to understand and manage those ecosystems.

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Software metadata

(executable) Software metadata description	
Current software version	1.0.1
Permanent link to executables of this version	https://github.com/onderbabur/samos/archive/refs/tags/v1.0.1.zip Virtual machine: https://doi.org/10.5281/zenodo.7074428
Legal Software License	MIT license
Computing platform/Operating System	MacOS, Linux, Windows
Installation requirements & dependencies	Java SE JDK 1.8, Eclipse Modeling Tools 2021-03, Eclipse plugin “m2e”, R version 3.6.1, R package “rJava” version 3.6.2 and custom package “vegan”
If available, link to user manual - if formally published include a reference to the publication in the reference list	https://onderbabur.github.io/samos/
Support email for questions	Onder.Babur@wur.nl

Code metadata

Code metadata description	
Current code version	1.0.1
Permanent link to code/repository used of this code version	https://github.com/ScienceofComputerProgramming/SCICO-D-21-00209
Legal Code License	MIT license
Code versioning system used	git
Software code languages, tools, and services used	Java SE JDK 1.8, Eclipse ModelingTools 2021-03, Eclipse plugin “m2e” version 1.18, R version 3.6.1, R package “rJava” version 3.6.2 and custom package “vegan”
Compilation requirements, operating environments & dependencies	MacOS, Linux, Windows
If available Link to developer documentation/manual	https://onderbabur.github.io/samos/
Support email for questions	Onder.Babur@wur.nl

1. Introduction

Model-* engineering approaches such as model-driven engineering and model-based engineering promote the use of models, metamodels and model transformations as first-class citizens to tackle the complexity of building and maintaining software-intensive systems. As such approaches have gained popularity and are applied to larger problems, however, the complexity, size and variety of the involved artifacts (notably models) increase. This observation holds for open source as well as industrial ecosystems [1,2].

In this paper we present SAMOS (Statistical Analysis of MOdelS), a framework to address the scalability issue in building and managing model-* ecosystems. It treats collections of models as data and offers various large-scale analysis techniques. It has so far been applied for different modeling languages such as metamodels, feature models, statecharts, domain-specific models, and business process models; and for scenarios such as domain analysis, repository management, clustering, outlier detection, language usage analysis, and clone detection [3–11]. In this initial public version (1.0), it includes the core framework, feature extraction for Ecore metamodels, as well as domain clustering and clone detection functionalities. We have followed the artifact sharing guidelines [12] to maintain high quality in our work.

The rest of this paper is organized as follows. Section 2 summarizes some background concepts. Section 3 outlines the SAMOS architecture and functionalities. We illustrate SAMOS for domain clustering and clone detection for Ecore metamodels (Section 4). Section 5 concludes with future work.

2. Background

Information Retrieval (IR) tackles the challenge of efficiently indexing, analyzing and searching various forms of content such as text documents [13]. IR consists of a typical workflow. First, documents are collected and indexed, e.g. using a Vector Space Model (VSM) with (1) a vector representation of vocabulary occurrence in a document, named *term frequency*, (2) *zones* (e.g. ‘author’, ‘title’), (3) weighting schemes such as inverse document frequency (idf), and zone weights, (4) NLP techniques for handling synonyms.

With the VSM we effectively transform each document into an n-dimen-sional vector, yielding an $m \times n$ matrix for m documents. Document similarity can be defined as the distance (e.g. Euclidean or cosine) between vectors in the VSM. We can use these distances for identifying similar groups of documents —i.e. clustering as an unsupervised machine learning (ML) technique.

Finally, n-grams [14] are used in computational linguistics to build probabilistic models of natural language text, e.g. for estimating the next word given a sequence of words, or comparing text collections based on their n-gram profiles. In essence, n-grams represent a linear encoding of structural context. Alternative (and increasingly more complex) fragmentations of structural context include sub-trees and sub-graphs. We will refer to n-grams and sub-trees while discussing SAMOS in the next section.

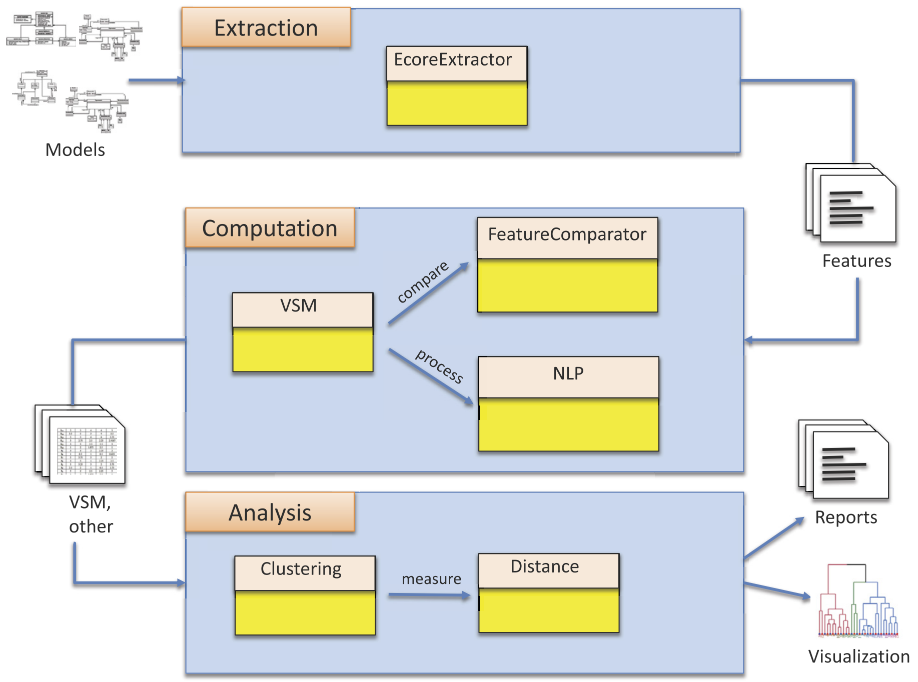

Fig. 1. Overview of SAMOS architecture.

3. SAMOS framework

SAMOS applies the IR and ML-inspired approaches as summarized above to models. In this section, we outline the overall architecture, implementation details and the current functionalities offered by SAMOS.

3.1. Architecture

The architecture, as depicted in Fig. 1, involves three main modules: extraction, computation and analysis. A typical workflow for analytics starts with a metamodel-driven extraction (i.e. in module *Extraction*) of features from a set of input models. Features can be, for instance, singleton names of model elements (very similar to the vocabulary of documents) or larger fragments of the underlying graph structure such as n-grams or sub-trees. In our context, an example n-gram for an EMF metamodel would be for $n = 2$ an EClass containing an EAttribute [5]. The feature files are then fed to the *Computation* module. SAMOS computes a term-frequency based VSM, using feature comparison schemes (for instance maximum similar subsequence for n-grams), weighting schemes (for instance EClass weighted higher than EAttribute) and NLP such as tokenization, filtering, stemming and synonym checking. The results include a vector space model and other metadata files, which are then moved to the *Analysis* module. The fact that the models are effectively transformed to their corresponding numerical vector representations allows the application of various analytics and machine learning techniques. Applying various distance measures suitable to the problem at hand, SAMOS applies different clustering algorithms and can output automatically derived cluster labels or diagrams for visualization and manual inspection and exploration. For more elaboration on the underlying techniques and a detailed example-driven demonstration of the workflow, please refer to our previous work [3,8].

3.2. Implementation

SAMOS is implemented in Java for feature extraction and VSM generation, and in R for the analytics and machine learning parts. SAMOS public version 1.0 as presented in this paper offers the following major functionalities:

- *Modeling languages:* SAMOS supports Ecore metamodels for feature extraction and subsequent steps of the analytics workflow.
- *Analyses:* SAMOS comes preconfigured to run in predefined settings for two types of analyses: domain clustering and clone detection.
- *Feature extraction:* Users can configure SAMOS to extract unigrams, bigrams and sub-trees with depth 1. Orthogonal to this configuration, they can choose to have basic vertex information (e.g. just the name of the model element) or the full details (i.e. all the attributes).

- *Fragmentation:* Users can specify the extraction and analysis scope: whole model or fragments (e.g. EPackages or EClasses in metamodels).
- *NLP components:* Users can configure NLP settings such as tokenization, lemmatization, WordNet synonym checking and threshold values.
- *Matching schemes:* Users can have type-based weights (e.g. EClass having more weight than EParameter) and idf (see Section 2).
- *Feature comparison:* Users can have different algorithms for feature comparison, e.g. maximum similar subsequence for n-grams or tree edit distance for subtrees [8].
- *Distance measures:* Different distance measures are used in the R scripts for different goals, e.g. cosine for domain clustering and masked Bray-Curtis for clone detection.
- *Clustering methods:* Similarly, different clustering methods are used for different goals, e.g. hierarchical clustering for domain clustering and density-based clustering for clone detection.

3.3. *Extension*

Beyond what the wide range of available configuration options as outlined in Section 3.2, SAMOS is highly flexible and extendable, due to its simple and modular architecture. The three main modules of extraction, computation and analysis, as depicted in Fig. 1, are independent of each other and the communication of data among them is achieved via a file-based pipeline. This approach so far has allowed us to plug-and-play different components, e.g. integrating an extractor for a different modeling language without changing the rest of the architecture.

Over the course of the years, parts of the workflow have been extended for various modeling languages and scenarios. Examples for the extraction component would include extending the *IExtractor* abstract class for UML2 models (ongoing work), or adding a completely new feature extractor SXFM feature models using its own Java-based parser [7], while reusing the computation and analysis components mostly as-is. Similarly, one can simply add a new statistical analysis component at the end of the workflow, as we have done in previous work by applying topic modeling on top of the vector space model we obtained from the computation module [9]. Additional extensions we have experimented with include attaching machine learning components on top of the computation output (i.e. the vector space model with its numerical vector representation), or even deep learning components directly on top of the extracted features. We plan to gradually integrate these extensions into future release versions of SAMOS.

4. Illustrative use cases

While the reference work for SAMOS already includes plenty of demonstration and evaluation of SAMOS, we provide two introductory scenarios in this version. The sample runs contain a prerequisite step of crawling 19 Ecore metamodels from ATL Zoo [15], and running the following scenarios.

Domain clustering scenario Users can run SAMOS with the domain clustering setting to see how conceptually related the model domains are. The predefined settings are: unigrams with just model element name information, whole model scoping, full components of NLP, type and idf weighting, simple n-gram comparison, cosine distance and hierarchical clustering. Clustering yields two types of output: one csv file with the list of cluster labels, and a pdf file visualizing the whole dataset in the form of a dendrogram. The dendrogram depicts how similar metamodels are to each other or other groups. The height values of the connection points of metamodels or groups map to intra-model or intra-group distances. The interpretation of the dendrogram in Fig. 2 is that most of the models on the left main branch of the tree are conceptually very similar; after manual investigation, they appear to be all conference management metamodels. The rightmost branch in turn has a cluster of bibliography management metamodels, although one item (Book.ecore) seems to be less similar to the rest of the cluster. For further reference on domain clustering on models, readers are referred to our previous work using SAMOS [3,7,9] and other related work [16].

Clone detection scenario Users can run SAMOS with the clone detection setting to see whether there are highly similar model fragments (*clones*) within or among metamodels. The predefined settings are: n-trees (depth 1) with just full model element attributes, EClass scoping, full components of NLP, type weighting only, Hungarian distance for subtree comparison, masked Bray-Curtis distance and density-based clustering. Clone detection yields three csv files corresponding to clusters of different clone types: Type A for identical fragments except layout and cosmetic differences, Type B for slightly different fragments (distance threshold 10%), and Type C for substantially different fragments (distance threshold 30%), with the threshold values chosen with respect to our previous work [8]. Table 1 depicts an excerpt for Type B clone fragments resulting from the sample run. Each row corresponds to a clone cluster with a cluster label (first column), list of model fragments separated by whitespace (second column), and the average size of the cluster in terms of total number of model elements. The model fragments are encoded in the format `MODEL_NAME$FRAGMENT_NAME`, and the clusters are sorted with respect to their average sizes.

SAMOS can also crawl our labeled dataset on Zenodo [17]. Users can apply domain clustering and clone detection on this significantly larger dataset. While there is no other related work for metamodel clone detection, readers can refer to literature for clone detection on other (non-meta-)model types, for instance, for Simulink models [18] and UML models [19].

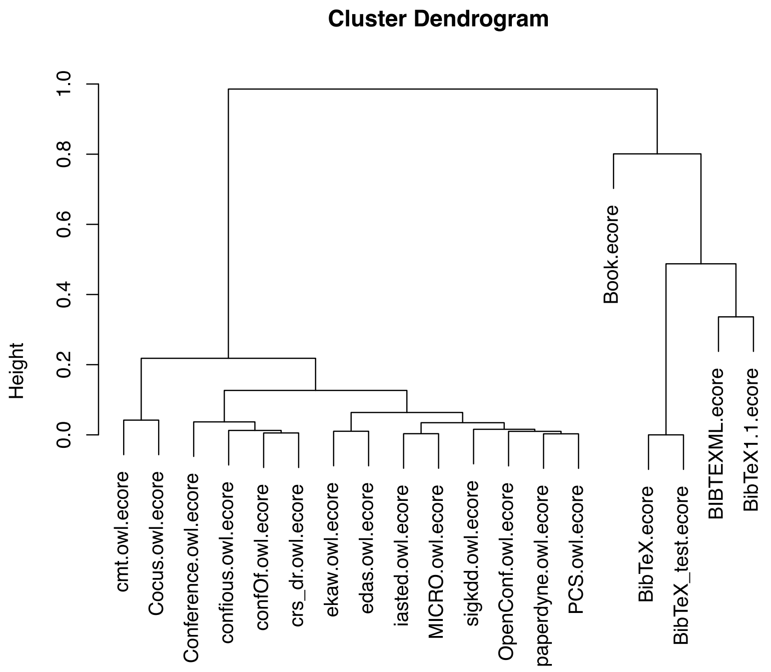

Fig. 2. Plot of the dendrogram as output of domain clustering.

Table 1
Clone detection results for Type B clones in the sample dataset.

Cluster label	Models	Average cluster size
4	MICRO.owl.ecore$Person sigkdd.owl.ecore$Person OpenConf.owl.ecore$Person ...	50.5
15	PCS.owl.ecore$Paper OpenConf.owl.ecore$Paper sigkdd.owl.ecore$Paper ...	46.5
14	MICRO.owl.ecore$Conference PCS.owl.ecore$Conference edas.owl.ecore$Conference ...	33.25
...	...	...

5. Conclusions and future work

In this paper, we presented the SAMOS framework for model analytics and management, in its public version 1.0. We briefly outlined the motivation for developing this framework, its workflow and main functionalities. We also provided two illustrative scenarios for domain clustering and clone detection. As already mentioned in the introduction, SAMOS has been in development for many years with a lot of (partly experimental, not all published) extensions for different languages, settings and analyses. We plan to gradually integrate those extensions into SAMOS, including but not limited to:

- Major performance optimizations, including iterative clone detection [8],
- Support for other languages: feature models [7], UML [6], BPMN [10], Simulink,
- Other analyses and ML algorithms such as topic modeling [9],
- High performance computing using Apache Spark [20],
- Mining software repositories and Neo4j bridges [11].

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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