Inexpensive Domain Adaptation of Pretrained Language Models: Case Studies on Biomedical NER and Covid-19 QA

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Abstract

Domain adaptation of Pretrained Language Models (PTLMs) is typically achieved by unsupervised pretraining on target-domain text. While successful, this approach is expensive in terms of hardware, runtime and CO₂ emissions. Here, we propose a cheaper alternative: We train Word2Vec on target-domain text and align the resulting word vectors with the wordpiece vectors of a general-domain PTLM.

We evaluate on eight biomedical Named Entity Recognition (NER) tasks and compare against the recently proposed BioBERT model. We cover over 50% of the BioBERT – BERT F1 delta, at 5% of BioBERT’s CO₂ footprint and 2% of its cloud compute cost. We also show how to quickly adapt an existing general-domain Question Answering (QA) model to an emerging domain: the Covid-19 pandemic. Models will be made available upon publication.

1 Introduction

Pretrained Language Models (PTLMs) such as BERT (Devlin et al., 2019) have spearheaded advances on many NLP tasks. Usually, PTLMs are pretrained on unlabeled general-domain and/or mixed-domain text, such as Wikipedia, digital books or the Common Crawl corpus.

When applying PTLMs to specific domains, it can be useful to domain-adapt them. Domain adaptation of PTLMs has typically been achieved by pretraining on target-domain text. One such model is BioBERT (Lee et al., 2020), which was initialized from general-domain BERT and then pretrained on biomedical scientific publications. The domain adaptation is shown to be helpful for target-domain tasks such as biomedical Named Entity Recognition (NER) or Question Answering (QA). On the downside, the computational cost of pretraining can be considerable: BioBERTv1.0 was adapted for ten days on eight large GPUs (see Table 1), which is expensive, environmentally unfriendly, prohibitive for small research labs and students, and may delay prototyping on emerging domains.

We therefore propose a fast, CPU-only domain-adaptation method for PTLMs: We train Word2Vec (Mikolov et al., 2013a) on target-domain text and align the resulting word vectors with the wordpiece vectors of an existing general-domain PTLM. The PTLM thus gains domain-specific lexical knowledge in the form of additional word vectors, but its deeper layers remain unchanged. Since Word2Vec and the vector space alignment are efficient models, the process requires a fraction of the resources associated with pretraining the PTLM itself, and it can be done on CPU.

In Section 4, we use the proposed method to domain-adapt BERT on PubMed+PMC (the data used for BioBERTv1.0) and/or CORD-19 (Covid-19 Open Research Dataset). We improve over general-domain BERT on eight out of eight biomedical NER tasks, using a fraction of the compute cost associated with BioBERT. In Section 5, we show how to quickly adapt an existing Question Answering model to text about the Covid-19 pandemic, without any target-domain Language Model pretraining or finetuning.

2 Related work

2.1 The BERT PTLM

For our purpose, a PTLM consists of three parts: A tokenizer $T_{LM} : L^+ \rightarrow \mathbb{L}_{LM}$, a wordpiece embedding function $\xi_{LM} : \mathbb{L}_{LM} \rightarrow \mathbb{R}^{d_{LM}}$ and an encoder function $\mathcal{F}_{LM}$. $\mathbb{L}_{LM}$ is a limited vocabulary of wordpieces. All words that are not in $\mathbb{L}_{LM}$ are tokenized into sequences of shorter wordpieces, e.g., tachycardia becomes ta ##chy ##card ##ia. Given a sentence $S = \{w_1, \ldots, w_T\}$, tokenized as $T_{LM}(S) = [T_{LM}(w_1); \ldots; T_{LM}(w_T)]$, $\xi_{LM}$ em-
Table 1: Domain adaptation cost. CO₂ emissions are calculated according to Strubell et al. (2019). Since our hardware configuration is not available on Google Cloud, we take an m1-ultramem-40 instance (40 vCPUs, 961GB RAM) to estimate an upper bound on our Google Cloud cost.

| Model                                      | Domain adaptation hardware | Power(W) | Time(h) | CO₂(lbs) | Google Cloud $ |
|---------------------------------------------|----------------------------|----------|---------|----------|----------------|
| BioBERTv1.0                                 | base 8 NVIDIA v100 GPUs (32GB) | 1505     | 240     | 544      | 1421 – 4762    |
| BioBERTv1.1                                 | base 8 NVIDIA v100 GPUs (32GB) | 1505     | 552     | 1252     | 3268 – 10952   |
| GreenBioBERT (Section 4)                    | base 12 Intel Xeon E7-8857 CPUs, 30GB RAM | 1560     | 12      | 28       | 16 – 76        |
| GreenCovidSQuADBERT (Section 5)             | large 12 Intel Xeon E7-8857 CPUs, 40GB RAM | 1560     | 24      | 56       | 32 – 152       |

2.4 Word vector space alignment

Word vector space alignment has most frequently been explored in the context of cross-lingual word embeddings. For instance, Mikolov et al. (2013b) align English and Spanish Word2Vec spaces by a simple linear transformation. Wang et al. (2019) use a related method to align cross-lingual word vectors and multilingual BERT wordpiece vectors.

3 Method

In the following, we assume access to a general-domain PTLM, as described in Section 2.1, and a corpus of unlabeled target-domain text.

3.1 Creating new input vectors

In a first step, we train Word2Vec on the target-domain corpus. In a second step, we take the intersection of $L_{LM}$ and $L_{W2V}$. In practice, the intersection mostly contains wordpieces from $L_{LM}$ that correspond to standalone words. It also contains single characters and other noise, however, we found that filtering them does not improve alignment quality. In a third step, we use the intersection to fit an unconstrained linear transformation $W \in \mathbb{R}^{d_{LM} \times d_{W2V}}$ via least squares:

$$\text{argmin}_W \sum_{x \in L_{LM} \cap L_{W2V}} ||W \hat{E}_{W2V}(x) - E_{LM}(x)||^2_2$$

Intuitively, $W$ makes Word2Vec vectors “look like” the PTLM’s native wordpiece vectors, just like cross-lingual alignment makes word vectors from one language “look like” word vectors from another language. In Table 2 (top), we show examples of within-space and cross-space nearest neighbors after alignment.

3.2 Updating the wordpiece embedding layer

Next, we redefine the wordpiece embedding layer of the PTLM. The most radical strategy would be to replace the entire layer with the aligned Word2Vec vectors:

$$\hat{E}_{LM} : L_{W2V} \rightarrow \mathbb{R}^{d_{LM}} ; \hat{E}_{LM}(x) = W \hat{E}_{W2V}(x)$$
In initial experiments, this strategy led to a drop in performance, presumably because function words are not well represented by Word2Vec, and replacing them disrupts BERT’s syntactic abilities. To prevent this problem, we leave existing wordpiece vectors intact and only add new ones:
\[
\hat{\mathcal{E}}_{LM} : \mathbb{L}_{LM} \cup \mathbb{L}_{W2V} \rightarrow \mathbb{E}_{dLM};
\]
\[
\hat{\mathcal{E}}_{LM}(x) = \begin{cases} 
\mathcal{E}_{LM}(x) & \text{if } x \in \mathbb{L}_{LM} \\
W\mathcal{E}_{W2V}(x) & \text{otherwise}
\end{cases}
\]

3.3 Updating the tokenizer

In a final step, we update the tokenizer to account for the added words. Let \( \hat{T}_{LM} \) be the standard BERT tokenizer, and let \( \bar{T}_{LM} \) be the tokenizer that treats all words in \( \mathbb{L}_{LM} \cup \mathbb{L}_{W2V} \) as one-wordpiece tokens, while tokenizing any other words as usual.

In practice, a given word may or may not benefit from being tokenized by \( \bar{T}_{LM} \) instead of \( \hat{T}_{LM} \). To give a concrete example, 82% of the words in the BC5CDR NER dataset that end in the suffix -ia are inside a disease entity (e.g., tachycardia). \( \bar{T}_{LM} \) tokenizes this word as ta ##ch ##card ##ia, thereby exposing the orthographic cue to the model. As a result, \( \bar{T}_{LM} \) leads to higher recall on -ia diseases. But there are many cases where wordpiece tokenization is meaningless or misleading. For instance euthymia (not a disease) is tokenized by \( \bar{T}_{LM} \) as e ##uth ##ym ##ia, making it likely to be classified as a disease. By contrast, \( \hat{T}_{LM} \) gives euthymia a one-wordpiece representation that depends only on distributional semantics. We find that using \( \bar{T}_{LM} \) improves precision on -ia diseases.

To combine these complementary strengths, we use a 50/50 mixture of \( \hat{T}_{LM} \)-tokenization and \( \bar{T}_{LM} \)-tokenization when finetuning the PTLM on a task. At test time, we use both tokenizers and mean-pool the outputs. Let \( o(T(S)) \) be some output of interest (e.g., a logit), given sentence S tokenized by T. We predict:
\[
\frac{1}{2} (o(T_{LM}(S)) + o(\bar{T}_{LM}(S))
\]

4 Experiment 1: Biomedical NER

In this section, we use the proposed method to create GreenBioBERT, an inexpensive and environmentally friendly alternative to BioBERT. Recall that BioBERTv1.0 (biobert_v1.0_pubmedPMC) was initialized from general-domain BERT (bert-base-cased) and pretrained on PubMed+PMC.

4.1 Domain adaptation

We train Word2Vec with vector size \( d_{W2V} = d_{LM} = 768 \) on PubMed+PMC (see Appendix for details). Then, we follow the procedure described in Section 3 to update the wordpiece embedding layer and tokenizer of general-domain BERT.
Figure 1: NER test set F1, transformed as \((x - BERT_{(ref)}) / (BioBERTv1.0_{(ref)} - BERT_{(ref)})\). A value of 0.5 means that 50% of the reported BioBERTv1.0 – BERT delta is covered. “ref”: Reference from Lee et al. (2020). “repr”: Our reproduction experiments. Error bars: Standard error of the mean.

4.3 Results and discussion

Table 2 (bottom) shows entity-level precision, recall and F1. For ease of visualization, Figure 1 shows what portion of the BioBERT – BERT F1 delta is covered. We improve over general-domain BERT on all tasks with varying effect sizes. Depending on the points of reference, we cover an average 52% to 60% of the BioBERT – BERT F1 delta (54% for BioBERTv1.0, 60% for BioBERTv1.1 and 52% for our reproduction experiments). Table 3 (top) shows the importance of vector space alignment: If we replace the aligned Word2Vec vectors with their non-aligned counterparts (by setting \(W = 1\)) or with randomly initialized vectors, F1 drops on all tasks.

5 Experiment 2: Covid-19 QA

In this section, we use the proposed method to quickly adapt an existing general-domain QA model to an emerging target domain: Covid-19. Our baseline model is SQuADBERT (bert-large-uncased-whole-word-maskin-finetuned-squad), a version of BERT that was finetuned on general-domain SQuAD (Rajpurkar et al., 2016). We evaluate on Deepset-AI Covid-QA, a SQuAD-style dataset with 1380 questions (see Appendix for details on data and preprocessing). We assume that there is no target-domain finetuning data, which is a realistic setup for a new domain.

5.1 Domain adaptation

We train Word2Vec with vector size \(d_{W2V} = d_{LM} = 1024\) on CORD-19 (Covid-19 Open Re-
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Inexpensive Domain Adaptation of Pretrained Language Models (Appendix)

Word2Vec training
We downloaded the PubMed, PMC and CORD-19 corpora from:
- https://ftp.ncbi.nlm.nih.gov/pub/PMC/oa_bulk/ [20 January 2020, 68GB raw text]
- https://ftp.ncbi.nlm.nih.gov/pubmed/baseline/ [20 January 2020, 24GB raw text]
- https://pages.semanticscholar.org/coronavirus-research [17 April 2020, 2GB raw text]

We extract all abstracts and text bodies and apply the BERT basic tokenizer (a word tokenizer that standard BERT uses before wordpiece tokenization). Then, we train CBOW Word2Vec\(^2\) with negative sampling. We use default parameters except for the vector size (which we set to \(d_{W2V} = d_{LM}\)).

Experiment 1: Biomedical NER

Pretrained models
General-domain BERT and BioBERTv1.0 were downloaded from:
- https://storage.googleapis.com/bert_models/2018_10_18/cased_L-12_H-768_A-12.zip
- https://github.com/ner/biobert-pretrained

Data
We downloaded the NER datasets by following instructions on https://github.com/dmis-lab/biobert#Datasets. For detailed dataset statistics, see Lee et al. (2020).

Preprocessing
We cut all sentences into chunks of 30 or fewer whitespace-tokenized words (without splitting inside labeled spans). Then, we tokenize every chunk \(S\) with \(T = T_{LM}\) or \(\hat{T} = T_{LM}\) and add special tokens:
\[
X = [CLS] T(S) [SEP]
\]

Word-initial wordpieces in \(T(S)\) are labeled as \(B(\text{egin})\), \(I(\text{inside})\) or \(O(\text{outside})\), while non-word-initial wordpieces are labeled as \(X(\text{ignore})\).

Modeling, training and inference
We follow Lee et al. (2020)'s implementation (https://github.com/dmis-lab/biobert): We add a randomly initialized softmax classifier on top of the last BERT layer to predict the labels. We finetune the entire model to minimize negative log likelihood, with the standard Adam optimizer (Kingma and Ba, 2014) and a linear learning rate scheduler (10% warmup). Like Lee et al. (2020), we finetune on the concatenation of the training and development set. All finetuning runs were done on a GeForce Titan X GPU (12GB).

Since we do not have the resources for an extensive hyperparameter search, we use defaults and recommendations from the BioBERT repository: Batch size of 32, peak learning rate of \(1 \cdot 10^{-5}\), and 100 epochs.

At inference time, we gather the output logits of word-initial wordpieces only. Since the number of word-initial wordpieces is the same for \(T_{LM}(S)\) and \(\hat{T}_{LM}(S)\), this makes mean-pooling the logits straightforward.

Note on our reproduction experiments
We found it easier to reproduce or exceed Lee et al. (2020)’s results for general-domain BERT, compared to their results for BioBERTv1.0 (see Figure 1, main paper). While this may be due to hyperparameters, it suggests that BioBERTv1.0 was more strongly tuned than BERT in the original BioBERT paper. This observation does not affect our conclusions, as GreenBioBERT performs better than reproduced BERT as well.

Experiment 2: Covid-19 QA

Pretrained model
We downloaded the SQuADBERT baseline from:
- https://huggingface.co/bert-large-uncased-whole-word-masking-finetuned-squad

Data
We downloaded the Deepset-AI Covid-QA dataset from:
- https://github.com/deepset-ai/COVID-QA/blob/master/data/question-answering/200423_covidQA.json [24 April 2020]

At the time of writing, the dataset contains 1380 questions and gold answer spans. Every question is associated with one of 98 research papers (contexts). We treat the entire dataset as a test set.
Note that there are some important differences between the dataset and SQuAD, which make the task challenging:

- The contexts are full documents rather than single paragraphs. Thus, the correct answer may appear several times, often with slightly different wordings. Only a single one of the occurrences is annotated as correct, e.g.:

  **Question:** What was the prevalence of Coronavirus OC43 in community samples in Ilorin, Nigeria?
  **Correct:** 13.3% (95% CI 6.9-23.6%) # from main text
  **Predicted:** (13.3%, 10/75). # from abstract

- SQuAD gold answers are defined as the “shortest span in the paragraph that answered the question” (Rajpurkar et al., 2016, p. 4), but many Covid-QA gold answers are longer and contain non-essential context, e.g.:

  **Question:** When was the Middle East Respiratory Syndrome Coronavirus isolated first?
  **Correct:** (MERS-CoV) was first isolated in 2012, in a 60-year-old man who died in Jeddah, KSA due to severe acute pneumonia and multiple organ failure
  **Predicted:** 2012,

Preprocessing

We tokenize every question-context pair \((Q, C)\) with \(T = T_{LM}\) or \(T = \hat{T}_{LM}\), which yields \((T(Q), T(C))\). Since \(T(C)\) is usually too long to be digested in a single forward pass, we define a sliding window with width and stride \(N = \left\lfloor \frac{509-|T(Q)|}{2} \right\rfloor\). At step \(n\), the “active” window is between \(a_n^{(l)} = nN\) and \(a_n^{(r)} = \min(|C|, nN + N)\). The input is defined as:

\[
X^{(n)} = [CLS] T(Q) [SEP] T(C) a_n^{(l)} - p_n^{(l)}, a_n^{(r)} + p_n^{(r)} [SEP]
\]

\(p_n^{(l)}\) and \(p_n^{(r)}\) are chosen such that \(|X^{(n)}| = 512\), and such that the active window is in the center of the input (if possible).

Modeling and inference

Feeding \(X^{(n)}\) into the pretrained QA model yields start logits \(h^{(\text{start},n)} \in \mathbb{R}^{|X^{(n)}|}\) and end logits \(h^{(\text{end},n)} \in \mathbb{R}^{|X^{(n)}|}\). We extract and concatenate the slices that correspond to the active windows of all steps:

\[
h^{(s)} \in \mathbb{R}^{|T(C)|}
\]

\[
h^{(s)} = [h^{(s,1)}_{a_1^{(l)}}, \ldots, h^{(s,n)}_{a_n^{(l)}, a_n^{(r)}}]
\]

Next, we map the logits from the wordpiece level to the word level. This allows us to mean-pool the outputs of \(T_{LM}\) and \(\hat{T}_{LM}\) even when \(|T_{LM}(C)| \neq |\hat{T}_{LM}(C)|\).

Let \(c_i\) be a whitespace-delimited word in \(C\). Let \(T(C)_{j:j+|T(c_i)|}\) be the corresponding wordpieces. The start and end logits of \(c_i\) are derived as:

\[
o_i^{(s)} = \max_{j \leq j' \leq j+|T(c_i)|} [h_{j'}^{(s)}]
\]

Finally, we return the answer span \(C_{k:k'}\) that maximizes \(o_k^{(\text{start})} + o_k^{(\text{end})}\), subject to the constraints that \(k'\) does not precede \(k\) and the answer span is not longer than 500 characters.