



Finding Similar Stack Traces

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Software crash



Software crash



Crash Report

```
1 Date: 2016-01-20T22:11:48.834Z
2 Product: XXXXXXXXXXXXX
3 Version: 144.3143
4 Action: null
5 OS: Mac OS X
6 Java: Oracle Corporation 1.8.0_40-release
7 Message: new child is an ancestor
8
9 java.lang.IllegalArgumentException: new child is an ancestor
10   at javax.swing.tree.DefaultMutableTreeNode.insert(DefaultMutableTreeNode.java:179)
11   at javax.swing.tree.DefaultMutableTreeNode.add(DefaultMutableTreeNode.java:411)
12   at com.openapi.application.impl.ApplicationImpl$.run(ApplicationImpl.java:374)
   ....
41   at java.util.concurrent.ThreadPoolExecutor$Worker.run(ThreadPoolExecutor.java:617)
42   at java.lang.Thread.run(Thread.java:745)
43   at org.ide.PooledThreadExecutor$2$1.run ....
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Stack Trace

- Compare the similarity between stack traces (crash dumps)
 - Useful for call stacks
- Group stack traces
 - **Prioritization bug fixing**: focus on the most frequent and critical issues
 - **Problem diagnosis**: complementary information about an error



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TF-IDF

Stack trace

```
java.lang.ArrayIndexOutOfBoundsException: 4
  at sat4j.pb.PseudoOptDecorator.model(Unknown Source)
  at sat4j.pb.OptToPBSATAdapter.model(Unknown Source)
  at eclipse.Projector.backToIU(Projector.java:67)
  at eclipse.Projector.invokeSolver(Projector.java:64)
  at eclipse.SimplePlanner.getPlan(SimplePlanner.java:24)
  at eclipse.PatchTest3.testCompleteScenario(PatchTest3.java:90)
  at reflect.NativeMethodImpl.invoke0(Native Method)
  at reflect.NativeMethodImpl.invoke(NativeMethodImpl.java:39)
```

Bag of words - Method names



```
sat4j.pb.PseudoOptDecorator.model,
sat4j.pb.OptToPBSATAdapter.model,
eclipse.Projector.backToIU,
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reflect.NativeMethodImpl.invoke0,
reflect.NativeMethodImpl.invoke
```

TF-IDF

$$\textit{similarity} = \sum_{\textit{word} \in \textit{query}} \textit{term_freq}(\textit{word}, \textit{doc}) * \textit{IDF}(\textit{word}, \textit{doc})$$



TF-IDF

Problem: position information is lost



Optimal Global Alignment

- Equivalent to Edit Distance
- Find the best alignment between sequences
 - Dynamic programming



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Global Alignment Types

```
- - A B B B B D F  
C C A B B K - - -
```



Global Alignment Types

-	-	A	B	B	B	B	D	F
C	C	A	B	B	K	-	-	-

Alignment between an element and a gap



Global alignment

```
- - A B B B B D F  
C C A B B K - - -
```

Match



Global Alignment Types

```
- - A B B B B D F  
C C A B B K - - -
```

Mismatch



Optimal Global Alignment

- Query: (q_1, q_2, \dots, q_i)
- Candidate: (c_1, c_2, \dots, c_j)
- Matrix M :
 - $M_{i,j}$ = optimal alignment score between q_i and c_j
 - Bottom-up strategy to progressively create M



Optimal Global Alignment

$$M_{i,j} = \max \begin{cases} M_{i-1,j} - \text{gap_score}(q_i) \\ M_{i,j-1} - \text{gap_score}(c_j) \\ M_{i-1,j-1} + S(q_i, c_j) \end{cases}$$

q_i is aligned with gap

c_j is aligned with gap

q_i is aligned with c_j



Optimal Global Alignment

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Optimal Global Alignment

$$S(q_i, c_j) = \begin{cases} \text{match_score}(q_i, c_j), & \text{if } q_i = c_j \\ - \text{mismatch_score}(q_i, c_j), & \text{otherwise} \end{cases},$$



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Optimal Global Alignment

- **match_score, mismatch_score and gap_score** are fixed
- Ignore two important pieces of information:
 - ① **Rarity**: the alignment of rare methods should have a higher impact on the similarity
 - ② **Position**: first positions are more relevant than the last ones



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Our solution

We modify how `match_score`, `mismatch_score` and `gap_score` are computed



Our solution

- For each method in a stack trace (s_k)
 - ① Global weight (gw): importance of s_k in a database
 - ② Local weight (lw): importance of s_k in a stack trace



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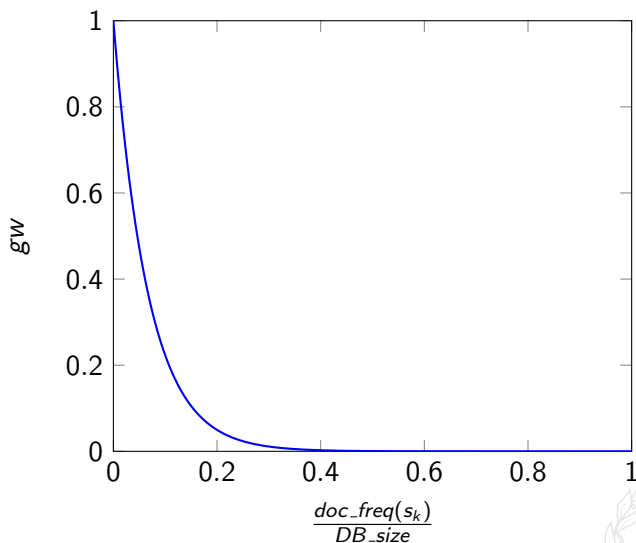


Global weight

$$gw(s_k) = e^{-\beta \frac{doc_freq(s_k)}{DB_size}}$$



Global weight: $\beta = 15$

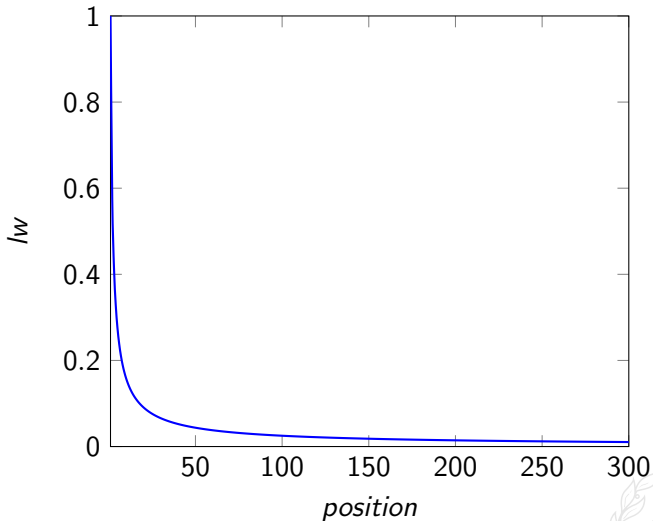


Local weight

$$lw(s_k) = k^{-\alpha}$$



Local weight: $\alpha = 0.8$



Frame weight

Frame weight: overall importance of a method

$$w(s_k) = lw(s_k) * gw(s_k)$$



Alignment Costs

- $gap_cost(s_k) = w(s_k)$
- $mismatch_cost(q_i, c_j) = w(q_i) + w(c_j)$
- $match_cost(q_i, c_j) = \max(w(q_i) + w(c_j)) * diff_pos(i, j)$



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Position Difference

$$\text{diff_pos}(i, j) = e^{-\gamma|i-j|}$$

Compare the matched frames positions



Experiments

- Task: Duplicate crash reports detection
- Datasets: Netbeans, Eclipse, OpenOffice, and Gnome
- 50 different runs
- Metrics
 - ① Area Under the ROC Curve (AUC)
 - ② Recall Rate@1 (RR@1): percentage of queries whose the first report in the recommend list is the correct duplicate.



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- Our method is compared to TF-IDF and Vanilla Optimal Global Alignment
 - Difference: ΔAUC and $\Delta RR@1$
 - Wilcoxon signed-rank test: statistical significance is indicated by ★



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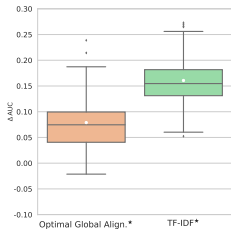
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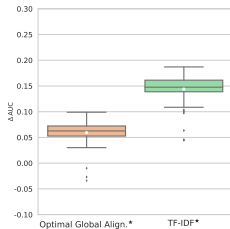
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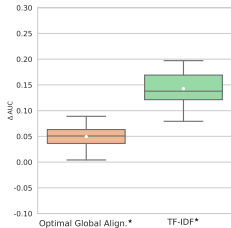


ΔAUC 

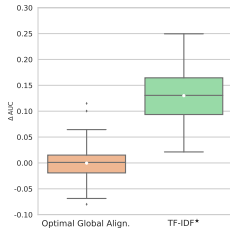
Ubuntu



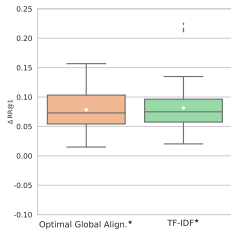
Eclipse



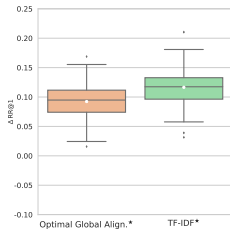
Netbeans



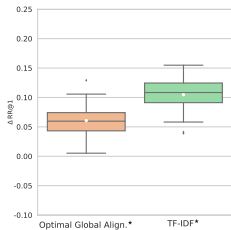
Gnome

$\Delta RR@1$ 

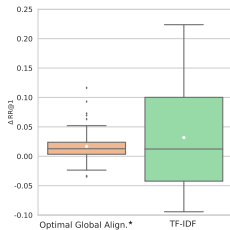
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Eclipse



Netbeans



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Concluding Remarks

- Our method significantly surpasses Vanilla Optimal Global Alignment and TF-IDF
- We developed a simple scheme to compute the alignment costs
 - 3 parameters
 - Computational cost is not significantly increased
- Unsupervised: parameter values might be manually chosen



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Future works

- Make our method available for our partners
 - Should we integrate it to a software?
 - Inputs and outputs?
- Please let us know how our method could be useful for your project!



Thank you for your attention!
Questions?

