

A Fast and Sound Tagging Method for Discontinuous Named-Entity Recognition

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Abstract

We introduce a novel tagging scheme for discontinuous named entity recognition based on an explicit description of the inner structure of discontinuous mentions. We rely on a weighted finite state automaton for both marginal and maximum *a posteriori* inference. As such, our method is sound in the sense that (1) well-formedness of predicted tag sequences is ensured via the automaton structure and (2) there is an unambiguous mapping between well-formed sequences of tags and (discontinuous) mentions. We evaluate our approach on three English datasets in the biomedical domain, and report comparable results to state-of-the-art while having a way simpler and faster model.

1 Introduction

Named Entity Recognition (NER) is a fundamental Natural Language Processing (NLP) task that aims at identifying mentions of named entities in texts. These mentions may for example refer to persons, organizations, locations or even dates, among others (Grishman and Sundheim, 1996; Chinchor and Robinson, 1998). Over the years, this task has been extensively studied by the community, with contributions including decoding algorithms, neural network architectures, loss functions and methods for learning in different data availability situations, *inter alia*.

There exists several variants of the NER problem, among which the most studied are *flat* NER and *nested* NER. The most common method for the flat case is BIO tagging (Ramshaw and Marcus, 1995), where each word in a sentence is tagged depending on whether it is the beginning of a mention (B), inside a mention (I) or outside a mention (O).¹ An important benefit of BIO tagging is that prediction has a linear time-complexity in the input length² using the Viterbi algorithm (Forney, 1973), contrary

to concurrent approaches like semi-Markov models that have a quadratic time-complexity (Janssen and Limnios, 1999; Sarawagi and Cohen, 2004).

A less studied task is *discontinuous* NER, where mentions are allowed to span discontinuous sequences of words. This problem is especially important for biomedical NLP. For example, pharmacovigilance aims to detect adversarial drug reactions after a product is distributed in the market via automatic analysis of medical reports or social media (Berlin et al., 2008; Coloma et al., 2013). Mentions of symptoms naturally occur in non-contiguous sequences, for example the sentence “The pain I was experiencing around the hipjoints was incredible” contains the symptom mention “pain hipjoints” with a five word gap in the middle.

Several methods for discontinuous NER have been proposed in the literature, including transition models (Dai et al., 2020) and other structured prediction approaches (Wang et al., 2021; Fei et al., 2021; Li et al., 2022). Unfortunately, they are more costly than BIO tagging and require specialized neural network architectures. There have also been attempts to propose tagging schemes for discontinuous NER (Tang et al., 2013, 2018; Metke-Jimenez and Karimi, 2016; Muis and Lu, 2016), but they all exhibit *structural ambiguity* (see Section 5).

In this work, we propose a novel tagging scheme for discontinuous NER that exploits the inner structure of discontinuous mentions. Contrary to previous attempts, our approach is *sound* in the sense that: (1) there is no encoding ambiguity between sets of mentions and sequences of tags (i.e. there is a one-to-one mapping between the two representations); and (2) our prediction algorithm is constrained to predict only well-formed sequences of tags (i.e. we can always reconstruct a set of mentions from a predicted tag sequence). To ensure

the number of possible mention labels. However, labels are not considered part of the input and are assumed to be fixed.

¹See (Ratinov and Roth, 2009) for other variants.

²It is quadratic in the number of tags, which depends on

well-formedness of predictions, we propose an algorithm based on inference in a weighted finite-state automaton. Using our approach, the time complexity of maximum *a posteriori* inference for prediction is linear in the length of the input. Moreover, our algorithm can be very efficiently implemented on GPU for batched inference (Argueta and Chiang, 2017; Rush, 2020).

Our contributions can be summarized as follows: (1) We propose to decompose discontinuous mentions in a new two-layer representation; (2) We propose a novel tagging scheme for this representation together with a linear-time tagging algorithm that ensures well-formedness of predictions; (3) We explain how labels in the inner structures can be inferred during training when the information is not available in the data; (4) We experiment on three English datasets and report competitive results while having a much faster model.

Our implementation is publicly available.³ Importantly, our decoding algorithm and all our loss functions can be used as a drop-in replacements in any BIO tagger. As such, any future research in the BIO tagging field may also be evaluated on discontinuous NER at no extra cost.

2 Reduction to Word Tagging

In this section, we explain how we map discontinuous mentions into a two-layer representation that allows us to derive a new tagging scheme. Although this transformation is generic, for ease of exposition we illustrate it on the particular case of adversarial drug reactions.

2.1 Inner Structure of Mentions

Discontinuous mentions of adversarial drug reactions (ADR) and disorders in biomedical NER mainly result from two linguistic phenomena. Firstly, mentions may be expressed as the combination of two non-contiguous syntactic constituents, due to linguistic word order rules. In the following example of an ADR, the discontinuity is caused by the verb position constraint in English:

(1) $\frac{\text{ADR}}{\text{toes are } \underline{\text{painful}}}$

Secondly, many languages allow alternative sentential structures for coordinations, including construction based on deletion operations. For example, consider the two following sentences:

(2) $\frac{\text{ADR}}{\text{pain in arms and } \underline{\text{pain in shoulders}}}$
 (3) $\frac{\text{ADR}}{\text{pain in arms and } \underline{\text{shoulders}}}$

The repeated element is eliminated in the second one, leading to the presence of a discontinuous mention, a phenomenon called coordination reduction (Lakoff and Peters, 1969). Although the underlying linguistic structures are different, we will treat both cases in the same way.

Change of representation. In practice, discontinuous mentions exhibit an inner structure. For example, a discontinuous ADR can be decomposed into a *body part* and an *event*. As such, we propose to transform discontinuous mentions into a two-layer representation:

- Upper layers identify *sets of mentions*;
- Lower layers identify *labeled components*.

We restrict the number of labels for components to be equal to two. The previous example is converted as follows:

(4) $\frac{\text{ADR(S)}}{\text{EVENT PART PART}}$
 pain in arms and shoulders

Note that the two mentions do not explicitly appear in this new representation. Nevertheless, the opposite transformation is then trivial: to rebuild all discontinuous mention in a discontinuous set, we simply take the Cartesian product between the two set of components, e.g.

$$\underbrace{\{\text{pain in}\}}_{\text{Components labeled EVENT}} \times \underbrace{\{\text{arms, shoulders}\}}_{\text{Components labeled PART}} \mapsto \underbrace{\{\text{pain in arms, pain in shoulders}\}}_{\text{Reconstructed discontinuous mentions}}$$

Note that this can result in some of the mentions being continuous, as in Ex. 4.

One obvious issue is that component labels are not annotated in datasets. We consider two solutions to tackle this challenge. First, we can use unsupervised and weakly-supervised learning methods to infer component labels during training, as explained in Section 4. Second, we can use component labels to mark if they share the same type as the leftmost one, no matter whether they refer to a body part of an event. In this setting, Ex. 1 and 3 are annotated as follows:

(5) $\frac{\text{ADR(S)}}{\text{FIRST OTHER}}$
 toes are painful

³<https://github.com/FilippoC/disc-ner-tagging>

ADR(S)

	FIRST	OTHER	OTHER
(6)	pain	in arms	and shoulders

In other words, component labels do not convey semantic information, only structural information.

Continuous mentions. There exists two forms of continuous mentions. First, continuous mentions that share one or more words with at least one other mention. In this case, we split the mention and we process it as described above. Second, there are continuous mentions that do not share any word with other mentions, see Ex. 2. In principle, we could also transform these mentions in the two layers representation. However, not only we lack information about component labels but we do not even know where to split them! In Ex. 3, we know that “pain in arms” should be splitted into “pain in” and “arms” as the first two words are shared with another mention. But for the two continuous mentions in Ex. 2, we do not have such information. Therefore, in this case, we treat them as standard continuous ones.

Comparison with nested NER. Although Dai et al. (2020) suggested the use of nested NER models for discontinuous NER using a similar yet different representation than ours, we argue that the two problems are quite different:

- The structures that we consider are not recursive, contrary to nested mentions, e.g. “[The president of [the United States of [America]]]”;
- The components are highly constrained, e.g. a set of ADRs must contain at least one body part and one event;
- The span of a set of mentions is fixed by its components: it begins (resp. ends) at the same word as its leftmost (resp. rightmost) component.

Therefore, we instead propose a tagging scheme tailored to discontinuous NER.

Beyond the biomedical domain. Our approach can be applied to other domains, e.g. we can transform the following mentions into our representation by differentiating first and last names:

	PER	PER	PER
(7)	Meg	and	Jack White

Unfortunately, these discontinuities have not been

annotated in standard datasets.⁴

2.2 Tagging Scheme

We now explain how we transform the two-layer structure into a sequence of tags. Without loss of generality, we assume that mentions are unlabeled in the original corpus, as practical datasets for discontinuous NER contain a single mention label.⁵ Moreover, we define the component labels as X and Y (e.g. *body part* and *event* in previous examples) to simplify notation and treat in a similar way semantic and structural component labels.

Our approach requires 10 tags. First, the 3 tags CB, CI and O are used in a similar way to BIO tags. CB and CI are used to identify first and following words in a continuous mention, respectively. The tag O is used to mark words that are neither part of a continuous mention or in the span of a set of mentions. In Ex. 2, word “and” is tagged with O whereas in Ex. 3 it is *not* tagged with O. This is due to the fact that in the second example, after transformation into the two layers representation, the word “and” will appear inside a set of mentions, see Ex. 4.

Second, tags to identify set of mentions and their components are of the form *-* where:

- the left-hand side is used to identify the span of the set of mentions, and can therefore take values DB (first word of the span) and DI (other words of the span);
- the right-hand side is used to identify labeled components, and can take values BX, IX, BY, IY and O.

The 7 tags used for discontinuous mentions are DB-BX, DB-BY, IB-BX, IB-BY, IB-IX, IB-IY and IB-O. Note that the leftmost word in a set of mentions must also be the beginning of a component, so the following combinations *are not* part of the tagset: DB-IX, DB-IY and DB-O. Figure 1 shows an example of tag conversion.

Importantly, any sequence of tags is *well-formed* if and only if:

⁴Wang et al. (2023) automatically extracted coordination structures from syntactic structures. However, note that (1) the resulting dataset does not contain discontinuous mentions that we are interested in and (2) conjunction reduction cannot always be inferred from the syntactic structure (Lakoff and Peters, 1969; Lechner, 2000; Wilder, 2018).

⁵It is trivial to augment the set of tags with labels if necessary, as done for standard BIO tagging.

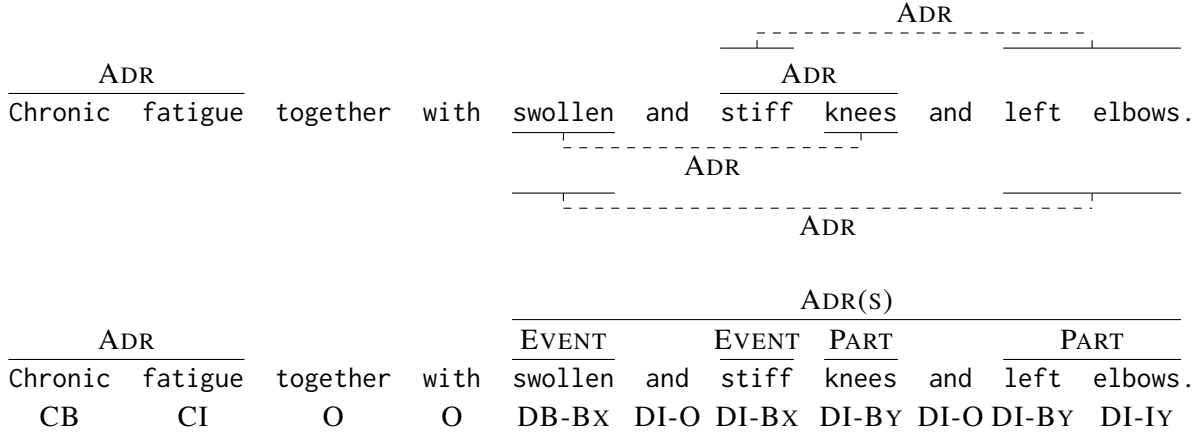


Figure 1: **(Top)** Sentence with its original annotation. It contains two continuous mentions (“Chronic fatigue” and “stiff knees”) and three discontinuous mentions (“swollen knees”, “swollen left elbows” and “stiff left elbows”). **(Bottom)** Sentence annotated with our two-layer representation and the associated tag sequence.

1. All CI tags are preceded by either BI or CI, as standard in BIO tagging;
2. All DI-* tags must be preceded by either DB-* or DI-*;
3. All *-IX tags must be preceded by either *-BX or *-IX (and similarly for the Y label);
4. A set of mentions must contain at least one component labeled X and one labeled Y, that is it must contain at least one word tagged with *-BX and one with *-BY.
5. A set of mentions must not yield a single continuous mention after reconstruction, i.e. the following sequence of tags is forbidden:

(8) $\begin{array}{ccccccccc} \text{some} & \text{pain} & \text{in} & \text{arms} & \text{and} & & & & \\ \text{O} & \text{DB-BX} & \text{DI-IX} & \text{DI-IY} & \text{O} & & & & \end{array}$

 as it would introduce ambiguity in the encoding of continuous mentions;
6. A discontinuous mention cannot end with tag DI-O, as this would result in the span of a set of mentions that do not end with the same word as its rightmost component.⁶

3 Decoding Algorithm

Without loss of generality, we assume all sentences have n words. Let T be the tagset, X be the set of sentences of n words and Y the set of well-formed tag sequences. We represent a sequence of tags $\mathbf{y} \in Y$ as a binary vector with $n \times |T|$ entries, where each entry is associated with a tag

⁶The analogous constraint on the first word is implicitly enforced by the absence of a DB-O tag in the tagging scheme.

and a word, i.e. $\mathbf{y} \in \{0, 1\}^{n|T|}$. If the value of an entry is 1 (resp. 0), the associated tag is assigned to the associated word (resp. not assigned). Note that $Y \subset \{0, 1\}^{n|T|}$ is a strict subset of all such vectors, as each word must be assigned exactly one tag and that the resulting tag sequence must satisfy the constraints described in Section 2.2.

Let $f_\theta : X \rightarrow \mathbb{R}^{n|T|}$ be a neural network parameterized by θ . We define the probability of a tag sequence $\mathbf{y} \in Y$ given the input \mathbf{x} as a Boltzmann-Gibbs distribution (or *softmax* over structures):

$$p_\theta(\mathbf{y}|\mathbf{x}) = \exp(\langle \mathbf{y}, f_\theta(\mathbf{x}) \rangle - A_Y(f_\theta(\mathbf{x}))),$$

where $\langle \cdot, \cdot \rangle$ denotes the dot product and A_Y is the log-partition function ensuring that the distribution is correctly normalized:

$$A_Y(\mathbf{w}) = \log \sum_{\mathbf{y} \in Y} \exp \langle \mathbf{y}, \mathbf{w} \rangle. \quad (1)$$

Computing $A_Y(\mathbf{w})$ is called *marginal inference* due to its link with marginal probabilities (Wainwright et al., 2008). Computing the most probable output is reduced to computing:

$$\hat{\mathbf{y}}_\theta(\mathbf{x}) = \arg \max_{\mathbf{y} \in Y} \langle \mathbf{y}, f_\theta(\mathbf{x}) \rangle, \quad (2)$$

called *maximum a posteriori (MAP) inference*.

In practice, we need to compute the term in Equation 1 for training the model and the term in Equation 2 for prediction. The difficulty stems from the restriction (in the sum and in the $\arg \max$ search space) to the set of well-formed outputs Y . We follow a long tradition in NLP (Koskenniemi, 1990;

Mohri et al., 1996; Karttunen et al., 1996; Kanthak and Ney, 2004; Tromble and Eisner, 2006; Rastogi et al., 2016; Lin et al., 2019; Papay et al., 2022, *inter alia*) and rely on a finite-state automaton to solve these inference problems while enforcing the well-formedness constraints.

3.1 Finite-State Automata

Definitions. Weighted Finite State Automata (WFSAs) are generalization of FSA (Eilenberg, 1974; Droste et al., 2009) that include weights on their transitions. Formally, a WFSAs over \mathbb{R} is a 5-tuple (Σ, Q, E, i, F) where: Σ is a finite alphabet with $\epsilon \notin \Sigma$; Q is the set of states; $E \subseteq Q \times \Sigma \times \mathbb{R} \times Q$ is the set of weighted transitions, where $(q, \sigma, w, r) \in E$ is a transition from state q to state r emitting symbol σ with weight w ; $i \in Q$ is an initial state and $F \subseteq Q$ are final states.

A *valid path* is a path starting at i and ending at any state in F . A valid path emits a sequence of symbols, and has a weight equal to the sum of the transition weights it contains. The symbol ϵ is used for transitions that do not emit any symbol. The language of a WFSAs is the set of emissions along all possible valid paths. A WFSAs is ϵ -free if there is no ϵ -transition.

Algorithms. Given an acyclic WFSAs, the path of maximum weight (Eq. 2) and the the log-sum-exp of all valid paths (Eq. 1) can be computed using variants of the Viterbi algorithm (Forney, 1973) and the Forward algorithm (Baum, 1972), respectively. These algorithms are in fact identical, but defined over different semirings (Goodman, 1999): the tropical semiring for the Viterbi and the thermodynamic semiring (Marcolli and Thorngren, 2014) for the Forward. We refer to (Mohri, 2009, Section 3) for an in-depth introduction. The time complexity of both algorithms is $\mathcal{O}(|E|)$ if a topological ordering of states is known.

Application to sequence tagging. We follow previous work and use the intersection of two WFSAs to constraint tag sequences (Koskenniemi, 1990; Koskenniemi et al., 1992). The *grammar automaton* $\mathcal{G} \triangleq (T \cup \{\epsilon\}, Q, E, i, F)$ is a cyclic WFSAs whose language is the set of all well-formed tag sequences (of any length). We assume \mathcal{G} is ϵ -free and deterministic.⁷ Without loss of generality, we fix all transition weights to 0. The *sentence automaton* $\mathcal{S} \triangleq (T \cup \{\epsilon\}, Q', E', i', F')$ is an acyclic FSA that represents all possible (not necessarily

valid) analyses for a given sentence of n words. States are $Q' \triangleq \{0, \dots, n\}$ and transitions are:

$$E' \triangleq \{(i-1, t, w_{(i,t)}, i) \mid i \in \{1 \dots n\} \wedge t \in T\}$$

where $w_{(i,t)}$ is the weight associated with tagging word at position i with tag t . Initial and final states are $i' \triangleq 0$ and $F' \triangleq \{n\}$. This WFSAs contains $n|T|$ transitions, and each transition correspond to tagging a given word with a given tag. By construction, it is always deterministic and ϵ -free.

We denote $G \cap S$ the intersection of G and S (Hopcroft et al., 2001, Section 4.2.1) composed of states $Q'' \triangleq Q \times Q'$, transitions

$$E'' \triangleq \left\{ \left((i-1, p), t, w_{(i,t)}, (i, q) \right) \mid \begin{array}{l} i \in \{1 \dots n\} \wedge \\ (p, t, 0, q) \in E \end{array} \right\},$$

initial state $i'' \triangleq (i, i')$ and final states $F'' \triangleq F \times F'$. Then, all valid paths in $G \cap S$ are well-formed sequences of tags for the input sentence of length n . We can then simply run the Viterbi or the Forward algorithm on $G \cap S$ to compute Eq. 1 and 2. Note that $|E''| \propto n$, therefore the time-complexity is linear in the number of words.

We refer the reader to Tapanainen (1997) for an introduction to this sequence tagging approach.

3.2 Grammar Automaton

The grammar automaton used to constraint prediction to well-formed sequences of tags is shown in Figure 2. We present the automaton with ϵ -transition for the sake of clarity, but they can be removed. We omit weights as they are null. States 1 and 2 recognize valid sequences of CB, CI and O tags. Moreover, the structure of the WFSAs recognizing discontinuous mentions is symmetric: the left-hand (resp. right-hand) side recognizes discontinuous mentions whose leftmost component is labeled X (resp. Y). Therefore, we present only the left-hand side.

Transition (1, DB-BX, 7) starts the recognition of a set of mentions whose leftmost component is labeled X. The self-loop in state 7 recognizes following words of the first component. Next we need to check that the inner structure of the set of mentions is well-formed. On the one hand, states 5 and 6 allows to recognize following X components and DI-O tags, until recognition of the first Y component via transition (5, DI-BY, 4). On the other hand, transition (7, DB-BX, 8) starts the recognition of an component labeled Y that directly follows the first component. Therefore, we need to check

⁷Procedures to determinize and remove ϵ -transitions can be found in Hopcroft et al. (2001, Section 2.3.5 and 2.5.5).

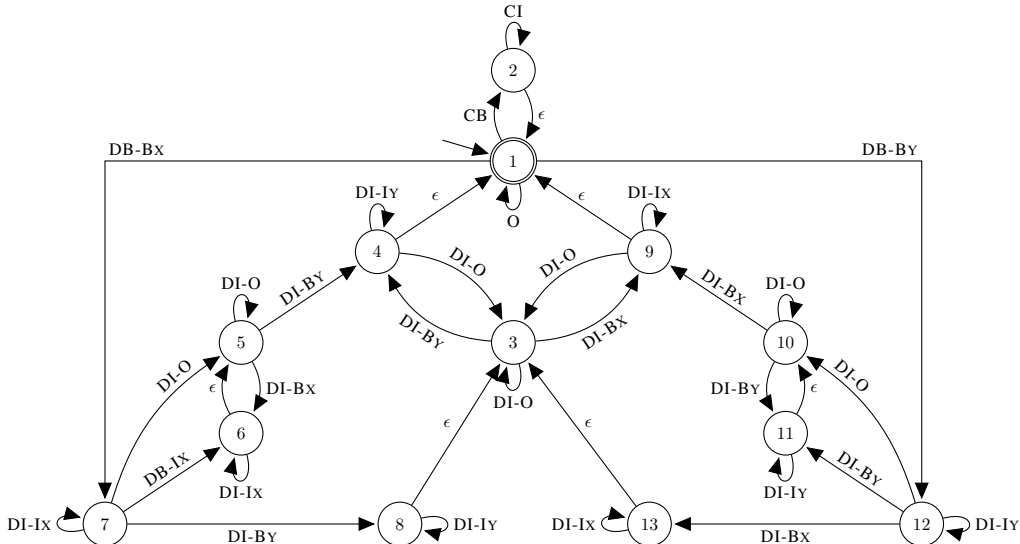


Figure 2: The grammar automaton we propose for discontinuous named-entity recognition.

that there is “something else” in the set of mentions, otherwise the sequence of tags could lead to an ambiguity in the encoding of continuous mentions. We ensure this via transition $(8, \epsilon, 3)$, that requires the generation of another component before reaching the final state. Finally, states 3, 4 and 9 recognizes extra X and Y in the set of mentions.

As such, the language of our grammar automaton is the set of well-formed tag sequences as described in Section 2.2. To use our grammar automaton, we need to remove ϵ -transitions. The resulting WFSA has 22 states.⁸ In the case of structural component labels, we can simply remove transition $(1, \text{DB-BY}, 12)$ to constrain the leftmost mention to be labeled X.

Practical implementation. The intersection of the grammar and the sentence automata does not result in a homogeneous Markov chain as transition weights correspond to tag weights for the next word, and are therefore different at each step. However, the resulting automaton has always a simple time-invariant structure. In term of implementation, this reduces to applying a mask at each step, and both Viterbi and forward algorithms can be implemented using basic differentiable tensor operations. For MAP inference, we compute the path of maximum weight and then rely on backpropagation to retrieve the sequence of tags (Mensch and Blondel, 2018, Section 2.1).

⁸Although 22 states is small and allows very fast computation, it is already too large for drawing a comprehensive figure.

4 Weakly-Supervised Learning

The negative log-likelihood (NLL) loss

$$\ell(\mathbf{w}; \mathbf{y}) = -\langle \mathbf{y}, \mathbf{w} \rangle + A_Y(\mathbf{w}),$$

requires knowledge of the gold output \mathbf{y} . Unfortunately, NER datasets only contains annotated mentions, but not their component labels (e.g. we do not know which components are body parts and events). Therefore, we need to resort on weakly-supervised learning to infer this information.

4.1 Learning with Partial Labels

Learning with partial labels refers to the case where the gold output is unknown but there is access to a subset of labels that includes the gold one (Grandvalet and Bengio, 2004; Nguyen and Caruana, 2008; Cour et al., 2011). Let $\tilde{Y} \subseteq Y$ be the set of tag sequences that recovers the gold discontinuous mentions. For the example in Figure 1, \tilde{Y} contain two sequences, one where components of the set of mentions are labeled X/X/Y/Y and the other Y/Y/X/X. For a sentence containing k sets of mentions, we have $|\tilde{Y}| = 2^k$.

Following Jin and Ghahramani (2002), we minimize the NLL after marginalizing over \tilde{Y} :

$$\begin{aligned} \tilde{\ell}(\mathbf{w}; \tilde{Y}) &= -\log p_{\theta}(\tilde{Y}|\mathbf{x}) = -\log \sum_{\mathbf{y} \in \tilde{Y}} p_{\theta}(\mathbf{y}|\mathbf{x}) \\ &= A_Y(f_{\theta}(\mathbf{x})) - \log \underbrace{\sum_{\mathbf{y} \in \tilde{Y}} \exp\langle \mathbf{y}, f_{\theta}(\mathbf{x}) \rangle}_{=A_{\tilde{Y}}(f_{\theta}(\mathbf{x}))}, \end{aligned} \quad (3)$$

where $A_{\tilde{Y}}$ is the *clamped* log-partition. In speech processing, $A_{\tilde{Y}}$ is called the alignment model (Povey et al., 2016; Hadian et al., 2018).

Relation with EM. We can interpret minimizing $\tilde{\ell}$ as an Expectation-Maximization (EM) procedure (Neal and Hinton, 1998). Indeed, the variational formulation of the clamped log-partition is:

$$A_{\tilde{Y}}(\mathbf{w}) = \sup_{\mu \in \text{conv } \tilde{Y}} \langle \mu, \mathbf{w} \rangle - \Omega_{\tilde{Y}}(\mu),$$

where conv denotes the convex hull and $\Omega_{\tilde{Y}}$ is a structured entropy term as described by Blondel et al. (2020, Section 7.1). Setting $\mathbf{w} = f_{\theta}(\mathbf{x})$, the gradient of A is (Danskin, 1966):

$$\hat{\mu}_{\tilde{Y}}(\mathbf{w}) = \nabla A_{\tilde{Y}}(\mathbf{w}) = \arg \max_{\mu \in \text{conv } \tilde{Y}} \langle \mu, \mathbf{w} \rangle - \Omega_{\tilde{Y}}(\mu).$$

We rewrite the minimization of $\tilde{\ell}$ as a two-step procedure:

1. **E step:** compute $\hat{\mu}_{\tilde{Y}}(\mathbf{w})$;
2. **M step:** take one gradient step over the network parameters using the marginal distribution computed in E step, yielding the loss:

$$\ell(\mathbf{w}; \hat{\mu}_{\tilde{Y}}(\mathbf{w})) = -\langle \mathbf{y}, \hat{\mu}(\mathbf{w}) \rangle + A_Y(\mathbf{w}).$$

It is important to note that $\hat{\mu}_{\tilde{Y}}(\mathbf{w})$ is considered as a constant in the M step, i.e. the gradient is:

$$\nabla \ell(\mathbf{w}; \hat{\mu}_{\tilde{Y}}(\mathbf{w})) = -\hat{\mu}(\mathbf{w}) + \nabla A_Y(\mathbf{w}) = \nabla \tilde{\ell}(\mathbf{w}; \tilde{Y}),$$

meaning that this EM procedure is equivalent to minimizing the loss in Equation 3.

This suggests a ‘‘Hard EM’’ alternative, where the E step computes the unregularized maximum:

$$\hat{\mathbf{y}}_{\tilde{Y}}(\mathbf{w}) = \arg \max_{\mathbf{y} \in \text{conv } \tilde{Y}} \langle \mathbf{y}, \mathbf{w} \rangle,$$

and then apply one step of gradient descent using the loss $\ell(\mathbf{w}; \hat{\mathbf{y}}_{\tilde{Y}}(\mathbf{w}))$ in the M step.

4.2 Silver Annotation of Components

In order to automatically annotate components, we collect names of body parts from the metathesaurus MRCONSO.RRF of the Unified Medical Language System (UMLS, version 2023ab).⁹ We select English entries corresponding to semantic types ‘‘Body Location or Region’’, ‘‘Body Part, Organ,

or Organ Component’’ and ‘‘Body Space or Junction’’, which corresponds to identifiers T029, T023 and T030, respectively.¹⁰ However, we remove all acronyms as they would introduce too many false positives in the annotation process (e.g. ‘‘in’’ and ‘‘am’’ are acronyms of body parts). This leads to 218 134 names of body parts.

Then, we try to match words of components with these entries. If at least one word of a component match an entry, we consider it as a body part. Note that a single match fully disambiguate a set of mentions.

5 Related Work

Tagging methods. Tang et al. (2013) proposed the BIOHD tagging scheme for discontinuous NER. A major issue of their approach is its *structural ambiguity*: several tag sequences can encode the same discontinuous mention, and different discontinuous mentions have the same associated tag sequence, see (Muis and Lu, 2016, Section 3.1). A choice to resolve ambiguity has to be made when making a prediction, meaning that there are structures that cannot be predicted. Moreover, this approach does not constrain the output tag sequence to be well-formed, i.e. it may not be possible to reconstruct mentions from a predicted tag sequence. The tagging scheme used by Metke-Jimenez and Karimi (2016) and Dai et al. (2017) has the same limitation. Muis and Lu (2016) proposed a graph-based method that ensures that predictions are well-formed, but their approach still exhibits structural ambiguity.

Other methods. Wang and Lu (2019) rely on a two-step model that first predicts continuous spans (i.e. components) and then uses a separate classifier that combines them together. Dai et al. (2020) proposed a novel transition-based model. These two approaches are based on sequential predictions that are trained using gold intermediate outputs, which can lead to error propagation once a single mistake is made at test time. To resolve this problem, Wang et al. (2021) proposed a method that jointly predicts spans and their combination based on the maximal clique problem. A downside of these approaches is that they are more computationally costly (and therefore slower) than tagging methods.

⁹https://www.ncbi.nlm.nih.gov/books/NBK9685/table/ch03.T.concept_names_and_sources_file_mr/

¹⁰<https://www.ncbi.nlm.nih.gov/books/NBK9685/table/ch03.Tf/>

	CADEC		SHARE2013		SHARE2014	
	F1	Disc. F1	F1	Disc. F1	F1	Disc. F1
Previous work						
Tang et al. (2013)			75.0			
Tang et al. (2018)	66.3					
Metke-Jimenez and Karimi (2016)	64.4		56.5		60.2	
Metke-Jimenez and Karimi (2016) [†]	67.4	1.8	74.9	18.8	76.6	6.0
Muis and Lu (2016) [†]	58.0	23.9	70.3	50.0	74.7	41.1
Dai et al. (2020)	69.0	37.9	77.7	52.5	79.6	49.2
Wang et al. (2021)	71.5	44.4	81.2	55.9	81.3	54.1
This work						
Soft EM	71.1	38.1	80.7	49.2	81.5	51.9
Hard EM	71.9	35.9	82.0	51.9	81.6	54.1
Weakly soft EM	71.8	37.6	82.0	52.0	81.4	46.2
Weakly hard EM	70.4	33.6	82.0	52.1	81.8	49.8
Structural labels	72.9	41.5	82.1	53.3	80.9	53.7

Table 1: Results on on three different datasets. Results marked with [†] are reproductions by Wang et al. (2021).

Split	CADEC	SHARE2013	SHARE2014
Train	5340 (306)	8508 (477)	17407 (777)
- filtered	5322 (288)	8432 (401)	17294 (667)
Dev.	1097 (59)	1250 (58)	1361 (59)
Test	1160 (74)	9009 (301)	15850 (411)

Table 2: Number of sentences in each split. The number in parentheses corresponds to the number of sentences with at least one discontinuous mention.

Model	CADEC	S2013	S2014
Dai et al. (2020)	36	41	40
Wang et al. (2021)	193	200	198
This work	8286	10216	10206

Table 3: Speed comparison in terms of sentence per seconds. Numbers for Dai et al. (2020) are BERT-based models, as reproduced by Wang et al. (2021).

6 Experiments

We evaluate our approach on three standard English datasets for named-entity recognition in the biomedical domain: CADEC (Karimi et al., 2015), SHARE2013 (Pradhan et al.) and SHARE2014 (Mowery et al.). We pre-process the data using the script of Dai et al. (2020). Note that our tagging scheme cannot predict all discontinuous mentions in the data, i.e. there are sentences that we cannot convert to our representation. Therefore, we remove these sentences from the training set.¹¹ Data statistics are given in Table 2.

Our neural network is excessively simple: we use the DEBERTA-V3 pretrained self-attentive network (He et al., 2021a,b) followed by a single linear

¹¹Obviously, we do not remove anything from the test set.

projection that maps context-sensitive embedding to tags. All training details are given in Appendix A. For each loss function, we train six models with six different seeds, and we select the best model using the development set.

Results. We report the F-measure on all mentions and on discontinuous mentions only in Table 1. The evaluation is conducted on the the original representation so results are comparable with previous work. Our approach leads to similar results to previous work. We do not observe significant differences between different loss functions.

Speed. All numbers are reported for computation on NVIDIA V100 GPUs. Training takes approximately 40, 60 and 80 minutes on CADEC, SHARE2013 and SHARE2014, respectively. Table 3 compares decoding with previous work of Dai et al. (2020) and Wang et al. (2021). The transition-based model of Dai et al. (2020) is particularly slow as their approach cannot fully exploit GPU parallelization. Our approach is \sim 40-50 times faster than the method of Wang et al. (2021). This is due to two reasons: (1) they use a complex neural network architecture on top of a BERT-like model and (2) for each input they must solve a NP-hard problem (maximum clique) to make the prediction.

7 Conclusion

In this work, we propose a novel tagging scheme for discontinuous NER based on a two-layer representation of discontinuous mentions. Our approach leads to result on par with state-of-the-art using a very simple neural network architecture. Importantly, decoding with our model is very fast com-

pared to previous work.

Our main objective with this work is to propose a simple plug-in method for discontinuous NER: any future work on models for BIO tagging can now also be trivially evaluated on discontinuous NER. Moreover, our approach is also fast to train, meaning that there is no significant cost overhead.

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A Training details

The model is trained for 20 epochs using the cosine learning rate scheduler as implemented in the HuggingFace library. The maximum learning rate is fixed to 10^{-5} . The warmup ratio is 10%. We apply dropout with a probability of 0.5 to BERT’s output. The gradient norm is clipped to 1. All parameters have a weight decay of 0.01. We use the Adam variant proposed in (Mosbach et al., 2021).