Tree-Adjoining Grammar Parsing and Applications

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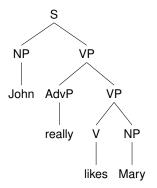
Outline

- Background and Motivations
- 2 Supertagging Models
- Parsing Models
- Vector Representations of Supertags
- Graph-based TAG Parsing
- 6 Applications of TAG

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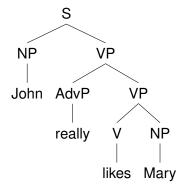
Syntactic Parsing



- Why do we need parsing?
- Does John love Mary? Does Mary love John?
- Understanding of a sentence depends on the structure



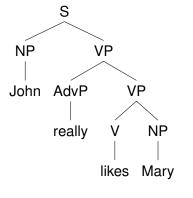
Context Free Grammars



$$S o NP \ VP$$
 $VP o AdvP \ VP$
 $AdvP o really$
 $VP o V \ NP$
 $NP o Mary$
 $NP o they$
 $NP o John$
 $V o like$
 $V o likes$

• These production rules generate sentences

Context Free Grammars



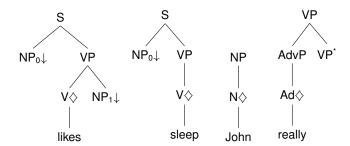
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 Fundamental problem: constraints are distributed over separate rules
 How do we choose V → like or V → likes?

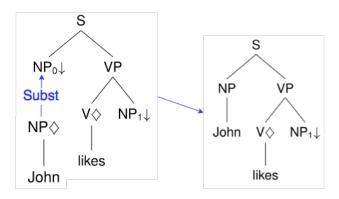


Tree-Adjoining Grammar (TAG) localizes grammatical constraints

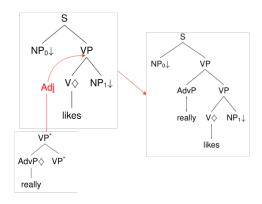
- Finite set of lexicalized elementary trees
- Finite set of operations (Substitution and Adjunction) are used to combine elementary trees

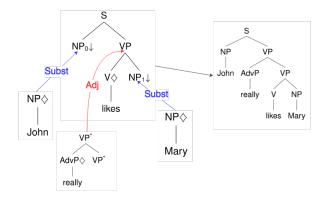


Substitution



Adjunction





Adjunction allows for unbounded recursion while still enforcing agreement.

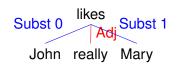
John smartly occasionally really only likes Mary...

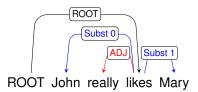


Derivation Tree

Derivation tree records the operations.

Forms a dependency tree (each token has exactly one parent)

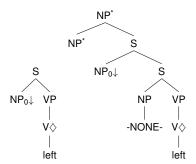




Two Steps in TAG Parsing

Now the reverse process.

- Supertagging
 Assign elementary trees (supertags) to each token. Similar to POS tagging.
- Parsing
 Predict operations on the elementary trees.



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Supertagging is a bottleneck

Supertagger	Parser	Stag Acc	UAS	LAS
Gold	Chart (MICA)	100.00	97.60	97.30
Maxent (MICA)	Chart (MICA)	88.52	87.60	85.80

- Supertagging is almost parsing
- There are about 5,000 supertags in the grammar
- About half of them occur only once in the training data (PTB WSJ Sections 1-22).

BiLSTM Supertagging

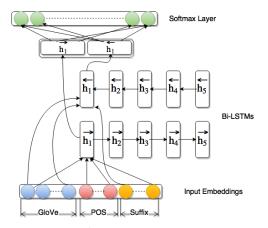


Figure: BiLSTM Supertagger Architecture.

Supertagging is still a bottleneck

Supertagger	Parser	Stag Acc	UAS	LAS
Maxent (MICA)	Chart (MICA)	88.52		
BiLSTM	Chart (MICA)	89.32		

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- We can compensate for supertagging errors by exploiting structural similarities across elementary trees.
- Similarities across supertags are not utilized by the chart parser.
- We use two alternative families of parsing algorithms

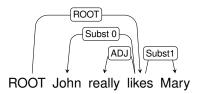
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Parsing Models

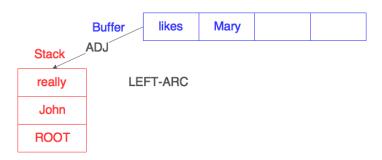
- Prior Work: Unlexicalized Chart-Parser (MICA)
 [Bangalore et al., 2009]
- Unlexicalized Transition-based Parser [Kasai et al., 2017, Friedman et al., 2017]
- Graph-based Parser [Kasai et al., 2018]

Arc-Eager System (MALT) [Nivre et al., 2006]

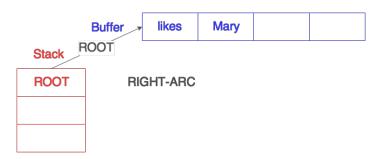


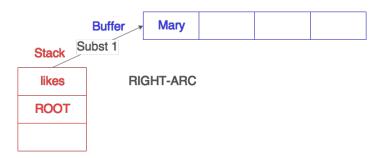












	Buffer			
Stack				
Mary	EN	ND		
likes				
ROOT				

How do we learn?

- Represent the configuration by the top k elements from stack and buffer: $\{s_i, b_i\}_{i=1}^k$ [Chen and Manning, 2014].
- Represent s_i (b_i) by the TAG elementary tree and the derived substitution operations performed into s_i .
- Encode the TAG elementary trees and the substitution operations with dense vectors.

NN Transition-based Parsing Model

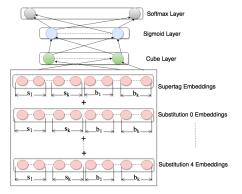
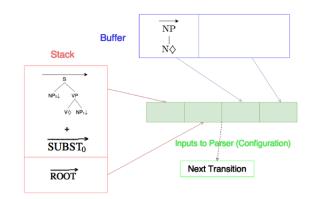


Figure: Transition-based Parser Neural Network Architecture.

Example

John really likes Mary

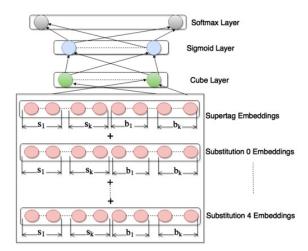
	Stack	Buffer	Relations	Action
ĺ	ROOT likes	Mary	$\{(ROOT, likes, ROOT), (likes, John, 0) \cdots \}$	RIGHT:1



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Embeddings for Elementary Trees



PCA Plots of Vector Representations

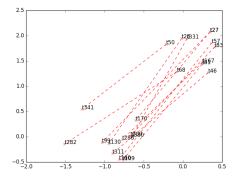


Figure: Declarative/subject relative alignment (Atomic embeddings) ex: the man **sneezed** vs. the man who **sneezed**

PCA Plots of Vector Representations

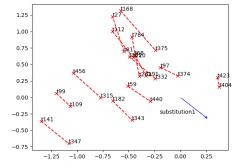


Figure: Transitive/intransitive alignment (Atomic embeddings). ex: the man who **devoured** the pizza vs. the man who **sneezed**

Analogy Test Results

n	# equations	% correct	Avg. position
300	246	50.40	7.98
4724	57220	4.62	289.48

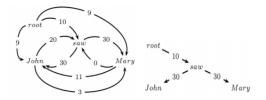
Table: Analogy task results. (n is a number used to restrict which supertags are considered: For a given n, only equations for which all supertags are among the n most common supertags are considered.)

- % **correct**: Percent of equations for which the left hand side's closest cosine neighbor was the right hand side.
- Avg. position: The position of the correct right hand side in the list of supertag embeddings ranked by cosine distance from the left hand side.

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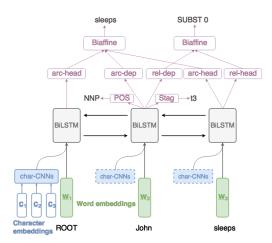
Graph-based Parsing



[McDonald et al., 2005]

- Score n² directed edges (n potential parents for each of the n tokens in a sentence) using features
- Find the maximum spanning tree (greedy + cycle fix)

Graph-based Parsing TAG Parsing



Comparison btw transition-based and graph-based

Rich feature representations with parse history v.s. global training/inference

- Transition-based parsers have parse history that naturally relates supertags that differ only by a certain operation (e.g. transitive/intransive)
- Transition-based parsers suffer from global error propagation
- Graph-based parsers assign scores independently
- Graph-based parser with BiLSTM feature representations (still no history)

New Results

Parser	UAS	LAS
MICA Chart	86.66	84.90
Transition-based Parsing	90.97	89.68
Joint Graph Parsing (POS+Stag)	93.26	91.89

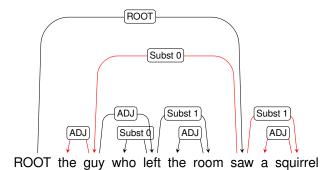
Table: Parsing results on the test set.

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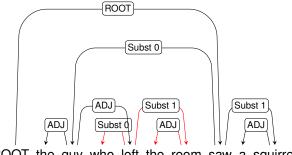
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[Xu et al., 2017]

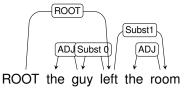
- E.g. The guy who left the room saw a squirrel
- ⇒ The guy left the room
- \implies The guy saw a squirrel
- \implies The room saw a squirrel
- → The guy saw an animal (not pure syntactic)
 - Parse the original sentence and hypothesis
 - Transform the parses using properties of supertags
 - If the original sentence parse subsumes the hypothesis one, YES.



ROOT Subst 1 ADJ S



ROOT the guy who left the room saw a squirrel

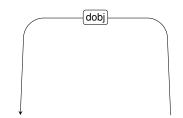




System	%A	%P	%R	F1
[Rimell and Clark, 2010]	72.4	79.6	62.8	70.2
[Ng et al., 2010]	70.4	68.3	80.1	73.7
[Lien, 2014]	70.7	88.6	50.0	63.9
Transition-based TAG Parsing	72.4	85.4	56.4	68.0
Graph-based Method	78.1	86.3	68.6	76.4

Table: PETE test results. Precision (P), recall (R), and F1 are calculated for "entails."

Unbounded Dependency Recovery



I met the guy who I think John saw

System	obRC	obRd	sbRC	free	obQ	rnr	sbEm	Total
C&C	59.3	62.6	80.0	72.6	72.6	49.4	22.4	53.6
Enju	<u>47.3</u>	<u>65.9</u>	82.1	76.2	32.5	47.1	32.9	<u>54.4</u>
Stanford	22.0	1.1	74.7	64.3	41.2	45.4	10.6	38.1
MST	34.1	47.3	78.9	65.5	41.2	45.4	<u>37.6</u>	49.7
MALT	40.7	50.5	84.2	70.2	31.2	39.7	23.5	48.0
Joint	72.5	78.0	81.1	85.7	56.3	47.1	49.4	64.9

Acknowledgement

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