Relieving the Computational Bottleneck: Joint Inference for Event Extraction with High-Dimensional Features

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Event Extraction

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  - BioNLP Genia event extraction task concerns the extraction of instances of bio-molecular event types (Kim et al., 2009)

An Example of BioNLP Events

… demonstrated that HOIL-1L interaction protein (HOIP) is recruited to CD40 in a TRAF2-dependent manner …

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Events can be nested.

Standard Pipeline Approach

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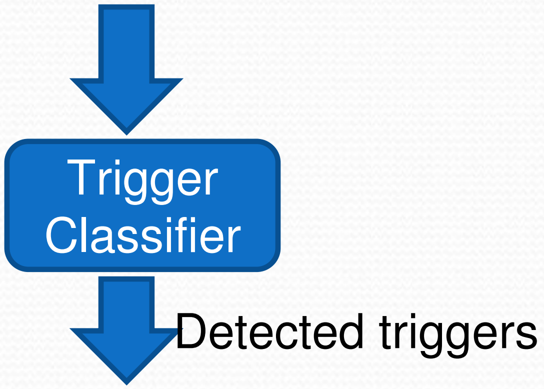
Step 1: Detect if a token is a trigger and if so, assign a event/trigger type to it



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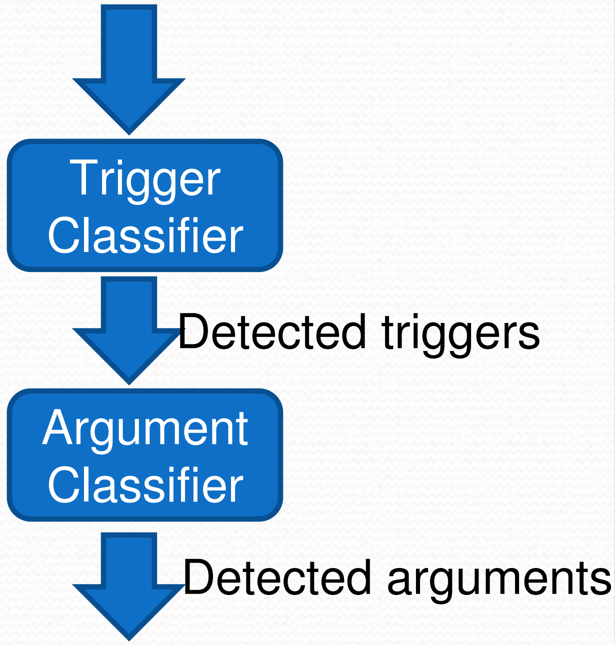

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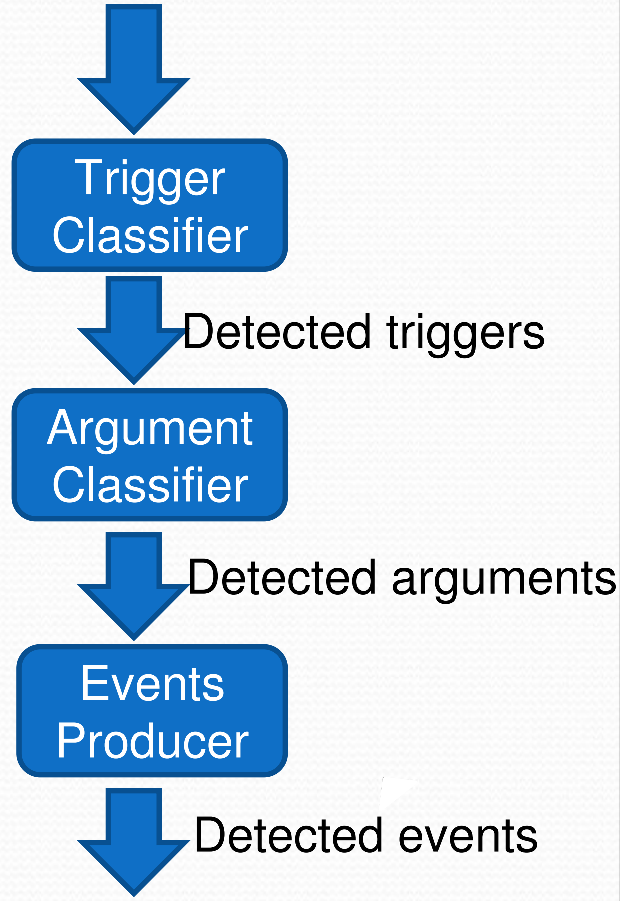

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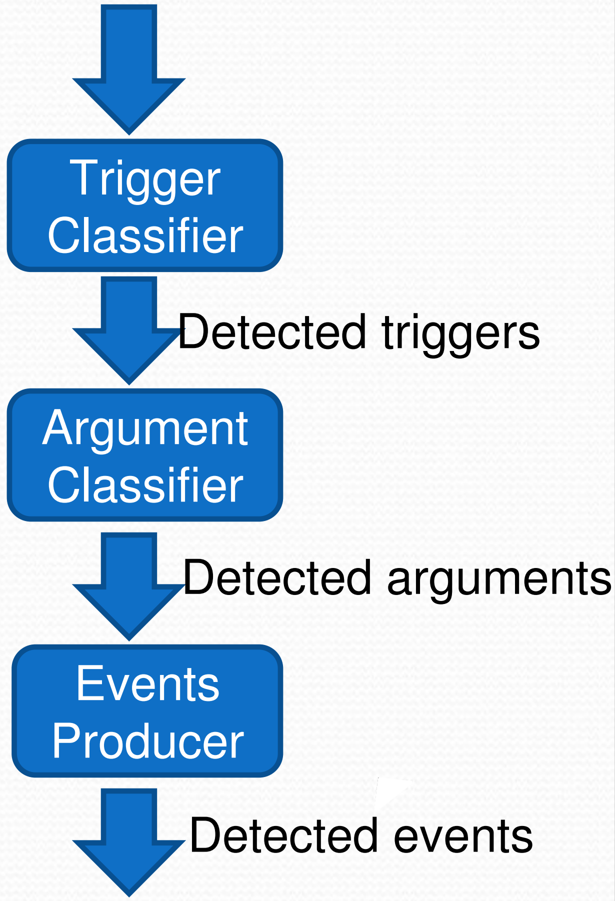

Steps 1 and 2 are difficult, while Step 3 is trivial

Pipeline Approach: Pros and Cons

- **Pros**
  - Approach is simple and straightforward
  - Uses an efficient learner (e.g., SVMs) in each step, thus enabling the use of high-dimensional features
    - Features such as n-grams of context words, n-grams of words/POS/dependency relations extracted from dependency paths are important for event extraction

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- **Cons**
  - Error may propagate from one stage to the next
  - Each trigger/argument is detected independently, thus failing to capture the relationships between neighboring triggers, neighboring arguments, etc.

Pipeline Approach

- achieved state-of-the-art results in BioNLP Genia event extraction despite its weaknesses
  - BioNLP’13: Hakala et al.(2013)
  - BioNLP’09 and BioNLP’11: Miwa et al. (2012)

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Can we improve further? If so, how?

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Try to overcome the weaknesses of the pipeline approach

Joint Inference

- **Markov Logic Networks (MLNs)**
  - Riedel et al. (2009), Poon and Vanderwende (2010)

- **Pros**
  - can avoid error propagation
    - by jointly detecting triggers and arguments
  - can model dependencies between triggers/arguments

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  - Because they include a highly simplified model ignoring powerful high-dimensional features
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  - The complexity of inference is high
    - E.g.: $Word(w_1,p-1) \wedge Word(w_2,p) \wedge Word(w_3,p+1) \rightarrow Type(p, T)$
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assignment of values to variables

Goal

- Combine the strengths of the pipeline approach and MLNs for event extraction

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Propose a model for event extraction based on **MLNs** that can handle **high-dimensional** features

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  - The Genia event extraction task
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  - **Regulation** event
    - One protein or event as its ***THEME*** argument and optionally one protein or event as its ***CAUSE*** argument

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  A weight specifies how important it is to satisfy the constraint
    - **hard formula**: infinite weight
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      - Mother(x,y) → Below45(x)
  - A **grounding** of a formula is an assignment of values to the variables in the formula
    - In Mother(x,y) → Below45(x), if each of x and y has 10 values, then the formula has 10 x 10 = 100 groundings

MLNs: Preliminaries

- A world $\boldsymbol{\omega}$ is an assignment of values to all ground predicates
  - Father(Bob,John)=T, Father(Bob,Ted)=F, Father(Jack,Matt)=T, Male(Bob)=T, Male(Jesse)=F, …

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ω is more probable if more formulas are satisfied more often

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MLNs: Preliminaries

- The key inference task over MLNs is finding the most probable world (a.k.a. the MAP task):

$$\arg\max_{\omega} P(\omega) = \arg\max_{\omega} \sum_{i} w_i N(f_i, \omega)$$

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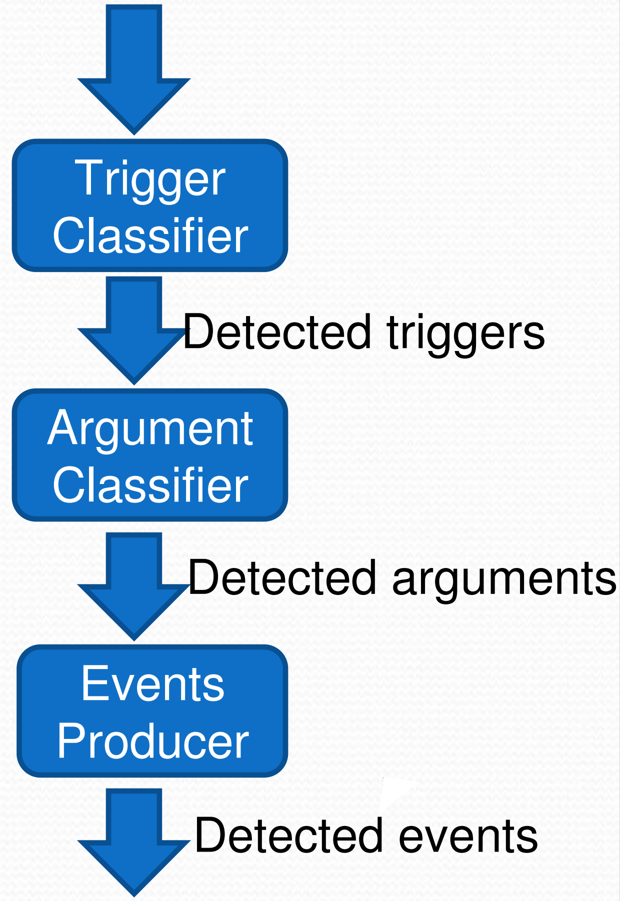
Baseline System

- Adopts the standard pipeline approach
  - trigger classification followed by argument classification



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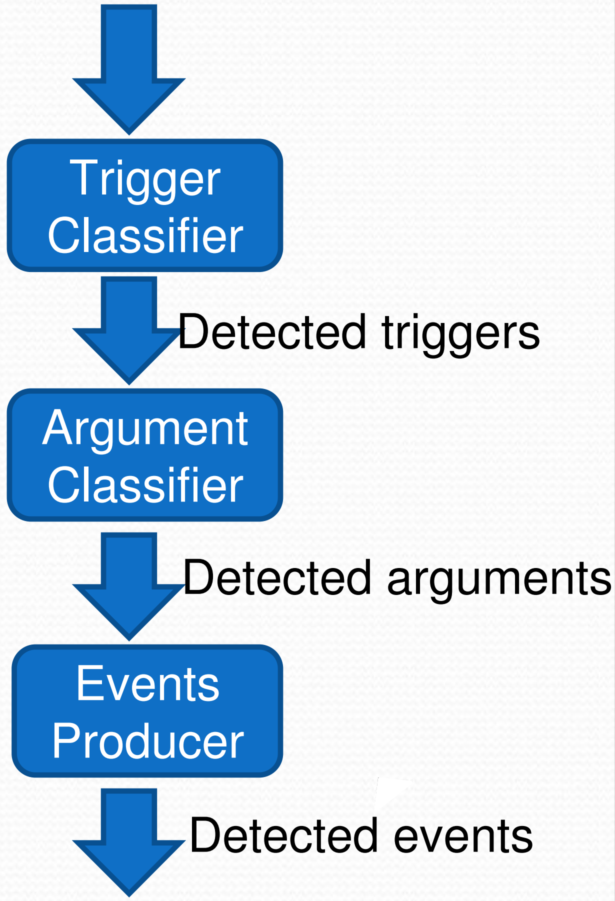

Training the Trigger Classifier

- **Training instance creation**
  - Create one training instance for each **candidate trigger** in each training document
    - Candidate triggers are verbs, nouns and adjectives in the text
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- **Learning algorithm**
  - SVM-multiclass

Training the Trigger Classifier

- Features computed on a candidate trigger t

Token features	The lexical string, lemma, stem, POS of t and its surrounding tokens in a window of 2; word n-grams (n=1,2,3) of t and its context words; whether t contains an uppercase letter or a symbol; …
Dependency features	Compute features based on the shortest dependency path p from t to the nearest protein: vertex walk in p; edge walk in p; n-grams (n-2,3,4) of the stemmed words associated with p's vertices; n-grams (n=2,3,4) of the POS tags of the words associated with p's vertices; …

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Over 3 million features

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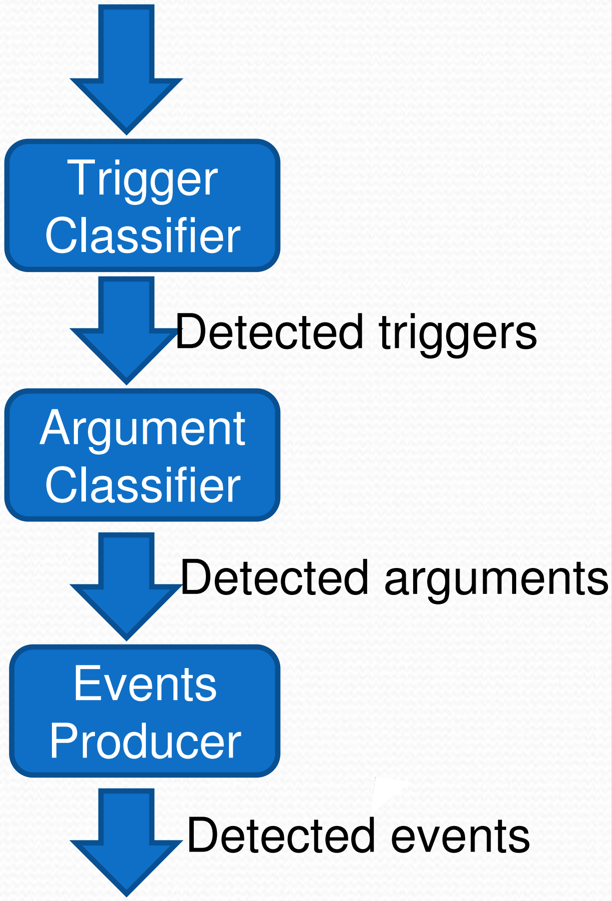

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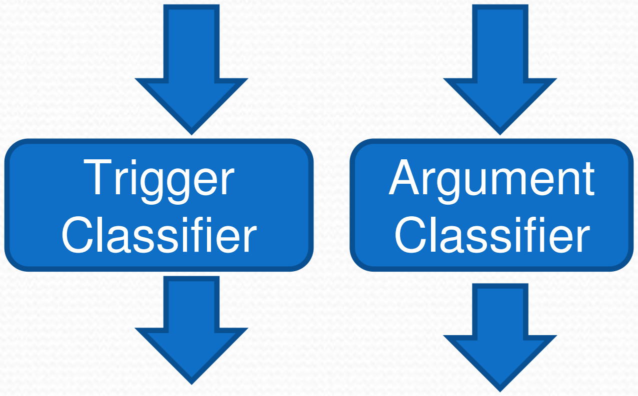
Our MLN Approach to Event Extraction

- **Goal**: design a model for event extraction that combines the strengths of SVMs and MLNs
  - can employ **high-dimensional** features
  - can model the **dependencies** between different data instances

Our Approach: An Overview

Step 1: Learn the SVM trigger and argument classifiers using high-dimensional features as in the **Baseline**



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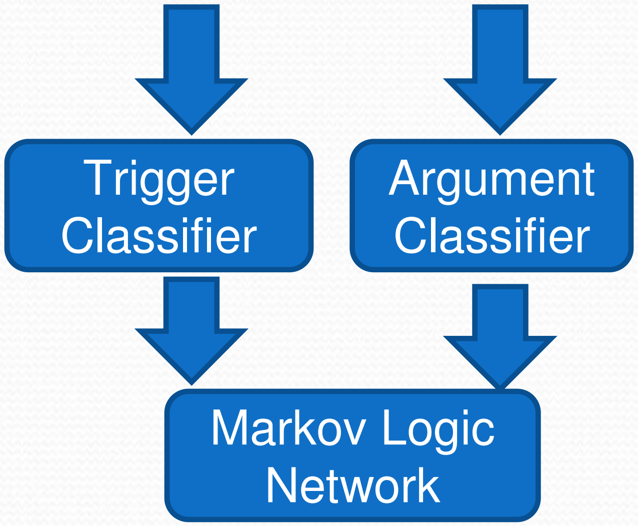

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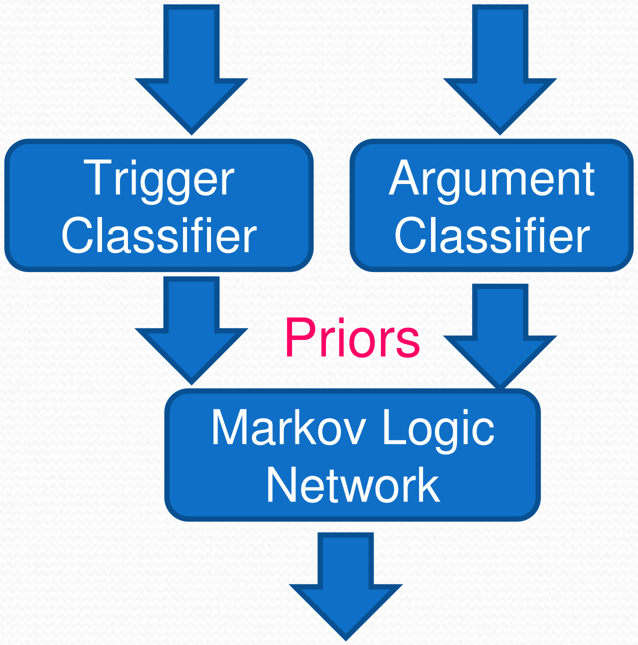

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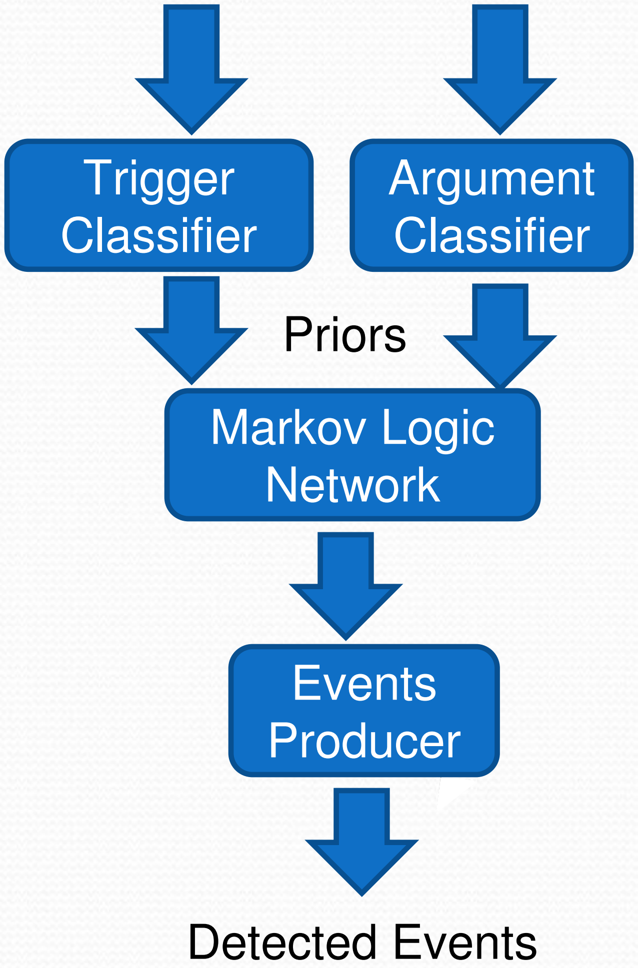

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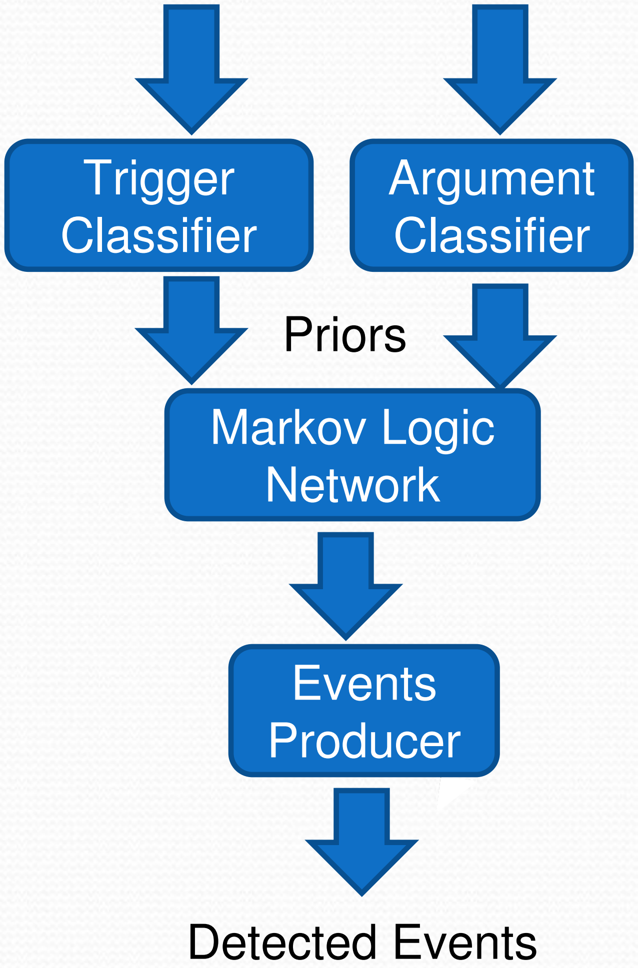

BioMLN: 3 kinds of Predicates

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"!" means that exactly one *ttype* makes the predicate true for each combination of *sid* and *tid*

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The token in sentence *sid* at position *tid* corresponds to a **Simple** or **Binding** event

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  $\texttt{TriggerType}(sid, tid, ttype!)$

  $\texttt{ArgumentRole}(sid, aid, tid, arole!)$

- **Hidden predicates:** model latent random processes

  $\texttt{Simple}(sid, tid)$

  $\texttt{Regulation}(sid, tid)$

The token in sentence *sid* at position *tid* corresponds to a **Simple** or **Binding** event trigger

The token in sentence *sid* at position *tid* corresponds to a **Regulation** event trigger

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dtype is the dependency type in the dependency parse tree that connects the token at position ***tid*** to the token at position ***aid*** in sentence ***sid***

BioMLN: 9 Formulas

1. $\exists t$ $\texttt{TriggerType}(i,j,t)$.

2. $\exists a$ $\texttt{ArgumentRole}(i,k,j,a)$.

3. $\neg\texttt{TriggerType}(i,j,None) \Rightarrow \exists k$ $\texttt{ArgumentRole}(i,k,j,Theme)$.

4. $\texttt{Simple}(i,j) \Rightarrow \neg \exists k$ $\texttt{ArgumentRole}(i,k,j,Cause)$.

5. $\texttt{TriggerType}(i,j,None) \Leftrightarrow \texttt{ArgumentRole}(i,k,j,None)$.

6. $\neg\texttt{ArgumentRole}(i,k,j,None) \wedge \neg\texttt{TriggerType}(i,k,None) \Rightarrow \texttt{Regulation}(i,j)$.

7. $\texttt{Simple}(i,j) \Leftrightarrow \texttt{TriggerType}(i,j,Simple1) \vee \ldots \vee \texttt{TriggerType}(i,j,Binding)$.

8. $\texttt{Regulation}(i,j) \Leftrightarrow \texttt{TriggerType}(i,j,Reg) \vee \texttt{TriggerType}(i,j,PosReg)$
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Each candidate trigger/argument has a type/role

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Hidden predicates are clusters of trigger types

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Capture dependencies between triggers and arguments

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MLN Structure – Joint Formulas

Hard constraints:
infinite weights

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Soft constraints: weights need to be learned

Weight Learning for Soft Formulas

- Could use gradient descent to maximize the conditional log-likelihood of the query and the hidden variables given an assignment to the evidence variables

$$w_j^{t+1} = w_j^t - \alpha(\mathbb{E}_{\mathbf{w}}(n_j) - n_j)$$

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expected number of groundings in which the j-th formula is satisfied given the current weight vector

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Computing the expectation requires performing inference over the MLN and is intractable

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Approximate the number of satisfied groundings in the MAP assignment

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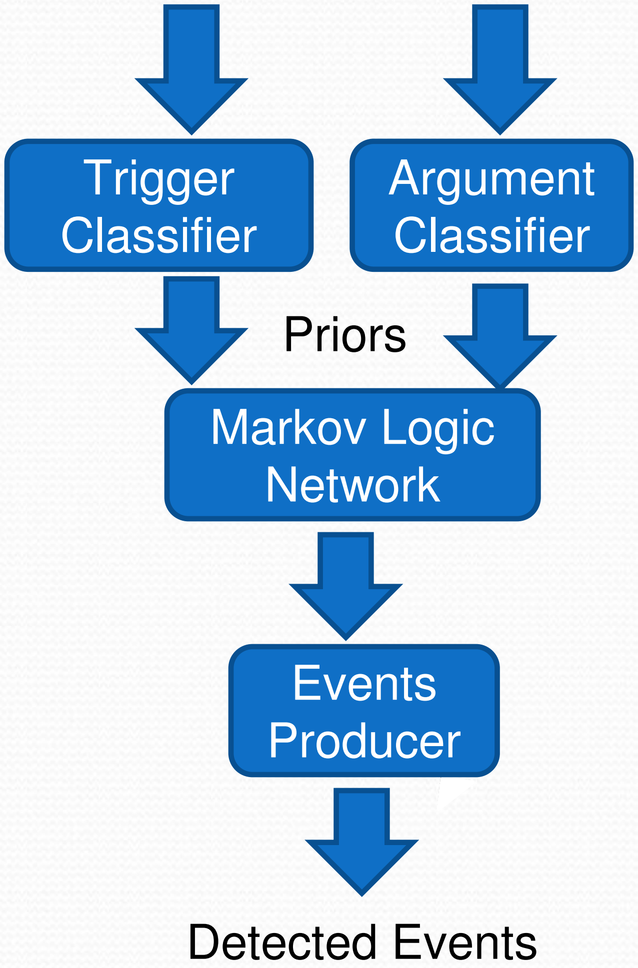
Approximate the number of satisfied groundings in the MAP assignment
Easier to compute the MAP assignment than the expectation

Our Approach: An Overview

Step 1: Learn the SVM trigger and argument classifiers using high-dimensional features as in the **Baseline**

Step 2: Design an MLN whose formulas encode the soft and hard constraints on the predicates

Step 3: Encode SVM output as prior knowledge in the MLNs



Using the SVM Output as Priors for the MLN

- Two soft clauses are added into the MLN:

$\texttt{TriggerType}(i,+j,+t)$ $\texttt{ArgumentRole}(i,+k,+j,+a)$

'+' means a separate weight is to be learned for each unique combination of j and t

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- Use these confidence values as the weights of these soft formulas
  - Provide prior knowledge for the MLN
    - High-dimensional features implicitly used by the MLN
  - In practice, we need to **scale** these confidence values

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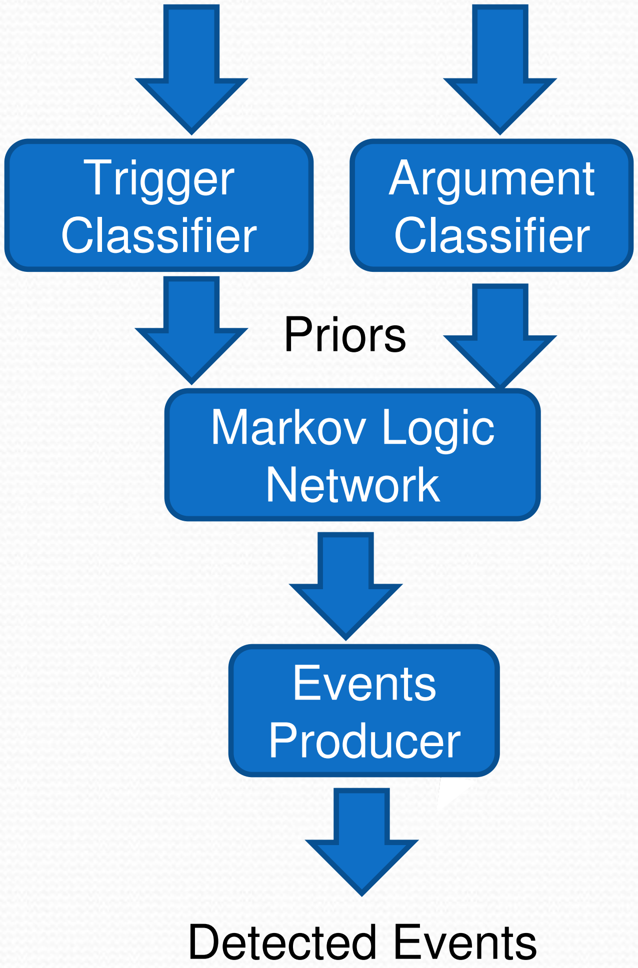

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- Perform MAP inference
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How?

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2. Compute the MAP solution using standard solvers

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- But.. this naive approach is infeasible because of the huge size of the network:
  - Assuming 1000 sentences and 10 tokens per sentence, 100K groundings will be generated for one formula:

$$\neg\texttt{TriggerType}(i,j,None) \Rightarrow \exists k\ \texttt{ArgumentRole}(i,k,j,Theme).$$

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  - Decompose the network into several disconnected components

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    - The MAP computation is decomposable
      - can perform MAP inference for each sentence independently
- So.. we can create one MLN per sentence
  - keep only one sentence's grounding in memory

Plan for the Talk

- Preliminaries
  - The Genia event extraction task
  - Markov Logic Networks
- Baseline system
- Our MLN approach
- Evaluation

Evaluation: Goal

- Evaluate our MLN approach to event extraction

Evaluation: Datasets and Statistics

Dataset	#Papers	#Abstracts	#Trigger types	#Events
BioNLP'13	(10,10,14)	(0,0,0)	13	(2817,3199,3348)
BioNLP'11	(5,5,4)	(800,150,260)	9	(10310,4690,5301)
BioNLP'09	(0,0,0)	(800,150,260)	9	(8597,1809,3182)

- (x,y,z): x in training, y in development, and z in test

Evaluation: Scoring Setting

- Scores obtained by submitting our output to the official online evaluation tool under the **approximate span**, **recursive evaluation** setting

Results on the BioNLP'13 Test Data

System	Rec.	Prec.	F1
Our System	48.95	59.24	**53.61**
EVEX (Hakala et al., 2013)	45.44	58.03	50.97
TEES-2.1 (Björne and Salakoski, 2013)	46.17	56.32	50.74
BIOSEM (Bui et al., 2013)	42.47	62.83	50.68
NCBI (Liu et al., 2013)	40.53	61.72	48.93
DLUTNLP (Li et al., 2013a)	40.81	57.00	47.56

- Best systems on this dataset:
  - EVEX, TEES-2.1 and DLUTNLP: pipeline learning systems
  - BIOSEM: a rule based system
  - NCBI: the only joint model using subgraph isomorphism
- Our system beats the best-performing system

Comparison with Baseline on BioNLP'13

	SVM			MLN+SVM		
Type	**Rec.**	**Prec.**	**F1**	**Rec.**	**Prec.**	**F1**
Simple	64.47	87.89	74.38	73.11	78.99	75.94
Protein-Mod	66.49	79.87	72.57	72.25	69.70	70.95
Binding	39.04	50.00	43.84	48.05	43.84	45.85
Regulation	23.51	56.21	33.15	36.47	50.86	42.48
Overall	37.90	67.88	**48.64**	48.95	59.24	**53.61**

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Overall	37.90	67.88	**48.64**	48.95	59.24	**53.61**

- MLN+SVM beats our SVM baseline by nearly 5 points
  - Joint inference using MLN is important
  - Performance on **Regulation** events improves by 9.33 points

Results on the BioNLP'11 Test Data

System	Rec.	Prec.	F1
Our System	53.42	63.61	**58.07**
Miwa12 (Miwa et al., 2012)	53.35	63.48	57.98
Riedel11 (Riedel et al., 2011)	—	—	56
UTurku (Björne and Salakoski, 2011)	49.56	57.65	53.30
MSR-NLP (Quirk et al., 2011)	48.64	54.71	51.50

- Best systems on this dataset:
  - Miwa12: a pipeline system using coreference features
  - Riedel11: a joint model using dual decomposition
  - Uturku and MSR-NLP: pipeline systems

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- Best systems on this dataset:
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- Even without using coreference features, our system
  - performs marginally better than Miwa12
  - beats the best joint model and other two best pipeline models

Results on the BioNLP'09 Test Data

System	Rec.	Prec.	F1
Miwa12 (Miwa et al., 2012)	52.67	65.19	58.27
Our System	53.96	63.08	**58.16**
Riedel11 (Riedel et al., 2011)	–	–	57.4
Miwa10 (Miwa et al., 2010a)	50.13	64.16	56.28
Bjorne (Björne et al., 2009)	46.73	58.48	51.95
PoonMLN (Poon&Vanderwende,2010)	43.7	58.6	50.0
RiedelMLN (Riedel et al., 2009)	36.9	55.6	44.4

- Best systems on this dataset:
  - Miwa12: a pipeline system with a coreference feature
  - Riedel11: a joint model using dual decomposition
  - Miwa10 and Bjorne: pipeline systems without coreference features
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RiedelMLN (Riedel et al., 2009)	36.9	55.6	44.4

- Our system
  - outperforms previous MLN-based systems, the best joint model, and pipeline systems without coreference features
  - is only marginally worse than Miwa12, which uses coreference features

Summary

- Presented a general approach for exploiting the power of high-dimensional features in MLNs
- Obtained the best or second best score on the three Genia event extraction datasets