#### Detecting Adverse Drug Reaction in Drug Labels using a Cascaded Sequence Labeling Approach

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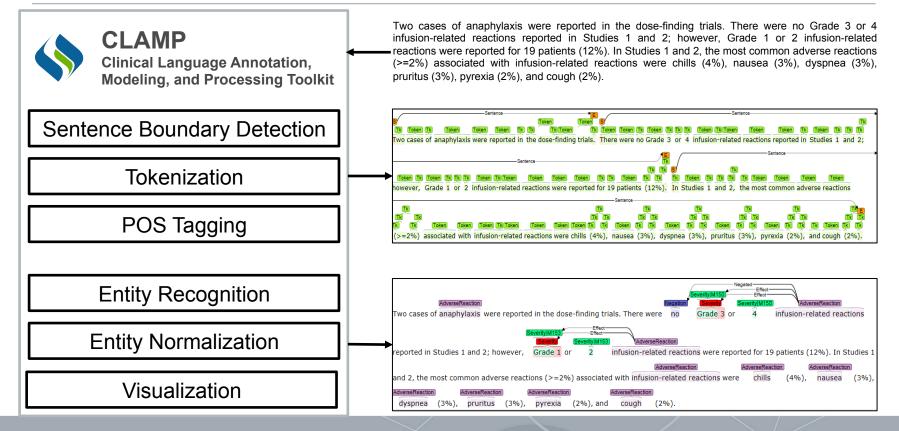
#### Introduction

- TAC 2017 ADR Challenge
  - Adverse Drug Reaction Extraction from Drug Labels
- We participated in all four tasks
  - Task 1 Extract mentions of *AdverseReactions* and modifier concepts (i.e., *Severity*, *Factor*, *DrugClass*, *Negation*, and *Animal*)
  - Task 2 Identify the relations between *AdverseReactions* and their modifier concepts (i.e., *Negated*, *Hypothetical*, and *Effect*)
  - Task 3 Identify positive *AdverseReaction* mentions in the labels
  - Task 4 Map recognized positive AdverseReaction to *MedDRA PT*(s) and *LLT*(s).



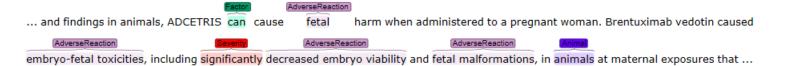
	#drug labels	Usage
Training	101	Developing models and optimizing parameters
Development	2,208	Training word embeddings and rule development
Test	99	Testing

#### **Pre-processing and baseline approaches**

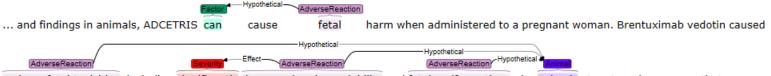


# Task 1&2: Extract *AdverseReactions*, related mentions, and their relations

Task 1: Named Entity Recognition



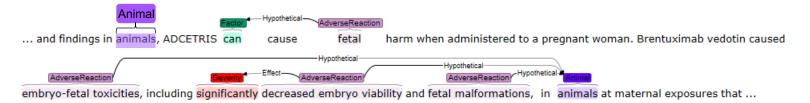
• Task 2: Relation Extraction



embryo-fetal toxicities, including significantly decreased embryo viability and fetal malformations, in animals at maternal exposures that ...

#### **Identified Issues – related mention recognition**

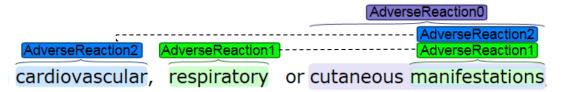
• A related mention is not annotated in the gold standard if it is not associated with any *AdverseReaction* 



- Issue 1: Cannot train a machine-learning based NER system directly
- **Issue 2**: Missing some negative relation samples, thus making it difficult for the traditional relation classification approach, which requires for both positive and negative candidates for training

### **Identified Issue – Disjoint/overlapping entities**

• Example of disjoint entities



- **Issue**: Cannot handle disjoint entities using the traditional NER approaches
  - Basic assumptions for a machine learning-based NER system
    - entities do not overlap with one another
    - each entity consists of contiguous words

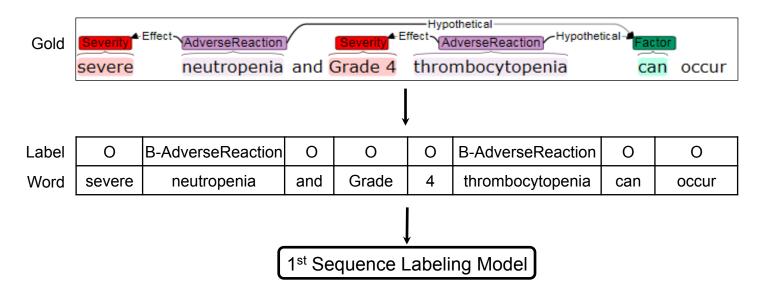
#### **Our approach - Cascaded Sequence Labeling Models**

• Model 1 – Sequence labeling model for AdverseReaction only

 Model 2 – Recognize both related mentions and their relations to the target AdverseReaction mentions at the same time, using one sequence labeling model

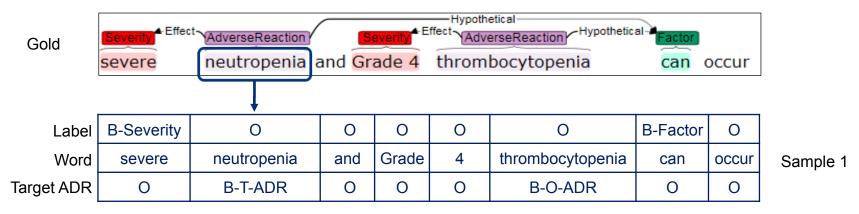
#### **Model 1 – AdverseReaction NER**

• Train 1<sup>st</sup> sequence labeling model, recognize AdverseReaction only



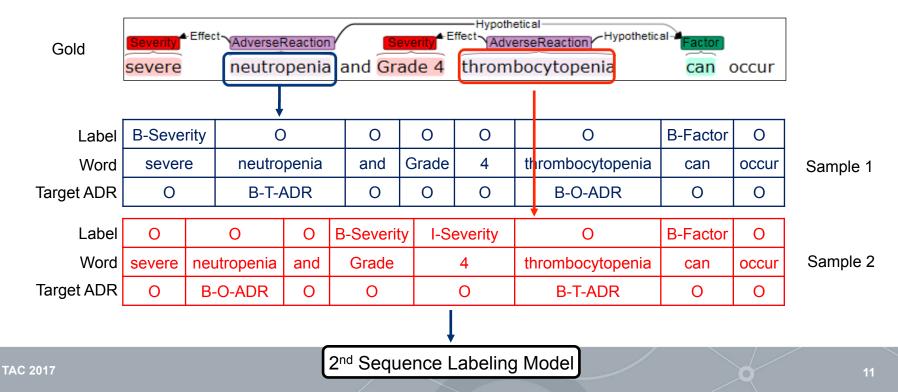
#### Model 2 – Related mentions and relations

 Train 2<sup>nd</sup> sequence labeling model, focus on modifier concepts and their relations with AdverseReactions together

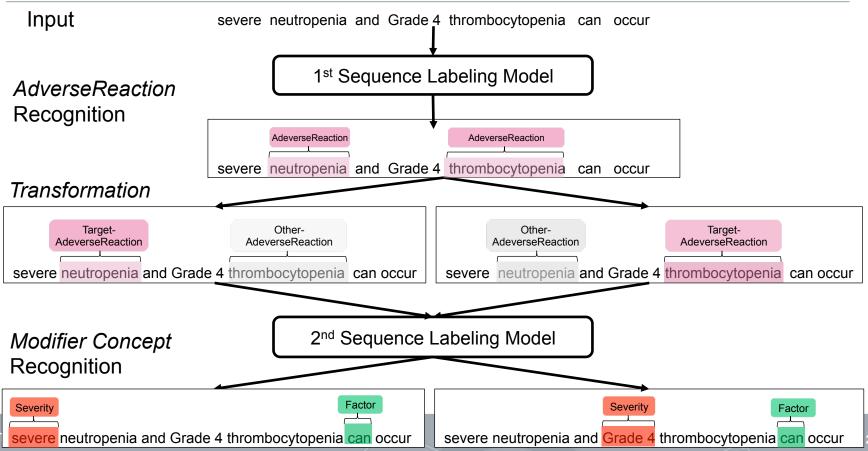


#### Model 2 – Related mentions and relations

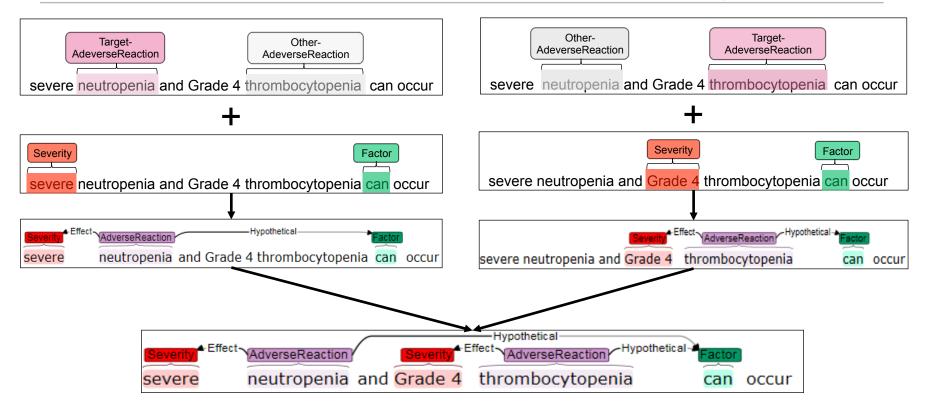
 Train 2<sup>nd</sup> sequence labeling model, focus on modifier concepts and their relations with AdverseReactions



#### **Predict with Cascaded Sequence Labeling Models**



#### **Predict with Cascaded Sequence Labeling Models**

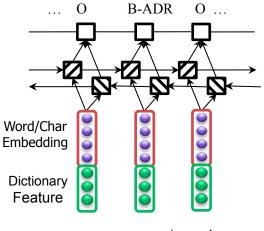


## **Sequence Labeling Models**

- Conditional Random Fields (CRF)
  - Linear-Chain CRF (Lafferty et al., 2001)
- Recurrent Neural Network (RNN)
  - LSTM-CRF: a bidirectional LSTM with a conditional random field layer above it (Lafferty et al., 2016)
    - Input layer: word embeddings + character embeddings
  - LSTM-CRF(Dict)
    - Use B-/I-/O to represent dictionary lookup results, initiate with random values
    - Input layer: word embeddings + character embeddings + dictionary features

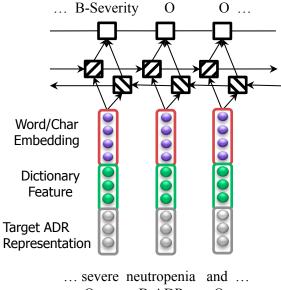
#### LSTM-CRF(Dict)

# 1<sup>st</sup> model for *AdverseReaction* recognition



... severe neutropenia and ...

## 2<sup>nd</sup> model for modifier concepts and relation extraction



#### **Our approach for disjoint entities**

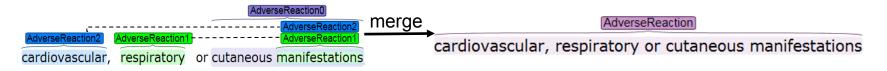
• Step 1 - Merge qualified disjoint entities into *pseudo* continuous entities

• Step 2 - Training NER models using *pseudo* continuous entities

• Step 3 - Split detected continuous entities using rules

## **Merge and Train disjoint entities**

- Merge qualified entities in gold standard
  - Discard, if
    - cross sentences, or
    - more than 3 segments, or
    - more than 5 tokens between two segments
  - Merge others



• Train NER models using 'continuous' entities

### **Split continuous entities**

#### Detect candidates

- has more than 4 tokens, or
- contain any of 'and', 'or', '/', ',', or '('
- Split using rules
  - Regular expression rules
    - $((grade|stage)\s+\d)\s^{(2)}and|or|\-|V)\s^{(d)} \rightarrow group(1)|group(2)+group(3)$
    - E.g. 'Grade 3 and 4'  $\rightarrow$  'Grade 3 ' and 'Grade ... 4'
  - Dictionary–based rules
    - Dictionary(~3000 pairs):<infections, viral>, <infections, protozoal>, <increase in, AST> etc.
      - Started from Training data, and
      - enriched with MedDRA terms
    - E.g. viral, or protozoal infections ' → 'viral ... infections' and 'protozoal infections'

#### Task 3 - Identify Positive AdverseReactions

• An AdverseReaction is positive if:

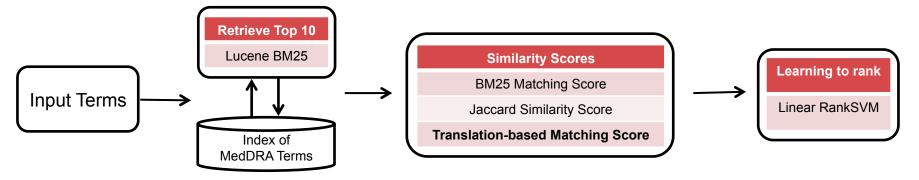
the AdverseReaction is not negated

AND

the *AdverseReaction* is not related by a *Hypothetical* relation to a *DrugClass* or *Animal* 

## Task 4 Link AdverseReactions to MedDRA codes

Work flow for MedDRA encoding

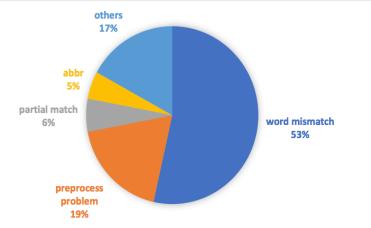


	Top 10 Concepts	Top 10 Concepts	BM25	Jaccard	TransLM	Top 10 Concepts	score
"elevations, lipids" →	Lipids	Lipids	11.12	0.5	-1.95	Lipids	0.73
	Lipid proteinosis	Lipid proteinosis	8.93	0.5	-5.74	Lipid proteinosis	0.63
	Lipid increased	Lipid increased	8.93	0.5	-0.76	Lipid increased	0.98

## **Translation-based similarity**

Motivation --- Word mismatch problem

Mention	Elevations, lipids
Simple Match	lipids
Ground-truth	lipids increased



- Machine translation model
  - Word-to-word translation probability
  - t = increased, w = elevations, p(w|t) = 0.6142

### **Train the word-to-word translation probabilities**

#### Prepare parallel corpus

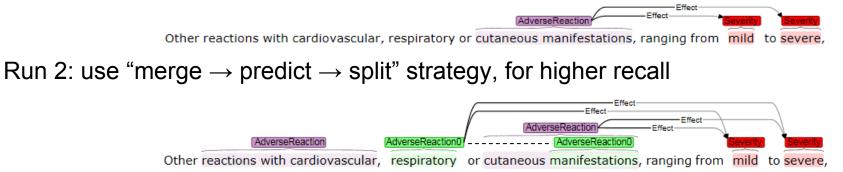
- From MedDRA, construct 53,368 mapping pairs <Low Level Term, Preferred Term>, e.g.
  - <Diseases of nail, Nail disorder>
  - <Bilirubin elevated, Blood bilirubin increased>
- From Training Data, construct 7,045 mapping pairs <Mention, Mapped MedDRA Term>, e.g.
  - <alt elevations, ALT increased>
  - <cardiovascular disease, cardiovascular disorder>
- Train word-to-word translation probability with IBM Model 1(Brown et al., 1993)

 $Pts = \epsilon/(l+1) \uparrow m \prod j = 1 \uparrow m \lim \sum i = 0 \uparrow l \lim p(t \downarrow j \mid s \downarrow i)$ 

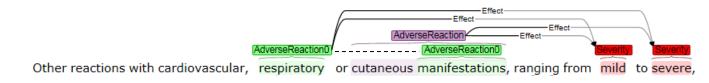
We use GIZA++ toolkit to train the translation probabilities

#### **Submissions**

• Run 1: discarded all disjoint *AdverseReactions*, for higher precision



• Run 3: combine Run 1 and Run 2, for higher F1



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#### **Results of submissions**

• The performances of the three runs of our system on all tasks

	Task 1		Task 2		Task 3			Task 4				
Run	+type		Full(+type)		Macro-			Macro-				
	Р	R	F1	Р	R	F1	Р	R	F1	Р	R	F1
1	83.78	79.74	81.71	51.67	44.45	47.79	82.61	81.88	81.65	84.04	86.67	84.79
2	80.22	84.40	82.26	46.24	48.32	47.26	78.77	85.62	81.39	80.83	89.90	84.53
3	82.54	82.42	82.48	50.24	47.82	49.00	80.69	85.05	82.19	83.02	89.06	85.33

#### **Results-1<sup>st</sup> model to recognize AdverseReactions**

#### CRF vs. RNN on non-disjoint AdverseReactions

- Training data set
- 5-fold cross validation
- Exact match

Model	Precision	Recall	F1-measure
CRF	88.05	77.60	82.50
LSTM-CRF	84.21	80.29	82.21
LSTM-CRF(Dict)	85.03	82.01	83.34

#### **Results- 1<sup>st</sup> model to recognize AdverseReactions**

#### • CRF vs. RNN, merged disjoint AdverseReactions

- Training data set
- 5-fold cross validation
- Exact match

Model	Precision	Recall	F1-measure
CRF	87.7	83.8	85.7
LSTM-CRF	85.4	87.8	86.6
LSTM-CRF(Dict)	86.7	90.0	88.3

# **Results- 2<sup>nd</sup> model to recognize related mentions and relations to AdverseReaction**

- CRF vs. RNN
  - Training data set, merged disjoint AdverseReactions
  - 5-fold cross validation
  - Gold AdverseReactions
  - Exact match

	Mentions	Mod	ifier Extra	ction	Relation Extraction			
Model	Type/To Entity	Р	R	F1	Р	R	F1	
	Animal	0.830	0.886	0.857	0.739	0.718	0.729	
	DrugClass	0.603	0.281	0.384	0.593	0.263	0.364	
CRF	Factor	0.747	0.681	0.712	0.711	0.625	0.665	
	Negation	0.833	0.561	0.671	0.789	0.504	0.615	
	Severity	0.881	0.698	0.779	0.788	0.625	0.697	
	Animal	0.884	0.864	0.874	0.815	0.746	0.779	
	DrugClass	0.528	0.305	0.387	0.547	0.272	0.363	
LSTM - CRF (Dict)	Factor	0.720	0.771	0.745	0.669	0.744	0.704	
	Negation	0.716	0.643	0.677	0.689	0.597	0.640	
	Severity	0.787	0.793	0.790	0.721	0.749	0.735	

### **Results of MedDRA encoding**

- Performances of different normalization methods
  - Training data set
  - 5-fold cross validation

	Macro-P	Macro-R	Macro-F1	%impr BM25
cTakes	88.39	75.55	81.28	
MetaMap	90.99	86.79	88.76	
BM25	87.82	90.56	89.11	
TransLM (MedDRA)	90.64	92.57	91.53	2.72
TransLM (MedDRA+TrainData)	93.09	94.42	93.70	5.15
Learning to Rank	93.18	94.58	93.83	5.30

#### **Discussion**

- A cascaded sequence labeling model for entity and relation extraction
  - Reasonable performance
  - Need further investigation to compare it with traditional relation classification methods
- RNN for entity and relation extraction
  - Better performance than CRF?
  - Knowledge/dictionary helps, worth further investigation
- Disjoint entities
  - What are the best strategies?
- Linking to MedDRA
  - Translation-based similarity methods

## Acknowledgement

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  - Qiang Wei M.S.
  - Hua Xu Ph.D.

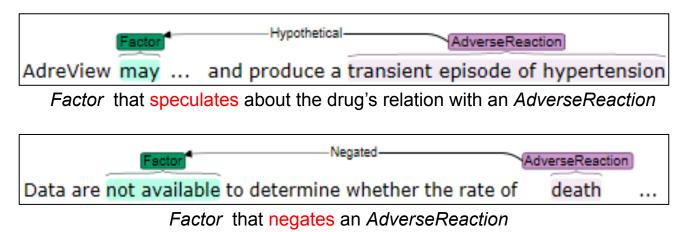
# Thank you!

#### Email me at: Hua.Xu@uth.tmc.edu



## **Detect Relation Type for** *<Factor*, *AdverseReaction>*

- Limitation of the Cascaded Sequence Labeling-based Approach
  - Cannot classify the relation type of a <modifier, AdverseReaction> pair



- Rule-based Post-processing
  - Negated: Factor is one of placebo, too small, other than, not available, no trial, etc.
  - Hypothetical: *Factor* is none of above