

Event Extraction as Dependency Parsing

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Stanford University

4.21.2011

Joint work with Mihai Surdeanu and Chris Manning
(to appear in ACL 2011)



Event Extraction from Biomedical Text

Goal: Determine which biological events occur within text



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We have found that the HTLV-1 transactivator protein, tax, acts as a costimulatory signal for GM-CSF and IL-2 gene transcription in that it can cooperate with TCR signals to mediate high level gene expression.



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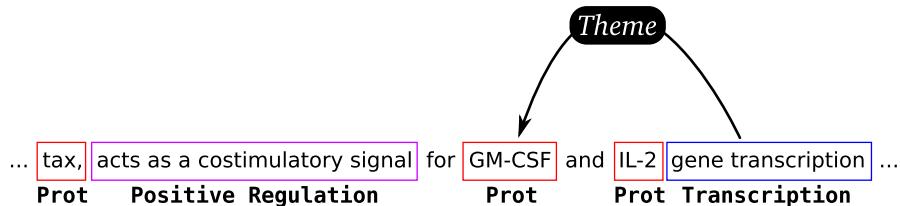


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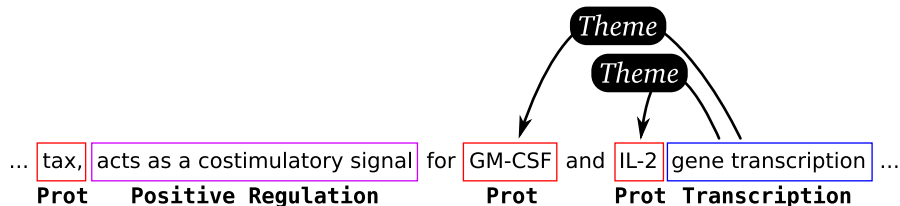


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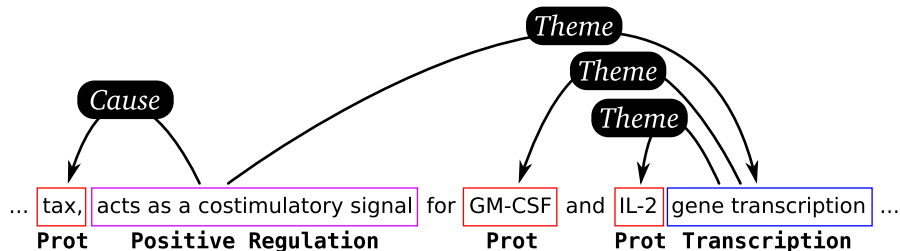


Hierarchical Event Extraction from Biomedical Text

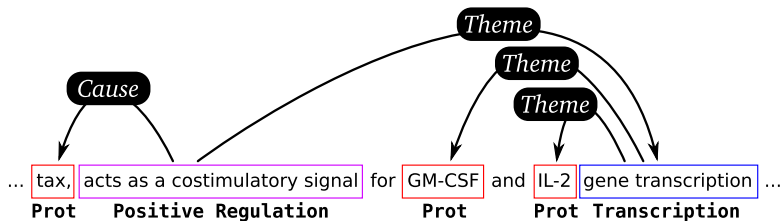
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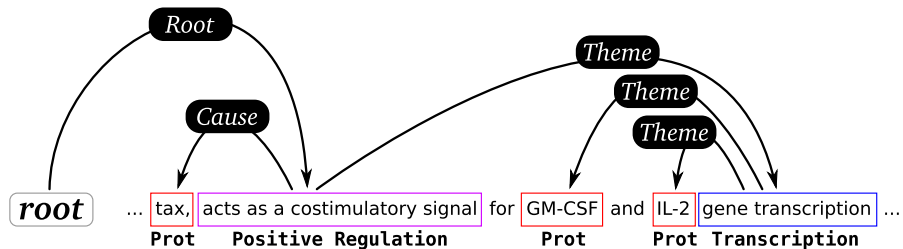
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This talk in two slides...



Spoiler alert!



A little bit about the BioNLP 2009 shared task

Type	Name	Arguments
Simple	Gene expression	<i>Theme</i> (Protein)
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- Protein entities given for free
 - ...but event anchors must be detected by the model
- Event anchors and proteins can participate in multiple events
- Events can span sentences ($\approx 7\%$ do)
- Actually the simplest BioNLP 2009 shared task (“Task 1”)
 - ...and BioNLP 2011 task includes two new domains



Outline

- 1 BioNLP shared task
- 2 Previous approaches**
 - Pipelined systems
 - Markov Logic
- 3 Event Parsing
- 4 Experiments
- 5 Future work
- 6 Conclusion



UTurku: Björne *et al.* (2009)

- Best scoring system in BioNLP 2009 shared task

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- Pipelined classifiers:
 - 1 Event anchor detection and classification
 - 2 Event linking
 - 3 Heuristic postprocessing rules
- 52.0% *f*-score

[Björne *et al.*, BioNLP 2009]



Miwa *et al.* (2010)

- **Outperforms** best scoring system in BioNLP 2009 shared task
- Pipelined classifiers:
 - 1 Event anchor detection and classification
 - 2 Event linking
 - 3 **Learned** postprocessing rules
- **53.3%** *f*-score
- More domain specific features, multiple syntactic parsers

[Miwa *et al.*, JBCB 2010]



Markov Logic

- Markov logic-based system using hard and soft constraints

[Poon and Vanderwende, NAACL 2010]

[Riedel *et al.*, NAACL 2009]



Markov Logic

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- Example formula schema:

$$\text{Token}(j, +\text{text}) \wedge \text{SyntacticDep}(i, j, \text{dep}) \implies \text{EventType}(i, +\text{type})$$

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- 50.0% *f*-score

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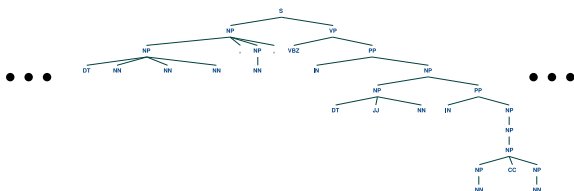
Overview of our model

... tax, acts as a costimulatory signal for GM-CSF and IL-2 gene transcription ...

Preprocessing: Segmentation, tokenization



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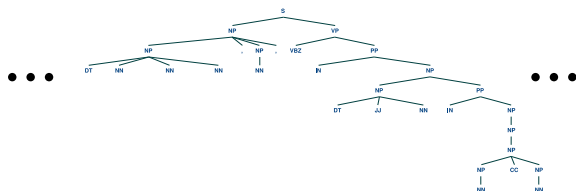
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[McClosky and Charniak, ACL 2008]



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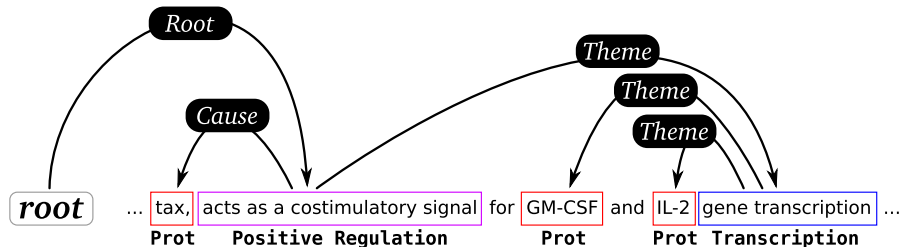
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Anchor classification: Essentially NER for event anchors



Overview of our model



Event parsing: Parse anchors and proteins using reranking parser



Anchor classification

- Anchors can be multiple words (13% have 2+ words)



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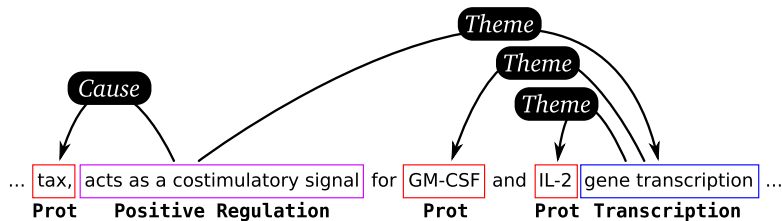


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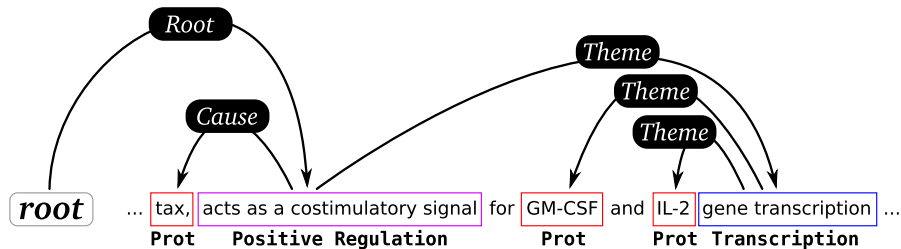
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- More recent work on boosting recall (distributional similarity features)



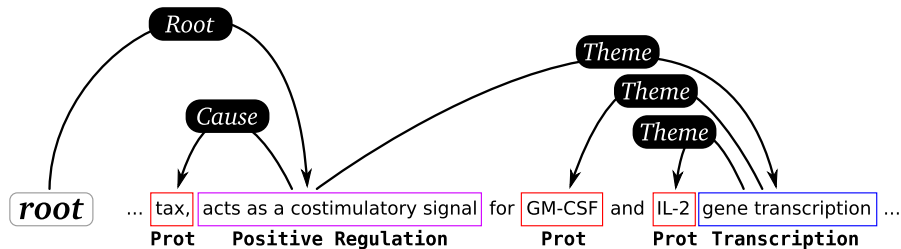
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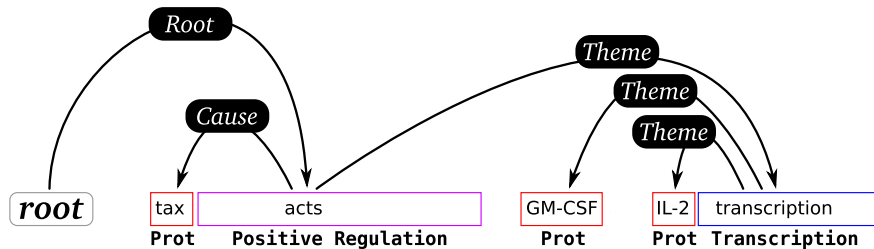
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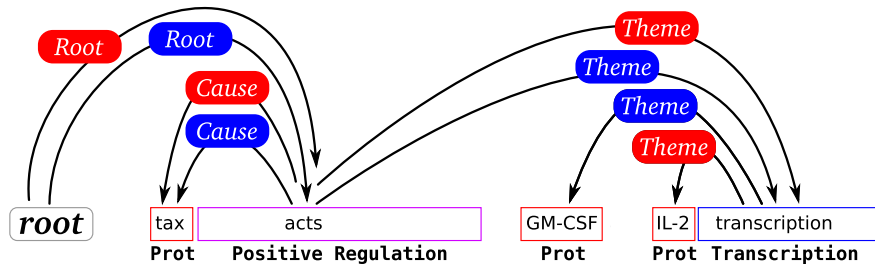
(Not pictured: Unused entities linked to the root as well.)



Event parsing with dependency parsers



DAGnabbit!



...but most duplicates can be merged

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- Binding is the only ambiguous case.



Maximum-spanning tree based parsing

Why a dependency parser?

- Event structures are non-projective (non-planar)



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Why MSTParser? [McDonald *et al.*, EMNLP 2005]

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Why MSTParser? [McDonald *et al.*, EMNLP 2005]

- Handles non-projective trees naturally
- Easy to extend feature extractor
- Support for n -best parsing



Crash course in MSTParser

- Parse trees represented as a **labeled graph** ($G = (V, E)$)
- Words are nodes ($i, j, \dots \in V$), dependency relations are edges ($e_{ij} \in E$)



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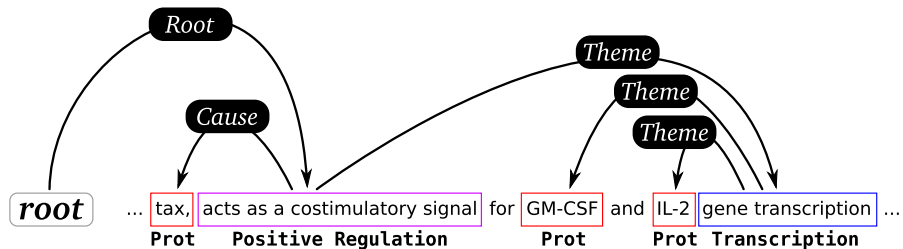


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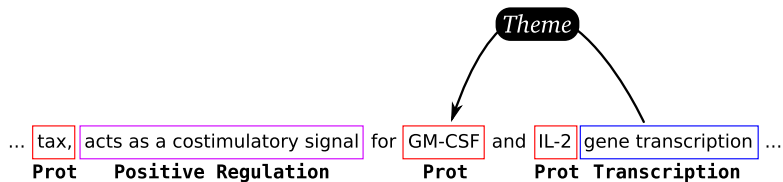
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- Features must be **edge-factored**



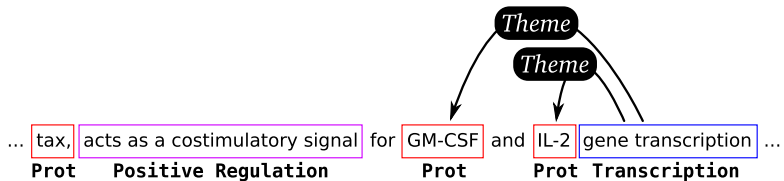
Edge-factored features



Edge-factored features



Second-order edge-factored features



Feature spaces

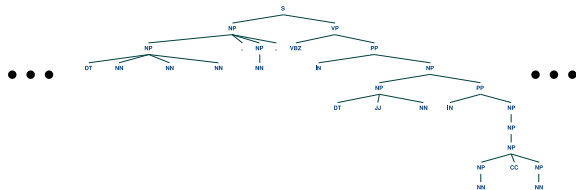
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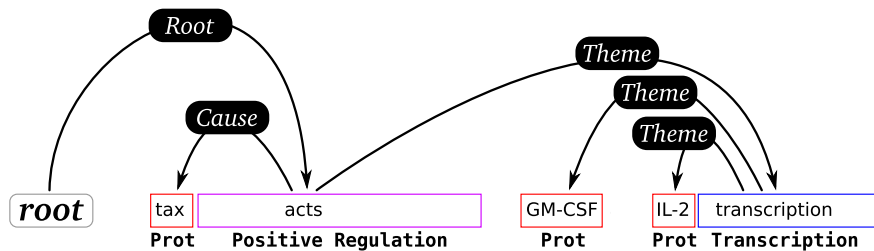
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“Full”

(includes original syntactic tree)



Feature spaces



“Reduced”



Features for BioNLP

Full sentence space:

- Surface words features (distance, n -grams)



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- Generalized type features
(e.g. *Positive Regulation* is a *Complex Event* is an *Event*)



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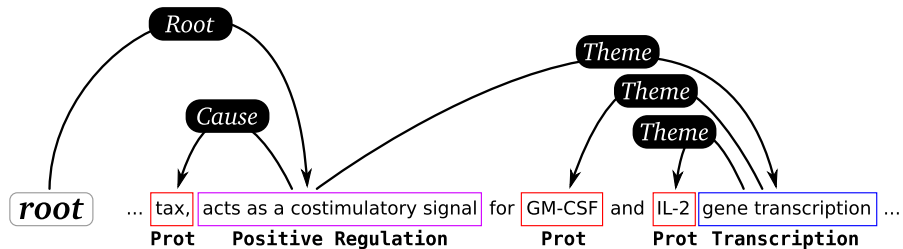


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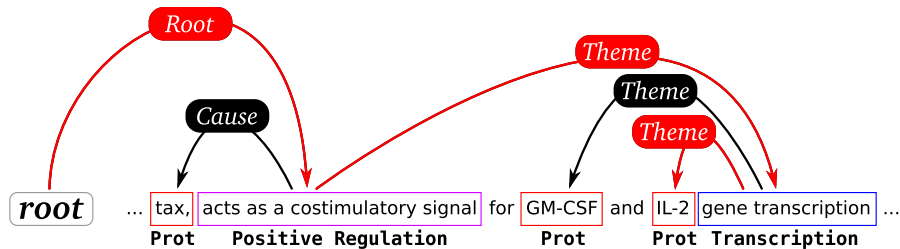
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[Johnson and Ural, NAACL 2010]
- k -best decoding in $O(kn^2)$, reranking takes $O(k)$ time



Reranker features



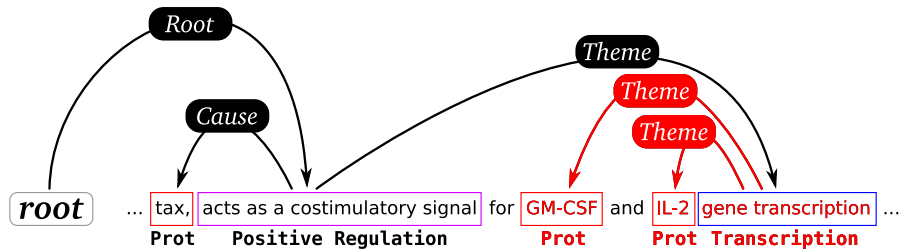
Reranker features



Paths to root



Reranker features

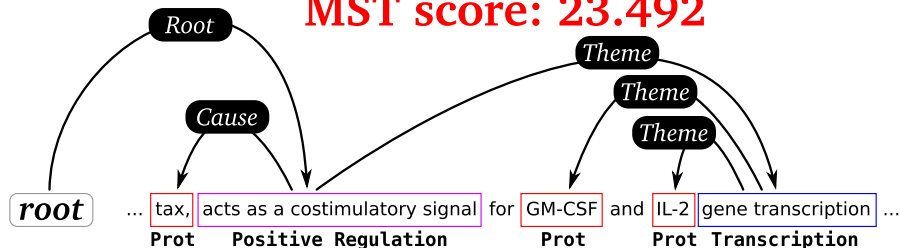


Event frames



Reranker features

MST score: 23.492



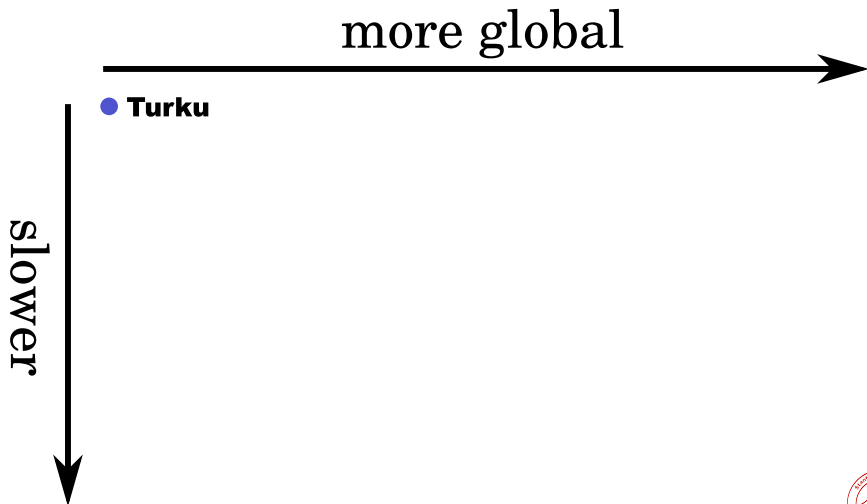
Score from parser



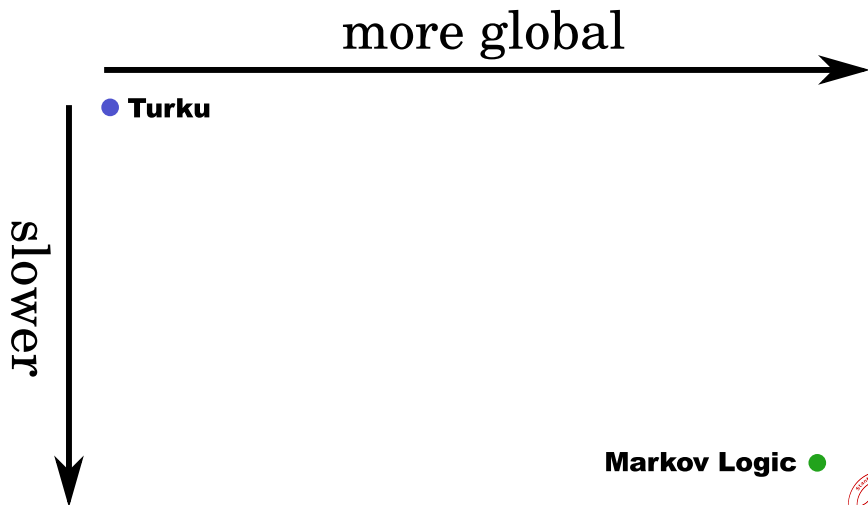
Relation to previous models



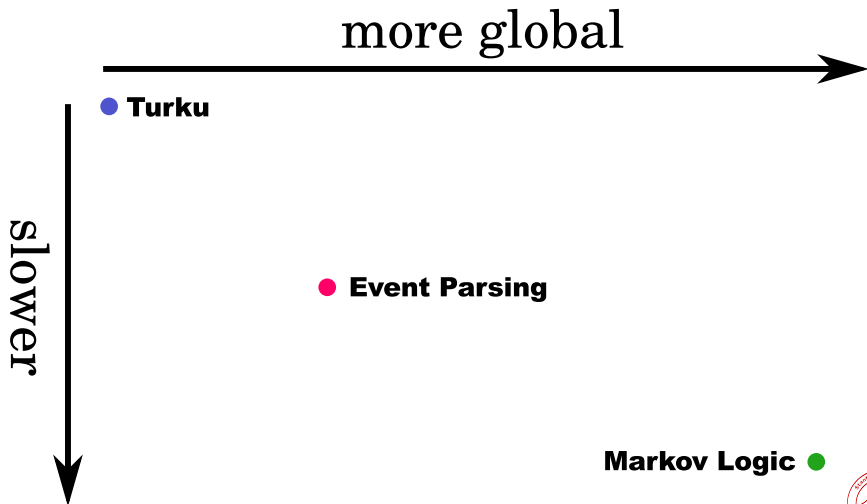
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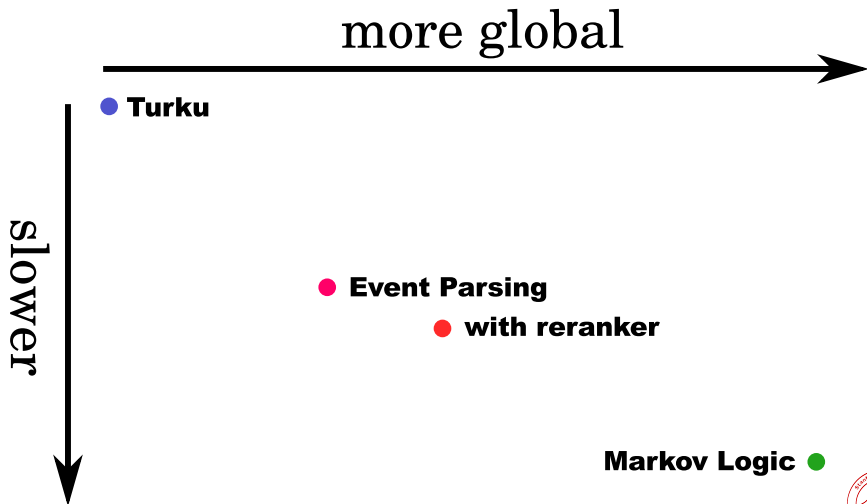
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- 800 articles for training, 150 for development, 260 for testing



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Anchors

- Two scenarios: Gold or predicted
- When predicted, train on the union of predicted and gold anchors



Performance of system components

Anchors	Parser	RR	Conv.	Rec	Prec	F ₁
Gold	Gold	Gold	✓	81.6	93.4	87.1

(performance on development corpus)



Performance of system components

Anchors	Parser	RR	Conv.	Rec	Prec	F ₁
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Anchors	Parser	RR	Conv.	Rec	Prec	F ₁
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Oracle reranker scores

		<i>n</i> -best parses considered			
Anchors	Parser(s)	1	2	10	All
Gold	2P	71.8	77.5	84.8	86.2
	1P, 2P, 2N	—	—	—	86.7
Predicted	2P	52.7	60.7	70.1	72.5
	1P, 2P, 2N	—	—	—	73.4

(performance on development corpus)



Oracle reranker scores

		<i>n</i> -best parses considered			
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Comparison with State-of-the-Art

System	<i>f</i> -score		
	dev _{GA}	dev	test
Event Parsing	73.1	53.5	48.6
[Björne <i>et al.</i> , 2009]	72.1	53.5	52.0
[Poon and Vanderwende, 2010]	N/A	55.5	50.0
[Miwa <i>et al.</i> , 2010]	—	56.3	53.3

(dev_{GA} is the development section with gold anchors)



Outline

- 1 BioNLP shared task
- 2 Previous approaches
- 3 Event Parsing
- 4 Experiments
- 5 Future work**
 - Document-level parsing
 - DAG parsing
- 6 Conclusion



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 - Dependency paths can cross sentences
- Currently performs $\approx 3\%$ worse than sentence-level parsing



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- Maybe TurboParser [Martins and Smith, ACL 2009] can do this by adjusting constraints



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Questions?

