

Graph Similarity Scoring

Applied to

Abstract Meaning Representation

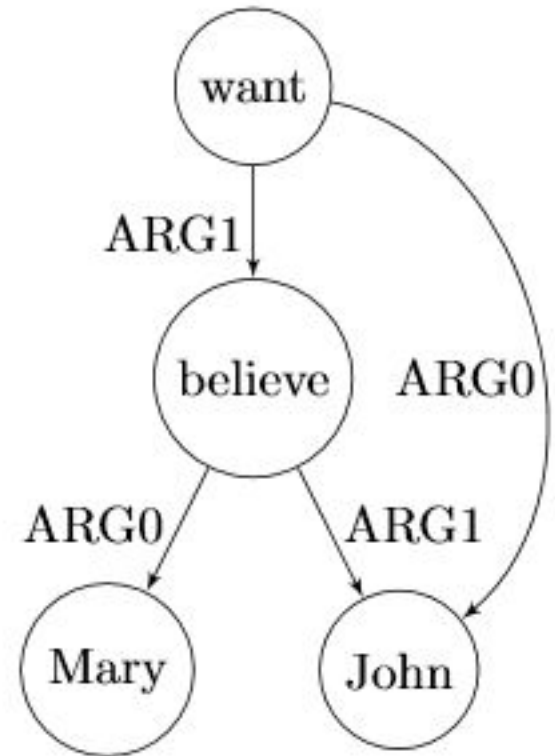
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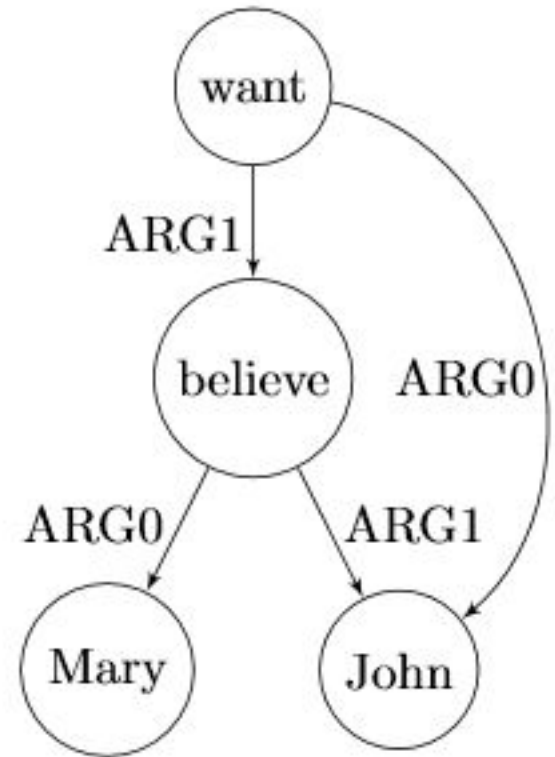
Abstract Meaning Representation (AMR)

- AMRs are a semantic formalism which models sentences



Abstract Meaning Representation (AMR)

- AMRs are a semantic formalism which models sentences
 - Nodes represent concepts
 - Edges represent relations between concepts
 - Semantic roles
 - ARG0 = Agent
 - ARG1 = Patient
 - Example AMR for sentence: “John wants Mary to believe him.”



Properties of AMRS as Graphs

- Some properties of AMRs
 - Directed Acyclic Graphs (DAGs)
 - Single rooted (focus of sentence)
 - Each AMR represents a sentence



Dataset

- Set of 10,312 AMRs from various news sources
- Average number of nodes is: 17.1
- Average number of edges is: 17.1
- More than half are trees



Kernel: Graph Similarity Scoring

- Use some AMRs for training
 - Given multiple candidate AMRs, choose best one
 - Need a way to score each choice
 - Want pairwise digraph similarity score
- Typical metric used for AMRs is SMATCH



SMATCH Score

- Semantic Match score
 - Find best matching of nodes
 - Score based on node and edge labels
 - F1 score
 - Node label
 - For each edge: edge type and end points



Basic Implementation Pseudocode

Algorithm 1 Basic SMATCH pseudocode

```
1: procedure GETSMATCH(A,B)
2:    $maxF1 \leftarrow 0$ 
3:   for mapping in nodeMapping(a,b) do
4:      $correct \leftarrow 0$ 
5:     for alignedPair in mapping do
6:       if labels match then
7:          $correct \leftarrow correct + 1$ 
8:     for edges in a do
9:       replace end-points with aligned nodes from b
10:      if new edge exists in b then
11:         $correct \leftarrow correct + 1$ 
12:       $precisionDenominator \leftarrow$  number of triples in b
13:       $recallDenominator \leftarrow$  number of triples in a
14:       $precision \leftarrow correct/precisionDenominator$ 
15:       $recall \leftarrow correct/recallDenominator$ 
16:       $f1 \leftarrow (recall + precision)/2$ 
17:      if  $f1 > maxF1$  then
18:         $maxF1 \leftarrow f1$ 
19:   return  $maxF1$ 
20: procedure NODEMAPPING(A,B)
21:   allAlignments  $\leftarrow$  empty
22:   Select  $node_a$  in a
23:   for  $node_b$  in b do
24:     newAlignments  $\leftarrow$  align  $node_a$  to  $node_b$ 
25:      $newA \leftarrow a - node_a$ 
26:      $newB \leftarrow b - node_b$ 
27:     newAlignments  $\leftarrow$  nodeMapping( $newA, newB$ )
28:     append newAlignments to allAlignments
29:   return allAlignments
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**Find all ways to
match nodes in A
with nodes in B**

Basic Implementation Pseudocode

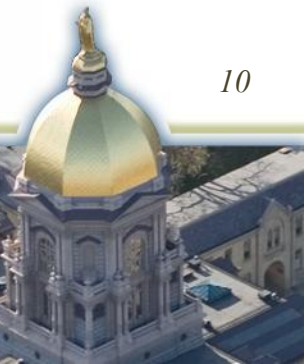
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Check if node labels match and if edge labels match

Complexity

- Most direct way (previous slide) has complexity $\sim O(N!/(N-M)! * |M+E|)$
 - N = number of nodes in larger graph
 - M = number of nodes in smaller graph
 - E = number of edges in smaller graph
- In practice, heuristics are used
 - Faster, but no optimality guarantee
 - I want to avoid heuristics



Improvements

- Combine mapping and scoring
 - Score nodes as they are matched
 - Avoids recomputing
- Score likely alignment first, use as cutoff
 - Number incorrect is cutoff threshold
 - Can avoid unnecessary computation
- Send subgraphs to worker processes for parallelism



New Complexity

- Previously $\sim O(N!/(N-M)! * |M+E|)$
- Now $\sim O(N!/(N-M)! * |E|)$ in worst case, $\sim O(N!/(N-M)!)$ in average case
- Worst case complexity not improved greatly
- Better in practice using cutoff to eliminate parts of search space
- Effectiveness increases as SMATCH increases



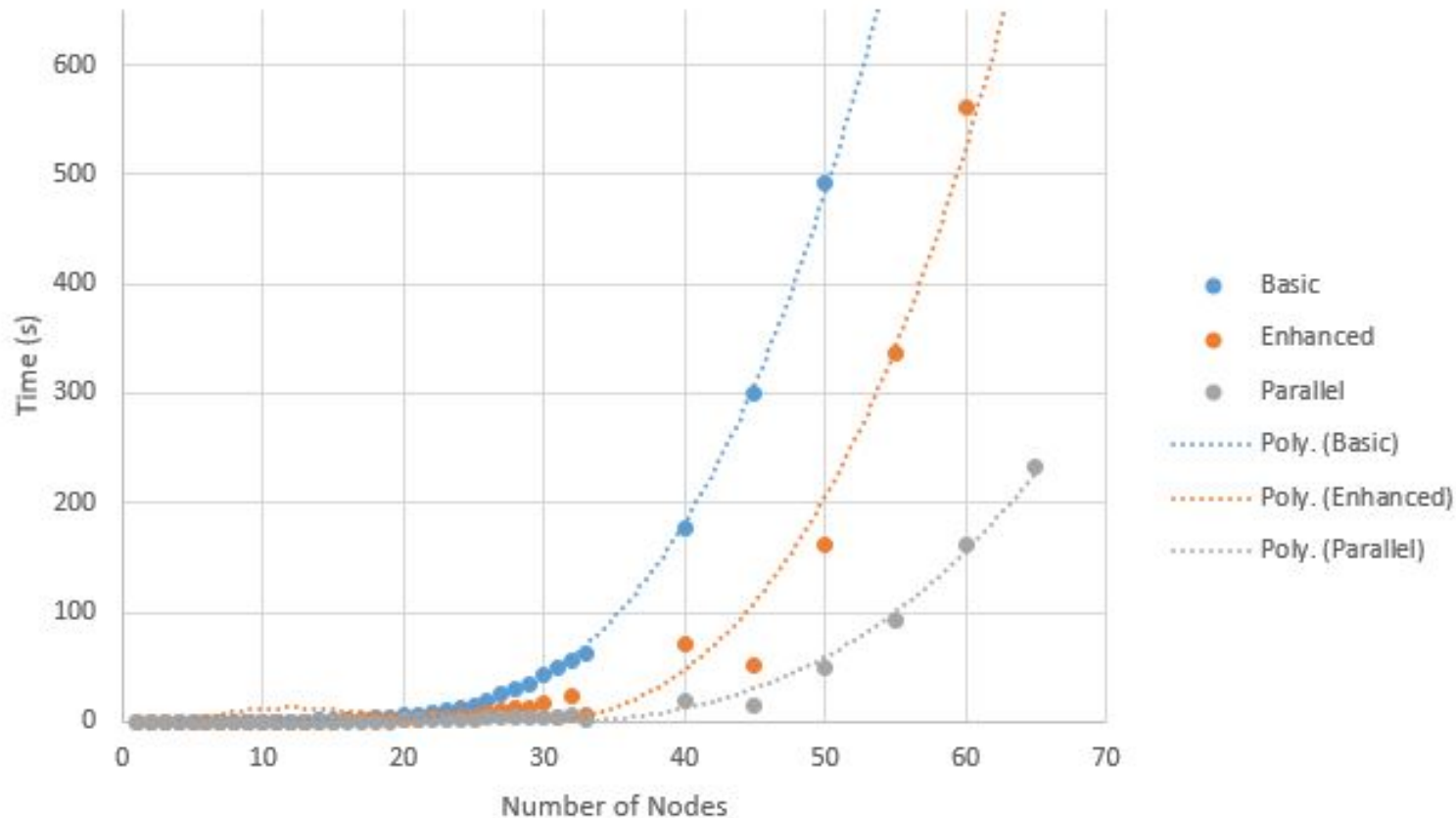
Implementation

- Implemented in Python 2.7
- Uses NetworkX
- Uses Multiprocessing library
- ~500 lines of code (separate functions for basic vs enhanced vs parallel, so some repetition)

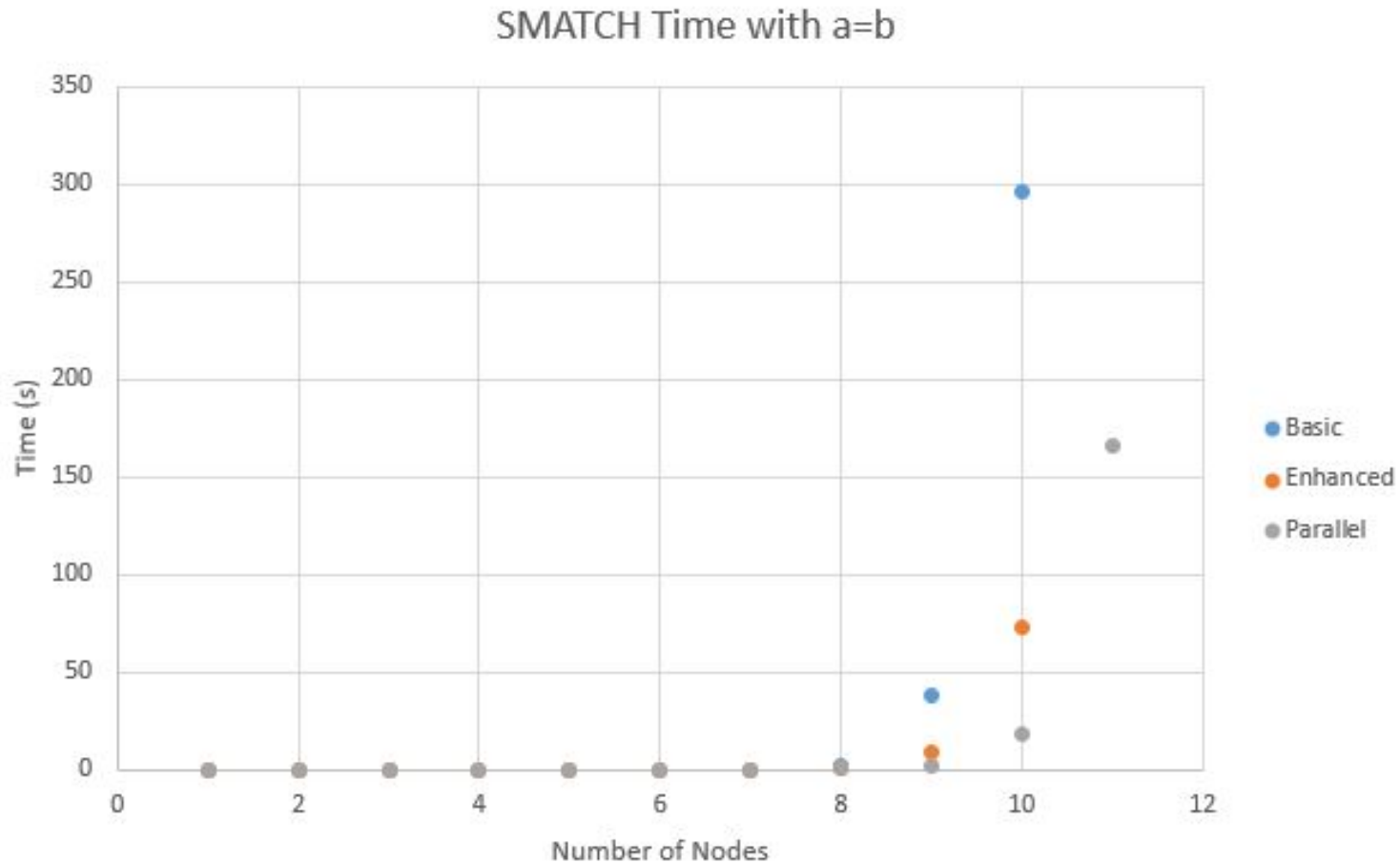


Timing Results

SMATCH Time with 4 node AMR



Timing Results

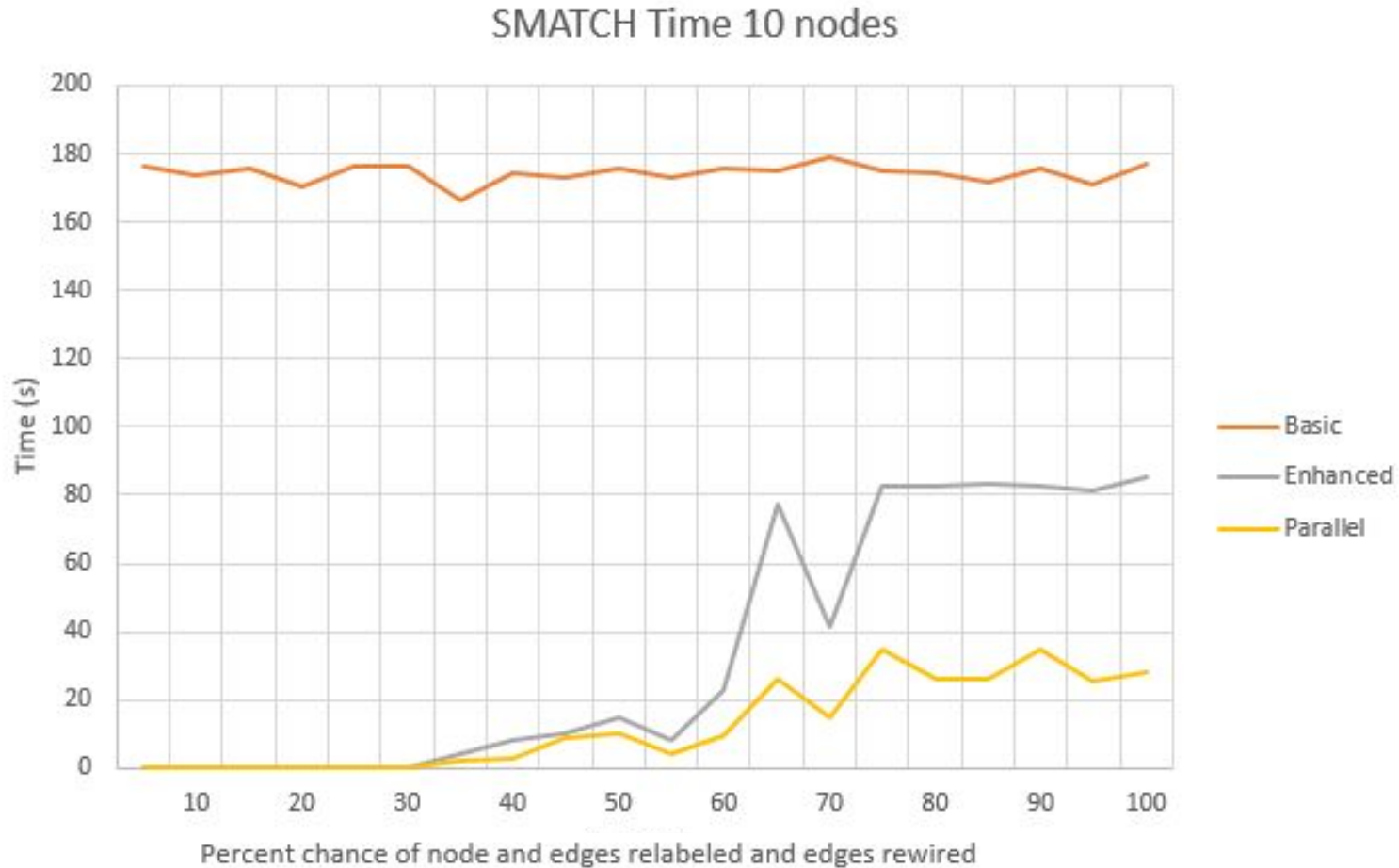


Generating Candidate AMRs

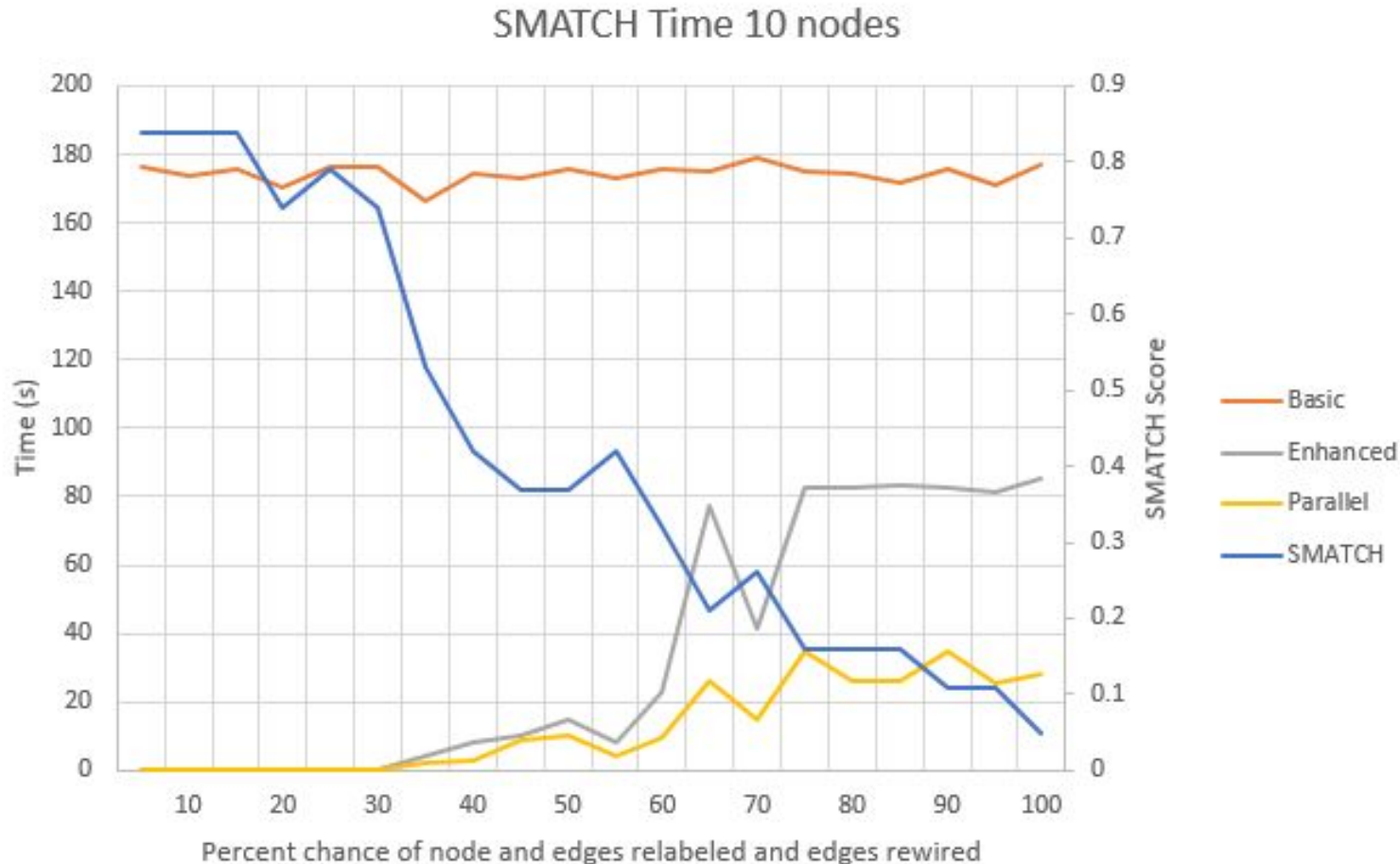
- In practice we use SMATCH on AMRs that are similar
- Imitate this by randomly rewiring edges, relabeling edges, and relabeling nodes



Timing Results



Timing Results



Conclusions

- While the worst case complexity remains bad, typical use can be made much better
- Prune search space by not pursuing bad subgraphs
- Parallelize subgraph search
- Most effective when candidate is close to correct (high SMATCH)

