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Research and Applications

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Biomedical and clinical English model packages for the Stanza Python NLP library

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ABSTRACT

Objective: The study sought to develop and evaluate neural natural language processing (NLP) packages for the syntactic analysis and named entity recognition of biomedical and clinical English text.

Materials and Methods: We implement and train biomedical and clinical English NLP pipelines by extending the widely used Stanza library originally designed for general NLP tasks. Our models are trained with a mix of public datasets such as the CRAFT treebank as well as with a private corpus of radiology reports annotated with 5 radiology-domain entities. The resulting pipelines are fully based on neural networks, and are able to perform tokenization, part-of-speech tagging, lemmatization, dependency parsing, and named entity recognition for both biomedical and clinical text. We compare our systems against popular open-source NLP libraries such as CoreNLP and scispaCy, state-of-the-art models such as the BioBERT models, and winning systems from the BioNLP CRAFT shared task.

Results: For syntactic analysis, our systems achieve much better performance compared with the released scispaCy models and CoreNLP models retrained on the same treebanks, and are on par with the winning system from the CRAFT shared task. For NER, our systems substantially outperform scispaCy, and are better or on par with the state-of-the-art performance from BioBERT, while being much more computationally efficient.

Conclusions: We introduce biomedical and clinical NLP packages built for the Stanza library. These packages offer performance that is similar to the state of the art, and are also optimized for ease of use. To facilitate research, we make all our models publicly available. We also provide an online demonstration (http://stanza.run/bio).

Key words: natural language processing, machine learning, syntactic analysis, dependency parsing, named entity recognition

INTRODUCTION

A large portion of biomedical knowledge and clinical communication is encoded in free-text biomedical literature or clinical notes.[1,2] The biomedical and clinical natural language processing (NLP) communities have made substantial efforts to unlock this knowledge, by building systems that are able to extract information,[3,4] answer questions,[5,6] or understand conversations[7] from biomedical and clinical text.

NLP toolkits that are able to understand the linguistic structure of biomedical and clinical textand extract information from it are often used as the first step of building such systems.[8,9] Existing general-purpose NLP toolkits are optimized for high performance and ease of use but are not easily adapted to the biomedical domain with state-of-the-art performance. For example, the Stanford CoreNLP library[10] and the spaCy library (https://spacy.io/), despite being widely used by the NLP community, do not provide customized models for biomedical language processing. The recent scispaCy toolkit[11] extends spaCy's coverage to the biomedical domain, yet it does not provide state-of-the-art performance on syntactic analysis or entity recognition tasks, and does not offer models customized to clinical text processing.

In addition to general-purpose NLP toolkits, several NLP toolkits specialized for processing biomedical or clinical text are available. For example, Mayo Clinic's cTAKES (Clinical Text Analysis and Knowledge Extraction System) provides a dictionary-based named-entity recognizer to find Unified Medical Language System Metathesaurus terms[12] in text, in addition to other NLP functionalities, such as tokenization, part of speech tagging, and parsing.[13] Other similar packages include the Health Information Text Extraction (HITEx) library,[14] the MetaMap toolkit,[15] and the CLAMP clinical NLP toolkit.[16] These packages often integrate sophisticated domain-specific features crafted by experts, yet they fall short of integrating modern deep learning–based models that offer much more accurate performance than traditional rule-based or machine learning methods. Moreover, as Python becomes a common language of choice in the biomedical data science community,[17] the lack of native Python support has significantly limited users' ability to adopt these toolkits and integrate them with modern computational libraries such as the deep learning libraries.

The recently introduced Stanza NLP library[18] offers state-of-the-art syntactic analysis and NER functionality with native Python support. Its fully neural pipeline design enables extension of its language processing capabilities to the biomedical and clinical domain. In this study, we present biomedical and clinical English model packages for the Stanza library (Figure 1). These packages are built on top of Stanza's neural system, and offer syntactic analysis support for biomedical and clinical text, including tokenization, lemmatization, part-of-speech (POS) tagging, and dependency parsing, based on the Universal Dependencies v2 (UDv2) formalism,[19] and highly accurate named entity recognition (NER) capabilities covering a wide variety of domains.

These packages include 2 UD-compatible biomedical syntactic analysis pipelines trained on the publicly available CRAFT[20] and GENIA[8] treebanks, respectively; a UD-compatible clinical syntactic analysis pipeline, trained with a silver-standard treebank created from clinical notes in the MIMIC-III (Medical Information Mart for Intensive Care-III) database[21]; 8 accurate biomedical NER models augmented with contextualized representations, achieving near state-of-the-art performance; and 2 clinical NER models, including a newly introduced model specialized in recognizing entities in clinical radiology reports.

We show through a variety of experiments that these packages achieve performance that meets or surpasses state-of-the-art results. We further show via examples and benchmarking that these packages are easy to use and do not compromise speed, especially when GPU acceleration is available. We hope that our packages will facilitate future research to analyze and understand biomedical and clinical text.

MATERIALS AND METHODS

Syntactic analysis modules and implementations

Stanza's syntactic analysis pipeline consists of modules for tokenization, sentence segmentation, POS tagging, lemmatization, and dependency parsing. All modules are implemented as neural network models. We briefly introduce each component in turn and refer readers to the Stanza system paper[18] for details.

Tokenization and sentence splitting

The first step of text analysis is usually tokenization and sentence segmentation. In Stanza, these 2 tasks are jointly modeled as a tagging problem over character sequences, in which the model predicts whether a given character is the end of a token, a sentence, or neither. This joint task is realized with a lightweight recurrent neural network. We choose to combine these tasks because they are usually context-sensitive and can benefit from joint inference to reduce ambiguity.

POS tagging

Once the text is tokenized, Stanza predicts the POS tags for each word in each sentence.

We adopt a bidirectional long short-term memory network (BiLSTM) as the basic architecture to predict both the language-specific POS (XPOS) tags and the universal POS (UPOS) tags.

We further adapt the biaffine scoring mechanism from the biaffine neural parser[22] to condition XPOS prediction on that of UPOS, which improves the prediction consistency between XPOS and UPOS tags.[23]

Lemmatization

In many practical downstream applications, it is useful to recover the canonical form of a word by lemmatizing it (eg, recovering the lemma form *do* from the word *did*) for better pattern matching. Stanza's lemmatizer is implemented as an ensemble of a dictionary-based lemmatizer and a neural sequence-to-sequence lemmatizer that operate on character sequences. An additional classifier is built on the encoder output of the seq2seq model, to predict *shortcut operations* such as lowercasing the input word or using an exact copy of the input word as lemma. These shortcut operations improve the robustness of the neural lemmatizer on long input character sequences such as URLs by avoiding the unnecessary generation of very long sequences.

Dependency parsing

To analyze the syntactic structure of each sentence, Stanza parses it into the UD format,[19] in which each word in a sentence is assigned a syntactic head that is either another word in the sentence, or in the case of the root word, an artificial *root* symbol. The dependency parser in Stanza is a variant of the BiLSTM-based deep biaffine neural dependency parser[22] that Qi et al[23] have modified for improved accuracy.

Biomedical syntactic analysis pipeline

We provide 2 separate syntactic analysis pipelines for biomedical text by training Stanza's neural syntactic pipeline on 2 publicly available biomedical treebanks: the CRAFT treebank[20] and the GENIA treebank.[8,24] The 2 treebanks differ in 2 main ways. First, while GENIA is collected from PubMed abstracts related to "human," "blood cells," and "transcription factors," CRAFT is collected from full-text articles related to the Mouse Genome Informatics database. Second, while the CRAFT treebank tokenizes segments of hyphenated words separately (eg, *up-regulation* tokenized into *up—regulation*), the GENIA treebank treats hyphenated words as single tokens.

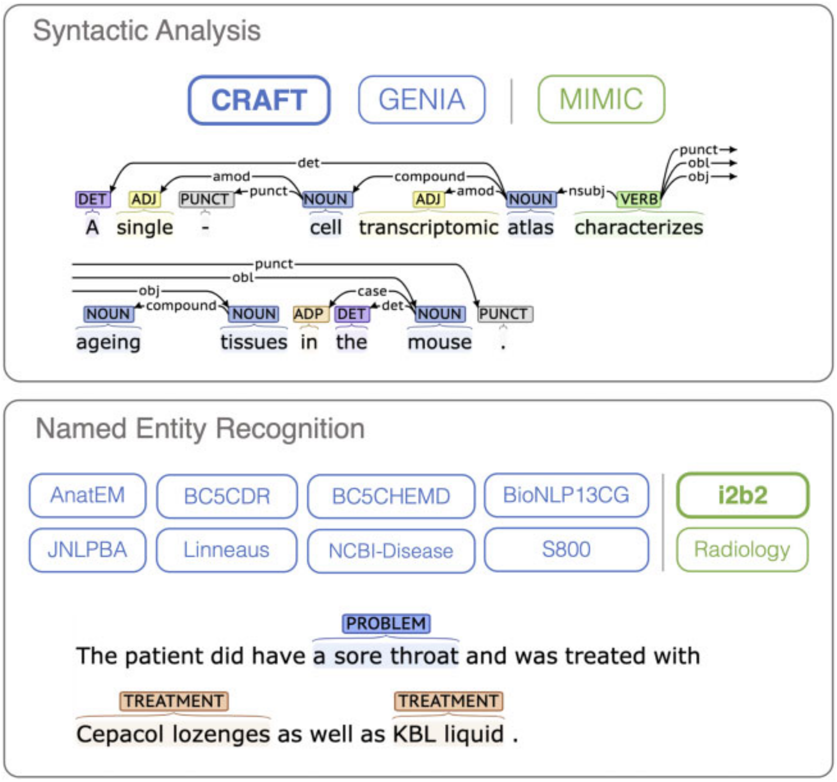

Syntactic Analysis
CRAFT
GENIA
MIMIC
DET ADJ PUNCT NOUN ADJ NOUN VERB
A single - cell transcriptomic atlas characterizes
det
amod
punct
compound
amod
nsubj
punct
obl
obj
NOUN NOUN ADP DET NOUN PUNCT
ageing tissues in the mouse .
punct
obl
obj
compound
case
det
Named Entity Recognition
AnatEM
BC5CDR
BC5CHEMD
BioNLP13CG
i2b2
JNLPBA
Linneaus
NCBI-Disease
S800
Radiology
PROBLEM
The patient did have a sore throat and was treated with
TREATMENT
TREATMENT
Cepacol lozenges as well as KBL liquid .

Figure 1. Overview of the biomedical and clinical English model packages in the Stanza NLP library. For syntactic analysis, an example output from the CRAFT biomedical pipeline is shown; for named entity recognition, an example output from the i2b2 clinical model is shown.

Because both treebanks provide only Penn Treebank annotations in their original releases, to train our neural pipeline, we first convert both of them into UDv2[19] format annotations, using the UD converter[25] in the Stanford CoreNLP library.[10] To facilitate future research we have made the converted files publicly available (https://nlp.stanford.edu/projects/stanza/bio/).

Treebank combination

Because the tokenization in the CRAFT treebank is fully compatible with that in the general UD English treebanks, in practice we found it beneficial to combine the English Web Treebank (EWT)[26] with the CRAFT treebank for training the CRAFT syntactic analysis pipeline. We show later via experiments that this treebank combination improves the robustness of the resulting pipeline on both general and in-domain text.

Clinical syntactic analysis pipeline

Unlike the biomedical domain, no large annotated treebanks for clinical text are publicly available.

Therefore, to build a syntactic analysis pipeline that generalizes well to the clinical domain, we created a silver-standard treebank by making use of the publicly available clinical notes in the MIMIC-III database.[21] The creation of this treebank is based on 2 main observations made via qualitative analysis over sampled clinical notes from the MIMIC-III database. First, we find that Stanza's neural syntactic analysis pipeline trained on general English treebanks generalizes reasonably well to well-formatted text in the clinical domain. Second, the highly optimized rule-based tokenizer in the Stanford CoreNLP library produces more accurate and consistent tokenization and sentence segmentation on clinical text than the neural tokenizer in Stanza trained on a single treebank. For example, while the neural tokenizer trained on a general English treebank tends to produce inconsistent sentence segmentations in the presence of consecutive punctuation marks or spaces in a sentence, the CoreNLP tokenizer handles these cases in a much more consistent and accurate manner.

Based on these observations, we create a silver-standard MIMIC treebank with the following procedure. First, we randomly sample 800 clinical notes of all types from the MIMIC-III database, and stratify the notes into training/dev/test splits with 600/100/100 clinical notes, respectively. These numbers are chosen to create a treebank of similar size to the general English EWT treebank. Second, we tokenize and sentence-segment the sampled notes with the default CoreNLP tokenizer. Third, we pretrain Stanza's general English syntactic analysis pipeline on the EWT treebank, then run it on the pretokenized notes, and produce syntactic annotations following the UDv2 format. Fourth, to improve the robustness of the resulting models trained on this treebank, similar to the CRAFT pipeline, we concatenate the training split of the original EWT treebank with this silver-standard MIMIC treebank. We show later via experiments that this treebank combination again improves the robustness of the resulting pipeline on syntactic analysis tasks. A diagram that illustrates this whole training procedure is shown in Figure 2.

NER models

Stanza's NER component adopts the architecture of the contextualized string representation-based sequence tagger.[27] For each domain, we train a forward and a backward LSTM character-level

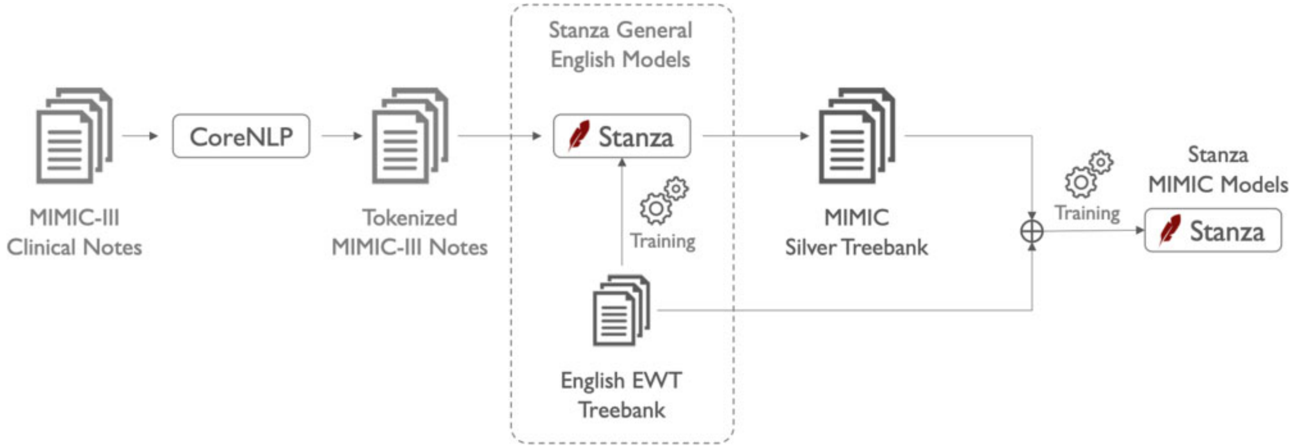


Figure 2. Training diagram of the Stanza MIMIC clinical syntactic analysis models. Sampled MIMIC-III (Medical Information Mart for Intensive Care-III) clinical notes are first tokenized and sentence-segmented with the CoreNLP tokenizer, and then syntactically annotated with the pretrained Stanza general English syntactic models. The derived silver-standard treebank is then concatenated with the original English Web Treebank (EWT) treebank and used for training the Stanza clinical syntactic models.

language model (CharLM) to supplement the word representation in each sentence. At tagging time, we concatenate the representations from these CharLMs at each word position with a word embedding, and feed the result into a standard 1-layer BiLSTM sequence tagger with a conditional random field–based decoder. The pretrained CharLMs provide rich domain-specific representations that notably improve the accuracy of the NER models.

Biomedical NER models

For the biomedical domain, we provide 8 individual NER models trained on 8 publicly available biomedical NER datasets: AnatEM,[28] BC5CDR,[29] BC4CHEMD,[30] BioNLP13CG,[31] JNLPBA,[32] Linnaeus,[33] NCBI-Disease,[34] and S800.[35] These models cover a wide variety of entity types in domains ranging from anatomical analysis to genetics and cellular biology. For training, we use preprocessed versions of these datasets provided by Wang et al.[36]

Clinical NER models

Our clinical-domain NER system contains 2 individually trained models. First, we provide a general-purpose NER model trained on the 2010 i2b2/VA dataset[37] that extracts problem, test, and treatment entities from various types of clinical notes. Second, we also provide a new radiology NER model, which extracts 5 types of entities from radiology reports: *anatomy*, *observation*, *anatomy modifier*, *observation modifier*, and *uncertainty*. The training dataset of this NER model consists of 150 chest computed tomography radiology reports collected from 3 individual hospitals.[38] Two radiologists were trained to annotate the reports with 5 entity types with an estimated Cohen's kappa interannotator agreement of 0.75. For full details of the entity types and corpora used in this dataset, we refer the readers to Hassanpour and Langlotz.[38]

For all biomedical and clinical NER datasets used in our study, we provide a detailed description of their supported entity types and their statistics in Supplementary Appendix B.

CharLM training corpora

For the biomedical NER models, we pretrain both the forward and backward CharLMs on the publicly available PubMed abstracts. For computational efficiency, we sampled about half of the 2020 PubMed Baseline dump (ftp://ftp.ncbi.nlm.nih.gov/pubmed/baseline) as our training corpus, which includes about 2.1 billion tokens. For the clinical NER models, we pretrain the CharLMs on all types of the MIMIC-III[21] clinical notes. During preprocessing of these notes, we exclude sentences in which at least 1 anonymization mask is applied (eg, *[**First Name8 (NamePattern2)**]*), to prevent the prevalence of such masks from polluting the representations learned by the CharLMs. The final corpus for training the clinical CharLMs includes about 0.4 billion tokens.

RESULTS

Syntactic analysis performance

We compare Stanza's syntactic analysis performance mainly with CoreNLP and scispaCy, and present the results in Table 1. We focus on evaluating the end-to-end performance of all toolkits starting from raw text. In this evaluation setup, a system takes raw text as input, and each module makes predictions by taking outputs from its previous modules. This setup is more challenging than using gold tokenized text and other annotations as input to downstream modules, as used in a lot of previous evaluations. For quantitative evaluation of the syntactic pipeline, we adopt the official evaluation metrics used in the CoNLL 2018 Universal Dependencies Shared Task. We include detailed descriptions of our metrics in Supplementary Appendix A, and refer the readers to the shared task official website for in-depth introductions (https://universaldependencies.org/conll18/evaluation.html).

For fair comparisons, for both CoreNLP and scispaCy, we present their results by retraining their pipelines on the corresponding treebanks using the official training scripts. scispaCy results are generated by retraining the *scispacy-large* models. For the MIMIC treebank, we do not include a comparison with scispaCy, mainly because we observed a severely degraded performance when applying it to tokenizing and sentence-segmenting clinical notes.

Notably, we find that Stanza's neural pipeline generalizes well to all treebanks we evaluate on, and achieves the best results for all components on all treebanks.

POS and parsing with gold input

The much lower tokenization performance of scispaCy on the CRAFT treebank is due to different tokenization rules adopted: the tokenizer in scispaCy is originally developed for the GENIA treebank and therefore segments hyphenated words differently from the CRAFT treebank annotations (see Biomedical Pipeline), leading to lower tokenization performance. To understand the underlying syntactic analysis performance without this tokenization difference, we run an individual evaluation on the CRAFT treebank with gold tokenization results provided to the POS tagger and parser at test time. We find that under this gold tokenization setup, Stanza is able to achieve an XPOS F_1 score of 98.40 and a parsing labeled attachment score (LAS) score of 92.10, while CoreNLP achieves 97.67 and 86.17, and scispaCy achieves 97.85 and 87.52 for XPOS and parsing LAS, respectively. Therefore, even with gold tokenization input (and gold POS tags for the parser), Stanza's neural pipeline still leads to substantially better performance for both POS tagging and UD parsing, with a notable gain of 5.93 and 4.58 LAS compared with CoreNLP and scispaCy, respectively. Our findings are in line with previous observations that a neural biaffine architecture outperforms other models on biomedical syntactic analysis tasks.[39]

Comparisons with CRAFT shared tasks 2019 systems

We further compare our end-to-end syntactic analysis results with the state-of-the-art system in the CRAFT Shared Tasks 2019,[9] for which CRAFT is also used as the evaluation treebank. For all systems, we also report results for the official morphology-aware LAS (MLAS) and bi-lexical dependency score (BLEX) metrics, which, apart from dependency predictions, also take POS tags and lemma outputs into account.

Under this setting, we find that the CRAFT shared task 2019 baseline system, which uses a combination of the NLTK tokenizer[40] and the SyntaxNet neural parser[41] retrained with the CRAFT treebank, achieves limited performance with LAS = 56.68 and MLAS = 44.22 (no BLEX score due to missing lemma outputs), while our syntactic pipeline trained on the CRAFT dataset achieves a much better performance: LAS = 89.67, MLAS = 86.06, and BLEX = 86.47. For comparisons, the shared task winning system[42] reports similar performance, with LAS = 89.70, MLAS = 85.55, and BLEX = 86.63. We note that the results from our system are not directly comparable to those from the shared task, owing to the different dependency parsing formalisms used (i.e., while we use UDv2 parse trees, the shared task used a parsing formalism similar to the older Stanford Dependencies formalism). Nevertheless, these results suggest that the accuracy of our pipeline is on par with that of the CRAFT shared task 2019 winning system, and substantially outperforms the shared task baseline system.

Table 1. Neural syntactic analysis pipeline performance

Treebank	System	Tokens	Sents.	UPOS	XPOS	Lemmas	UAS	LAS
CRAFT	Stanza	99.66	99.16	98.18	97.95	98.92	91.09	89.67
	CoreNLP	98.80	98.45	93.65	96.56	97.99	83.59	81.81
	scispaCy	91.49	97.47	83.81	89.67	89.39	79.08	77.74
GENIA	Stanza	99.81	99.78	98.81	98.76	99.58	91.01	89.48
	CoreNLP	98.22	97.20	93.40	96.98	97.97	84.75	83.16
	scispaCy	98.88	97.18	89.84	97.55	97.02	88.15	86.57
MIMIC	Stanza	99.18	97.11	95.64	95.25	97.37	85.44	82.81
	CoreNLP	100.00	100.00	94.08	94.53	95.84	78.92	74.94

All results are F_1 scores produced by the 2018 UD Shared Task official evaluation script. All CoreNLP (v4.0.0) and scispaCy (v0.2.5) results are from models retrained on the corresponding treebanks. UPOS results for scispaCy are generated by manually converting XPOS predictions to UPOS tags with the conversion script provided by spaCy. For scispaCy results, the *scispacy-large* models are used. Note that the MIMIC results are based on silver-standard training and evaluation data as described previously.

LAS: labeled attachment score; MIMIC: Medical Information Mart for Intensive Care; UAS: unlabeled attachment score; UPOS: universal part of speech; XPOS: language part of speech.

Effects of using combined treebanks

To evaluate the effect of using combined treebanks, we train Stanza's biomedical and clinical syntactic analysis pipeline on each individual treebank as well as the combined treebanks and evaluate their performance on the test set of each individual treebank. We present the results in Table 2. We find that by combining the biomedical or clinical treebanks with the general English EWT treebank, the resulting model not only is able to preserve its high performance on processing general-domain text, but also achieves marginally better in-domain performance compared with using the biomedical and clinical treebanks alone. For example, while the pipeline trained on the EWT treebank alone is only able to achieve an LAS scoreof 68.99 on the CRAFT test set, the pipeline trained on the combined dataset achieves the overall best LAS score of 89.57 on the CRAFT test set, with only a drop in LAS of 1.2 on the EWT test set. These results suggest that compared with using the in-domain treebank alone, using the combined treebanks improves the robustness of Stanza's pipeline on both in-domain and general English text.

NER performance

We mainly compare Stanza's NER performance to BioBERT, which achieves state-of-the-art performance on most of the datasets tested, and scispaCy in Table 3. For both toolkits, we compare with their official reported results.[4,11] We find that on most datasets tested, Stanza's NER performance is on par with or superior to the strong performance achieved by BioBERT, despite using considerably more compact models. A substantial difference is observed on the BC4CHEMD and NCBI-Disease datasets, where BioBERT leads by 2.71 and 2.22 in F_1, respectively, and on the S800 dataset, in which Stanza leads by 2.29 in F_1 score. Compared with scispaCy, Stanza achieves substantially higher performance on all datasets tested. On the newly introduced Radiology dataset, Stanza achieves an overall F_1 score of 84.80 micro-averaged over 5 entity types.

In addition to BioBERT, we also compare Stanza's performance with SciBERT,[43] which achieves F_1 scores of 90.01, 77.28, and 88.57 on the BC5CDR, JNLPBA, and NCBI-Disease datasets, respectively, and ClinicalBERT,[44] which achieves an F_1 score of 86.4 on the i2b2 dataset. We find that Stanza's performance is on par with or better than the strong performance offered by SciBERT and ClinicalBERT, too.

Effects of pretrained character LMs

To understand the effect of using the domain-specific pretrained CharLMs in NER models, on each dataset we also trained a baseline NER model in which the pretrained LM is replaced by a randomly initialized character-level BiLSTM, which is fine-tuned with other components during training. We compare Stanza's full NER performance with this baseline model in Table 4. We find that by pretrain-

Table 2. Comparisons of using combined treebanks vs single treebanks for the biomedical and clinical syntactic analysis pipelines

Biomedical Syntactic Analysis Pipelines				
	EWT Test		CRAFT Test	
Training Corpus	**Token F_1**	**LAS**	**Token F_1**	**LAS**
EWT	99.01	83.59	96.09	68.99
CRAFT	93.67	60.42	99.66	89.58
Combined	98.99	82.37	99.66	89.67
Clinical Syntactic Analysis Pipelines				
	EWT Test		MIMIC Test	
Training Corpus	**Token F_1**	**LAS**	**Token F_1**	**LAS**
EWT	99.01	83.59	92.97	75.97
MIMIC	94.39	66.63	98.70	81.46
Combined	98.84	82.57	99.18	82.81

For the biomedical pipeline we show results for the English EWT treebank and the CRAFT treebank; for the clinical pipeline we show results for the English EWT treebank and a silver-standard MIMIC treebank. For each test set, tokenization F_1 and LAS scores are shown for models trained with each treebank alone and a combined treebank.

EWT: English Web Treebank; LAS: labeled attachment score; MIMIC: Medical Information Mart for Intensive Care.

ing Stanza's CharLMs on large corpora, we are able to achieve an average gain of in F_1 score of 2.91 and 1.94 on the biomedical and clinical NER datasets, respectively.

Speed comparisons

We compare the speed of Stanza with CoreNLP and scispaCy on syntactic analysis tasks, and with scispaCy and BioBERT on the NER task (for BioBERT, we implemented our own code to run inference on the test data, as an inference API is not provided in the BioBERT official repository). We use the CRAFT test set, which contains about 1.2 million raw characters, for benchmarking the syntactic analysis pipeline, and the test split of the JNLPBA NER dataset, which contains about 101k tokens, for benchmarking the NER task. Apart from CPU speed, we also benchmark a toolkit's speed on GPU whenever GPU acceleration is available. Experiments are run on a machine with 2 Intel Xeon Gold 5222 CPUs (14 cores each). For GPU tests, we use a single NVIDIA Titan RTX card.

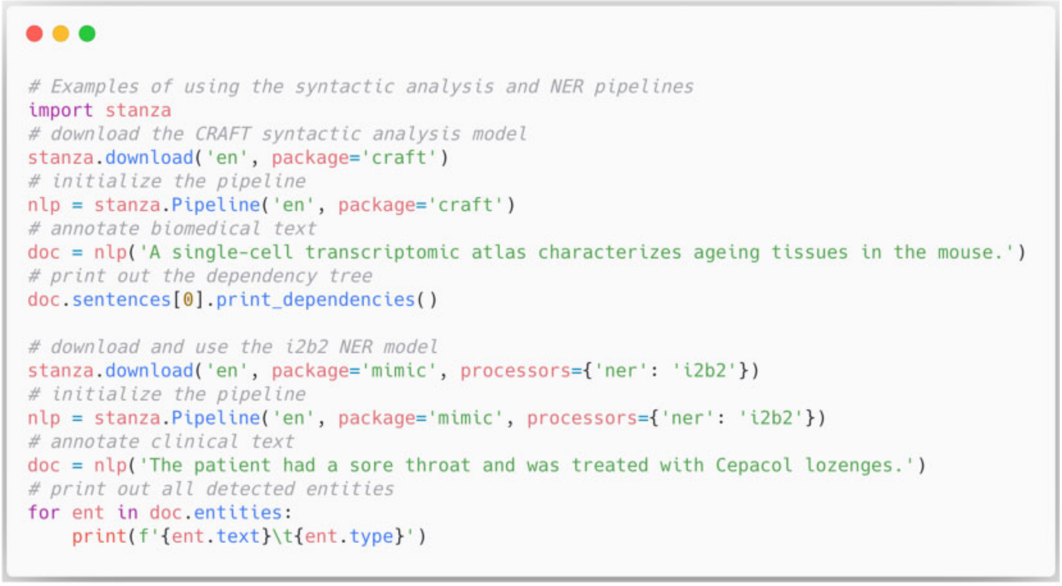
For each of the tasks, we focus on comparing the runtime of each toolkit relative to scispaCy. We find that for syntactic analysis, Stanza's speed is on par with scispaCy when a GPU is used (1.42× runtime), although it is much slower when only a CPU is available (6.83× runtime vs scispaCy). Even in the CPU setting, Stanza's biomedical syntactic analysis pipeline is still slightly faster than CoreNLP, which uses 7.23× runtime compared with scispaCy. For NER with GPU acceleration, Stanza's biomedical models are marginally faster than scispaCy (0.95× runtime vs scispaCy) and are considerably faster than BioBERT (4.59× runtime vs scispaCy). When only CPU is available, Stanza's biomedical models take much longer time to process text than scispaCy (14.8× runtime) but remain much faster than BioBERT which uses 121× runtime compared with scispaCy.

DISCUSSION

System usage

We provide a fully unified Python interface for using Stanza's biomedical/clinical models and general NLP models. The biomedical and clinical syntactic analysis pipelines can be specified with a *package* keyword. We demonstrate how to download the CRAFT biomedical package and run syntactic analysis for an example sentence in Figure 3. For NER, Stanza's biomedical and clinical models can be specified with a *processors* keyword. We demonstrate how to download the i2b2 clinical NER model along with the MIMIC clinical pipeline, and run NER annotation over an example clinical text in Figure 3. To easily integrate with external tokenization libraries, Stanza's biomedical and clinical pipelines also support annotating text that is pretokenized and sentence-segmented. This can be easily specified with a *tokenize_pretokenized* keyword when initializing the pipelines.

We provide full details on how to use the biomedical and clinical models via online documentation (https://stanfordnlp.github.io/stanza/).



```
# Examples of using the syntactic analysis and NER pipelines
import stanza
# download the CRAFT syntactic analysis model
stanza.download('en', package='craft')
# initialize the pipeline
nlp = stanza.Pipeline('en', package='craft')
# annotate biomedical text
doc = nlp('A single-cell transcriptomic atlas characterizes ageing tissues in the mouse.')
# print out the dependency tree
doc.sentences[0].print_dependencies()

# download and use the i2b2 NER model
stanza.download('en', package='mimic', processors={'ner': 'i2b2'})
# initialize the pipeline
nlp = stanza.Pipeline('en', package='mimic', processors={'ner': 'i2b2'})
# annotate clinical text
doc = nlp('The patient had a sore throat and was treated with Cepacol lozenges.')
# print out all detected entities
for ent in doc.entities:
    print(f'{ent.text}\t{ent.type}')
```

Figure 3. Example code for using the biomedical syntactic analysis and named entity recognition pipelines in Stanza.

Table 3. Named entity recognition performance across different datasets in the biomedical and clinical domains

Category	Dataset	Domain (# of Entities)	Stanza	BioBERT	scispaCy
Bio	AnatEM	Anatomy (1)	88.18	–	84.14
	BC5CDR	Chemical, Disease (2)	88.08	–	83.92
	BC4CHEMD	Chemical (1)	89.65	92.36	84.55
	BioNLP13CG	Cancer Genetics (16)	84.34	–	77.60
	JNLPBA	Protein, DNA, RNA, Cell line, Cell type (5)	76.09	77.49	73.21
	Linnaeus	Species (1)	88.27	88.24	81.74
	NCBI-Disease	Disease (1)	87.49	89.71	81.65
	S800	Species (1)	76.35	74.06	–
Clinical	i2b2	Problem, Test, Treatment (3)	88.13	86.73	–
	Radiology	Radiology Report (5)	84.80	–	–

All scores reported are entity micro-averaged test F_1. For each dataset, we also list the domain and number of its entity types. BioBERT results are from the v1.1 models reported by Lee et al[4]; scispaCy results are from the *scispacy-medium* models reported by Neumann et al.[11]

Table 4. Named entity recognition performance comparison between Stanza and a baseline BiLSTM-CRF model without character language models pretrained on large corpora

Category	Dataset	Baseline	Stanza	Δ
Bio	AnatEM	85.14	88.18	+3.04
	BC5CDR	86.14	88.08	+1.94
	BC4CHEMD	87.45	89.65	+2.20
	BioNLP13CG	82.09	84.34	+2.25
	JNLPBA	75.29	76.09	+0.80
	Linnaeus	83.74	88.27	+4.53
	NCBI-Disease	84.04	87.49	+3.45
	S800	71.30	76.35	+5.05
	Average (8 datasets)	81.90	84.81	+2.91
Clinical	i2b2	86.04	88.08	+2.04
	Radiology	83.01	84.80	+1.79
	Average (2 datasets)	84.53	86.47	+1.94

For both the biomedical and clinical models, an average difference over 8 models and 2 models are shown in the last column, respectively.

BiLSTM-CRF: bidirectional long short-term memory network conditional random field.

CONCLUSION

We present the biomedical and clinical model packages in the Stanza Python NLP toolkit. We show that Stanza's biomedical and clinical packages offer highly accurate syntactic analysis and named entity recognition capabilities, while maintaining competitive speed with existing toolkits, especially when GPU acceleration is available. These packages are highly integrated with Stanza's existing Python NLP interface, and require no additional effort to use. We hope to continuously maintain and expand these packages as new resources become available.

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AUTHOR CONTRIBUTIONS

YuhaZ, YuhuZ, and PQ implemented the models used in this article. YuhaZ and YuhuZ performed the data collection, data processing and experiments. YuhaZ created the figures and tables, and drafted the manuscript. All authors conceived of the idea for the article. All authors were involved in the design of the methodologies and experiments, and in the preparation of the final manuscript.

SUPPLEMENTARY MATERIAL

Supplementary material is available at *Journal of the American Medical Informatics Association* online.

CONFLICT OF INTEREST STATEMENT

Curtis P. Langlotzis in the board of directors and a shareholder of BunkerHill Health and is an advisor and option holder of whiterabbit.ai, Nines, GalileoCDS, and Sirona Medical.

DATA AVAILABILITY STATEMENT

The source code used in this paper is available at https://github.com/stanfordnlp/stanza. All pretrained models used in this paper can be downloaded by following the instructions at: https://stanfordnlp.github.io/stanza/biomed.html. An online demo of the models is available at: http://stanza.run/bio. The preprocessed biomedical treebanks used in this paper are available at: https://nlp.stanford.edu/projects/.

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