



Reconstruction of Coordination Ellipsis from Clinical Trial Eligibility Criteria Text

Using Natural Language Processing with Deep Learning

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Example Coordination Ellipsis In Criteria Text

- Participant has active infection with **hepatitis B or hepatitis C virus**.
- **Histologically or cytologically confirmed breast cancer** that is metastatic of unresectable.
- Documented **germline mutation in BRA1 or BRCA2** that is predicted to be deleterious or suspected deleterious
- **major stomach or bowel resections**
- Participants with **a personal or family history of long QT syndrome**

SCIENTIFIC DATA



OPEN

DATA DESCRIPTOR

Chia, a large annotated corpus of clinical trial eligibility criteria

Fabrício Kury^{1,4}, Alex Butler^{1,4}, ChiYuan^{1,4}, Li-heng Fu¹, Yingcheng Sun¹, Hao Liu^{1,2}, Ida Sim³, Simona Carini³ & Chunhua Weng¹✉

We present Chia, a novel, large annotated corpus of patient eligibility criteria extracted from 1,000 interventional, Phase IV clinical trials registered in ClinicalTrials.gov. This dataset includes 12,409 annotated eligibility criteria, represented by 41,487 distinctive entities of 15 entity types and 25,017 relationships of 12 relationship types. Each criterion is represented as a directed acyclic graph, which can be easily transformed into Boolean logic to form a database query. Chia can serve as a shared benchmark to develop and test future machine learning, rule-based, or hybrid methods for information extraction from free-text clinical trial eligibility criteria.

The Capstone Project Goals

- To leverage the CHIA dataset to improve biomedical NER
- To develop deep learning NLP models

Our Contributions

- We designed new tagging schemas for named entity recognition in Clinical Trial Summaries
 - We developed start-end labeling, E-label, Question Answering tagging schemas to mitigate ellipsis entity problems
 - We integrated domain knowledge from dictionary into model architecture
- We successfully extracted Ellipsis entities from CHIA
- Our enhanced model achieved 0.88 F1 score on CHIA data

Architecture

Model:

None-Transformers(Flair, SpaCy,sklearn-crfsuite)
Transformers(BERT, Bio-Clinical BERT, Pubmed-BERT)
Ensemble models
Dictionary enhancement

Data:

CHIA, a human-annotated clinical trial corpus (the largest so far)
COVID-19 for testing, the latest COVID-19 clinical trial corpus

Entity Labels:

Standard labeling method:
B(Begin), I(Inside), O(Outside)
Novel labeling method for ellipsis :
boundary label,
ellipsis label

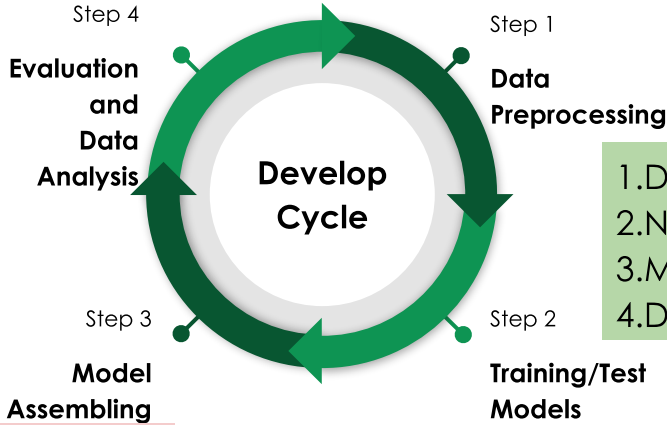
```
clinical 0  
central B-Condition  
nervous I-Condition  
dysfunction I-Condition
```

Major activities

1. Online deployment
2. UI: **Demo**

- Add datasets:
1. Dictionary
 2. Covid-19 dataset (generalizability)

1. Exact-match (new ver)
2. Relaxed-evaluation:
Token level
Character level
3. Definition: Inclusion Relation

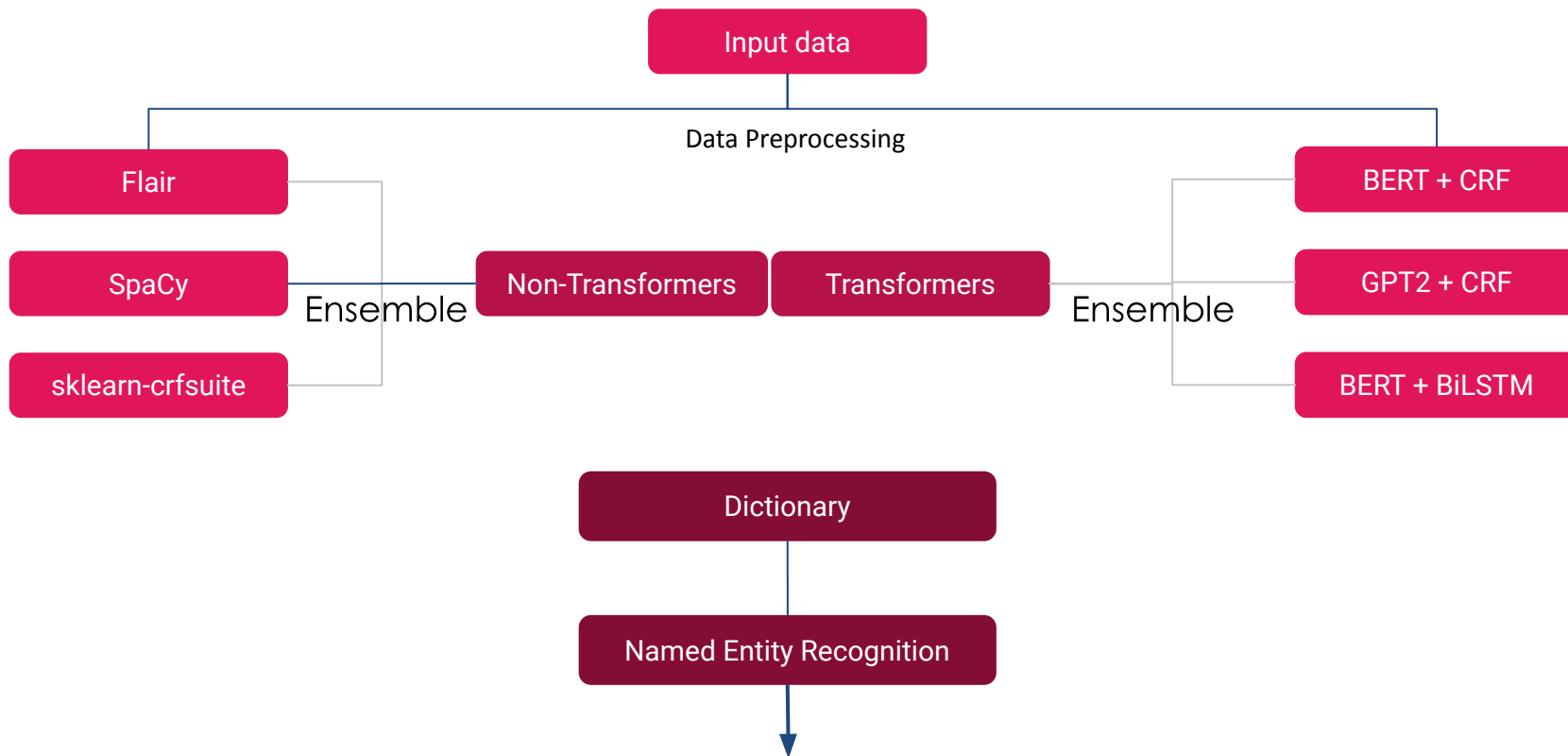


1. Dictionary preprocessing
2. New labeling method
3. Multi-Domain preprocessing
4. Data Imbalance (refine)

1. Training/Test on multi-domain entities
2. Covid-19 Test

1. **Model Ensembles**
2. Non-BERT, BERT
3. Relaxed-ensemble:
Token level
Character level
4. vector-ensemble

Pipeline



Four Level Evaluation Architecture

Strict

Exact Matching

I

word	,	lactose	malabsorption	,
label	O	B	I	O
pred	O	B	I	O

Label Refining

II

word	chronic	renal	failure
label	O	B	I
pred	B	I	I

Inclusion Relaxation

III

word	Extension	of	Local	tumor
label	B	I	I	I
pred	O	O	B	I

Position Relaxation

IV

word	tear	film	dysfunction	syndrome
label	B	I	I	O
pred	O	B	I	I

Relax

Baseline

Datasets vs model performances

%	Flair	SpaCy	Microsoft-BERT	Flair+BERT	Flair+SpaCy
CHIA	79.42 85	74.98 83	78.73 87	77.33 86	77.45 80.52
COVID-19	75.48 85.41	65.30 77.64	\	\	68.67
	sk-crfsuite	GPT2+CRF	BERT+CRF	BERT+CNN	BERT+BiLSTM
CHIA	69.65 76	67.50	82.23 87	80.45	72.67
COVID-19	60.07	\	76.73	77.89	\

Baseline Error Analysis

1. **HBV, HCV and HIV infections:**

Patient with Hepatitis B Virus (HBV) , Hepatitis C Virus (HCV) and Human

○ ○ B I I ○ B ○ ○ B I I ○ B ○ ○ B
Immunodeficiency Virus (HIV) infections
I I ○ B ○ I

2. **allergic disease or allergic reactions:**

history of allergic disease or reactions likely to be exacerbated by any

○ ○ B I ○ I ○ ○ ○ ○ ○ ○
component of the vaccine

○ ○ ○ ○

3. **alcohol or drug abuse**

Patients used to alcohol or drug (medication) abuse

○ ○ ○ B ○ B ○ B ○ I

Enhanced Architecture - I

Model: BiLSTM + CRF

Label: Ellipsis labels (E-label)

```
Exposure      E-common  
to E-common  
sun E-B  
or 0  
UV E-B  
radiations  E-I
```

```
Type      E-common  
I E-B  
or 0  
II E-B  
diabetes  E-common
```

```
History 0  
of 0  
blood E-B  
clotting E-I  
or 0  
bleeding E-B  
abnormalities E-common
```

Enhanced - Ellipsis Result

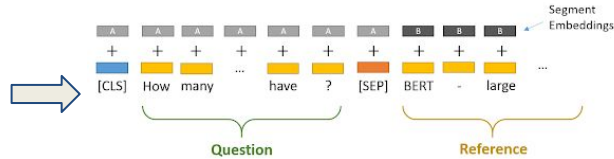
Datasets vs model performances Ellipsis
Evaluation on CHIA

BiLSTM	entity	test sentences
Total	128	54
Exactly correct	96	41
Rate	0.75	0.76

Enhanced Architecture - II

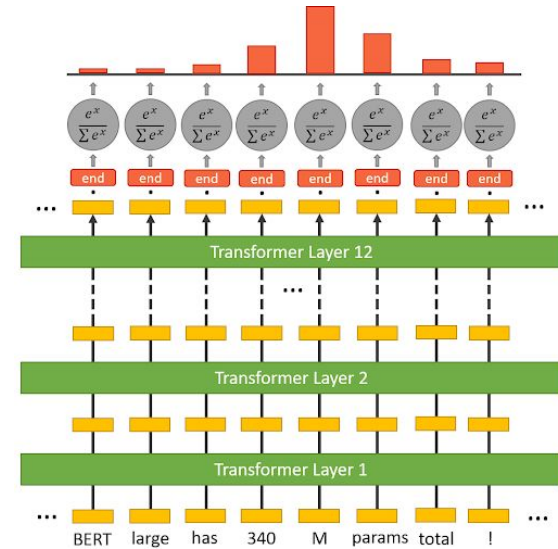
Model: Question Answering

Help extract boundary position.



Question: How many parameters does BERT-large have?

Reference Text: BERT-large is really big... it has 24 layers and an embedding size of 1,024, for a total of 340M parameters! Altogether it is 1.34GB, so expect it to take a couple minutes to download to your Colab instance.



Source: Chris McCormick

basal START E2
 or NA 0
 squamous MID E1
 cell MID E-common
 carcinoma MID E-common
 of MID E-common
 the MID E-common
 skin END E-common

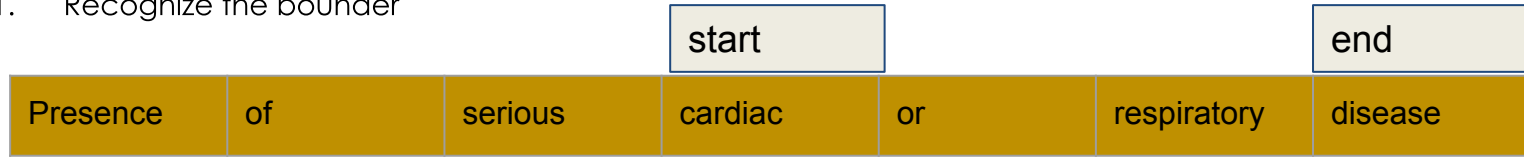


Corresponding labeling method

Enhanced Architecture - II

Procedure to recover ellipsis entity:

1. Recognize the boundary



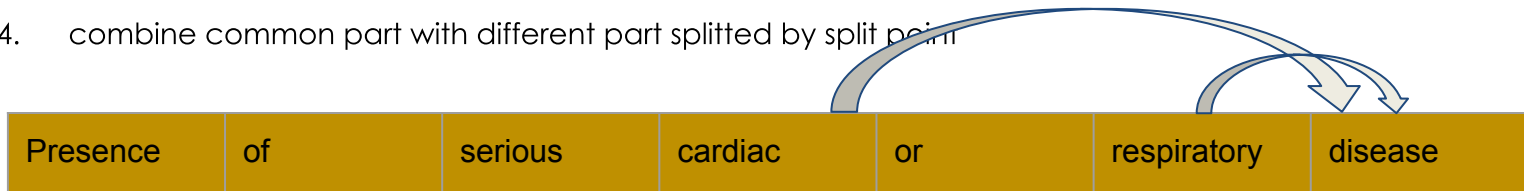
2. Finding split point like 'OR' 'AND' or punctuation



3. Finding common part



4. combine common part with different part splitted by split point



Ellipsis Test Result

Two type of errors:

1. boundary detection error:

Boundary detection error	boundary to be detected	correctly identified	rate
Total	54	48	88%

2. Ellipsis recovery error:

Ellipsis extraction error	entity to be extracted	correctly identified	rate
Total	108	97	89.8%

Discussion-Error Analysis(ellipsis)

1. Problems:
 - a. “abnormal physical examination , vital signs or 12 lead ECG” (OOV)
 - b. “Severe and/or chronic renal failure” (“and”, “/”)

2. In a nutshell, small training dataset

UI

A basic functioning version of the named entity tagging web application has been completed, which can be accessed at:

<http://34.121.40.143:9006>. One can use the website to submit clinical trials to go through named entity recognition.

The screenshot shows a web application interface for "Clinical Trial Summaries Demo". The header includes "Home" and "About Us" links. The main heading is "The Columbia Clinical Trial Summarizer" with the subtitle "Using Natural Language Processing with Deep Learning for Clinical Trial Summaries". A green "REFRESH" button is present. Below is the "Input Clinical Trial" section with a text area containing the sentence: "Adult patients with T2DM who are indicated to receive liraglutide ,not as first-line therapy , in addition to diet and exercise to improve glycemic control". Underneath are two dropdown menus: "Select Models:" with "ensemble" selected, and "Select Domain:" with "ALL" selected. The "Recognized Entities" section displays the same sentence with colored boxes around specific words: "Adult" (purple), "PER" (purple), "patients with" (grey), "T2DM" (green), "CON" (green), "who are indicated to receive" (grey), "liraglutide" (cyan), "DRU" (cyan), ".not as" (grey), "first-line" (orange), "therapy" (orange), and "PRO" (orange). A blue "RESET" button is at the bottom.

Summary

1. We have developed both traditional and deep learning models to the Named Entity Recognition task on CHIA data, in an End-to-End way.
2. We have implemented Question Answering, Dictionary, and Ensemble Learning to improve the boundary recognition
3. We have designed and implemented new labeling methods to solve Ellipsis Entity problems
4. We have proposed and implemented new evaluating methods for relaxed match

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Thank You!