SMARAGD\textcolor{green}{\textbullet}: Synthesized sMatch for Accurate and Rapid AMR Graph Distance

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Abstract

The semantic similarity of graph-based meaning representations, such as Abstract Meaning Representation (AMR), is typically assessed using graph matching algorithms, such as SMATCH (Cai and Knight, 2013). However, SMATCH suffers from NP-completeness, making its large-scale application, e.g., for AMR clustering or semantic search, infeasible.

To mitigate this issue, we propose SMARAGD\textcolor{green}{\textbullet} (Synthesized sMatch for accurate and rapid AMR graph distance). We show the potential of neural networks to approximate the SMATCH scores and graph alignments, i) in linear time using a machine translation framework to predict the alignments, or ii) in constant time using a Siamese CNN to directly predict SMATCH scores. We show that the approximation error can be substantially reduced by applying data augmentation and AMR graph anonymization.

1 Introduction

Abstract Meaning Representation (AMR) (Banerrescu et al., 2013) represents the meaning of sentences in a graph format. The directed, rooted and acyclic AMR graph indicates the events and entities of a sentence, showing semantic roles and other key relations such as cause, time, purpose, instrument, etc. Because of these properties, AMR graphs are potentially useful for many natural language processing tasks: E.g., AMR has been used for summarization (Liu et al., 2015; Dohare et al., 2017; Liao et al., 2018) and Machine Translation (Song et al., 2019).

Often, pairs of AMRs need to be studied, using AMR metrics. Classically, AMRs are compared to assess Inter Annotator Agreement in SemBanking or for the purpose of parser evaluation, e.g., using the structural SMATCH metric (Cai and Knight, 2013). Going beyond these applications, researchers have leveraged SMATCH-based AMR metrics for NLG evaluation (Opitz and Frank, 2021; Manning and Schneider, 2021), as a basis for a COVID-19 semantics-based search engine (Bonial et al., 2020), comparison of cross-lingual AMR (Uhrig et al., 2021), and fine-grained argument similarity assessment (Opitz et al., 2021b). Many of these extended scenarios, such as AMR-based corpus search (Bonial et al., 2020), greatly profit from a quick similarity computation.

But AMR graph metrics typically suffer from a great time-complexity: Computation of SMATCH is NP-hard (Nagarajan and Sviridenko, 2009), and it can take more than a minute to compare some 1,000 AMR pairs (Song and Gildea, 2019). To understand that this can become problematic in many setups, consider a hypothetical user who desires exploring a (small) AMR-parsed corpus with only \(n = 1,000\) instances via clustering. The (symmetric) SMatch metric needs to be executed over \((n^2 - n)/2 = 499,500\) pairs, resulting in a total time of more than 6 hours. Given recent interest into meaning representations that cover multiple sentences, such as multi-sentence AMR (O’Gorman et al., 2018), dialogue AMR (Bonial et al., 2021) or discourse representation structures (Kamp, 1981), where the alignment search space is much larger (van Noord et al., 2018), we can anticipate that this problem will aggravate in the future.

Testing ways to mitigate these issues, we propose a method that learns to match AMR graphs from a teacher SMATCH, thereby reducing AMR clustering time from hours to seconds.

Our contributions are:

1. We explore three different neural approaches to synthesize the canonical AMR metric SMATCH from scratch.
2. We show that we can approximate SMATCH up to a small error, by leveraging novel data augmentation tricks.

Our code will be publicly released.
2 Related work

AMR similarity Recently, researchers have proposed AMR metrics beyond SMATCH. We can distinguish two branches: i) metrics that aim at extreme efficiency by skipping the alignment and extracting structure-sets from AMRs via breadth-first traversal (Song and Gildea, 2019; Anchiêta et al., 2019). ii) Wasserstein-alignment based and Weisfeiler-Leman graph metrics that aim to reflect human similarity ratings (Opitz et al., 2021a). Note that Opitz et al. (2020) show that skipping the alignment step risks safety hazards in parsing evaluation, underlining the importance of graph alignment.

Algorithm synthesis Researchers have sought to synthesize other algorithms. E.g., Parisotto et al. (2016); Chen et al. (2018); Austin et al. (2021) use neural networks to synthesize computer programs. Lample and Charton (2019) show that neural networks can be surprisingly good at more elaborated tasks in mathematics, such as symbolic integration. Work from other fields synthesize algorithms for tracking aircraft (Pudovkin et al., 2018), controlling wind-turbines (Saenz-Aguirre et al., 2019), or medical image analysis (Lee et al., 2018). The ‘long-range arena’ benchmark (Tay et al., 2021) for long-sequence models also includes synthesizing tasks, e.g., ‘listOps’ (learning to calculate) and Xpath (tracing a squiggly line), which prove challenging even for SOTA architectures.

3 Learning NP-hard graph alignment

The SMATCH metric measures the structural overlap of two AMRs. We i) compute an alignment between variable nodes of AMRs and ii) assess triple matches based on the provided alignment. Formally, we start with two AMR graphs $G$ and $G'$ with variable nodes $X = (x_1,...,x_n)$ and $Y = (y_1,...,y_m)$. The goal is then to find an optimal alignment:

$$map : X \rightarrow Y, \quad (1)$$

searching for a $map$ that maximizes the number of triple matches for the two graphs. E.g., assume $(a, ARG0, b) \in G$ and $(c, ARG0, d) \in G'$. If $a = c$ and $b = d$, we count one triple match. Finally:

$$SMATCH = \max_{map} score(G, G', map) \quad (2)$$

Researchers typically use a harmonic mean based overlap $score = F1 = 2PR/(P + R)$, where $P = (triples(G) \cap triples(G'))/triples(G)$ and $R = (triples(G) \cap triples(G'))/triples(G')$.  

3.1 Setup

Experimental data creation We create training, development and testing data as follows: 1. We parse 59,255 sentences of the LDC2020T02 data with a parser (Lyu and Titov, 2018) to obtain graph pairs that can be aligned; 2. For every parallel graph pair $(G, G')$, we use SMATCH (ORACLE) to compute an F1 score $s$, and the alignment $a$. Thus, our data set is $\{(G_i, G'_i, a_i, s_i)\}_{i=1}^n$. We shuffle the data and split it into training, development and test set (54255-2500-2500).

Objective and approach The task is to reproduce the teacher ORACLE as precisely as possible. We design and test three different approaches. The first is indirect, in that it predicts the alignment, from which we compute the score. The second directly predicts the scores. The third approach enhances the second, to make it even more efficient.

3.2 Synthesis option I: Learning SMATCH alignment explicitly

Here, we aim to synthesize the alignment itself (Eq. 1) into an NMT model, as illustrated in Figure 1. The input to the model is as follows: we linearize the two AMRs and concatenate the linearized token sequences with a special $<$SEP$>$ token. The output consists of a sequence $x_1;y_k;...;x_i;y_m;...$ where in every pair $i:u$, $u$ is a variable node from the first AMR, which is mapped to a node $v$ from the second AMR. The SMATCH score is then calculated based on the predicted alignment.

To predict the node alignments/mapping of variables, we use a transformer based encoder-decoder NMT model. Details about the network structure and hyperparameters are stated in Appendix A.1.

3.3 Synthesis option II: Learning SMATCH alignment implicitly

In this setup, we aim to predict SMATCH F1 scores for pairs of AMRs directly, in a single step. This means that we directly synthesize Eq. 2 into a neural network and our target is the ORACLE F1 score.

To facilitate this mapping, we adapt the convolutional neural network (CNN) of Opitz (2020), as shown in Figure 2. The model was originally intended to assess AMR accuracy (Opitz and Frank,
2019), i.e., measuring AMR parse quality without a reference. Taking inspiration from human annotators, who exploit a spatial ‘Penman’ arrangement of AMR graphs for better understanding, it models directed-acyclic and rooted graphs as 2d structures, employing a CNN for processing. To feed a pair of AMRs, we remove the dependency encoder of the model and replace it with an AMR graph encoder. Moreover, we increase the depth of the network by adding one additional MLP layer after convolutional encoding. A standard mean squared error is employed as loss function. More details about hyperparameters are stated in Appendix A.2.

3.4 Synthesis option III: tuning AMR vectors with SMATCH distance

Inspired by Reimers and Gurevych (2019), we aim to make the CNN even more efficient, by alleviating the need for pair-wise model inferences. Hence, instead of computing a shared representation of two CNN-encoded AMRs, we process each representation with an MLP (w/ shared parameters), to obtain two AMR vectors $NN(G)$ and $NN(G')$. These vectors are then tuned with a distance loss $\mathcal{L}$ against ORACLE $s$:

$$\mathcal{L} = \sum_{(G,G',s)} \left( 1 - |NN(G) - NN(G')| - s \right)^2$$

This approach enables extremely fast search and clustering: the required (clustering-)model inferences are $O(n)$ instead of $O(n^2)$, since the similarity is achieved with simple linear vector algebra.

3.5 Data compression and extension tricks

Vocabulary reduction trick We observe that SMATCH is a metric that measures the structural overlap of two graphs. This means that we can greatly reduce our vocabulary, by assigning each graph pair a local vocabulary (see Figure 3, ‘anonymize’). First, we gather all nodes from AMR pairs $a$ and $b$, computing a joint vocabulary over the concept nodes. We then relabel the concepts with integers starting from 1. E.g., consider AMR $a$: (r / run-01 :ARG0 (d / duck)), and AMR $b$: (x / run-01 :ARG0 (y / duck) :mod (z / fast)). The best alignment is $map^* = \{(r,x),(d,y),(\emptyset,z)\}$. Now, we set the shared concepts and relations to the same index $run=run=1$ and $duck=duck=2$ and $:ARG0=:ARG0=3$ and distribute the rest of the indices $r=4, d=5, x=6, y=7, z=8, fast=9, :mod=10$. This yields equivalent AMRs $a' = (4 / 1 :3 (5 / 2))$ and $b' = (6 / 1 :3 (7 / 2)) :10 (8 / 9)$. The target alignment then equals $map^* = \{(4,6),(5,7),\emptyset,8\}$. This strategy greatly reduces the vocabulary size, in our case from 40k tokens to less than 700.

Auxiliary data creation trick We also find that we can cheaply create auxiliary gold data. We
We expect that, with this strategy, the model will directly obtain the estimated $S^*$, which in turn will help it synthesize the algorithm.

From a random alignment (Fig. 3, ‘permute’). In our experiments, we permute the existing token-index vocabularies 10 times, resulting in a ten-fold increase of the training data. We expect that, with this strategy, the model will better learn properties of permutation invariance, which in turn will help it synthesize the algorithm.

3.6 Evaluation

Output post-processing In the implicitly synthesized alignment algorithm (score & vector synthesis), no further post-processing is required, since we directly obtain the estimated SMATCH scores as output. In the explicitly synthesized alignment algorithm, however, we get \( \text{map} \), which is the predicted alignment from the sequence-to-sequence model. In this case, we simply feed \( \text{map} \) as an argument into Eq. 2, to obtain the scores.

Evaluation We compare the predicted scores \( \hat{y} \) against the gold scores \( y \) with Pearson’s \( \rho \). However, for the model that predicts the explicit alignment (synthesizer I), we can compute another interesting and meaningful metric. For this, we first calculate the average SMATCH score over AMR pairs given the gold alignment \( \text{map}^* \), and then we calculate the average SMATCH score over AMR pairs given the predicted alignment \( \hat{\text{map}} \). Note, that the SMATCH score based on the gold alignment constitutes an upper bound (\( \text{max} \)). Therefore, the SMATCH score based on the predicted alignment shows us how close we are to this upper bound. Our baseline consists of scores that are computed from a random alignment (random).

| data trick     | SMATCH | Pea’s \( \rho \) | time (secs) |
|---------------|--------|-----------------|-------------|
| ORACLE        | na     | 77.5            | 100         | 28680       |
| rand. baseline| na     | 13.5            | 22.2        | 0.4         |
| align. synthesis | na     | 39.0            | 52.8        | 1089        |
| align. synthesis | voc   | 64.5            | 80.0        | 1089        |
| align. synthesis | voc+aug | 76.4        | 98.4        | 1089        |
| score synthesis | na     | 87.5            | 140         |
| score synthesis | voc   | 82.0            | 140         |
| score synthesis | voc+aug | 96.8        | 140         |
| vector synthesis | na     | 84.7            | 0.7         |
| vector synthesis | voc   | 75.6            | 0.7         |
| vector synthesis | voc+aug | 94.2        | 0.7         |

Table 1: Results of experiments. time: Approximate time for computing a pair-wise distance matrix on 1k AMRs on a TI 1080 GPU.

Results (Table 1) Our best model is the NMT approach using both data augmentation tricks. Obtaining 98.4 \( \rho \), it very closely approximates the ORACLE, while being about 30 times faster than ORACLE and 76.2 points better then the random baseline. Perhaps the best tradeoff between speed and approximation performance is gained by the simple CNN score synthesis (96.8 \( \rho \), 200x faster than ORACLE), also using both data tricks. The vector synthesizer falls a bit shorter in performance (94.2 \( \rho \)), but it is extremely fast and achieves a 40,000x speed-up compared to ORACLE and about 1500x compared to the NMT approach.

Consistently, the data extension \( \text{(aug)} \) is very useful. On the other hand, the vocabulary reduction \( \text{(voc)} \) is only useful for the NMT model (+27.2 points), whereas the scores are lowered for the CNN-based models (−5.5 for score synthesis, −9.1 for vector synthesis). We conjecture that the CNNs learn SMATCH more indirectly by exploiting token similarities in the global vocabulary, and therefore struggle more to understand the algorithm itself, in contrast to the heavily parameterized NMT transformer that can learn to assess tokens fully from their given graph context.

4 Conclusion

We proposed methods to synthesize the NP-hard AMR alignment algorithm SMATCH, exploring different neural architectures, and data augmentation strategies that help all models to generalize. Our best models increase SMATCH calculation speed by a large factor while incurring only small losses in accuracy that can be tolerated in many use cases.
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| parameter          | value                                                                 |
|--------------------|----------------------------------------------------------------------|
| embedding size     | 512                                                                  |
| encoder            | 4 transformer layers w/ 4 heads                                      |
| decoder            | 4 transformer layers w/ 4 heads                                      |
| feed forw. dim     | 2048                                                                 |
| loss               | cross-entropy                                                        |
| weight init        | xavier                                                               |
| optimizer          | adam                                                                  |
| learning rate      | 0.0002                                                               |
| batch size         | 8192 (tokens)                                                        |

Table 2: Overview of NMT hyper-parameters.

| parameter          | value                                                                 |
|--------------------|----------------------------------------------------------------------|
| emb. dimension     | 100                                                                  |
| 'pixels'           | 60x15                                                                |
| CNN encoder        | concatenate(256 3x3 convs, 3x3 max pool, 128 5x5 convs, 5x5 max pool) |
| MLP                | relu layer followed by linear regressor                               |
| weight init        | xavier                                                               |
| optimizer          | adam                                                                  |
| learning rate      | 0.001                                                                |
| batch size         | 64                                                                   |

Table 3: Overview of CNN hyper-parameters.

A Appendix

A.1 Sequence-to-sequence network parameters

Hyper-parameters for the NMT approach are displayed in Table 2. The best model is determined on the development data by calculating BLEU against the reference alignments.

A.2 CNN network parameters

Hyper-parameters for the CNN approach are displayed in Table 2. The best model is determined on the development data by calculating Pearson’s $\rho$ correlation of predicted scores and gold scores.