

A Graph Database Repository and Performance Evaluation Metrics for Graph Edit Distance

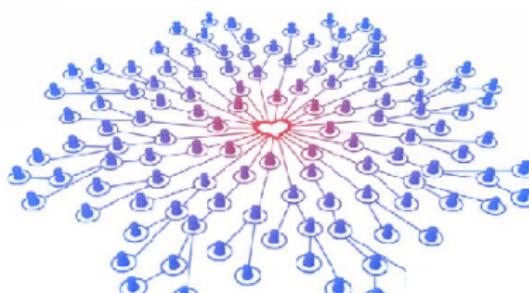
Zeina Abu-Aisheh, Romain Raveaux and Jean-Yves Ramel

Université de Tours - France
Equipe RFAI du Laboratoire Informatique (LI)

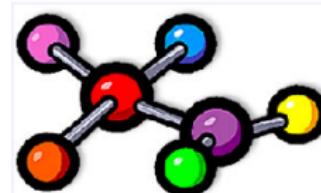
May 14, 2015



"Real-world graphs are everywhere" but how to compare them?



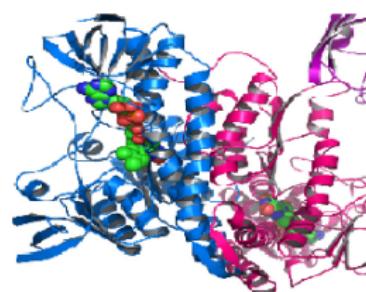
Social Networks



Chemical Bounds

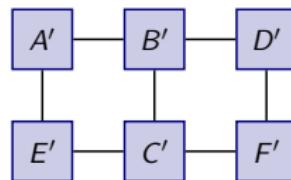
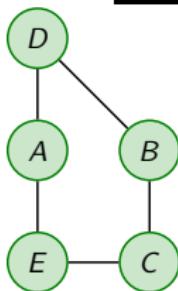


Characters

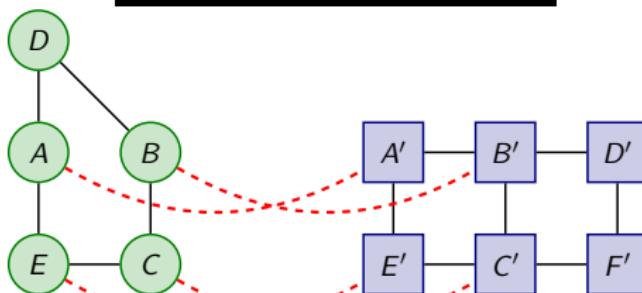


Protein Structures

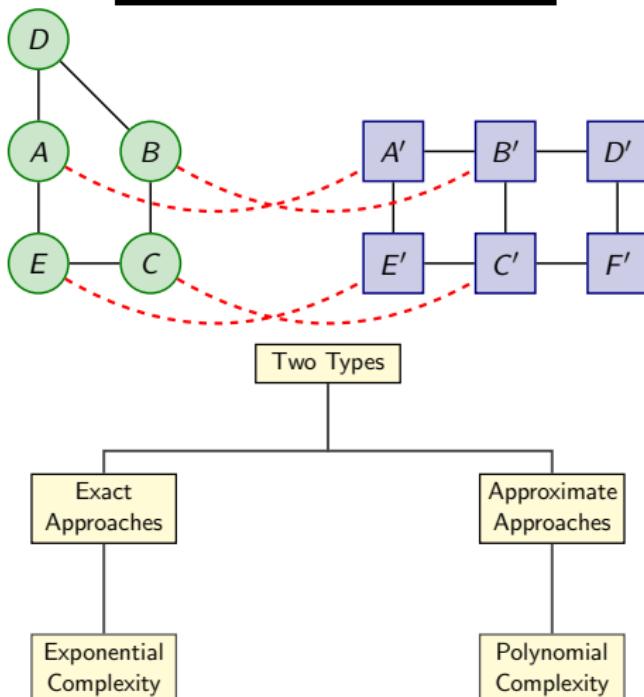
Inexact Graph Matching



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Inexact Graph Matching



Raised Questions

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- **Q1: How to evaluate error tolerant graph comparison methods ?**

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 - Speed.

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- **Q1: How to evaluate error tolerant graph comparison methods ?**
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- Q2: How to choose graph matching databases?

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- **Q2: How to choose graph matching databases?**
 - Graphs size.

Raised Questions

■ Q2: How to choose graph matching databases?

- Graphs size.
- Graphs types:
 - ★ Different typologies (dense, sparse, etc.).
 - ★ Different kinds of attributes (nominal, numeric, etc.).

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- Graphs size.
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- Applications types:
 - ★ Not only databases dedicated to classification (e.g., IAM [Riesen2008]).

Raised Questions

■ Q2: How to choose graph matching databases?

- Graphs size.
- Graphs types:
 - ★ Different typologies (dense, sparse, etc.).
 - ★ Different kinds of attributes (nominal, numeric, etc.).
- Applications types:
 - ★ Not only databases dedicated to classification (e.g., IAM [Riesen2008]).
 - ★ Other databases dedicated to other applications (e.g., matching quality).

Outline

- 1 Introduction**
- 2 Related Works**
- 3 Graph Repository**
- 4 Performance Evaluation Metrics**
- 5 Use Case**
- 6 Conclusions and Perspectives**

Plan

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Graph Edit Distance

Graph Edit Distance

Let $g_m = (V_m, E_m, \mu_m, \zeta_m)$ be the model graph and $g_t = (V_t, E_t, \mu_t, \zeta_t)$ be the target graph. The graph edit distance between G_1 and G_2 is defined by:

$$d_{plain}(g_m, g_t) = \min_{e_1, \dots, e_k \in \gamma(g_1, g_2)} \sum_{i=1}^k c(e_i)$$



Figure: Graph Edit Distance operations

Related Works

Ref	Problem Type	Graph Type	Database Type	Measure Type	Purpose
Santo2003	Exact GM	Non-attributed	Synthetic	Accuracy and scalability	Matching
CMU DataBase	Error-tolerant GM	Attributed	Real-world	Memory consumption, accuracy and matching quality	Matching
Riesen2008	Error-tolerant GM	Attributed	Real-world	Accuracy and running time	Classification
Conte2007, Foggia2001	Exact GM	Attributed	Synthetic	Accuracy and scalability	Matching
Carletti2013	Exact GM	(Non)attributed	Real-world	Scalability	Matching

Table: Synthesis of graph databases.

CMU Database: <http://vasc.ri.cmu.edu/idb/html/motion>

Conclusions of the state of the art

- Lack of performance comparison measures for error-tolerant GM methods.

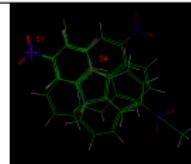
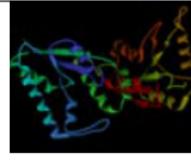
Conclusions of the state of the art

- Lack of performance comparison measures for error-tolerant GM methods.
- None of the repositories was dedicated to assessing the performance of GED.

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Databases

Database	Decomposition	Overview	Purpose
GREC	MIX, 5, 10, 15 and 20 vertices		Classification
MUTA	MIX, 10, 20, ... , 70 vertices		Classification
Protein	MIX, 20, 30 and 40 vertices		Classification
CMU	30 vertices		Matching

Databases

Database	# subsets	Max Graphs Size	# graphs per subset	# comparisons per subset	# optimal solutions
GREC	5 subsets	20	10 graphs	100	441
MUTA	8 subsets	70	10 graphs	100	189
Protein	5 subsets	40	10 graphs	100	47
CMU	1 subset	30	111 graphs	660	128

Table: Overview about the subsets included in the repository.

Repository link: [http://www.rfai.li.univ-tours.fr/
PagesPerso/zabuaisqueh/GED-benchmark.html](http://www.rfai.li.univ-tours.fr/PagesPerso/zabuaisqueh/GED-benchmark.html).

Added Low Level Information

- 6 methods:

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 - ★ Hausdorff [Fischer2013].

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- For each graph matching pair:

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 - Distance between each pair of graphs.

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G1Name	G2Name	Method	Distance	Optimal	Matching
image3.23	image3.25	BS-100	135.178	true	Vertex:0 → 0=37.476/ Vertex:1 → 1=6.519/ Vertex:2 → 2=32.070/ Vertex:4 → 4=34.409/ Vertex:3 → 3=24.703/ Edge:2 ↔ 3 → 2 ↔ 3 =0.0/ Edge:0 ↔ 4 → 0 ↔ 4=0.0

Table: Low level information (taken from the file GREC5.csv)

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- **Detailed answers:** <http://www.rfai.li.univ-tours.fr/PagesPerso/zabuaisqueh/GED-benchmark.html>.

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Performance Evaluation Metrics

- All metrics can be tested under:

Performance Evaluation Metrics

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Performance Evaluation Metrics

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- Given the reference answer R :

Performance Evaluation Metrics

- Given the reference answer R :
 - Deviation.

Performance Evaluation Metrics

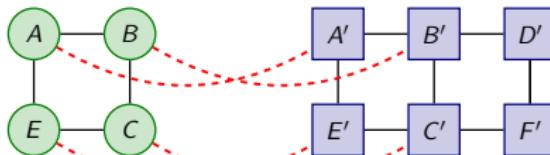
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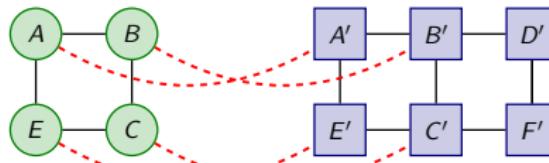
- Reference Distance (RD) = 5
- Reference Matching (RM):



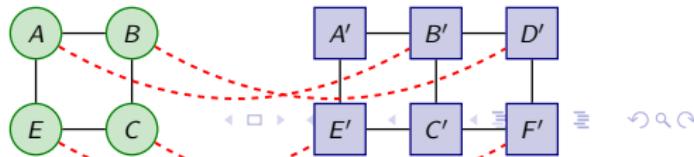
- Given the reference answer R :
 - Deviation.
 - Matching
 - Dissimilarity.

Performance Evaluation Metrics

- Reference Distance (RD) = 5
- Reference Matching (RM):



- Given the reference answer R :
 - Deviation.
 - Matching Dissimilarity.
- Distance found by method (m) = 6.
 - Deviation = 20%.
- Matching found by method (m):
 - Matching Dissimilarity = 75%.



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Performance Evaluation Metrics

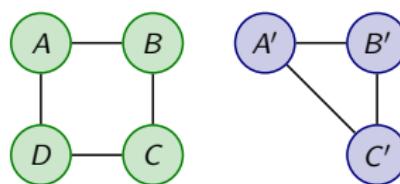
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- **Running time-Deviation plot:**

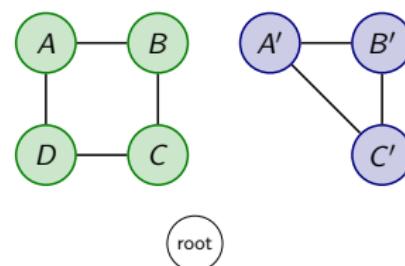
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 - Mean number of explored nodes.
 - Mean running time in milliseconds.
 - Running time-Deviation plot:
 - ★ Projection on a two-dimensional space (\mathbb{R}^2).

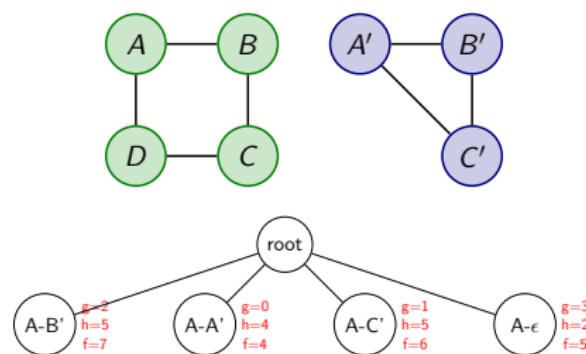
Performance Evaluation Metrics - Example



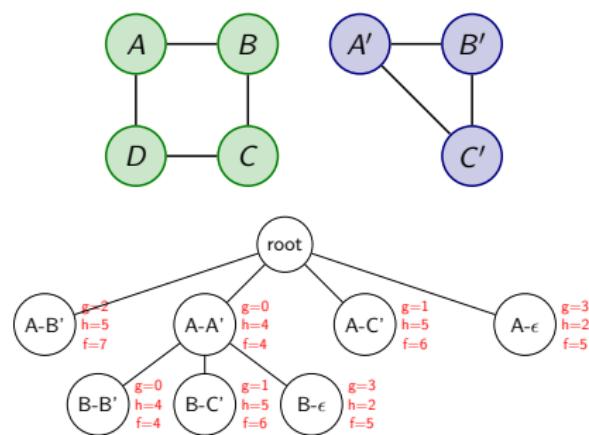
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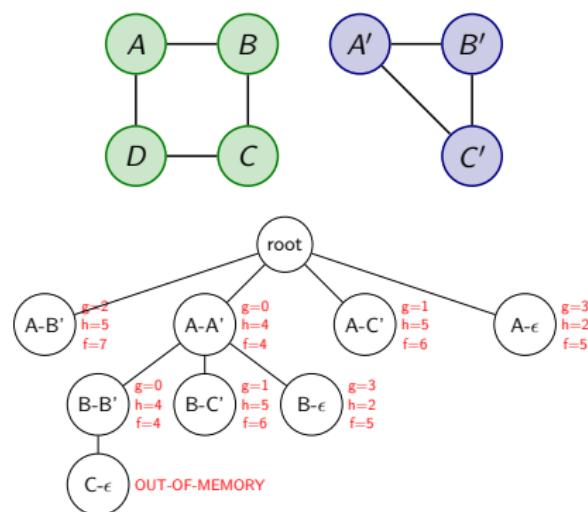
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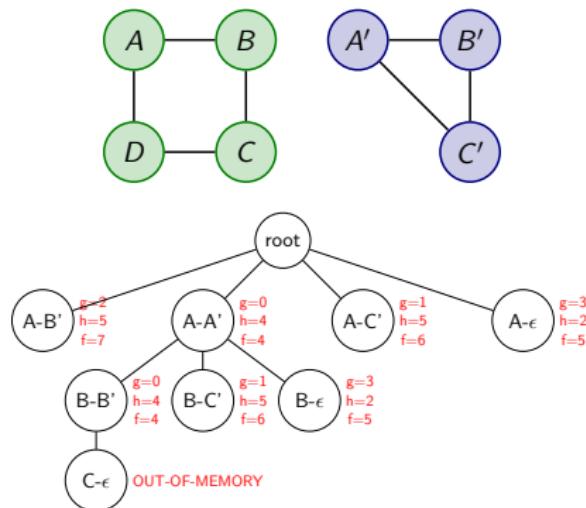
Performance Evaluation Metrics - Example



Performance Evaluation Metrics - Example



Performance Evaluation Metrics - Example



- Out-of-memory.
- Unfeasible solution.
- # of explored nodes = 3.

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Use Case

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■ Database: Mutagenicity.

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■ Constraints:

- $C_T = 300$ seconds.

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■ Database: Mutagenicity.

■ Constraints:

- $C_T = 300$ seconds.
- $C_M = 1024$ MB.

Results - Comparing with Reference Answers

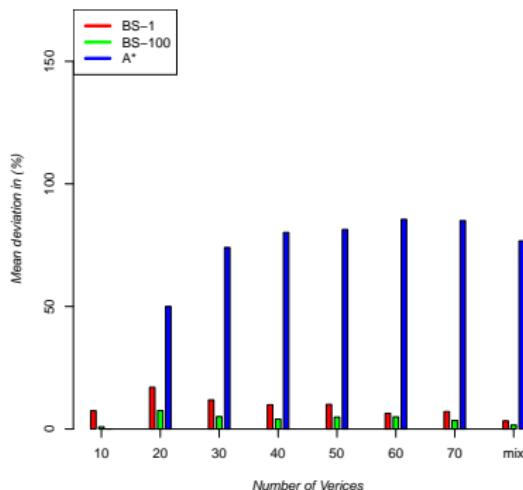


Figure: Deviation

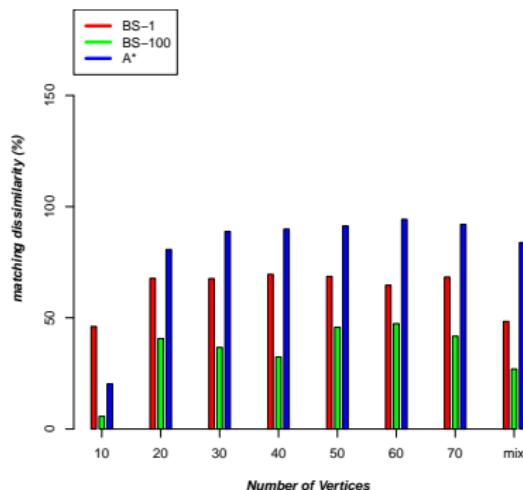


Figure: Matching Dissimilarity

The closer to 0, the better

Results - General Information

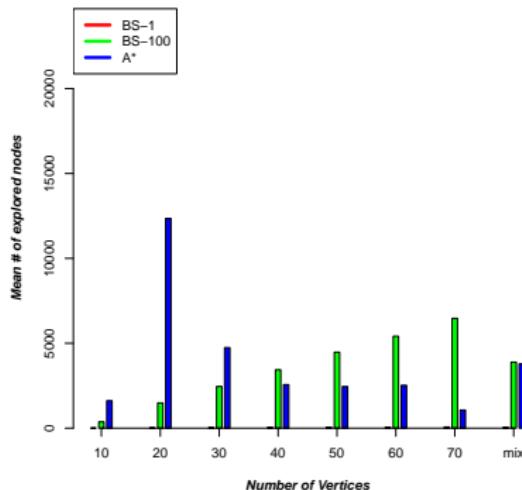


Figure: No of Explored Nodes

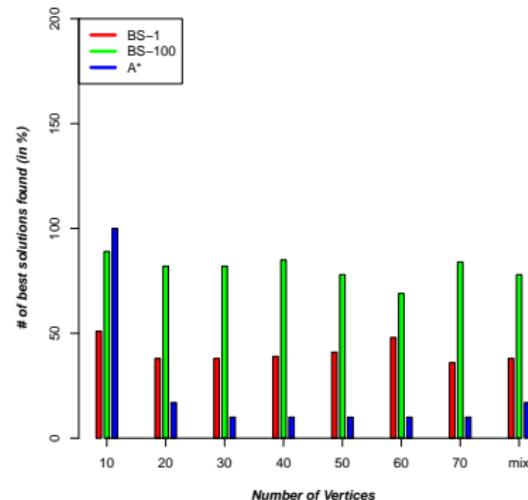


Figure: No of Best Found Solutions

Results - General Information

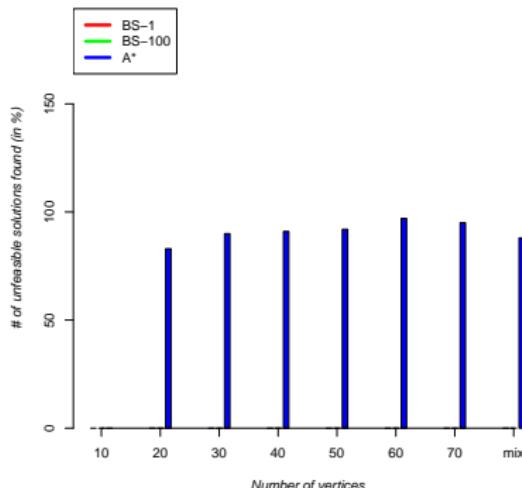


Figure: No of Unfeasible Solutions

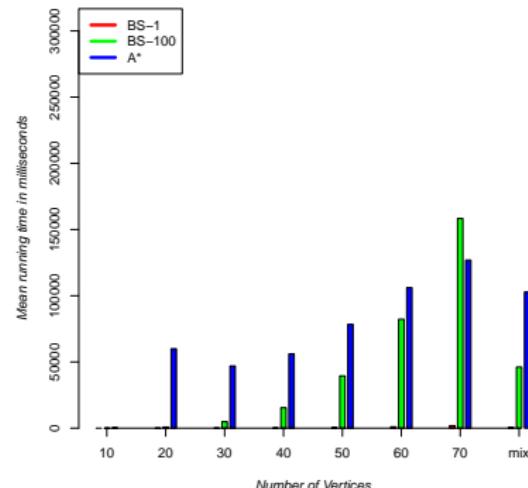


Figure: Running Time

Results - General Information

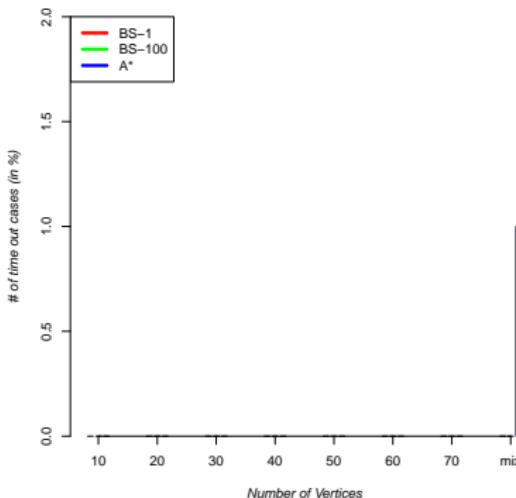


Figure: No of Time-Outs

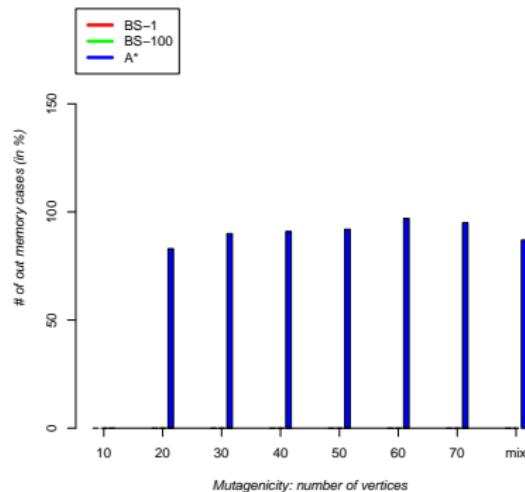
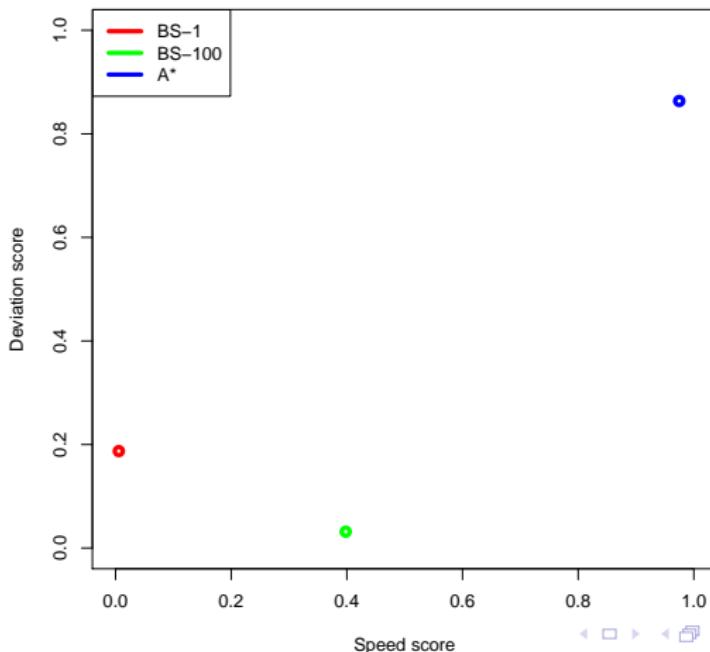


Figure: No of Memory-Outs

Results - Plot



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- **Additional low level annotation:**
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 - Four databases (GREC, Mutagenicity, Protein and CMU).

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 - Best distance and vertex-vertex matchings.
 - 6 methods (3 exact and 3 approximate).
 - Four databases (GREC, Mutagenicity, Protein and CMU).
 - **Scalability:** database decomposition.

Second Contribution

- **Performance evaluation metrics:**

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 - Under time and memory constraints.

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Second Contribution

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 - ★ **Deviation-Running time plot.**

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- **Metrics:**
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 - ★ Number of optimal solutions.

Perspectives

- Integrating better answers in the database (if found).

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- Expanding this repository by integrating other publicly available databases.

