# Unsupervised Multilingual Grammar Induction



- Languages exhibit variations in patterns of ambiguity
- Variations as natural supervison

در معرر در مر معرد المر المر المرام المرام الله الله الله الله والارض في البداء خلق الله السموات والارض

Morphology: acl 2008

POS tagging: emnlp 2008 naacl 2009

Syntax: acl 2009 (this talk)



English: I saw the student from MIT

English: I saw the student from MIT

```
English:

I saw the student from MIT

Urdu:

I MIT of student saw
```

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English: [I saw] the student from MIT
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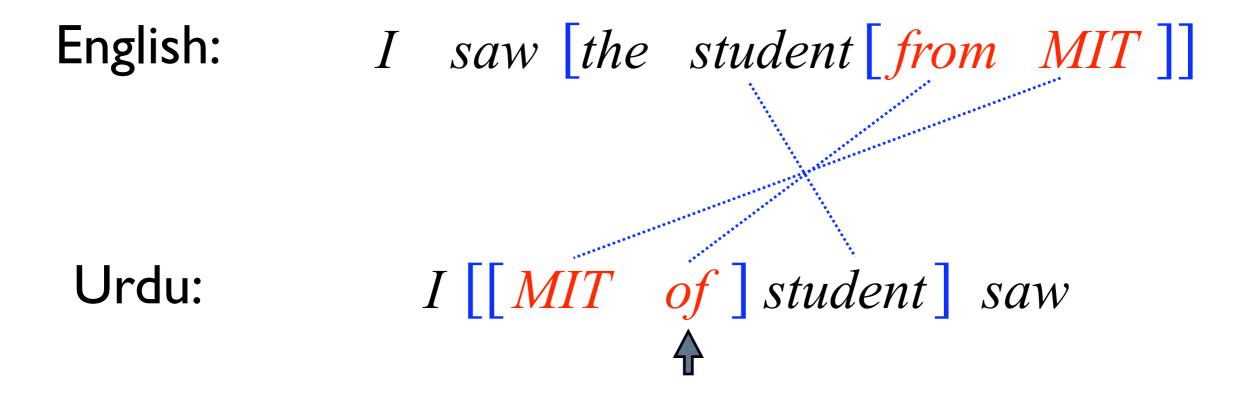
♠
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Urdu: I \quad \begin{bmatrix} MIT \quad of \end{bmatrix} student \end{bmatrix} \quad saw
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Main idea: learn from systematic variations in phrase order and expression

# Key Technical Challenge

# Represent shared cross-lingual syntactic structure

- Linguistically plausible
  - Allow full range of syntactic divergence and translational freedom
- Computationally tractable
  - Support probabilistic operations: argmax, marginalization, sampling

## Prior Representations

## Synchronous Grammars [Wu 1997; Melamed 2003; Chiang 2005; Smith&Smith 2004; Eisner 2005; Blunsom et al 2008]

- Employed for modeling phrase reordering in MT
- In basic form, isomorphic trees (up to sibling order)

### Node Matching [Burkett&Klein 2008]

- Ignores tree structure
- Marginalization is #P-complete

# Our Proposal

# Probabilistic adaptation of Unordered Tree Alignment [Jiang et al 1995]

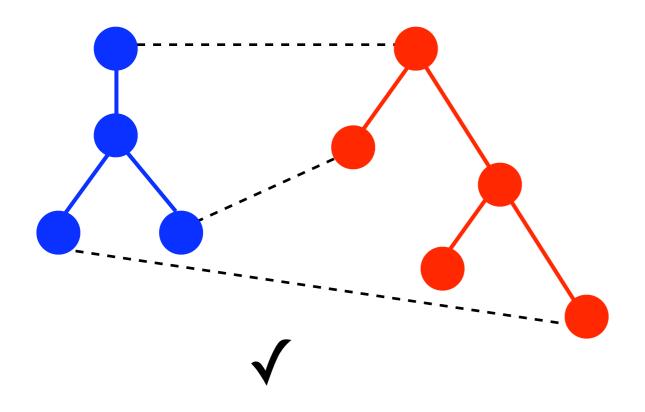
- Node alignments must respect tree structures
- Yet any number of nodes may remain unaligned
- Can marginalize and sample all possible alignments in linear time with dynamic program

# For trees $T_1$ and $T_2$ , an alignment A is obtained in the following way:

- I. Insert empty nodes into  $T_1$  and  $T_2$  and swap sibling order, until they are isomorphic
- 2. Overlay the resulting trees  $T_1$  and  $T_2$  to obtain A

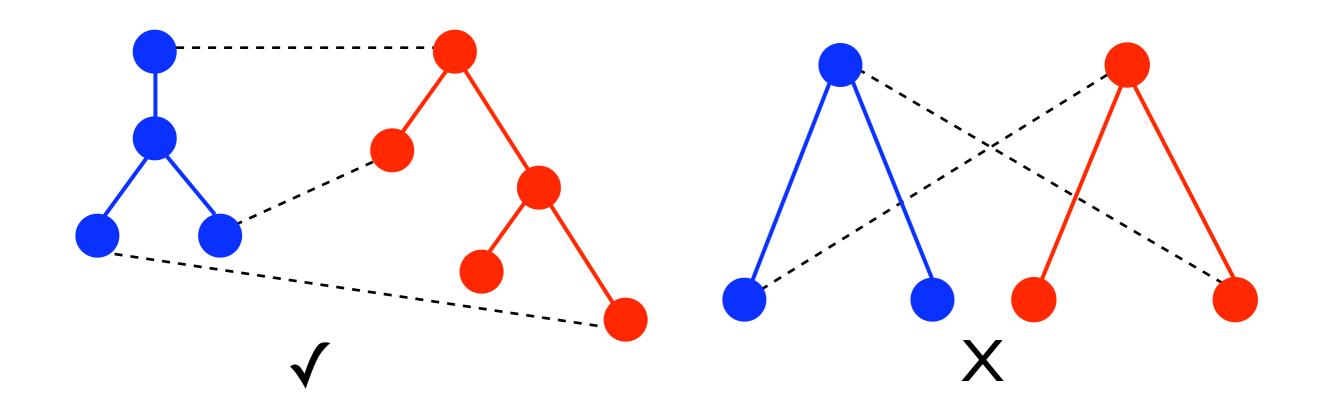
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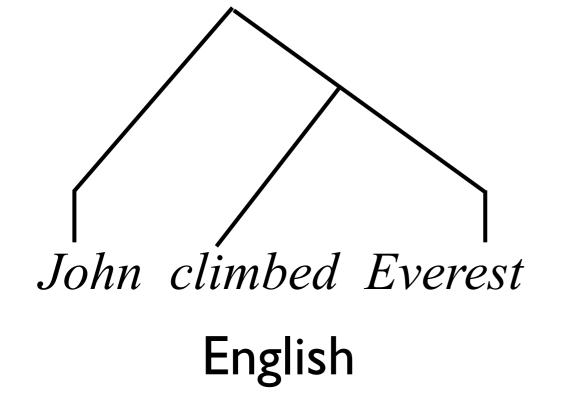
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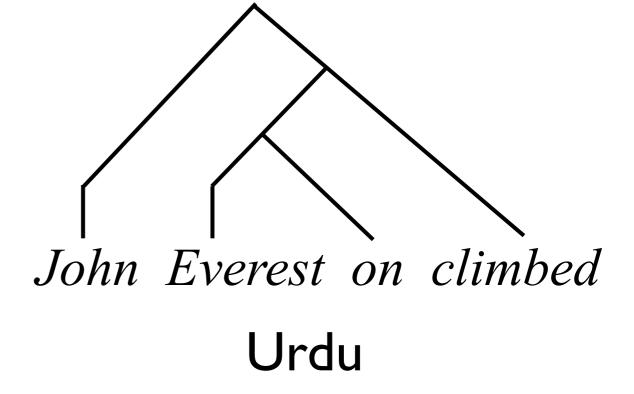


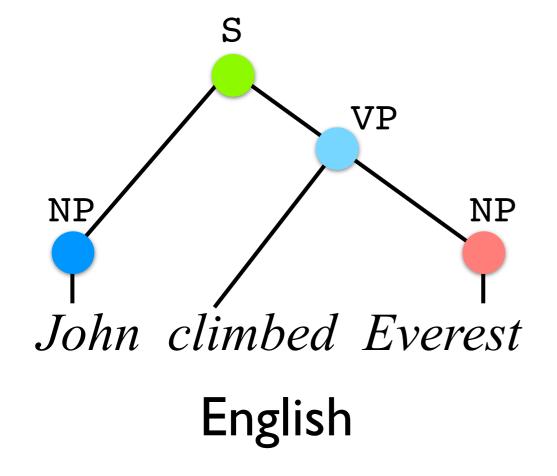
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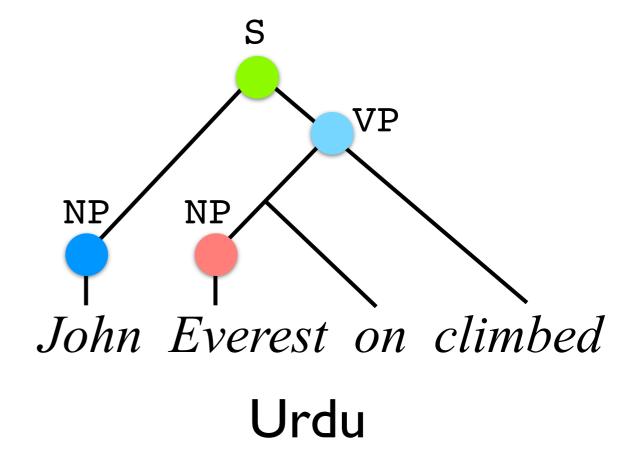
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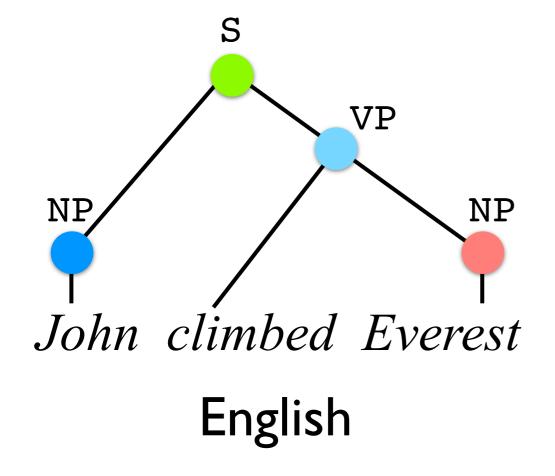


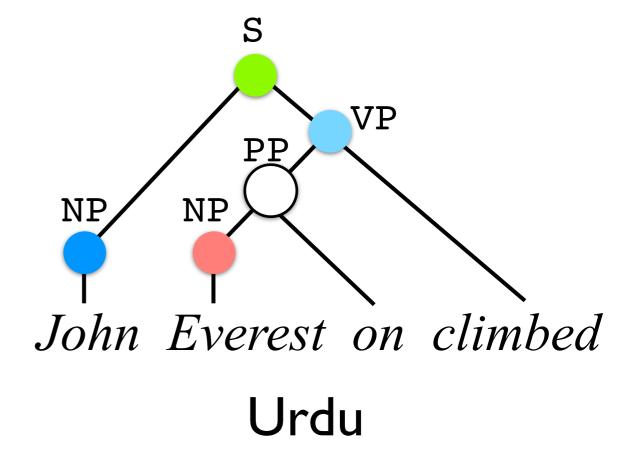


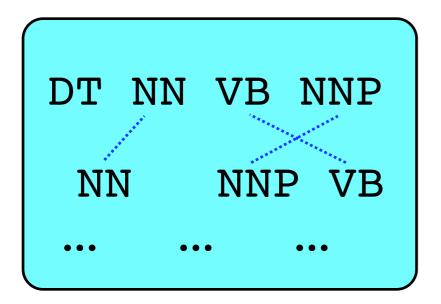


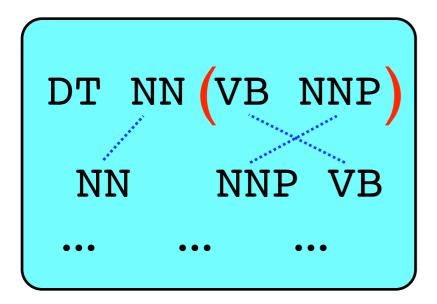




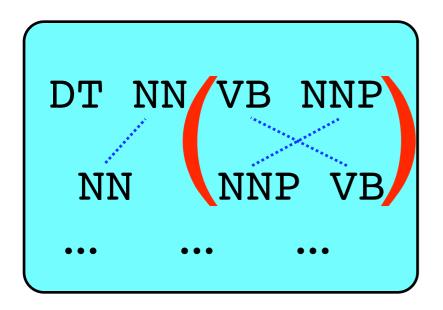




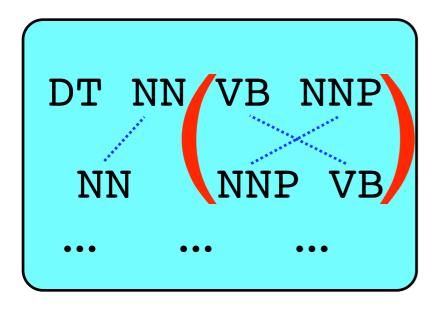




```
DT NN (VB NNP)
NN (NNP VB)
```



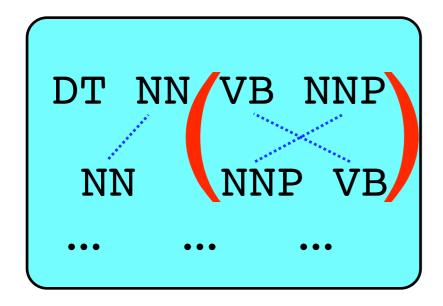
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Hypothesize aligned trees that best explain:

- frequent POS sequence pairs
- lexical alignments

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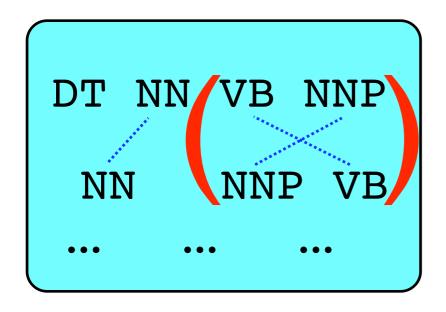


Parameters to learn

Hypothesize aligned trees that best explain:

- frequent POS sequence pairs
- lexical alignments

#### We observe:



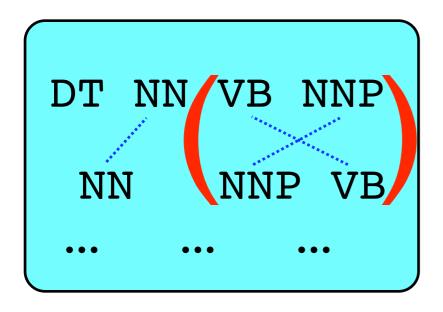
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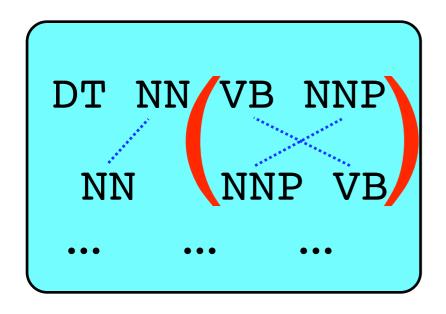
### Parameters to learn

 $\omega$  Probability of constituent pairs of aligned nodes

 $\phi^+$  Distribution on num. of word alignments between aligned nodes

Distribution on num. of word alignments between unaligned nodes

#### We observe:



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### Parameters to learn

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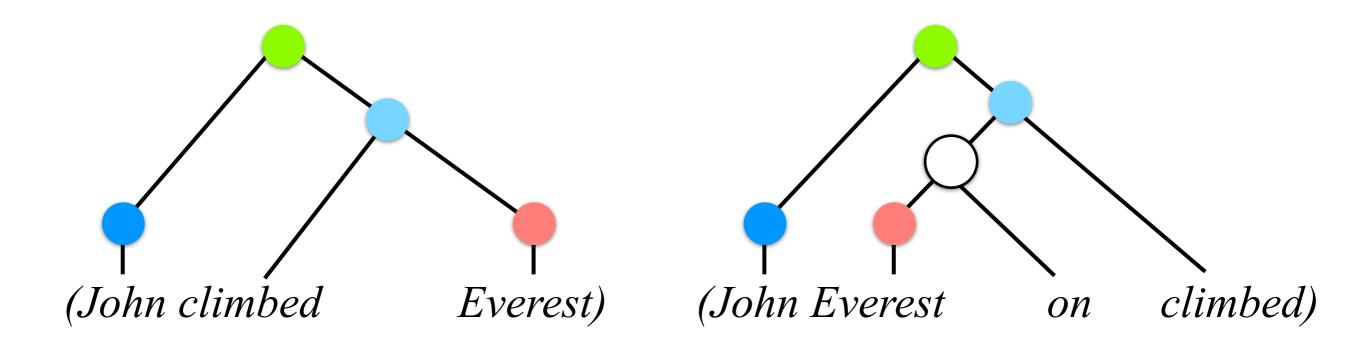
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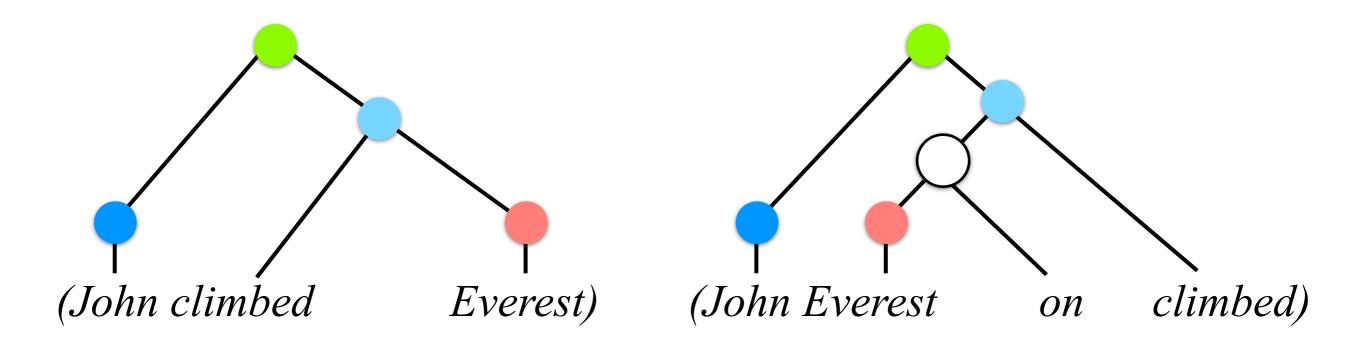
 $\phi^-$  Distribution on num. of word alignments between unaligned nodes

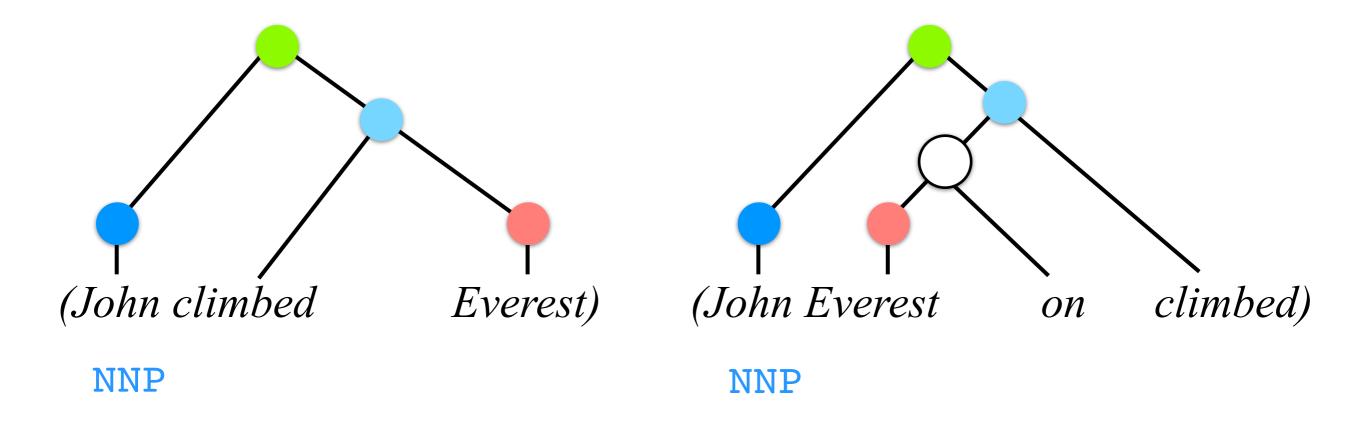
(language-specific parameters for unaligned nodes [Klein&Manning 2002])

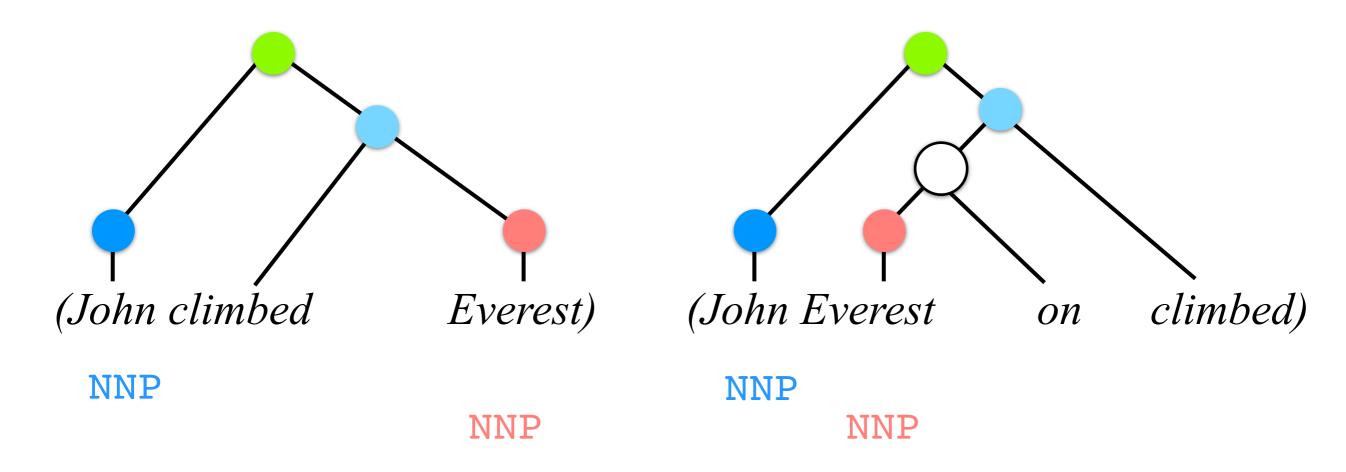
## Generative Story

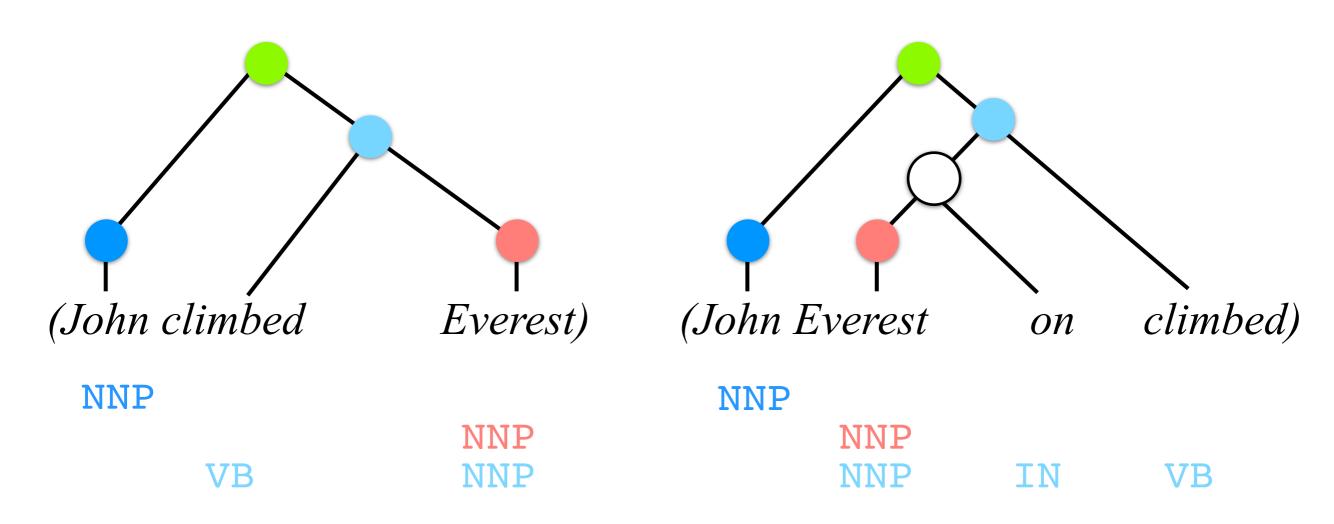
Draw alignment tree template  $(T_1, T_2, A)$  from uniform distribution:

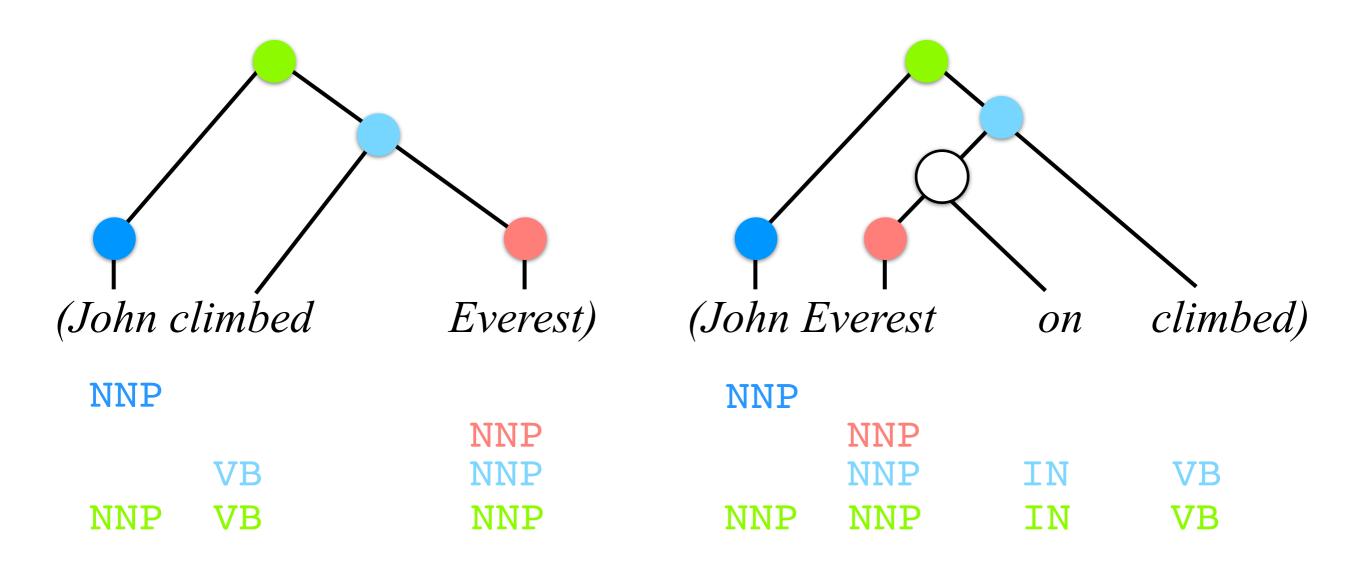




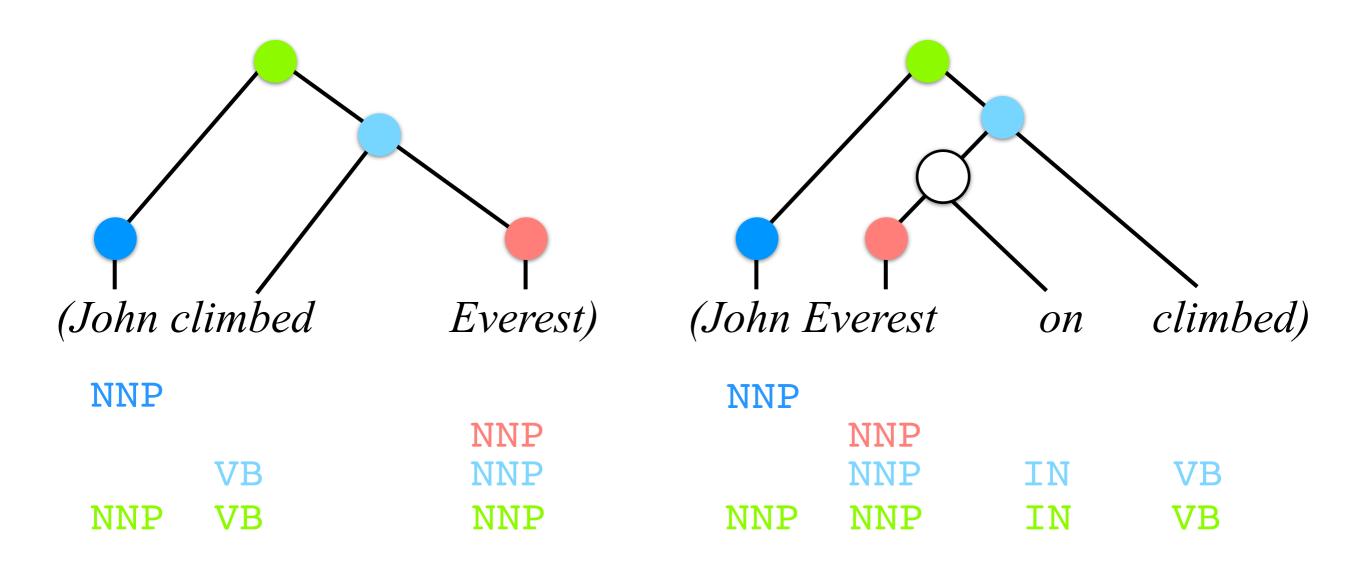




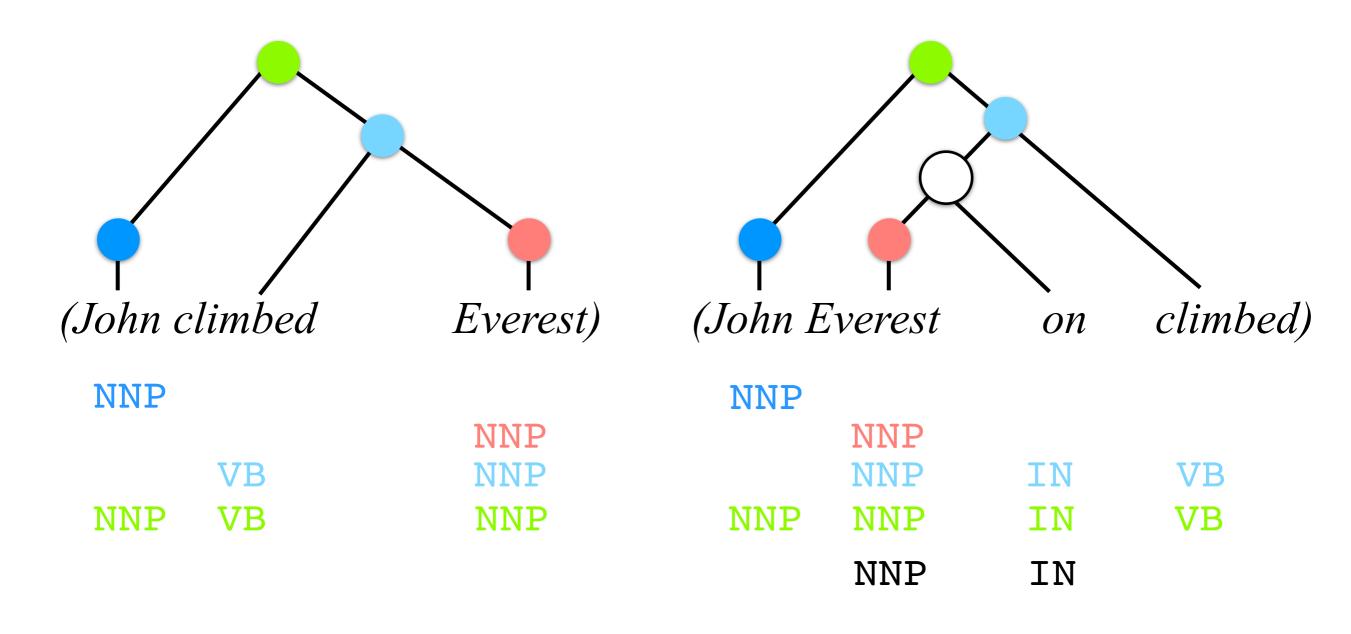




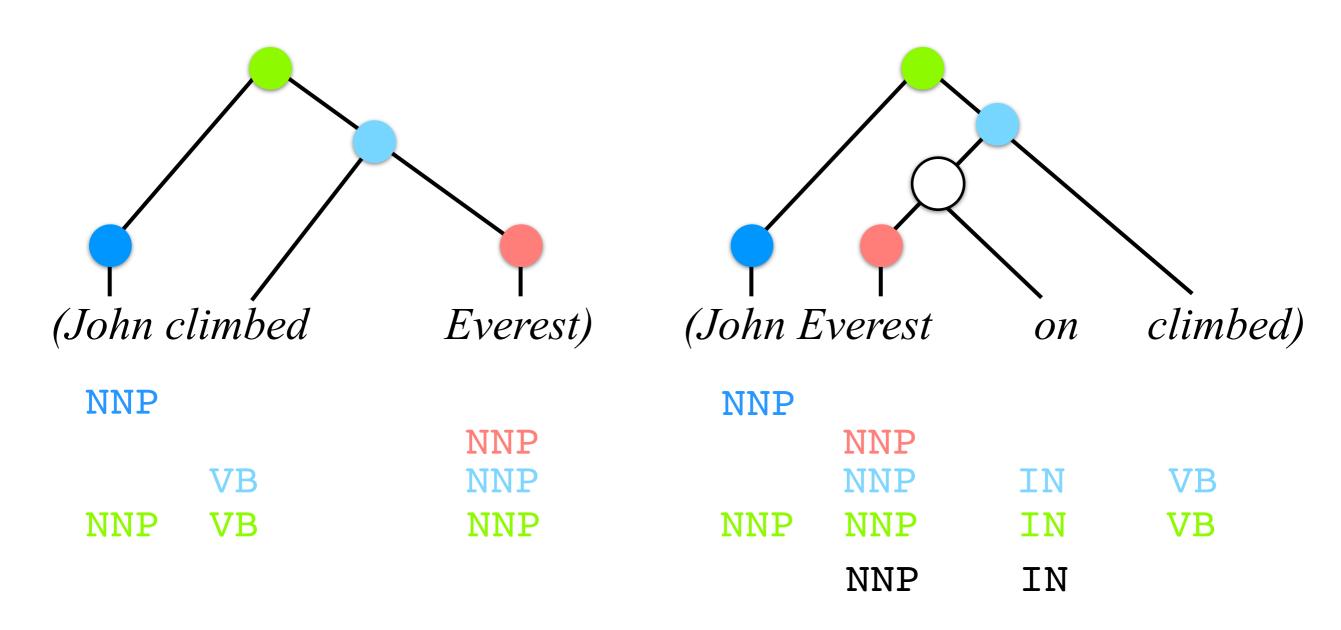
For each unaligned node, draw a constituent from language-specific parameters:



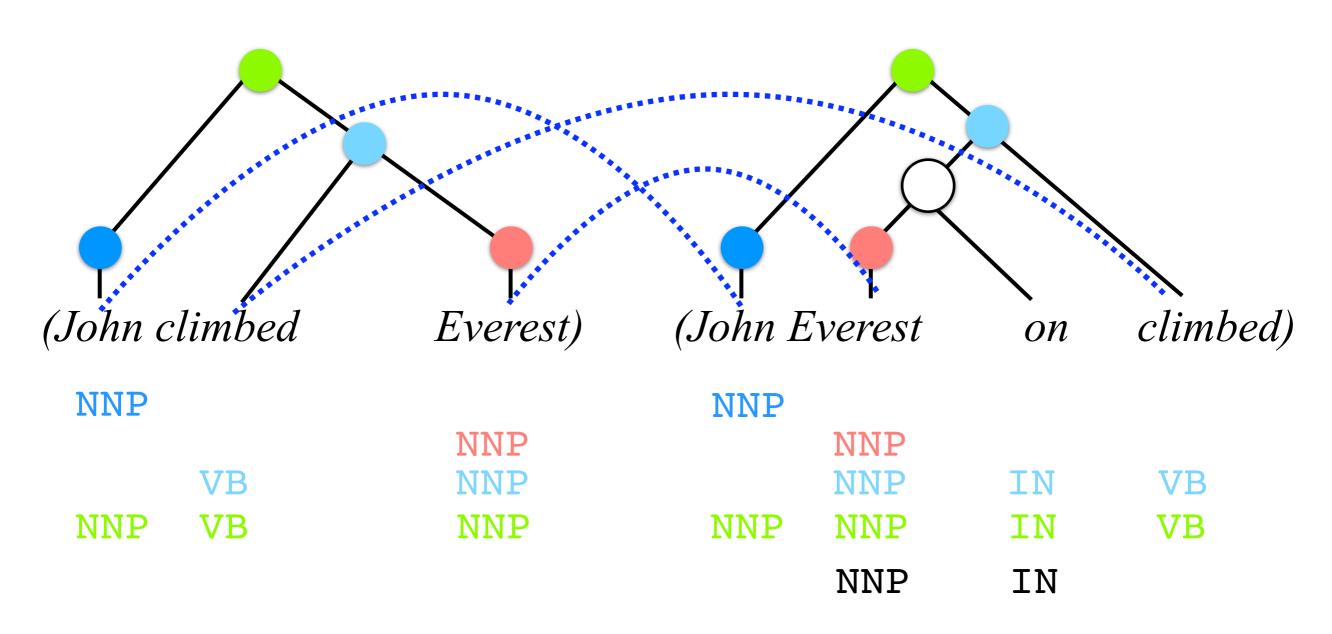
For each unaligned node, draw a constituent from language-specific parameters:



Draw word alignments between aligned and unaligned nodes according to  $\phi^+$  and  $\phi^-$ :



Draw word alignments between aligned and unaligned nodes according to  $\phi^+$  and  $\phi^-$ :



## Inference: Gibbs Sampling

 Sample each aligned tree pair conditioned on others:

$$P((T_1, T_2, A)_i | (\mathbf{T_1}, \mathbf{T_2}, \mathbf{A})_{-i})$$

 Marginalize over all parameter values using standard closed forms (accumulated counts + hyperparameters)

• Hard to sample aligned tree pair:  $(T_1, T_2, A)$ 

- ullet Hard to sample aligned tree pair:  $(T_1,T_2,A)$
- Use proposal distribution Q, which assumes no nodes are aligned, to separately sample  $T_1^st, T_2^st$

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- Accept with probability:

$$\min \left\{ 1, \frac{P(T_1^*, T_2^*) \ Q(T_1, T_2)}{P(T_1, T_2) \ Q(T_1^*, T_2^*)} \right\}$$
 (Metropolis-Hastings)

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separately sample  $T_1^st, T_2^st$ 

# Sampling each Tree: Inside-Outside

- Recursively sample split-points from the top down
- Calculate probability of each split-point by marginalizing over all possible subtrees ("inside" table of inside-outside)

```
DT NN VB IN DT JJ NN
The boy ran through the haunted house
```

need to marginalize over all possible alignments  $\boldsymbol{A}$ 

 $\Rightarrow$ 

need to marginalize over all possible alignments  ${\cal A}$ 

- For  $n_1 \in T_1, n_2 \in T_2$  table D stores marginal probability of subtrees rooted at  $n_1, n_2$
- Bottom-up dynamic program computes D in time  $O(|T_1||T_2|)$

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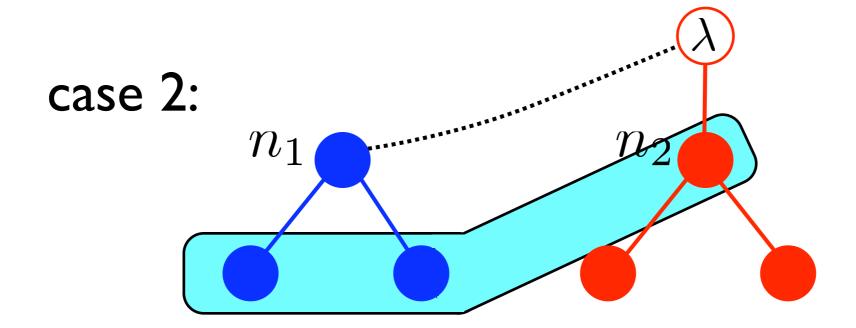
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case 1:  $n_1$ 

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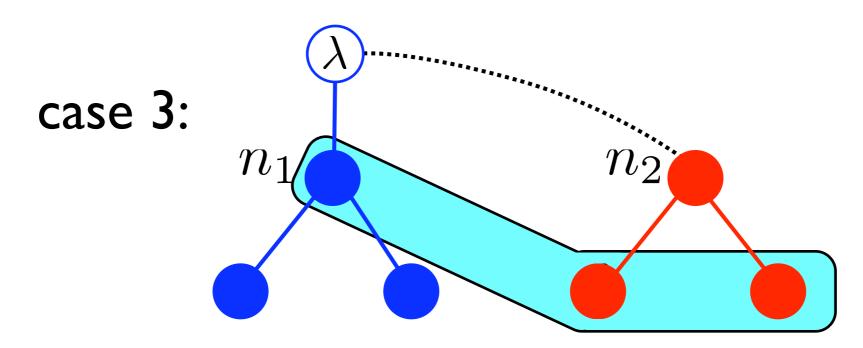
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case 3:  $n_1$   $n_2$ 



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similar for sampling

 $A|T_1,T_2$ 

## Experiments

Input: Bilingual POS sequences (w/ giza alignments)

Output: Binary tree bracketings

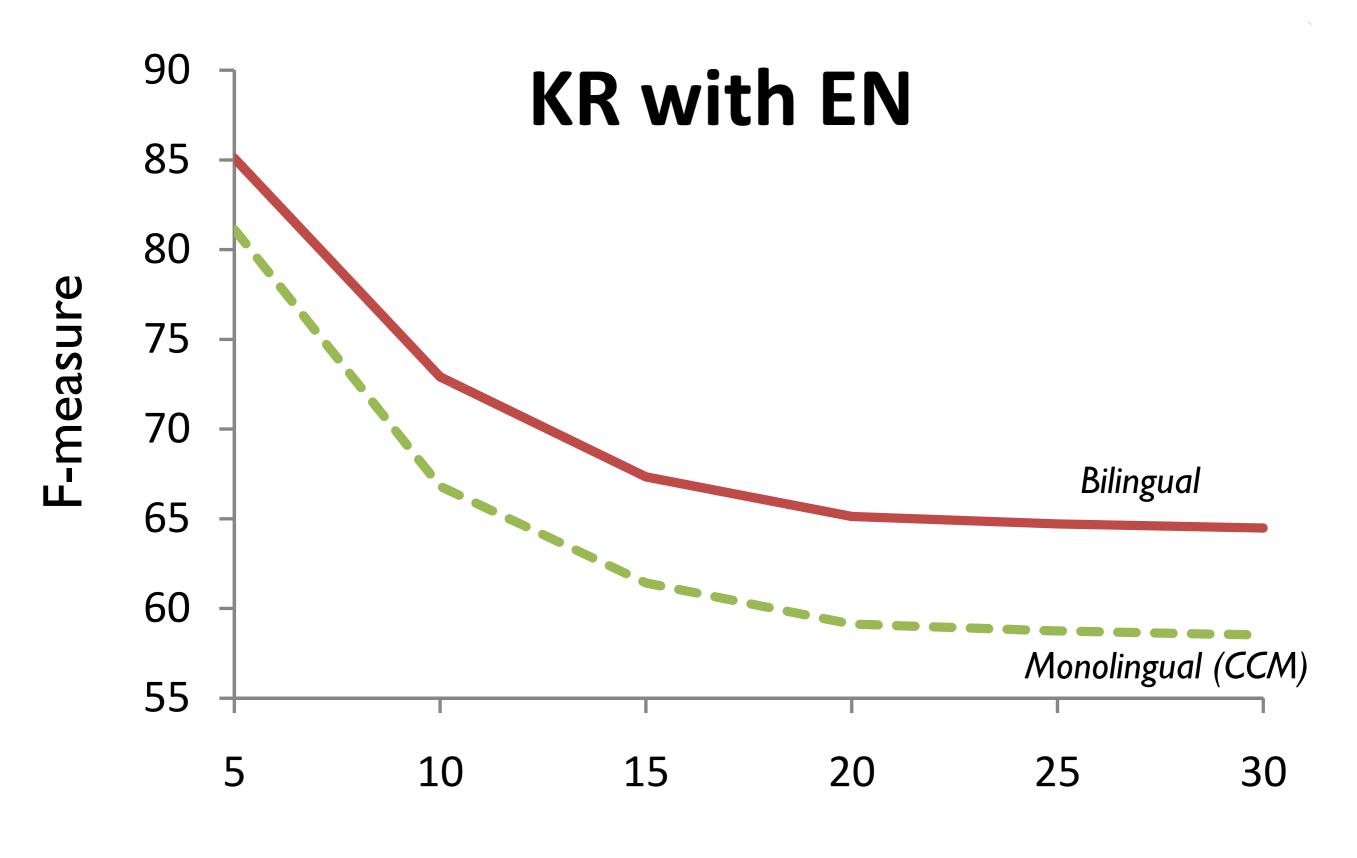
Evaluate: Bracket precision, recall, F-measure, on held-out monolingual test data.

Baseline: (Bayesian) CCM [Klein & Manning 2002]

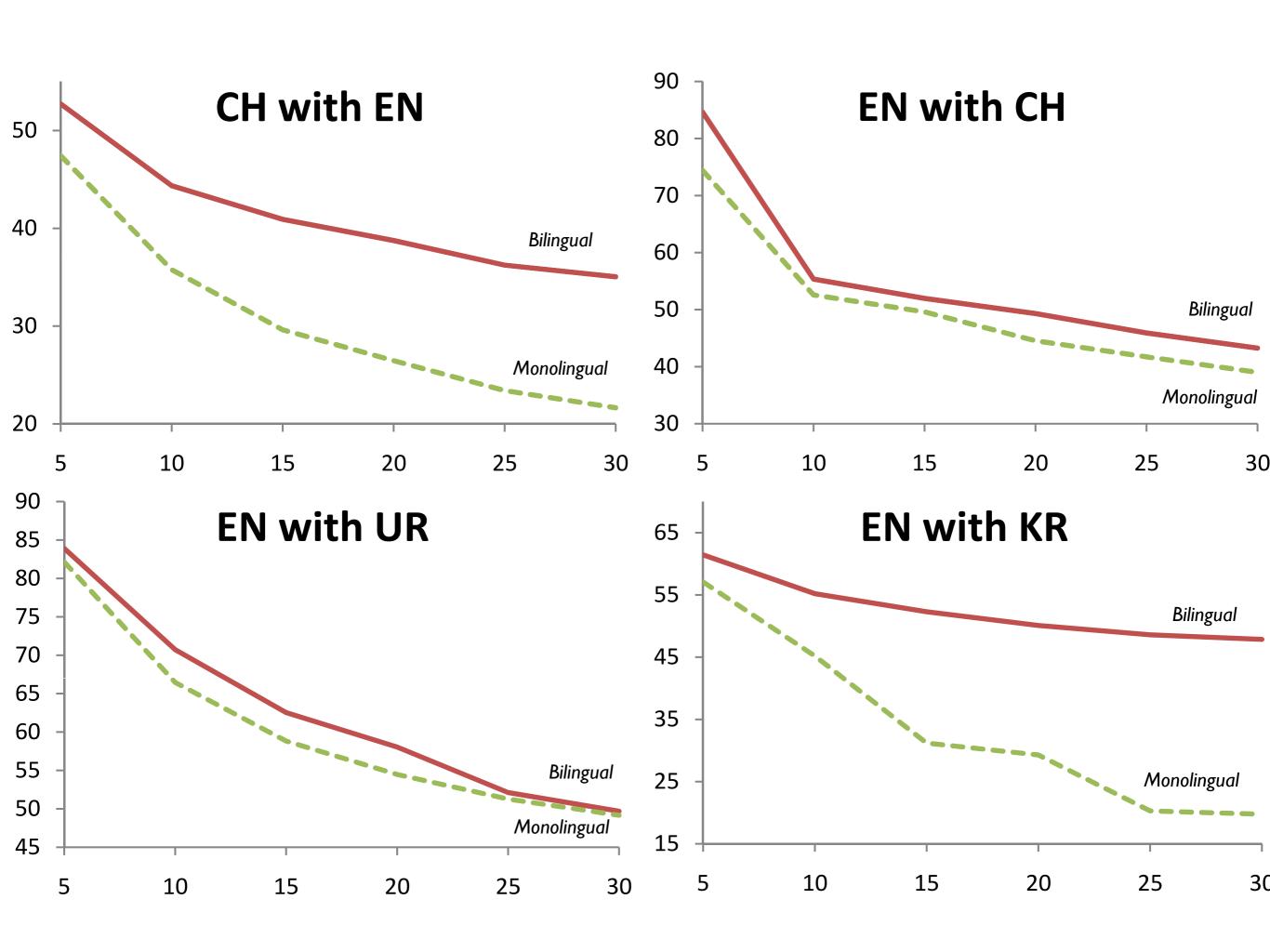
# Corpora

- Korean-English Treebank: 5,000 sentences
- Urdu translation of WSJ: 4,300 sentences
  - no Urdu gold brackets
- English-Chinese Treebank: 3,850 sentences

Evaluate on various maximum sentence lengths (5 - 30)



Max Sentence Length



#### Results

Average improvement across all scenarios:

Precision: +10

Recall: +8

F-measure: +9

 Average reduction in error relative to binary tree oracle: 19%

Percentage of tree nodes aligned

CH-EN	
UR-EN	
KR-EN	

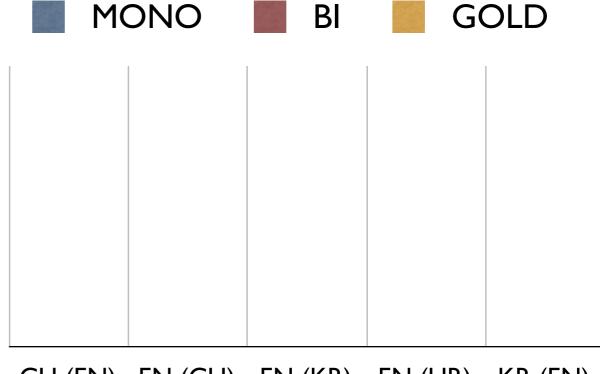
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# Entropy of bracketed POS sequences

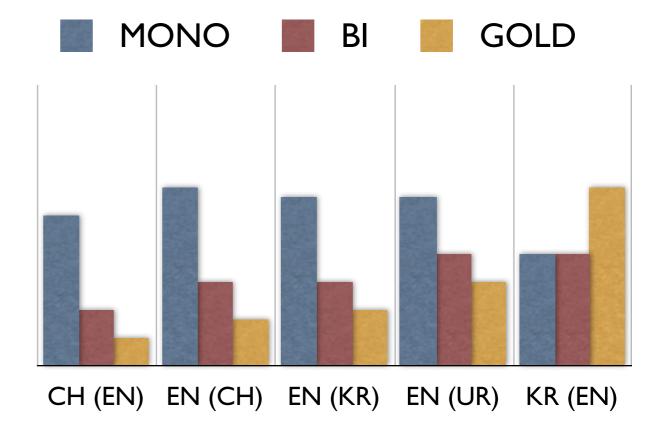


CH (EN) EN (CH) EN (KR) EN (UR) KR (EN)

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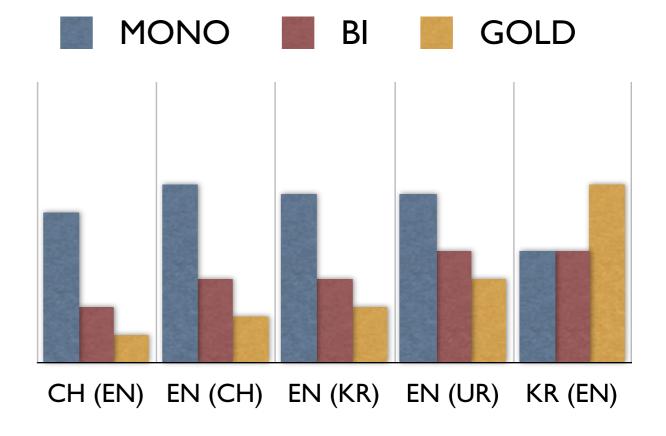
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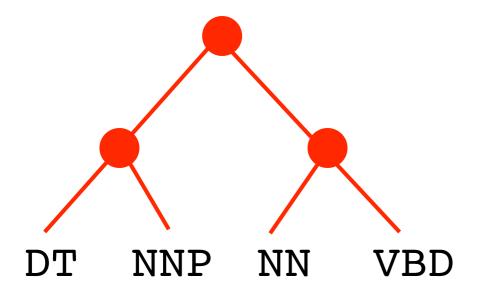
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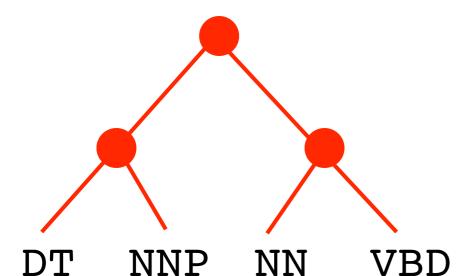


MONO	BI	GOLD
6.7	6.0	5.8

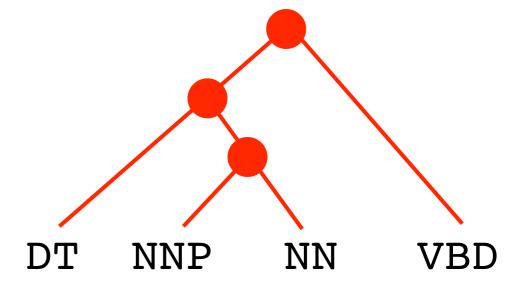
Monolingual X

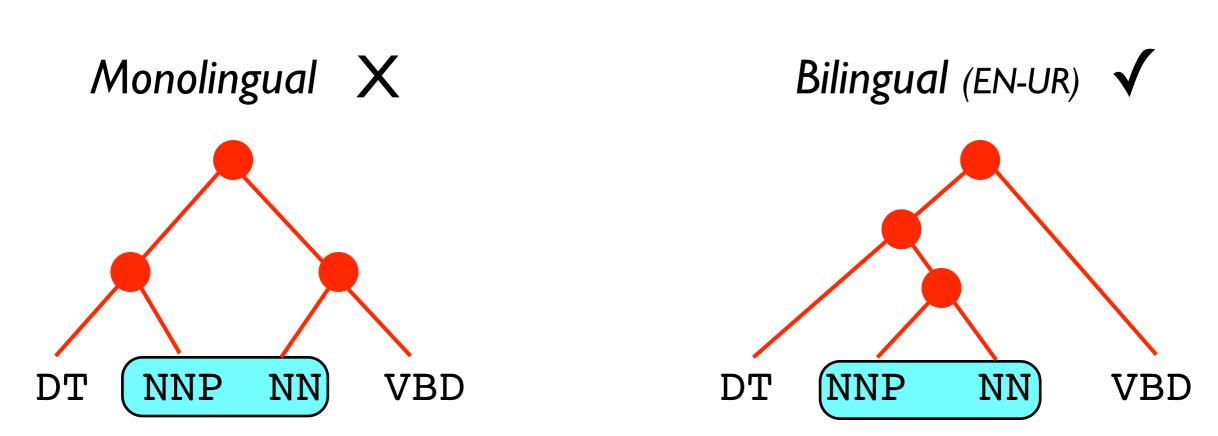


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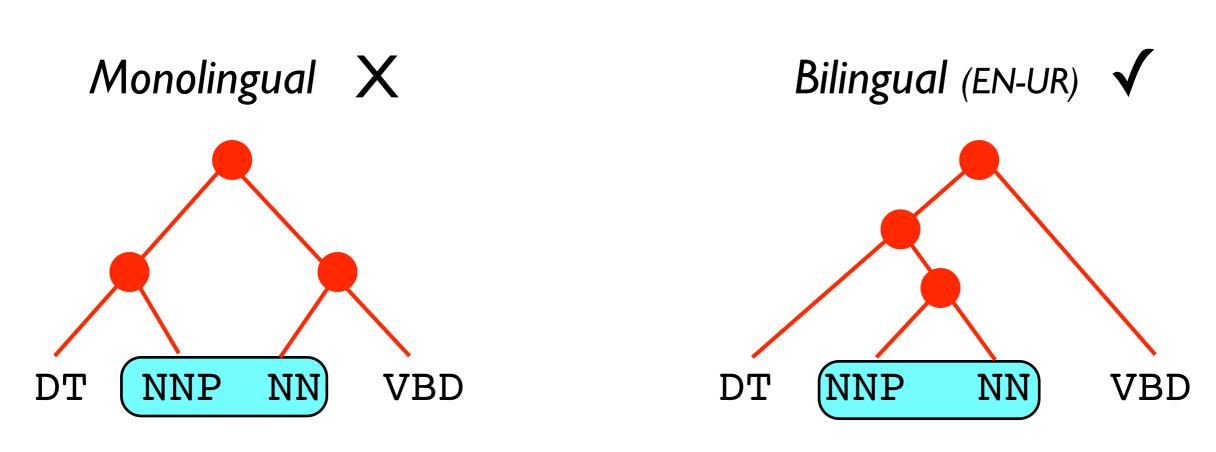


Bilingual (EN-UR) ✓





 $Pr_{mono}$  (NNP NN) <  $Pr_{bi}$  (NNP NN)



 $Pr_{mono}$  (NNP NN) <  $Pr_{bi}$  (NNP NN)

English: NNP NN
Urdu: NNP OF NN

#### Conclusions

Key idea: Use bilingual cues to learn better unsupervised monolingual models of grammar

- Adapt Tree Alignment to probabilistic setting:
  - Discover partial shared structure
  - Allow language-specific divergence
  - Computationally tractable
- Achieve improved performance on five corpora, across all sentence lengths

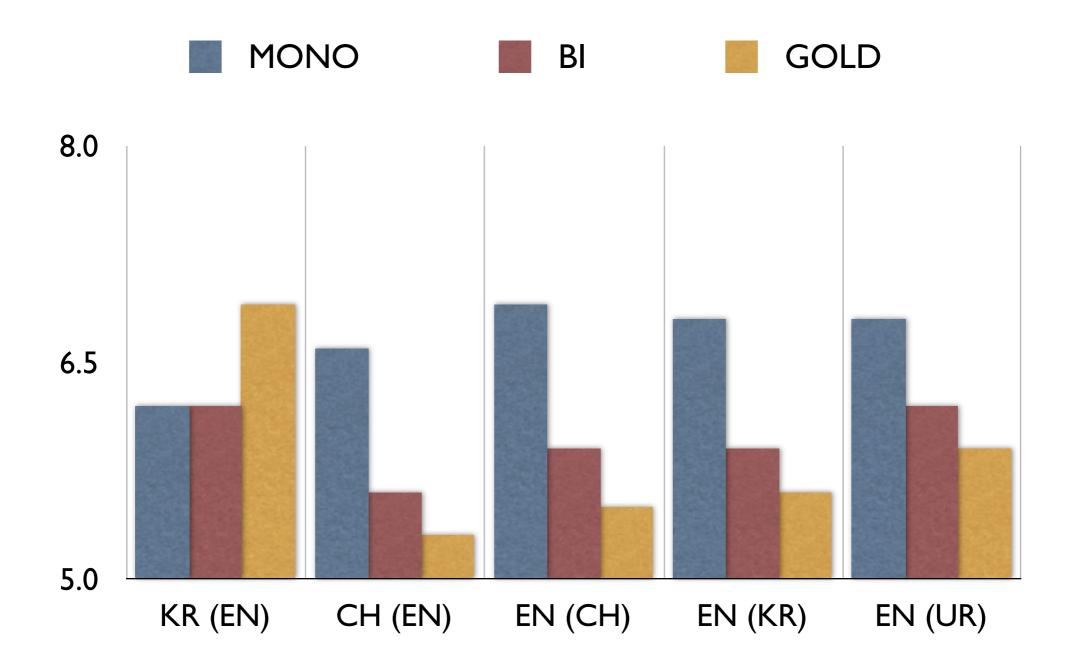
# Thank you!

# Analysis Entropy of constituent tag sequences

Percentage of a		MONO	BI	GOLD
tree node	CHEN	6.6	5.6	5.3
CH-EN	ENCH	6.9	5.9	5.5
UR-EN	KREN	6.2	6.2	6.9
KR-EN	ENKR	6.8	5.9	5.6
	ENur	6.8	6.2	5.9
	avg	6.7	6.0	5.8

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