Biomedical Named Entity Recognition at Scale

Veysel Kocaman John Snow Labs Inc. 16192 Coastal Highway Lewes, DE, USA 19958 veysel@johnsnowlabs.com David Talby John Snow Labs Inc. 16192 Coastal Highway Lewes, DE, USA 19958 david@johnsnowlabs.com

Abstract—Named entity recognition (NER) is a widely applicable natural language processing task and building block of question answering, topic modeling, information retrieval, etc. In the medical domain, NER plays a crucial role by extracting meaningful chunks from clinical notes and reports, which are then fed to downstream tasks like assertion status detection, entity resolution, relation extraction, and de-identification. Reimplementing a Bi-LSTM-CNN-Char deep learning architecture on top of Apache Spark, we present a single trainable NER model that obtains new state-of-the-art results on seven public biomedical benchmarks without using heavy contextual embeddings like BERT. This includes improving BC4CHEMD to 93.72% (4.1% gain), Species800 to 80.91% (4.6% gain), and JNLPBA to 81.29% (5.2% gain). In addition, this model is freely available within a production-grade code base as part of the open-source Spark NLP library; can scale up for training and inference in any Spark cluster; has GPU support and libraries for popular programming languages such as Python, R, Scala and Java; and can be extended to support other human languages with no code changes.

I. Introduction

Electronic health records (EHRs) are the primary source of information for clinicians tracking the care of their patients. Information fed into these systems may be found in structured fields for which values are inputted electronically (e.g. laboratory test orders or results) Liede et al. [2015] but most of the time information in these records is unstructured making it largely inaccessible for statistical analysis Murdoch and Detsky [2013]. These records include information such as the reason for administering drugs, previous disorders of the patient or the outcome of past treatments, and they are the largest source of empirical data in biomedical research, allowing for major scientific findings in highly relevant disorders such as cancer and Alzheimer's disease Perera et al. [2014]. Unlocking this information can bring a significant advancement to biomedical research.

The widespread adoption of EHRs and the growing wealth of digitized information sources about patients are opening new doors to uncover previously unidentified associations and accelerating knowledge discovery via state-of-the-art Machine Learning (ML) algorithms and new statistical methods. Due to innate obstacles in extracting information from unstructured text data and the high level of preciseness dictated in healthcare domain, manual abstraction has been prevalent in the industry. As the manual abstraction is highly expensive, time consuming and error prone process, there has been a growing trend in natural language processing (NLP) applications in clinical and

biomedical domain to automate the abstraction process as well as making the EHR data available through high-performant and fail-safe pipelines.

As the key ingredient of any NLP system, named entity recognition (NER) is regarded as the first building block of question answering, topic modelling, information retrieval, etc Yadav and Bethard [2019]. In the medical domain, NER plays the most crucial role by giving out the first meaningful chunks of a clinical note, and then feeding them as an input to the subsequent downstream tasks such as clinical assertion status Uzuner et al. [2011], clinical entity resolvers Tzitzivacos [2007] and de-identification of the sensitive data Uzuner et al. [2007]. However, segmentation of clinical and drug entities is considered to be a difficult task in biomedical NER systems because of complex orthographic structures of named entities Liu et al. [2015].

ML methods formulate the clinical NER task as a sequence labeling problem that aims to find the best label sequence (e.g., BIO format labels) for a given input sequence (individual words from clinical text) Wu et al. [2017]. Many top-ranked NER systems applied the Conditional Random Fields (CRFs) model Lafferty et al. [2001], which is the most popular solution among conventional ML algorithms. A typical stateof-the-art clinical NER system usually utilizes features from different linguistic levels, including orthographic information (e.g., capitalization of letters, prefix and suffix), syntactic information (e.g. POS tags), word n-grams, word embeddings, and semantic information (e.g., the UMLS concept unique identifier) Wu et al. [2017]. These features are usually utilized in LSTM Hochreiter and Schmidhuber [1997] based neural network frameworks Huang et al. [2015], Chiu and Nichols [2016], Ma and Hovy [2016] and gained popularity among researchers due to their effectiveness of modeling the sequential patterns.

In the last few months, pretraining large neural language models and rich contextual embeddings, such as BERT Devlin et al. [2018] and ELMO Peters et al. [2018], have also led to impressive gains on NER systems and many clinical variants of BERT models such as BioBert LEE et al. [2019], ClinicalBert Alsentzer et al. [2019], BlueBert Peng et al. [2019], SciBert Beltagy et al. [2019] and PubmedBert Gu et al. [2020] have been crafted to address biomedical and clinical NER tasks with state-of-the-art results. However, since these methods require significant computational resources during both

pretraining and getting prediction, using them in production is impractical under the restricted computational resources compared to classical pretrained embeddings (e.g. Glove). A recent study Arora et al. [2020] empirically shows that classical pretrained embeddings can match contextual embeddings on industry-scale data, and often perform within 5 to 10% accuracy (absolute) on benchmark tasks.

Despite the growing interest and all these ground breaking advances in NER systems, easy to use production ready models and tools are scarce and it is one of the major obstacles for clinical NLP researchers to implement the latest algorithms into their workflow and start using immediately. On the other hand, NLP tool kits specialized for processing biomedical and clinical text, such as MetaMap Aronson and Lang [2010] and cTAKES Savova et al. [2010] typically do not make use of new research innovations such as word representations or neural networks discussed above, hence producing less accurate results Zhang et al. [2020], Neumann et al. [2019]. In the last year, two new libraries, Stanza Zhang et al. [2020] and SciSpacy Neumann et al. [2019] took the stage to find a solution to the issues discussed above and released Python-based, de facto language of data science, production grade libraries. Both libraries offer out of the box clinical and biomedical pretrained NER models utilizing state-of-the-art deep learning frameworks mentioned above. However, none of these libraries or tools can scale up in clusters in terms of distributed data processing principles and do not support in-memory distributed data processing solutions such as Spark.

In this study, we show through extensive experiments that our NER module in Spark NLP library, one of the most widely used NLP libraries in industry, exceeds the biomedical NER benchmarks reported by Stanza in 7 out of 8 benchmark datasets and in every dataset reported by SciSpacy. Using the modified version of the well known BiLSTM-CNN-Char NER architecture Chiu and Nichols [2016] into Spark environment, Spark NLP's NER module can also be extended to other spoken languages with zero code changes and can scale up in Spark clusters.

The specific novel contributions of this paper are the following:

- Delivering the first production-grade scalable NER model implementation.
- Delivering a state-of-the-art NER model that exceeds the biomedical NER benchmarks reported by Stanza and SciSpaCy.
- Comparing the effectiveness of domain specific clinical word embeddings with general purpose GloVe embeddings inside the same NER architecture.
- Explaining the NER model implementation in Spark NLP which is the only NLP library that can scale up in Spark clusters while supporting popular programming languages (Python, R, Scala and Java).

The remainder of the paper is organized as follows: Section II introduces Spark NLP and explains the NER model framework implemented in Spark NLP. Section III elaborates the implementation details, datasets and settings for our experiments

and presents results for Spark NLP, Stanza and SciSpacy on the same benchmark datasets. Section IV concludes this paper by pointing out key points and future directions.

II. NER MODEL IMPLEMENTATION IN SPARK NLP

The deep neural network architecture for NER model in Spark NLP is BiLSTM-CNN-Char framework, a slightly modified version of the architecture proposed by Chiu et.al. Chiu and Nichols [2016]. It is a neural network architecture that automatically detects word and character-level features using a hybrid bidirectional LSTM and CNN architecture, eliminating the need for most feature engineering steps.

In the original framework, the CNN extracts a fixed length feature vector from character-level features. For each word, these vectors are concatenated and fed to the BLSTM network and then to the output layers. They employed a stacked bi-directional recurrent neural network with long short-term memory units to transform word features into named entity tag scores. The extracted features of each word are fed into a forward LSTM network and a backward LSTM network. The output of each network at each time step is decoded by a linear layer and a log-softmax layer into log-probabilities for each tag category. These two vectors are then simply added together to produce the final output Chiu and Nichols [2016]. The detailed architecture of the proposed framework in the original paper is illustrated at Figure 1. In sum, 50-dimensional pretrained word embeddings is used for word features, 25-dimension character embeddings is used for char features, and capitalization features (allCaps, upperInitial, lowercase, mixedCaps, noinfo) are used for case features. They also made use of lexicons as a form of external knowledge as proposed in Ratinov and Roth [2009].

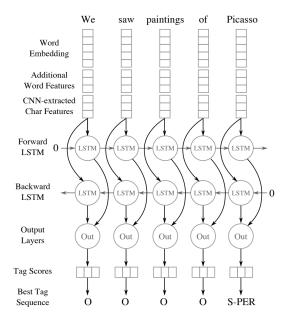


Fig. 1: Overview of the original BiLSTM-CNN-Char architecture Chiu and Nichols [2016].

In Spark NLP, we modified this framework as follows:

- Habibi et al. [2017] compared the performance of LSTM-CRF approach on 33 data sets covering five different entity classes with that of best-of-class NER tools and an entity-agnostic CRF implementation. On average, F1-score of LSTM-CRF is 5% above that of the baselines, using WikiPubMed-PMC word embeddings.
 - Using a similar neural network architecture, we trained our own biomedical word embeddings with skip-gram model on PubMed abstracts and case studies, as described in Mikolov et al. [2013], for learning distributed representations of words using contextual information. The trained word embeddings has 200-dimensions and a vocabulary size of 2.2 million. In order to compare the effectiveness of this embeddings, we also used 300-dimension pretrained GloVe embeddings with 6 billion tokens, trained on Wikipedia and Gigaword-5 dataset Pennington et al. [2014]. Both embeddings are ported into Spark through an annotator concept specifically designed for Spark NLP. The average word coverage of our implementation of domain specific word embeddings (we call it Spark-Biomedical embeddings in this study) is 99.5% and the coverage of Glove6B embeddings is 96.1% on the biomedical datasets used in this study (see Table I).
- Even though better results were reported by Ghaddar and Langlais [2018] through robust lexical features, after experimenting with different parameters and components, we decided to remove lexical features in order to reduce the complexity and relied on pretrained biomedical embeddings, casing features and char features through CNN. As sentences are represented through 2 nested sequences (words & chars), a CNN is applied in a way that each character is embedded in a character embedding matrix, of dimension 25. Then, a 1D Convolution layer processes the sequence of embedded char vectors, followed by a MaxPooling operation. This way, each word gets a vector representation. We used 25 filters and kernel size of 3. It is worth to mention that char features are proved to be highly useful in NER models and had provided a level of immunity to typos and spelling errors.
- We built a modified version of the framework Chiu and Nichols [2016] in Tensorflow (TF) and used LSTM-BlockFusedCell. This is an extremely efficient LSTM implementation based on Zaremba et al. [2014], that uses a single TF operation for the entire LSTM. Our experiments show that it is both faster and more memoryefficient than LSTMBlockCell. Then we implemented this framework in Scala using TensorFlow API. This setup is ported into Spark and let the driver node run the entire training using all the available cores on the driver node. We also added CuDA version of each TF component to be able to train our models on GPU when available.

Due to architectural design choices by Tensorflow implementation in JVM at the time of writing this paper, distributing the model training over the worker nodes in the cluster was not viable and effective, and putting the burden of

entire training process on the driver node mandated some limitations in terms of training speed and computational resources. Nevertheless, being able to get predictions on scale from voluminous data with state-of-the-art accuracy would overwhelm the aforementioned disadvantage.

III. IMPLEMENTATION DETAILS AND EXPERIMENTAL RESULTS

In this section, we describe the datasets, evaluation metrics, and provide an overview of experimental setup.

A. Datasets

In this study, we trained individual NER models on 8 publicly available biomedical NER datasets provided by Wang et al. [2019]: AnatEM Pyysalo and Ananiadou [2014], BC5CDR Li et al. [2016], BC4CHEMD Krallinger et al. [2015], BioNLP13CG Pyysalo et al. [2015], JNLPBA Kim et al. [2004], Linnaeus Gerner et al. [2010], NCBI-Disease Doğan et al. [2014] and S800 Pafilis et al. [2013]. These models cover a wide variety of entity types in domains ranging from anatomical analysis to genetics and cellular biology. For the sake of brevity, we didn't include details about the nature of the data sets and readers can refer to cited papers for more information. We trained several other clinical and biomedical NER models in Spark NLP, but we just report metrics on these 8 biomedical data sets as Stanza and SciSpacy also reported their benchmarks on these data sets that are freely available without any restrictions.

B. Overview of Experimental Setup

Biomedical NER datasets provided by Wang et al. [2019] are already in BIO and BIOES schemes for encoding entity annotations as token tags. IOB (or BIO) stands for Begin, Inside and Outside. Words tagged with O are outside of named entities and the I-XXX tag is used for words inside a named entity of type XXX. Whenever two entities of type XXX are immediately next to each other, the first word of the second entity will be tagged B-XXX to highlight that it starts another entity. On the other hand, BIOES (also known as BIOLU) is a little bit sophisticated annotation method that distinguishes between the end of a named entity and single entities. BIOES stands for Begin, Inside, Outside, End, Single. In this scheme, for example, a word describing a gene entity is tagged with "B-Gene" if it is at the beginning of the entity, "I-Gene" if it is in the middle of the entity, and "E-Gene" if it is at the end of the entity. Single-word gene entities are tagged with "S-Gene". All other words not describing entities of interest are tagged as 'O'.

BIOES scheme was also used in the original implementation of our NER architecture and considerable performance improvements over BIO are reported Chiu and Nichols [2016]. Ratinov and Roth [2009] also showed that the minimal BIO scheme was more difficult to learn than the BIOES scheme, which explicitly marks boundary tokens. However, we experienced various performance issues when we used BIOES schema (converging very fast in the early epochs but then fail to

TABLE I: Word embeddings coverage ratios on biomedical datasets. Our domain specific embeddings have near-perfect word coverages. The average word coverage of our implementation of domain specific word embeddings (we call it Spark-Biomedical Embeddings in this study) is 99.5% and the average word coverage of Glove6B embeddings is 96.1% on the biomedical datasets used in this study)

Detect	Spark-Biomedical Embeddings		Spark-Glove6B Embeddings		
Dataset	Training set	Test set	Training set	Test set	
NBCI-Disease	99.700	99.695	96.703	96.710	
BC5CDR	99.171	99.106	96.059	95.795	
BC4CHEMD	99.571	99.551	96.409	96.434	
Linnaeus	99.162	99.181	96.801	96.867	
Species800	99.350	99.345	95.909	96.258	
JNLPBA	99.530	99.496	92.566	92.690	
AnatEM	99.580	99.623	96.992	96.945	
BioNLP-CG	99.859	99.814	97.750	96.663	

generalize further and stuck at local minima), and then decided to use BIO scheme.

In terms of hyperparameter tuning, we run experiments by tuning the hyperparameters with the following parameter ranges through Random Search Bergstra and Bengio [2012] and found out that the following parameters would produce the best results (figures within the parenthesis represent the parameter ranges tested):

LSTM state size: 200 (200, 250)
Dropout rate: 0.5 (0.3, 0.7)
Batch size: 8 (4, 256)

• Learning rate: 0.001 (0.01, 0.0003)

Epoch: 10-15 (10, 100)Optimizer: Adam

• Learning rate decay coefficient (po) (real learning rate = lr/(1 + po * epoch) Smith [2018] : 0.005 (0.001, 0.01))

C. Experiment Results

We run our experiments on Colab¹ server provided by Google (2vCPU @ 2.2GHz, 13GB RAM) and used Apache Spark in local mode (no cluster). We present our results at Table II and Figure 2. As the only NLP library that scales up for training and inference in any Spark cluster, Spark NLP NER architecture obtains new state-of-the-art results on seven public biomedical benchmarks without using heavy contextual embeddings like BERT. This includes improving BC4CHEMD to 93.72% (4.1% gain), Species800 to 80.91% (4.6% gain), and JNLPBA to 81.29% (5.2% gain). Given that Stanza already claims that its NER performance is on par with or superior to the strong performance achieved by BioBERT, our proposed NER model can get better results despite using considerably more compact model. Moreover, this model is available within a productiongrade code base as part of the open-source Spark NLP library and a new NER model can be trained with a single line of code as presented in Appendix A.

As you can see on the leaderboard given at Table III, our NER model with pretrained biomedical embeddings produces better results than Stanza in 7 out of 8 biomedical datasets and

1https://colab.research.google.com/

exceeds SciSpacy in all the benchmarks. It is also surprising to see that our NER model with GloVe6B embeddings, despite being a general purpose embeddings, can also exceed Stanza's (also using domain specific embeddings, CharLM - characterlevel language model Akbik et al. [2018]) benchmarks in half of the benchmarks and again exceeds SciSpacy in all the benchmarks.

IV. CONCLUSION

Despite the growing interest and ground breaking advances in NLP research and NER systems, easy to use production ready models and tools are scarce in Biomedical domain and it is one of the major obstacles for clinical NLP researchers to implement the latest algorithms into their workflow and start using immediately.

In this study, we show through extensive experiments that NER module in Spark NLP library, one of the most widely used NLP libraries in industry, exceeds the biomedical NER benchmarks reported by Stanza in 7 out of 8 benchmark datasets and in every dataset reported by SciSpacy without using heavy contextual embeddings like BERT. Using the modified version of the well known BiLSTM-CNN-Char NER architecture Chiu and Nichols [2016] into Spark environment, we also presented that even with a general purpose GloVe embeddings (GloVe6B) and with no lexical features, we were able to achieve state-of-the-art results in biomedical domain and produces better results than Stanza in 4 out of 8 benchmark datasets. Given that Stanza also uses domain specific clinical embeddings, exceeding its benchmarks with general purpose embeddings is also another important observation.

Spark NLP's NER module can also be extended to other spoken languages with zero code changes and can scale up in Spark clusters. In addition, this model is available within a production-grade code base as part of the Spark NLP library; can scale up for training and inference in any Spark cluster; has GPU support and libraries for popular programming languages such as Python, R, Scala and Java; and is already extended to support other human languages with no code changes.

TABLE II: NER performance across different datasets in the biomedical domain. All scores reported are micro-averaged test F1 excluding O's. Stanza results are from the paper reported in Zhang et al. [2020], SciSpaCy results are from the scispacy-medium models reported in Neumann et al. [2019]. The official training and validation sets are merged and used for training and then the models are evaluated on the original test sets. For reproducibility purposes, we use the preprocessed versions of these datasets provided by Wang et al. [2019] and also used by Stanza. Spark-x prefix in the table indicates our implementation. Bold scores represent the best scores in the respective row.

Dataset	Entities	Spark - Biomedical	Spark - GloVe 6B	Stanza	SciSpacy
NBCI-Disease	Disease	89.13	87.19	87.49	81.65
BC5CDR	Chemical, Disease	89.73	88.32	88.08	83.92
BC4CHEMD	Chemical	93.72	92.32	89.65	84.55
Linnaeus	Species	86.26	85.51	88.27	81.74
Species800	Species	80.91	79.22	76.35	74.06
JNLPBA	5 types in cellular	81.29	79.78	76.09	73.21
AnatEM	Anatomy	89.13	87.74	88.18	84.14
BioNLP13-CG	16 types in Cancer Genetics	85.58	84.3	84.34	77.6

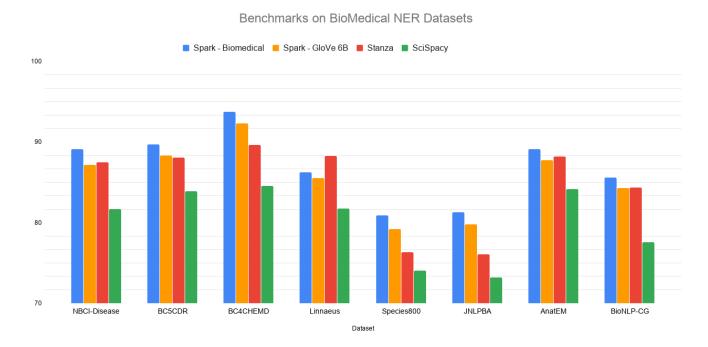


Fig. 2: NER performance across different biomedical benchmark datasets. Our implementation of NER model with domain specific embeddings exceeds Stanza in 7 out of 8 datasets and exceeds SciSpacy in all the benchmarks. The same implementation with general purpose GloVe embeddings is also better than SciSpacy in every dataset and exceeds Stanza in 4 out of 8 datasets.

REFERENCES

Alexander Liede, Rohini K Hernandez, Maayan Roth, Geoffrey Calkins, Katherine Larrabee, and Leo Nicacio. Validation of international classification of diseases coding for bone metastases in electronic health records using technology-enabled abstraction. *Clinical epidemiology*, 7:441, 2015.

Travis B Murdoch and Allan S Detsky. The inevitable application of big data to health care. *Jama*, 309(13):1351–1352, 2013.

Gayan Perera, Mizanur Khondoker, Matthew Broadbent, Gerome Breen, and Robert Stewart. Factors associated with response to acetylcholinesterase inhibition in dementia: a cohort study from a secondary mental health care case register in london. *PloS one*, 9(11):e109484, 2014.

Vikas Yadav and Steven Bethard. A survey on recent advances in named entity recognition from deep learning models. *arXiv preprint arXiv:1910.11470*, 2019.

Özlem Uzuner, Brett R South, Shuying Shen, and Scott L DuVall. 2010 i2b2/va challenge on concepts, assertions, and relations in clinical text. *Journal of the American Medical Informatics Association*, 18(5):552–556, 2011.

D Tzitzivacos. International classification of diseases 10th edition (icd-10):: main article. CME: Your SA Journal of

TABLE III: Biomedical NER benchmarks leaderboard. Spark-x prefix indicates our implementation.

	Best		2nd Best		3rd Best	
Dataset	Model	Score	Model	Score	Model	Score
NBCI-Disease	Spark-Biomedical	89.13	Stanza	87.49	Spark-GloVe6B	87.19
BC5CDR	Spark-Biomedical	89.73	Spark-GloVe6B	88.32	Stanza	88.08
BC4CHEMD	Spark-Biomedical	93.72	Spark-GloVe6B	92.32	Stanza	89.65
Linnaeus	Stanza	88.27	Spark-Biomedical	86.26	Spark-GloVe6B	85.51
Species800	Spark-Biomedical	81.29	Spark-GloVe6B	79.78	Stanza	76.09
AnatEM	Spark-Biomedical	89.13	Stanza	88.18	Spark-GloVe6B	87.74
BioNLP-CG	Spark-Biomedical	85.58	Stanza	84.34	Spark-GloVe6B	84.3

- CPD, 25(1):8-10, 2007.
- Özlem Uzuner, Yuan Luo, and Peter Szolovits. Evaluating the state-of-the-art in automatic de-identification. *Journal of the American Medical Informatics Association*, 14(5):550–563, 2007.
- Shengyu Liu, Buzhou Tang, Qingcai Chen, and Xiaolong Wang. Effects of semantic features on machine learning-based drug name recognition systems: word embeddings vs. manually constructed dictionaries. *Information*, 6(4):848–865, 2015.
- Yonghui Wu, Min Jiang, Jun Xu, Degui Zhi, and Hua Xu. Clinical named entity recognition using deep learning models. In *AMIA Annual Symposium Proceedings*, volume 2017, page 1812. American Medical Informatics Association, 2017.
- John Lafferty, Andrew McCallum, and Fernando CN Pereira. Conditional random fields: Probabilistic models for segmenting and labeling sequence data. 2001.
- Sepp Hochreiter and Jürgen Schmidhuber. Long short-term memory. *Neural computation*, 9(8):1735–1780, 1997.
- Zhiheng Huang, Wei Xu, and Kai Yu. Bidirectional lstm-crf models for sequence tagging. arXiv preprint arXiv:1508.01991, 2015.
- Jason PC Chiu and Eric Nichols. Named entity recognition with bidirectional lstm-cnns. *Transactions of the Association for Computational Linguistics*, 4:357–370, 2016.
- Xuezhe Ma and Eduard Hovy. End-to-end sequence labeling via bi-directional lstm-cnns-crf. *arXiv preprint arXiv:1603.01354*, 2016.
- Jacob Devlin, Ming-Wei Chang, Kenton Lee, and Kristina Toutanova. Bert: Pre-training of deep bidirectional transformers for language understanding. *arXiv preprint arXiv:1810.04805*, 2018.
- Matthew E Peters, Mark Neumann, Mohit Iyyer, Matt Gardner, Christopher Clark, Kenton Lee, and Luke Zettlemoyer. Deep contextualized word representations. *arXiv preprint arXiv:1802.05365*, 2018.
- J LEE, W YOON, S KIM, D KIM, and S KIM. So ch & kang j.(2019). biobert: a pretrained biomedical language representation model for biomedical text mining. *arXiv* preprint arXiv:1901.08746, 2019.
- Emily Alsentzer, John R Murphy, Willie Boag, Wei-Hung Weng, Di Jin, Tristan Naumann, and Matthew McDermott.

- Publicly available clinical bert embeddings. *arXiv preprint arXiv:1904.03323*, 2019.
- Yifan Peng, Shankai Yan, and Zhiyong Lu. Transfer learning in biomedical natural language processing: An evaluation of bert and elmo on ten benchmarking datasets. *arXiv* preprint *arXiv*:1906.05474, 2019.
- Iz Beltagy, Kyle Lo, and Arman Cohan. Scibert: A pretrained language model for scientific text. *arXiv preprint arXiv:1903.10676*, 2019.
- Yu Gu, Robert Tinn, Hao Cheng, Michael Lucas, Naoto Usuyama, Xiaodong Liu, Tristan Naumann, Jianfeng Gao, and Hoifung Poon. Domain-specific language model pretraining for biomedical natural language processing. *arXiv* preprint arXiv:2007.15779, 2020.
- Simran Arora, Avner May, Jian Zhang, and Christopher Ré. Contextual embeddings: When are they worth it? *arXiv* preprint arXiv:2005.09117, 2020.
- Alan R Aronson and François-Michel Lang. An overview of metamap: historical perspective and recent advances. *Journal* of the American Medical Informatics Association, 17(3):229– 236, 2010.
- Guergana K Savova, James J Masanz, Philip V Ogren, Jiaping Zheng, Sunghwan Sohn, Karin C Kipper-Schuler, and Christopher G Chute. Mayo clinical text analysis and knowledge extraction system (ctakes): architecture, component evaluation and applications. *Journal of the American Medical Informatics Association*, 17(5):507–513, 2010.
- Yuhao Zhang, Yuhui Zhang, Peng Qi, Christopher D Manning, and Curtis P Langlotz. Biomedical and clinical english model packages in the stanza python nlp library. *arXiv* preprint *arXiv*:2007.14640, 2020.
- Mark Neumann, Daniel King, Iz Beltagy, and Waleed Ammar. Scispacy: Fast and robust models for biomedical natural language processing. *arXiv* preprint arXiv:1902.07669, 2019.
- Lev Ratinov and Dan Roth. Design challenges and misconceptions in named entity recognition. In *Proceedings of the Thirteenth Conference on Computational Natural Language Learning (CoNLL-2009)*, pages 147–155, 2009.
- Maryam Habibi, Leon Weber, Mariana Neves, David Luis Wiegandt, and Ulf Leser. Deep learning with word em-

- beddings improves biomedical named entity recognition. *Bioinformatics*, 33(14):i37–i48, 2017.
- Tomas Mikolov, Kai Chen, Greg Corrado, and Jeffrey Dean. Efficient estimation of word representations in vector space. *arXiv* preprint arXiv:1301.3781, 2013.
- Jeffrey Pennington, Richard Socher, and Christopher D Manning. Glove: Global vectors for word representation. In *Proceedings of the 2014 conference on empirical methods in natural language processing (EMNLP)*, pages 1532–1543, 2014.
- Abbas Ghaddar and Philippe Langlais. Robust lexical features for improved neural network named-entity recognition. *arXiv* preprint arXiv:1806.03489, 2018.
- Wojciech Zaremba, Ilya Sutskever, and Oriol Vinyals. Recurrent neural network regularization. *arXiv preprint* arXiv:1409.2329, 2014.
- Xuan Wang, Yu Zhang, Xiang Ren, Yuhao Zhang, Marinka Zitnik, Jingbo Shang, Curtis Langlotz, and Jiawei Han. Crosstype biomedical named entity recognition with deep multitask learning. *Bioinformatics*, 35(10):1745–1752, 2019.
- Sampo Pyysalo and Sophia Ananiadou. Anatomical entity mention recognition at literature scale. *Bioinformatics*, 30 (6):868–875, 2014.
- Jiao Li, Yueping Sun, Robin J Johnson, Daniela Sciaky, Chih-Hsuan Wei, Robert Leaman, Allan Peter Davis, Carolyn J Mattingly, Thomas C Wiegers, and Zhiyong Lu. Biocreative v cdr task corpus: a resource for chemical disease relation extraction. *Database*, 2016, 2016.
- Martin Krallinger, Obdulia Rabal, Florian Leitner, Miguel Vazquez, David Salgado, Zhiyong Lu, Robert Leaman, Yanan Lu, Donghong Ji, Daniel M Lowe, et al. The chemdner corpus of chemicals and drugs and its annotation principles. *Journal of cheminformatics*, 7(1):1–17, 2015.
- Sampo Pyysalo, Tomoko Ohta, Rafal Rak, Andrew Rowley, Hong-Woo Chun, Sung-Jae Jung, Sung-Pil Choi, Jun'ichi Tsujii, and Sophia Ananiadou. Overview of the cancer genetics and pathway curation tasks of bionlp shared task 2013. *BMC bioinformatics*, 16(S10):S2, 2015.
- Jin-Dong Kim, Tomoko Ohta, Yoshimasa Tsuruoka, Yuka Tateisi, and Nigel Collier. Introduction to the bio-entity recognition task at jnlpba. In *Proceedings of the international joint workshop on natural language processing in biomedicine and its applications*, pages 70–75. Citeseer, 2004.
- Martin Gerner, Goran Nenadic, and Casey M Bergman. Linnaeus: a species name identification system for biomedical literature. *BMC bioinformatics*, 11(1):85, 2010.
- Rezarta Islamaj Doğan, Robert Leaman, and Zhiyong Lu. Ncbi disease corpus: a resource for disease name recognition and concept normalization. *Journal of biomedical informatics*, 47:1–10, 2014.
- Evangelos Pafilis, Sune P Frankild, Lucia Fanini, Sarah Faulwetter, Christina Pavloudi, Aikaterini Vasileiadou, Christos Arvanitidis, and Lars Juhl Jensen. The species and organisms resources for fast and accurate identification of taxonomic names in text. *PloS one*, 8(6):e65390, 2013.

- James Bergstra and Yoshua Bengio. Random search for hyperparameter optimization. *The Journal of Machine Learning Research*, 13(1):281–305, 2012.
- Leslie N Smith. A disciplined approach to neural network hyperparameters: Part 1-learning rate, batch size, momentum, and weight decay. *arXiv* preprint arXiv:1803.09820, 2018.
- Alan Akbik, Duncan Blythe, and Roland Vollgraf. Contextual string embeddings for sequence labeling. In *Proceedings* of the 27th International Conference on Computational Linguistics, pages 1638–1649, 2018.

APPENDIX

```
from pyspark.ml import Pipeline
import sparknlp
from sparknlp.training import CoNLL
from sparknlp.annotator import *
spark = sparknlp.start()
training_data = CoNLL().readDataset(spark, '
    BC5CDR_train.conll')
word_embedder = WordEmbeddings.pretrained('
    wikiner_6B_300', 'xx')
 .setInputCols(["sentence",'token'])\
 .setOutputCol("embeddings")
nerTagger = NerDLApproach() \
  .setInputCols(["sentence", "token", "embeddings"])
  .setLabelColumn("label") \
  .setOutputCol("ner") \
  .setMaxEpochs(10)\
  .setDropout(0.5)\
  .setLr(0.001) \
  .setPo(0.005)\
  .setBatchSize(8) \
  .setValidationSplit(0.2)\
pipeline = Pipeline(
   stages = [
   word embedder,
   nerTagger
ner_model = pipeline.fit(training_data)
```