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Measuring Differences To Compare Sets Of Models And Improve Diversity In MDE

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Synopsis

Context & Introduction

Model Driven Engineering

- Intensive use of models during software development process.
- A model is defined by a modelling language (meta-model).
- Models are manipulated by programs called model transformations.

Context & Introduction

Models play the key role

- Validate concepts (meta-model).
- test model transformations.

Solution to get sets of models

- Automated generation is preferred.

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Many generators exist

- $\mathcal{G}$RIMM.
- emftocsp.
- PRAMANA, etc.

Generated sets of models suffer from

- Close to each other in structure.
- Element naming is poor.
- Solutions' space is not covered.

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Our objectives

1. Measure the quality of a set of models.
2. Improve the quality of a set of models.

Solutions we propose

1. Compare two models.
2. Handle a whole set of models.
3. Increase the diversity of generated sets.

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Measuring model differences

Comparing two models with 4 distance measures.

Inspired from well-known distances.

- Mathematics.
- Natural language processing.
- Graph theory.

Adapted to models in MDE.

- structure of models.
- semantics of models.

Hamming distance

Original Hamming Distance

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- Compares vectors.
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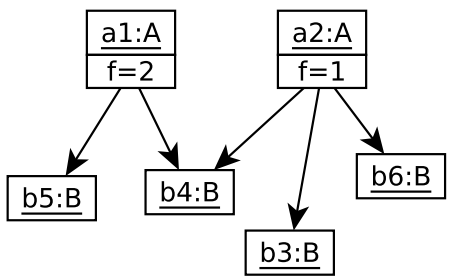
Our version for models

- Vectorial representation for models

$$a = (\overbrace{\underbrace{5,4,0,}_{links}\ \underbrace{2,}_{attributes}}^{instance\ a1}\ \overbrace{\underbrace{4,3,6,}_{links}\ \underbrace{1}_{attributes}}^{instance\ a2})$$



model *a*

Hamming distance

Counting differences

$$
\begin{aligned}
\text{a} &= (5, 4, 0, 2, 4, 3, 6, 1) \\
&= \textcircled{1}\ \textcircled{1}\ \textcircled{1}\ \textcircled{1}\ \textcircled{0}\ \textcircled{1}\ \textcircled{1}\ \textcircled{0} \\
\text{b} &= (6, 5, 3, 3, 4, 7, 0, 1) \\
\text{d(a,b)} &= 6/8
\end{aligned}
$$

Optimisations: permutation sensitive.

Levenshtein distance

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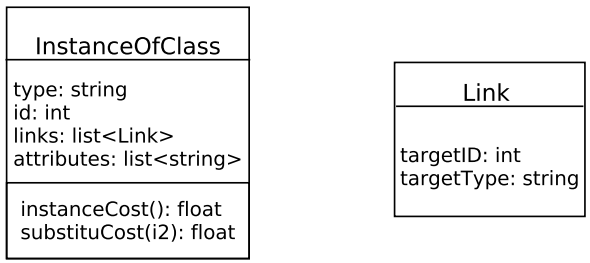

Model for vectorial representation

- Computing distance
  - Classical Levenshtein algorithm
  - Based on addition, suppression and substitution costs.

Centrality distance

Centrality measure

- In graphs, a function associating a value to each node.
- Many well-known centrality functions: `degree`, `betweenness`, `closeness`, etc.

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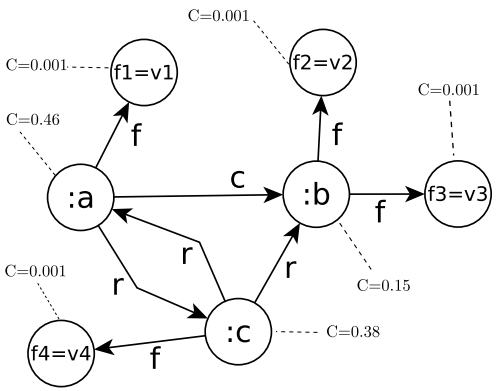
Custom centrality measure

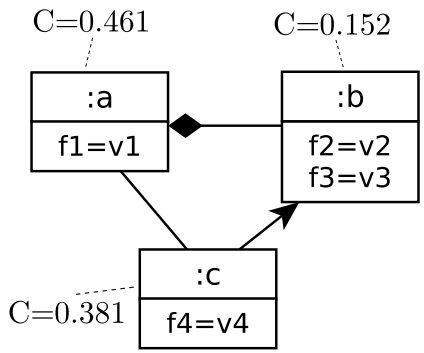
- Based on `eigenvector` centrality (used by `Google` in `Pagerank` algo.)

Centrality distance

Computation

- Transforming models into graphs
- Example of centrality vector





- Comparing two models using (euclidean) norm(s).

Handle sets of models

Objectives

- Compare the models of a set.
- Select the most representative ones.
- Bring a graphical view of the inter-model diversity.

Usefulness

- Reduce the amount of models for testing.
- Achieve a good coverage of meta-models.

Compare the models of a set

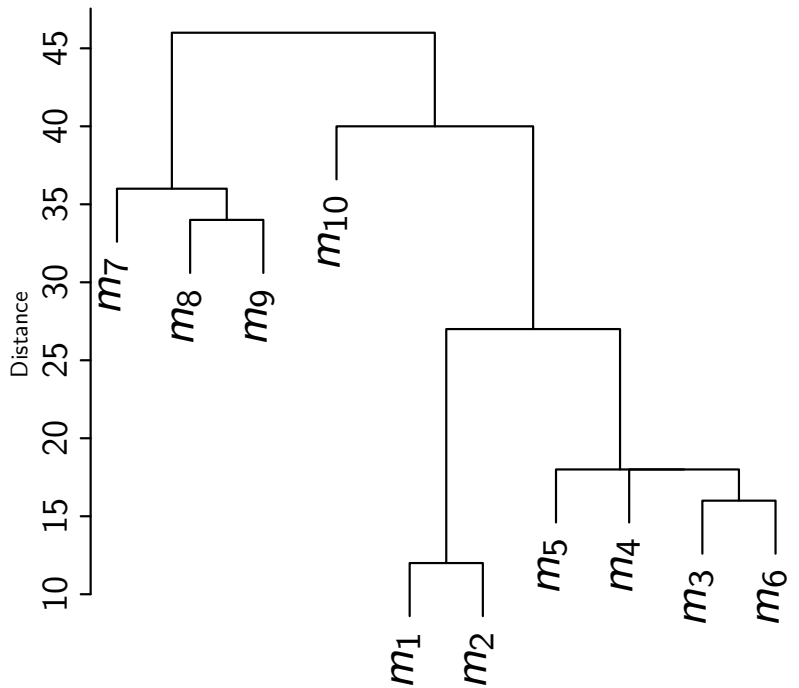
- Use distance metrics.
- Compute distances for each pair of models.
- Produce a distance matrix

	m_1	m_2	m_3	m_4	m_5	m_6	m_7	m_8	m_9	m_{10}
m_1	0	12	27	27	27	26	46	44	45	39
m_2	12	0	27	26	27	27	45	45	43	40
m_3	27	27	0	18	17	16	46	45	46	39
m_4	27	26	18	0	18	18	45	44	45	40
m_5	27	27	17	18	0	18	45	43	44	38
m_6	26	27	16	18	18	0	45	44	46	40
m_7	46	45	46	45	45	45	0	36	36	41
m_8	44	45	45	44	43	44	36	0	34	37
m_9	45	43	46	45	44	46	36	34	0	39
m_{10}	39	40	39	40	38	40	41	37	39	0

Select representative models

Hierarchical clustering of matrix

- Construct the clustering tree.
- Derive the clusters using a proximity threshold.
- Pick the representative models.



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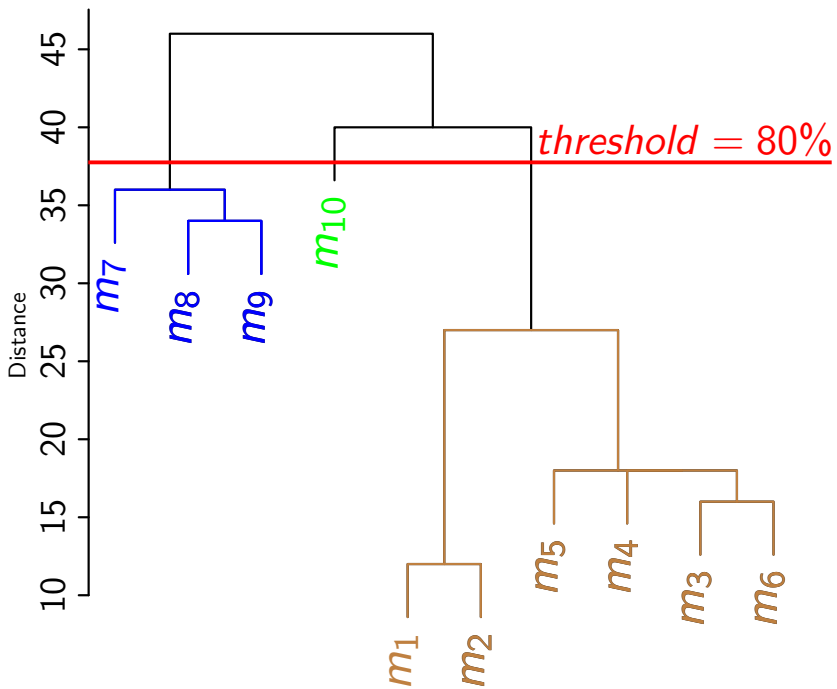

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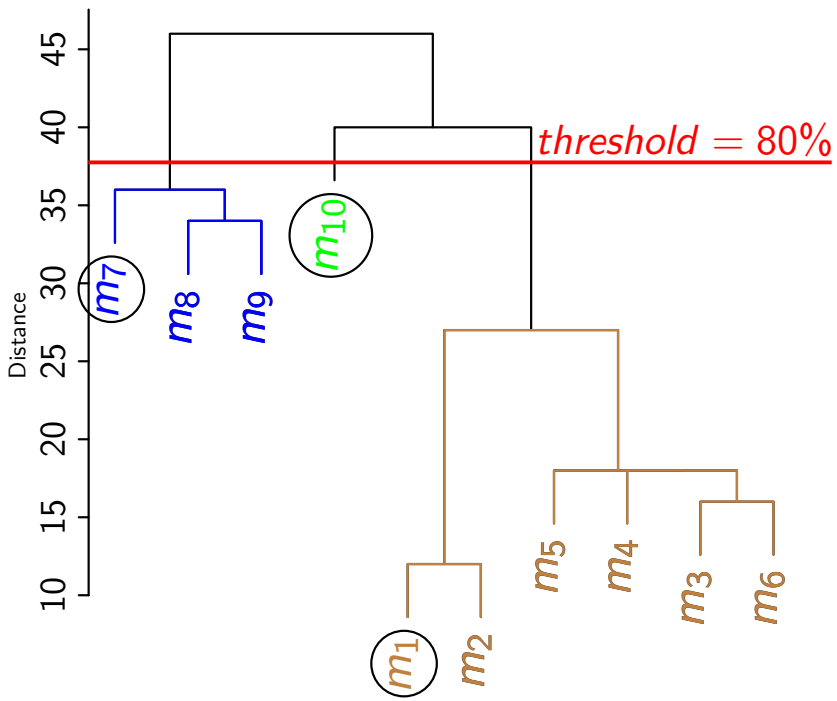
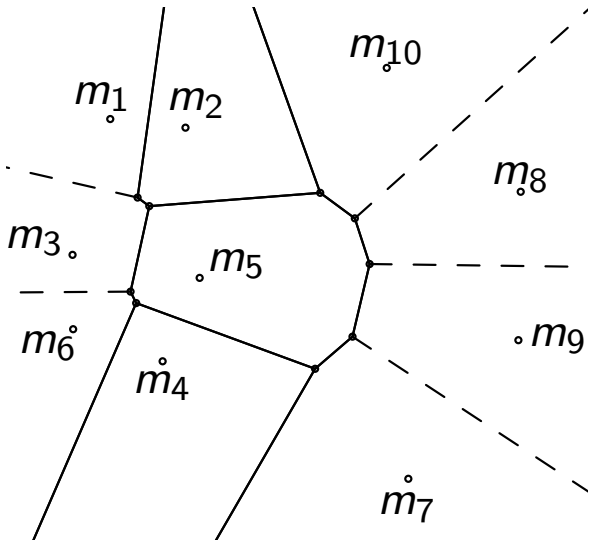


Graphical view of diversity

Voronoi Diagram

- 2D representation of models and distance between them.
- Manual selection of representative models.
- Manual comparison of model sets.



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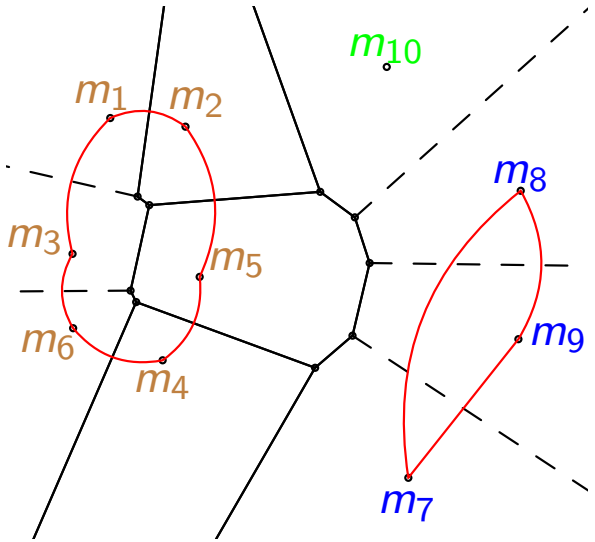

Application: improve diversity

Case study for application

- Scaffolding process in Bioinformatcis.
- Particular graphs.
- Lack of data.

With our approach

- Improve diversity of a set of generated models.
- Diverse sizes, structures, element naming.

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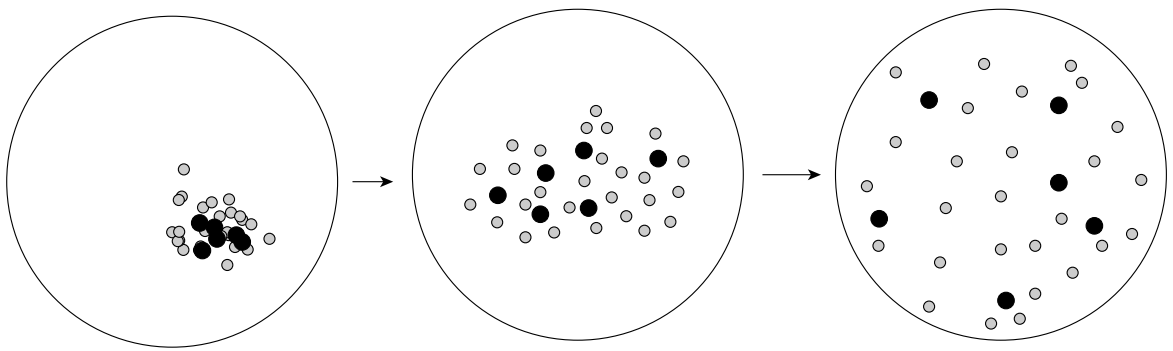


Genetic algorithm

Generate a first set of 100 models.

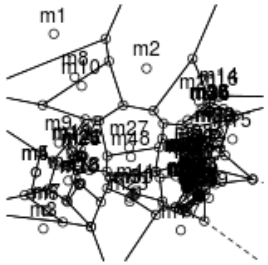
Genetic algorithm (NSGAII)

- Model the problem as a genetic algorithm.

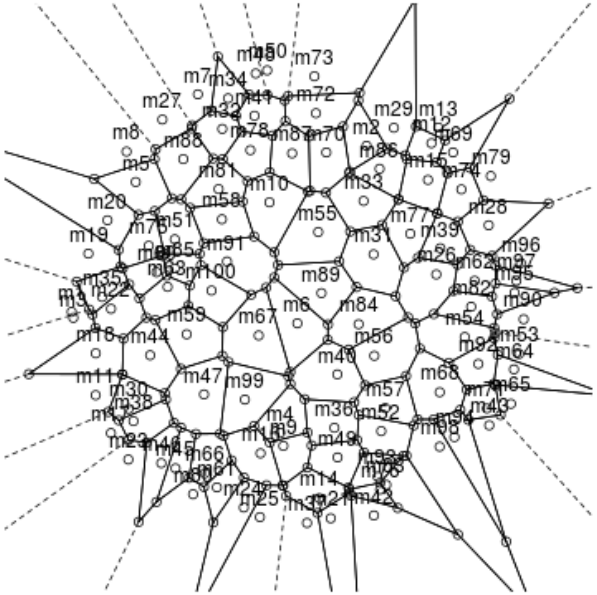
Running the GA (500 times)

- At each round, compute model distances and select representative models (S).
- Use S to produce the next population.

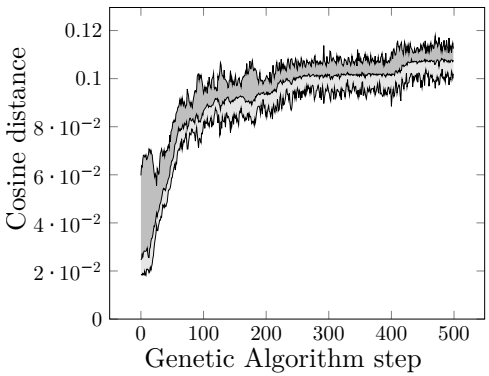
Experimental results

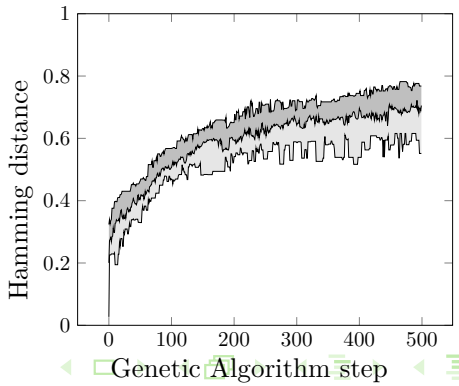


Round 0



Round 500





Conclusion & future work

Generated models suffer from

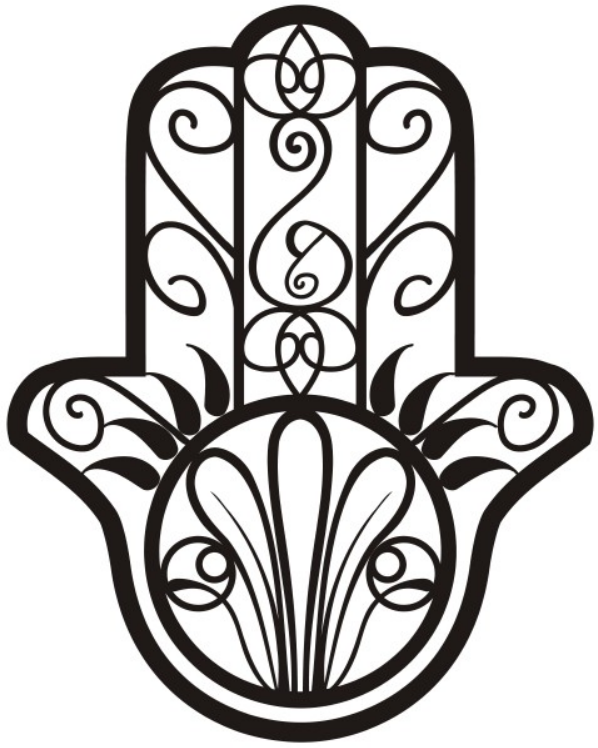
- Close to each other in structure.
- Element naming is poor.
- Solutions' space is not covered.

Contributions

- Four different measures for comparing models
- A method for comparing sets of models
- Select representative models (matrix clustering)
- Graphical viewing of covering (Voronoi diagrams)

Application

- Generate scaffold graphs in bio-informatics
- Improve diversity of generated models



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