# AMR Normalization for Fairer Evaluation

Michael Wayne Goodman goodmami@uw.edu Nanyang Technological University, Singapore 2019-09-13

#### Introduction: AMR, PENMAN, and Smatch

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#### Abstract Meaning Representation

- Compact encoding of sentential semantics as a DAG
- Independent of any syntactic analyses
- Hand-annotated gold data: some free, most LDC
- The "Penn Treebank of semantics" (Banarescu et al., 2013)

#### Example

"I had let my tools drop from my hands."
 (The Little Prince Corpus, id: lpp\_1943.355)

```
(l / let-01
  :ARG0 (i / i)
  :ARG1 (d / drop-01
        :ARG1 (t / tool
            :poss i)
        :ARG3 (h / hand
            :part-of i)))
```

# **PENMAN** Notation

### AMR is encoded in PENMAN notation

- l is node id, let-01 is node label, :ARG0 is edge label
- Bracketing alone forms a tree
  - Node ids allow re-entrancy
  - Inverted edges (:part-of) allow multiple roots

Triples

#### PENMAN graphs translate to a conjunction of triples

```
(l / let-01
   :ARG0 (i / i)
   :ARG1 (d / drop-01
            :ARG1 (t / tool
                      :poss i)
            :ARG3 (h / hand
```

instance(l, let-01) ^ ARG0(l, i) ^ instance(i. i) ^ ARG1(l. d) ^ instance(d, drop-01)  $ARG1(d. t)^{-1}$ instance(t, tool) ^ poss(t. i) ^  $ARG3(d, h)^{-1}$ instance(h, hand) ^ :part-of i))) part-of(h, i)

### What is AMR beyond PENMAN graphs?

- AMR is the model, PENMAN the encoding scheme
- Made up of "concepts" (nodes) and "relations" (edges)
- Verbal concepts taken from OntoNotes (Weischedel et al., 2011), others invented as necessary
- $\cdot\,$  Defined by the AMR Specification  $^1$  and annotator docs
- Mostly finite inventory of roles (except :opN, :sntN)
- Constraints (e.g., no cycles), and valid transformations (inversions, reification)

<sup>&</sup>lt;sup>1</sup>https://github.com/amrisi/amr-guidelines/blob/master/amr.md

### Smatch

# Smatch is the prevailing evaluation metric for AMR

- For two AMR graphs, find mappings of node ids
- Choose the mapping that maximizes matching triples
- Calculate precision, recall, and F1 (the Smatch score)
- Example:

```
(s / see-01 (s / see-01
:ARG0 (g / girl) :ARG1 (d / dog :quant 2)) (s / see-01
:ARG0 (g / girl) :ARG0 (g / girl)
:ARG1 (c / cat))
```

Left: 7 triples, Right: 6, Matching: 5 Precision: 5/7 = 0.71; Recall: 5/6 = 0.83; F1 = 0.77

# What's the Problem?

AMR has alternations that are meaning-equivalent according to the specification

- Some idiosyncratic role inversions, e.g.:
  - .:mod <-> :domain
  - · :consist-of <-> :consist-of-of
- Edge reifications, e.g.:

(a / ... :cause (b / ...)

...can reify **:cause** to...

```
(a / ...
:ARG1-of (c / cause-01
:ARG0 (c / ...)))
```

 $\cdot$  These result in differences in the triples, and thus the Smatch score

There is no partial credit for almost-correct triples

	Gold		Нур1	Hyp2		
( c	/ chapter	(c	/ chapter	(c / chapter)		
	:mod 7)		:quant 5)			
	CAMR		JAMR	AMREager		
( c	/ chapter	(c	/ chapter	(c / chapter		
	:quant 7)		:li 7)	:op1 7)		

- Getting the role wrong (CAMR, JAMR, AMREager) gets the same score as getting both the role and value wrong (Hyp1)
- Omitting the relation altogether (Hyp2) yields a higher score than having an incorrect relation.

### Some "equivalent" alternations are invalid graphs

Gold Bad (c / chapter (c / chapter :mod 7) :domain-of 5)

• If :domain-of is inverted, then 5 must be a node id, but it is a constant.

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Question: Can we address these problems in evaluation by normalizing the triples?

### Meaning-preserving normalization:

- Canonical Role Inversion
- Edge Reification

### Meaning-augmenting normalization:

- Attribute Reification
- Structure Preservation

### Replace non-canonical role with canonical ones

- .:mod-of -> :domain
- · :domain-of -> :mod
- · :consist -> :consist-of-of
- etc.
- (Also useful for general data cleaning)

Always reify edges

```
(d / drive-01)
  :ARGO (h / he)
  :manner (c / care-04 <----.
            :polarity -)) <-----
(d / drive-01
  :ARGO (h / he)
  :ARG1-of (m / have-manner-91 <-'
             :ARG2 (c / care-04
                     :ARG1-of (h2 / have-polarity-91 <-'
                                 :ARG2 -)))))
```

#### Make constants into node labels

#### Make the tree structure evident in the triples (using the Little Prince example, adding TOP relations)

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Test the relative effects of normalization on parsing evaluation for multiple parsers

- Use the Little Prince corpus with gold annotations
- Parse using JAMR (Flanigan et al., 2016)
- Parse using CAMR (Wang et al., 2016)
- Parse using AMREager (Damonte et al., 2017)
- Normalize each of the four above (various configurations)
- Compare:
  - Gold-orig × { JAMR-orig, CAMR-orig, AMREager-orig }
  - Gold-norm  $\times$  { JAMR-norm, CAMR-norm, AMREager-norm }

#### Results

	Normalization			Score			
System	Ι	А	R	S	Р	R	F
					0.60	0.56	0.58
	$\checkmark$				0.60	0.55	0.57
JAMR		$\checkmark$			0.61	0.56	0.58
			$\checkmark$		0.63	0.57	0.60
				$\checkmark$	0.59	0.55	0.57
					0.67	0.56	0.61
	$\checkmark$				0.67	0.56	0.61
CAMR		$\checkmark$			0.67	0.55	0.60
			$\checkmark$		0.70	0.57	0.63
				$\checkmark$	0.68	0.58	0.63
					0.57	0.52	0.55
	$\checkmark$				0.57	0.52	0.55
AMREager		$\checkmark$			0.57	0.53	0.55
			$\checkmark$		0.61	0.57	0.59
				./	0 5 9	054	056

#### Results

	Normalization			Score			
System	1	А	R	S	Р	R	F
					0.60	0.56	0.58
	$\checkmark$		$\checkmark$		0.63	0.57	0.60
JAMR		$\checkmark$	$\checkmark$		0.64	0.57	0.60
	$\checkmark$	$\checkmark$	$\checkmark$		0.64	0.57	0.60
	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	0.61	0.56	0.59
					0.67	0.56	0.61
	$\checkmark$		$\checkmark$		0.69	0.57	0.63
CAMR		$\checkmark$	$\checkmark$		0.70	0.56	0.62
	$\checkmark$	$\checkmark$	$\checkmark$		0.70	0.56	0.62
	$\checkmark$	$\checkmark$	$\checkmark$	$\checkmark$	0.70	0.58	0.63
					0.57	0.52	0.55
	$\checkmark$		$\checkmark$		0.61	0.57	0.59
AMREager		$\checkmark$	$\checkmark$		0.60	0.58	0.59
	$\checkmark$	$\checkmark$	$\checkmark$		0.60	0.58	0.59
	1	1	1	1	0.61	0 57	0 59

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# Discussion

- Normalization slightly increases scores on this dataset
  - mainly due to partial credit
- Sometimes it does worse
  - making available previously ignored triples
  - more triples -> larger denominator in Smatch
- Effects on a single system are unimportant
- Rather, relative effects for multiple systems is interesting
- Although, relative effects on this experiment are slight
  - Role inversion harmed JAMR but not others
  - AMREager improves compared to others
- Next step: try on other corpora (Bio-AMR, LDC, ...)

- Normalization is not promoted as a postprocessing step (in general)
- $\cdot\,$  Rather as preprocessing to evaluation
- Thus it allows parser developers to take risks
- Although reduced variation may benefit sequence-based models
- Similar procedures possibly useful for non-AMR representations (e.g., EDS, DMRS)

#### Thank you!

Software Available:

- Normalization
  https://github.com/goodmami/norman
- PENMAN graph library https://github.com/goodmami/penman

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