A Neural Candidate-Selector Architecture for Automatic Structured Clinical Text Annotation

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Problem: Text Annotation

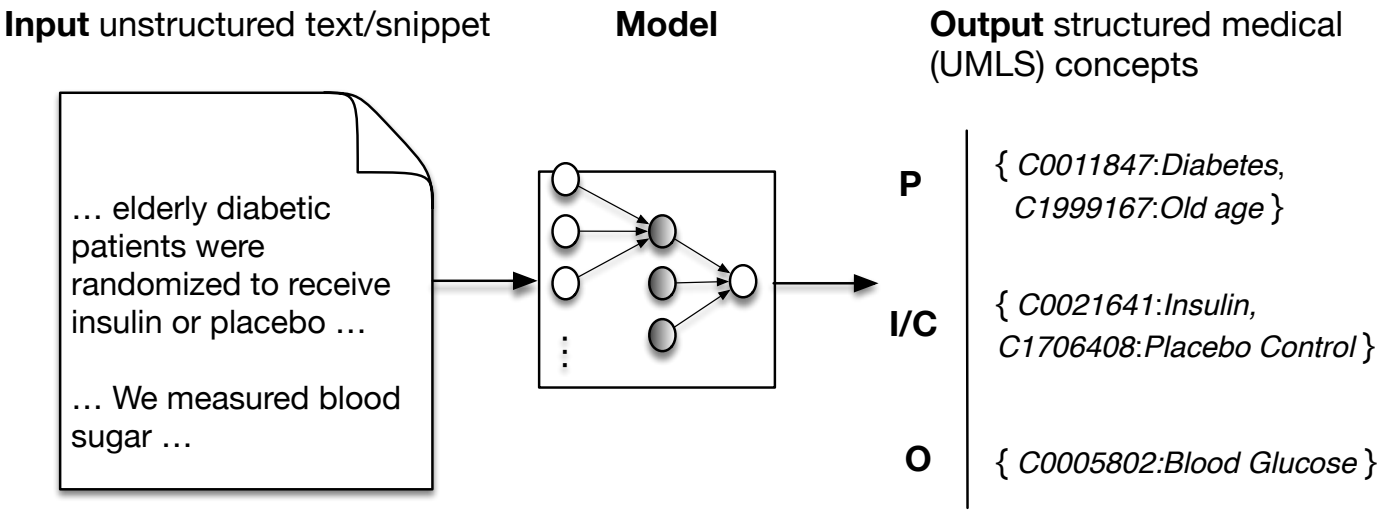


Figure: Illustration of the annotation task.

Problem: Clinical Trial Annotation

- Each clinical trial needs to be associated to multiple labels
- Labels are drawn from a controlled medical vocabulary
- Labels are associated to following disjoint categories:
  - Population
  - Intervention/Control
  - Outcome
- Vast output space for prediction
- Limited labelled training data

Motivation: Clinical Trial Annotation

- Correct labels are crucial during search for relevant literature
- Risk-of-bias is reduced with precise annotation
- Requires extensive human-effort to annotate the trials
- Takes time to annotate labels manually

Method: Candidate-Selector Architecture

- **Candidate Generation**: We generate candidate labels with high recall, to be passed on to the selector
- **Candidate Selection**: We prune the candidate set to obtain labels with high precision

Candidate Selection: Deep Model

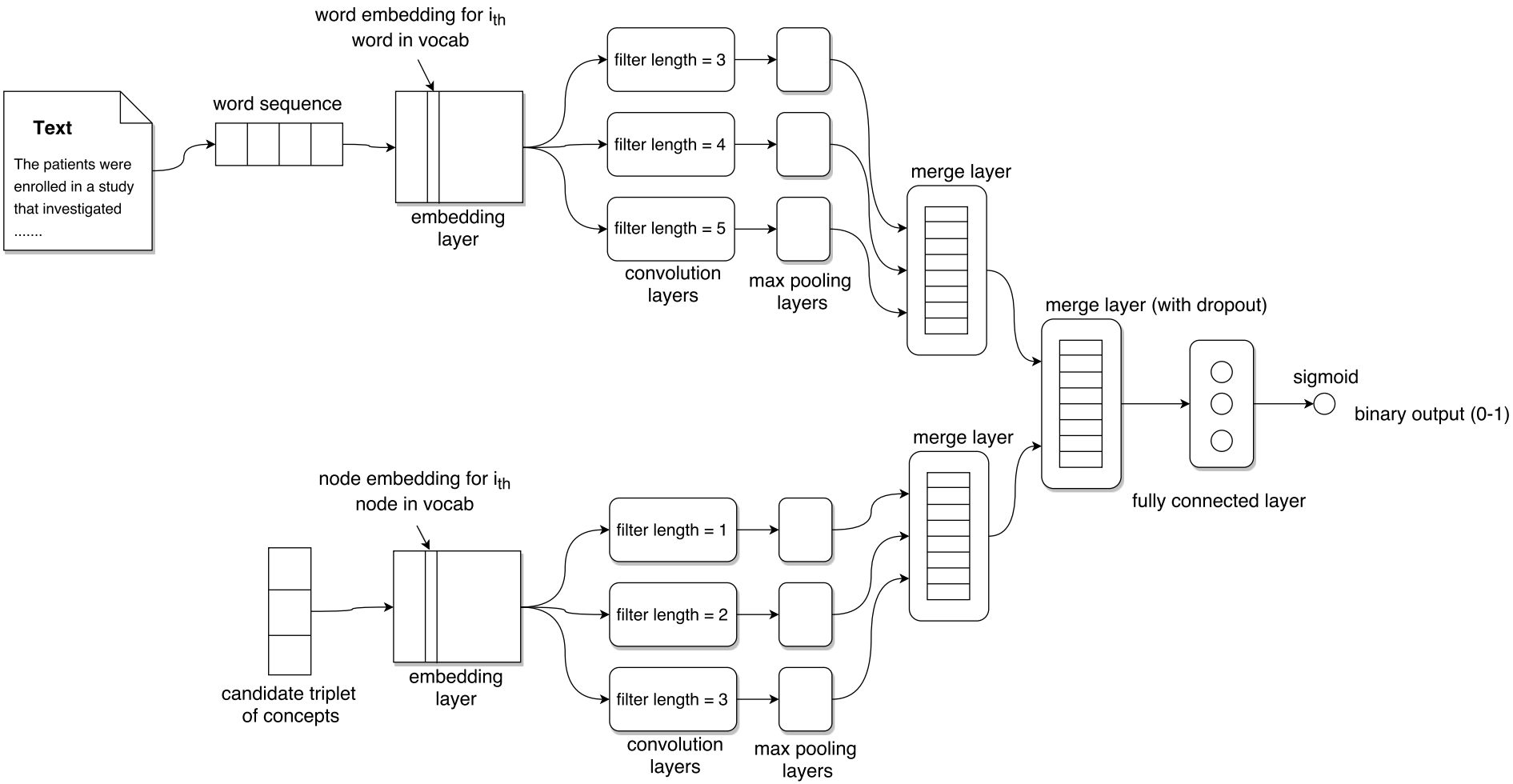


Figure: Candidate Selector Model

Candidate Selector: Model Training

- The model inputs during training are:
  - Free text (or abstract) that needs to be annotated
  - Candidate label triplets obtained for the given text
- Model output is a binary decision $\{0,1\}$
- Two types of triplets are constructed:
  - Positive triplets
  - Negative triplets

Candidate Selector: Model Training

- Positive triplets:
  - Formed by choosing one label each from P, I/C and O
  - Constructed from the ground truth annotations for P, I/C and O
  - All possible triplets are constructed using the given annotations.
- Negative triplets:
  - Non-existent triplets are constructed as negative samples
  - Help the model distinguish between relevant and irrelevant triplets

Candidate Selector: Model Training

- Two types of triplets used:
  - Complete triplets of the form $(c_P, c_{I/C}, c_O)$
  - Incomplete triplets of the form $\{(c_P, \_, \_), (c_P, c_{I/C}, \_)\}$
- Complete triplets used to learn joint distribution of labels
- Incomplete triplets useful for learning of marginals
- Ratio of # of positive triplets to # of negative triplets is 1:5

Candidate Generation

- At test time:
  - We generate candidates for each of the categories i.e. P, I/C and O
  - Using following two methods:
    - Metamap: It is a software deigned over the years to generate a list of concepts associated to a clinical text.
    - Multitask learning: We train a traditional multi-task deep learning model that can predict possible candidates during test time for a given text.

Metamap Service

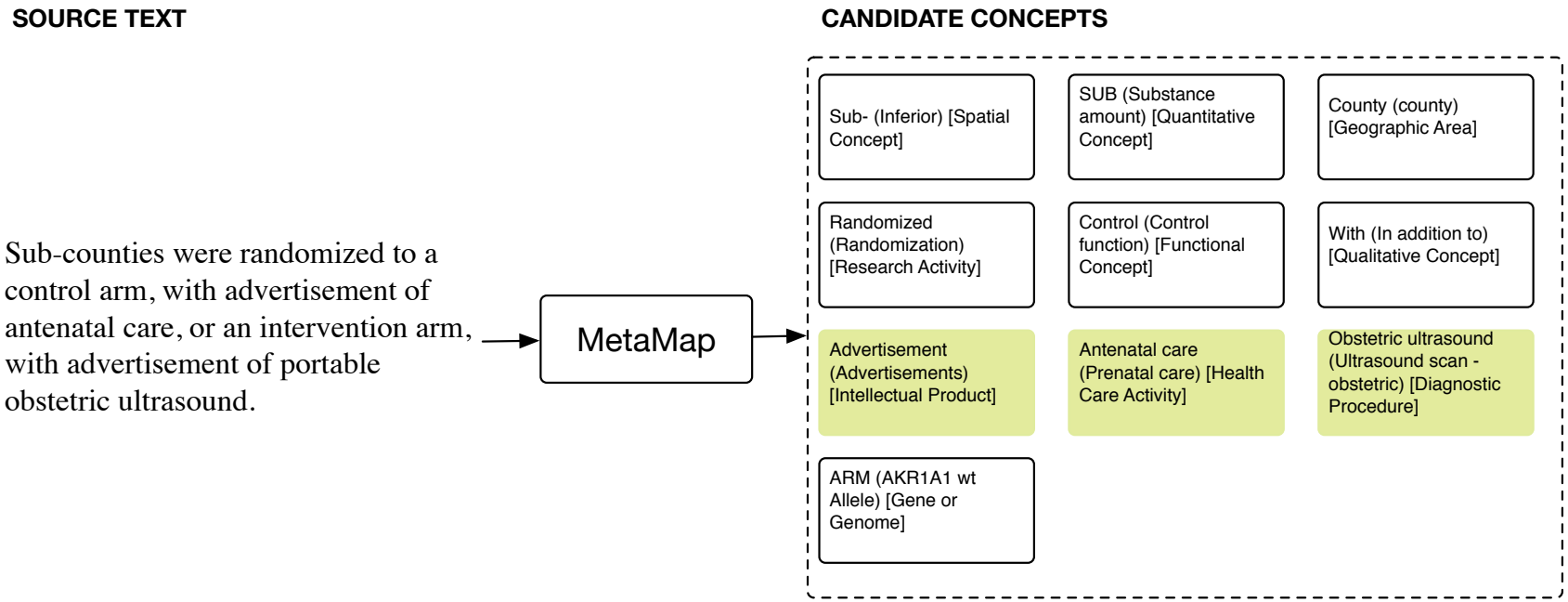


Figure: Metamap Service

- Returns a list of concepts based on the text
- Generates concepts in an unsupervised way
- Returns relevant concepts not seen during training

Multitask Model

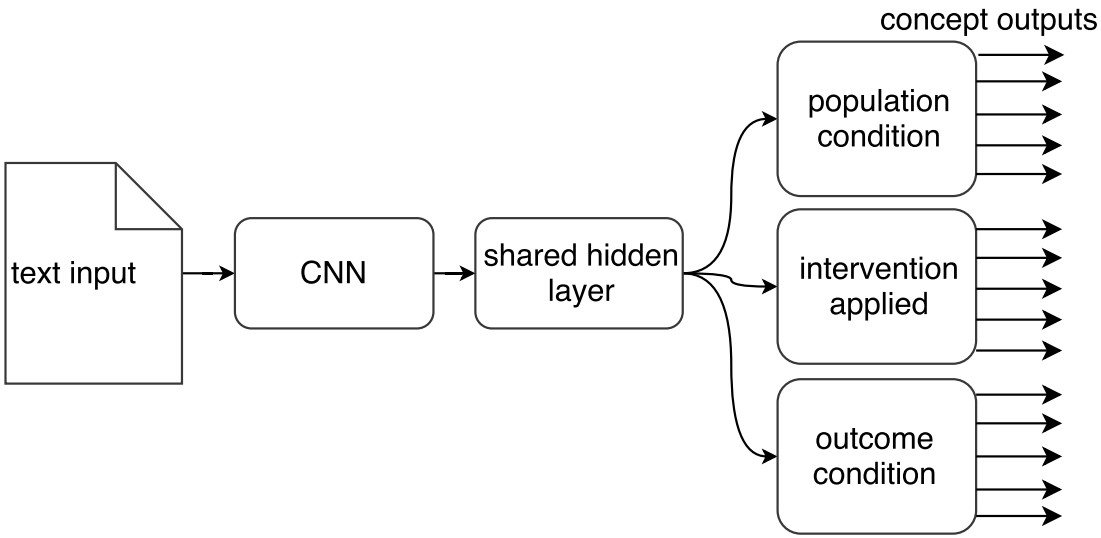


Figure: Multitask Model

- Used to generate candidate terms from those seen in the training set
- Provides a precise list of candidate terms that are relevant to the text

Dataset: Statistics

samples (clinical trials)	4306
distinct population concepts	875
distinct intervention concepts	1115
distinct outcome concepts	1731
population concepts	9387
intervention concepts	5458
outcome concepts	13800

Table: Dataset statistics.

Dataset: Characteristics

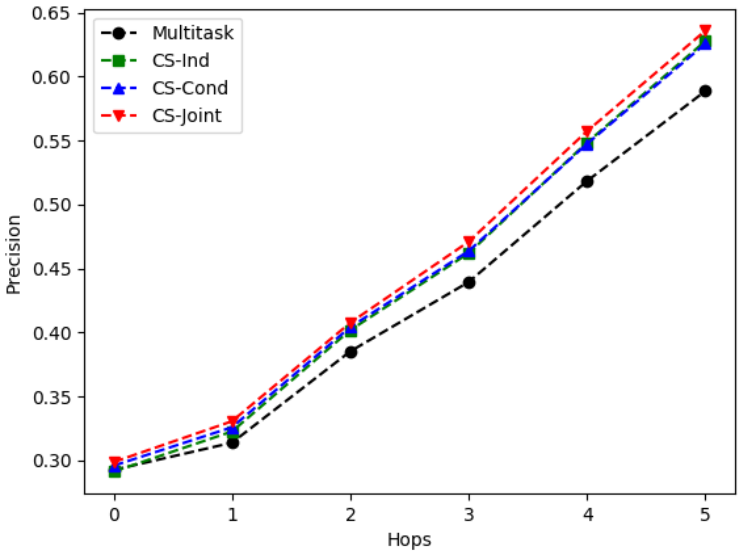
- Dataset consists of text describing clinical trials
- Concepts drawn from a restricted Unified Medical Language System (UML) vocabulary corresponding to PICO elements
- The PICO element corresponds to Population, Intervention/Control and Outcome
  - P: **P**opulation concerns the characteristics shared by trial participants (e.g., diabetic males)
  - I/C: **I**nterventions are the active treatments being studied (e.g., aspirin)/**C**omparators are baseline or alternative treatments to which these are compared (e.g., placebo).
  - O: **O**utcomes are the variables measured to assess the efficacy of different treatments (e.g., headache severity)

Experimental Results

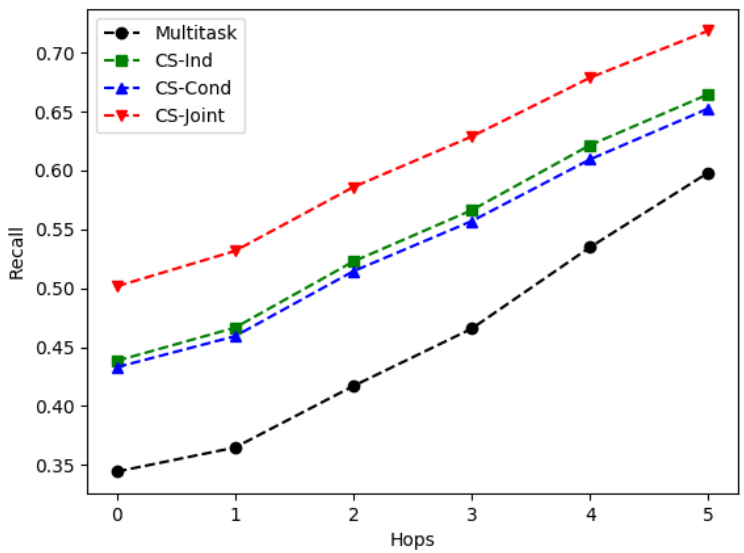
Category	Model	Precision	Recall	F1-score	Pr-2hops	Re-2hops	F1-2hops
Population	MetaMap	0.134	0.280	0.181	0.262	0.489	0.341
	Multitask	0.358	0.383	0.370	0.501	0.502	0.501
	CS-Ind	**0.385**	0.529	0.446	**0.557**	0.636	**0.594**
	CS-Cond	0.384	0.535	**0.447**	0.553	0.640	0.593
	CS-Joint	0.318	**0.594**	0.415	0.485	**0.709**	0.576
Interventions/Comparator	MetaMap	0.108	0.288	0.157	0.163	0.387	0.230
	Multitask	0.248	0.245	0.246	0.264	0.262	0.263
	CS-Ind	0.226	0.272	0.247	0.274	0.322	0.296
	CS-Cond	0.225	0.282	0.250	0.275	0.331	0.300
	CS-Joint	**0.265**	**0.421**	**0.326**	**0.314**	**0.473**	**0.378**
Outcomes	MetaMap	0.209	0.391	0.273	0.314	0.518	0.391
	Multitask	0.198	0.211	0.204	0.283	0.290	0.286
	CS-Ind	0.272	0.497	0.352	0.380	0.593	0.464
	CS-Cond	0.268	0.497	0.348	0.378	0.591	0.461
	CS-Joint	**0.279**	**0.503**	**0.359**	**0.38**	**0.595**	**0.468**

Table: Precisions, recalls and f1 measures realized by different models on the respective PICO elements.

Experimental Results



(a) Precision



(b) Recall

Figure: Average (over PICO elements) r-precisions (a) and recalls (b) for each method as a function of r, counts a predicted concept as matching the truth concept when it is $\leq r$ hops away.

Experimental Results

Category	Model	Precision	Recall	F1-score	Pr-2hops	Re-2hops	F1-2hops
Population	CS-Joint random	**0.268**	**0.251**	**0.259**	0.386	0.382	0.384
	CS-Joint pre-trained	0.264	0.250	0.257	**0.392**	**0.392**	**0.392**
Interventions/Comparator	CS-Joint random	0.219	0.248	0.233	0.272	**0.294**	**0.283**
	CS-Joint pre-trained	**0.233**	**0.257**	**0.244**	**0.273**	0.293	0.282
Outcomes	CS-Joint random	0.315	0.302	0.308	0.412	0.404	0.408
	CS-Joint pre-trained	**0.341**	**0.356**	**0.348**	**0.440**	**0.449**	**0.445**

Table: The performance of the CS-Joint model when using randomly initialized versus pre-trained embeddings.

Experimental Results

Category	Model	Precision	Recall	F1-score	Pr-2hops	Re-2hops	F1-2hops
Population	CS-Joint Complete	0.197	0.145	0.167	0.267	0.216	0.239
	CS-Joint +Marginals	**0.264**	**0.250**	**0.257**	**0.392**	**0.392**	**0.392**
Interventions/Comparator	CS-Joint Complete	0.156	0.149	0.153	0.180	0.168	0.174
	CS-Joint +Marginals	**0.233**	**0.257**	**0.244**	**0.273**	**0.293**	**0.282**
Outcomes	CS-Joint Complete	0.182	0.138	0.157	0.224	0.182	0.201
	CS-Joint +Marginals	**0.341**	**0.356**	**0.348**	**0.440**	**0.449**	**0.445**

Table: The performance of the CS-Joint model trained using only completely specified candidate triplets of the form $(c_P, c_{I/C}, c_O)$ versus a variant that accepts partially specified frames like $(\_, \_, c_O)$ or $(c_P, \_, c_O)$

Experimental Results

Category	Unseen concepts	Correctly classified
Population	193	24
Intervention	326	54
Outcome	423	77

Table: The number of unseen concepts identified correctly by the proposed CS-Joint model.

Conclusion

- We developed a new model for structured clinical text annotation that can work effectively with limited training data
- Our model learns to infer terms from the UMLS metathesaurus that describe the individual PICO elements relevant to a given study, as described in an input free-text
- It solves an important practical task for biomedical natural language processing.

Future Work

- Moving forward, we will further improve upon this model within the same framework, by exploiting the ontological structure underlying UMLS.
- We also hope to focus efforts on improving the recognition of novel terms, as this is important for the present task.

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Thank You!