Evaluating the Utility of Model Configurations and Data Augmentation on Clinical Semantic Textual Similarity

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Abstract

In this paper, we apply pre-trained language models to the Semantic Textual Similarity (STS) task, with a specific focus on the clinical domain. In low-resource setting of clinical STS, these large models tend to be impractical and prone to overfitting. Building on BERT, we study the impact of a number of model design choices, namely different fine-tuning and pooling strategies. We observe that the impact of domain-specific fine-tuning on clinical STS is much less than that in the general domain, likely due to the concept richness of the domain. Based on this, we propose two data augmentation techniques. Experimental results on N2C2-STS\(^1\) demonstrate substantial improvements, validating the utility of the proposed methods.

1 Introduction

Semantic Textual Similarity (STS) is a language understanding task, involving assessing the degree of semantic equivalence between two pieces of text based on a graded numerical score (Corley and Mihalcea, 2005). It has application in tasks such as information retrieval (Hliaoutakis et al., 2006), question answering (Hoogeveen et al., 2018), and summarization (AL-Khassawneh et al., 2016). In this paper, we focus on STS in the clinical domain, in the context of a recent task within the framework of N2C2 (the National NLP Clinical Challenges)\(^1\), which makes use of the extended MedSTS data set (Wang et al., 2018), referring to N2C2-STS, with limited annotated sentences pairs (1.6K) that are rich in domain terms.

Neural STS models typically consist of encoders to generate text representations, and a regression layer to measure the similarity score (He et al., 2015; Mueller and Thyagarajan, 2016; He and Lin, 2016; Reimers and Gurevych, 2019). These architectures require a large amount of training data, an unrealistic requirement in low resource settings.

Recently, pre-trained language models (LMs) such as GPT-2 (Radford et al., 2018) and BERT (Devlin et al., 2019) have been shown to benefit from pre-training over large corpora followed by fine tuning over specific tasks. However, for small-scale datasets, only limited fine-tuning can be done. For example, GPT-2 achieved strong results across four large natural language inference (NLI) datasets, but was less successful over the small-scale RTE corpus (Bentivogli et al., 2009), performing below a multi-task biLSTM model. Similarly, while the large-scale pre-training of BERT has led to impressive improvements on a range of tasks, only very modest improvements have been achieved on STS tasks such as STS-B (Cer et al., 2017) and MRPC (Dolan and Brockett, 2005) (with 5.7k and 3.6k training instances, resp.). Compared to general-domain STS benchmarks, labeled clinical STS data is more scarce, which tends to cause overfitting during fine-tuning. Moreover, further model scaling is a challenge due to GPU/TPU memory limitations and longer training time (Lan et al., 2019). This motivates us to search for model configurations which strike a balance between model flexibility and overfitting.

In this paper, we study the impact of a number of model design choices. First, following Reimers and Gurevych (2019), we study the impact of various pooling methods on STS, and find that convolution filters coupled with max and mean pooling outperform a number of alternative approaches. This can largely be attributed to their improved model expressiveness and ability to capture local interactions (Yu et al., 2019). Next, we consider different parameter fine-tuning strategies, with varying degrees of flexibility, ranging from keeping all parameters frozen during training to allowing all pa-

\(^1\)https://portal.dbmi.hms.harvard.edu/projects/n2c2-2019-t1/
rameters to be updated. This allows us to identify the optimal model flexibility without over-tuning, thereby further improving model performance.

Finally, inspired by recent studies, including sentence ordering prediction (Lan et al., 2019) and data-augmented question answering (Yu et al., 2019), we focus on data augmentation methods to expand the modest amount of training data. We first consider segment reordering (SR), in permuting segments that are delimited by commas or semicolons. Our second method increases linguistic diversity with back translation (BT). Extensive experiments on N2C2-STS reveal the effectiveness of data augmentation on clinical STS, particularly when combined with the best parameter fine-tuning and pooling strategies identified in Section 3, achieving an absolute gain in performance.

2 Related Work

2.1 Model Configurations

In pre-training, a spectrum of design choices have been proposed to optimize models, such as the pre-training objective, training corpus, and hyperparameter selection. Specific examples of objective functions include masked language modeling in BERT, permutation language modeling in XLNet (Yang et al., 2019), and sentence order prediction (SOP) in ALBERT (Lan et al., 2019). Additionally, RoBERTa (Liu et al., 2019) explored benefits from a larger mini-batch size, a dynamic masking strategy, and increasing the size of the training corpus (16G to 160G). However, all these efforts are targeted at improving downstream tasks indirectly by optimizing the capability and generalizability of LMs, while adapting a single fully-connected layer to capture task features.

Sentence-BERT (Reimers and Gurevych, 2019) makes use of task-specific structures to optimize STS, concentrating on computational and time efficiency, and is evaluated on relatively larger datasets in the general domain. For evaluating the impact of number of layers transferred to the supervised target task from the pre-trained language model, GPT-2 has been analyzed on two datasets. However, they are both large: MultiNLI (Williams et al., 2018) with >390k instances, and RACE (Lai et al., 2017) with >97k instances. These tasks also both involve reasoning-related classification, as opposed to the nuanced regression task of STS.

2.2 Data Augmentation

Synonym replacement is one of the most commonly used data augmentation methods to simulate linguistic diversity, but it introduces ambiguity if accurate context-dependent disambiguation is not performed. Moreover, random selection and replacement of a single word used in general texts is not plausible for term-rich clinical text, resulting in too much semantic divergence (e.g., patient to affected role and discharge to home to spark to home). By contrast, replacing a complete mention of the concept can increase error propagation due to the prerequisite concept extraction and normalization.

Random insertion, deletion, and swapping of words have been demonstrated to be effective on five text classification tasks (Wei and Zou, 2019). But those experiments targeted topic prediction, in contrast to semantic reasoning such as STS and MultiNLI. Intuitively, they do not change the overall topic of a text, but can skew the meaning of a sentence, undermining the STS task. Swapping an entire semantic segment may mitigate the risk of introducing label noise to the STS task.

Compared to semantic and syntactic distortion potentially caused by aforementioned methods, back translation (BT) (Sennrich et al., 2016) — translating to a target language then back to the original language — presents fluent augmented data and reliable improvements for tasks demanding for adequate semantic understanding, such as low-resource machine translation (Xia et al., 2019) and question answering (Yu et al., 2019). This motivates our application of BT on low-resource clinical STS, to bridge linguistic variation between two sentences. This work represents the first exploration of applying BT for STS.

3 STS Model Configurations

In this section, we study the impact of a number of model design choices on BERT for STS, using a 12-layer base model initialized with pretrained weights.

3.1 Hierarchical Convolution (HConv)

The resource-poor and concept-rich nature of clinical STS makes it difficult to train a large model end-to-end on sentence pairs. To address this, most recent studies have made use of pre-trained language models, such as BERT. The most straightforward way to use BERT is the feature-based approach, where the output of the last transformer block is
taken as input to the task-specific classifier. Many
have proposed the use of a dummy CLS token to
generate the feature vector, where CLS is a special
symbol added in front of every sequence during
pre-training, with its final hidden state always used
as the aggregate sequence representation for clas-
sification tasks, referring to CLS pooling. Other
types of pooling, such as mean and max pooling,
are investigated by Reimers and Gurevych (2019).

However, this results in inferior performance
as shown in the first row of Table 1. As a con-
sequence, the best strategy for extracting feature
vectors to represent a sentence remains an open
question.

In this work, we first experiment with the feature-
based approach, coupled with convolutional filters.
This is inspired by the use of convolutional filters
in QANet (Yu et al., 2019) to capture local interac-
tions. The difference lies in where convolutional
filters are applied. With QANet, multiple conv
filters are incorporated into each transformer en-
coder block to process the input from the previous
layer. In contrast, HConv-BERT is largely based
on BERT, with the addition of a single task-specific
classifier placed on top of BERT consisting of conv
filters organised in a hierarchical fashion. This
results in a much simplified model, making HConv-
BERT less prone to overfitting.

Specifically, we run a collection of convolutional
filters with a kernel of size $k \in \{2, 4\}$, each with
$J = 768$ output channels (indexed by $j \in [1, J]$),
over the temporal axis (indexed by $i \in [1, T]$):

$$c_{i,k} = w_{k,j} \ast x_{i+k-1} + b_{k,j} \quad (1)$$

where $x_{i+k-1}$ is the output BERT features for the
token span $i$ to $i + k - 1$, $\ast$ is the convolu-
tion operation, $w_{k,j}$ and $b_{k,j}$ are the convolution filter
and bias term for the $j$-th kernel of size $k$, and
[a; b] denotes the concatenation of a and b.

To capture interactions between distant elements,
we feed the output $c_{i,k}$ into another convolution
layer of kernel size 2 with $M = 128$ output chan-
els (indexed by $m \in [1, M]$):

$$c_{i,m} = w_m \ast c_{i+1,k} + b_m \quad (3)$$

$$c_{i,k} = [c_{i,1}; \ldots; c_{i,M}] \quad (4)$$

$$c_{i+1,k} = [c_{i+1,1}; \ldots; c_{i+1,M}] \quad (5)$$

where $c_{i+1,k}$ is the output of the first convolu-
tional layer over the span $i$ to $i + 1$ as defined in
Equation (2), and $w_m$ and $b_m$ are the filter and
bias term for the second convolutional layer with a
kernel size of 2 and output dimension of $M = 128$.

Lastly, we extract feature vectors by max and
mean pooling over the temporal axis and then con-
catenation:

$$v_{\text{max}} = \max \left( c_{i,k}^k \right) \quad v_{\text{mean}} = \text{avg} \left( c_{i,k}^k \right) \quad (5)$$

$$v = \left[ v_{\text{max}}^2; v_{\text{max}}^3; v_{\text{max}}^4; v_{\text{avg}}^2; v_{\text{avg}}^3; v_{\text{avg}}^4 \right] \quad (6)$$

The upper half of Table 1 shows that the pro-
posed hierarchical convolutional (HConv) architec-
ture provides substantial performance gains.

| Model         | SICK-R | STS-B | N2C2-STS |
|---------------|--------|-------|----------|
| Feature-based:|        |       |          |
| CLS-BERT      | 53.6/52.1 | 49.3/67.9 | 14.6/28.4 |
| HConv-BERT    | 80.1/73.6 | 83.0/83.2 | 79.4/74.4 |
| Fine-tuning:  |        |       |          |
| CLS-BERT      | 88.6/82.9 | 90.0/89.6 | 86.7/81.9 |
| HConv-BERT    | 88.7/83.5 | 90.1/89.6 | 87.7/80.7 |

Table 1: Pearson and Spearman correlation ($r/\rho$) be-
tween the predicted score and the gold labels for three
STS datasets using the feature-based approach (upper
half) and fine-tuning (bottom half) with CLS-BERT
and HConv-BERT. Performance is reported by conven-
tion as $r/\rho \times 100$.

3Due to space constraints, we limit our comparison to the
CLS pooling strategy, based on the observation of little
improvements when using other types of pooling (mean, max)
and concatenation, or sequence processing recurrent units.

32 Model Flexibility

We also evaluate the utility of this mechanism in the
fine-tuning setting with varying modelling flexibil-
ity. Concretely, we progressively increase the num-
ber of trainable parameters by transformer blocks.
That is, for the base BERT model with 12 layers,
we allow errors to be back-propagated through the
last $l$ layers while keeping the rest $(12 - l)$ fixed.

The results on STS-B and N2C2-STS are shown
in Figure 1. We observe performance crossover of
HConv and CLS-pooling on both datasets as the
number of trainable transformer layers increases.
While HConv reaches peak performance before the
crossover, CLS-pooling often requires more blocks
to be trainable to achieve comparable accuracy,
rendering the model much slower. Notably, the pro-
posed mechanism peaks with much fewer trainable
blocks on N2C2-STS than STS-B. We speculate
that this is due to the size difference between the
two datasets. To verify this hypothesis, we further
look into the relationship between the number of
The number of trainable transformer encoder layers on STS-B

| r     | CLS-BERT | HConv-BERT |
|-------|----------|------------|
| 86.0  |          |            |
| 86.5  |          |            |
| 87.0  |          |            |
| 87.5  |          |            |
| 88.0  |          |            |
| 88.5  |          |            |
| 89.0  |          |            |
| 89.5  |          |            |
| 90.0  |          |            |

Table 1, with HConv outperforming CLS-pooling.

4 Data Augmentation

The accuracy of an STS model unsurprisingly depends on the amount of labeled data. This is reflected in Figure 2, where models trained with more data outperform those with fewer training instances. In this section, we propose two data augmentation methods, namely segment reordering (SR) and back translation (BT), to address the data sparsity issue in clinical STS.

**Segment reordering.** Clinical texts often consist of text segments describing multiple events and patient symptoms. Each segment is often an independent semantic unit, separated by commas or semicolons. Inspired by the random word swapping of Wei and Zou (2019), we exploit this property and propose a heuristic, named segment reordering (SR), to generate permutations of the original sequence based on these segments. While we expect this to introduce some noise to the training data, our hypothesis is that the increase in training data size will outweigh this. For instance, consider the text new confusion or inability to stay alert and awake; feeling like you are going to pass out. Flipping the order of the two segments will not hinder the overall understanding of the text. More formally, for a given pair of sentences $S_1$ and $S_2$, each consisting of a sequence of segments $S_1 = \{s_{11}, \ldots, s_{1m}\}$ and $S_2 = \{s_{21}, \ldots, s_{2n}\}$, we generate a new pair by randomly permuting the segment order, effectively doubling the size of the training corpus.

Based on this, we set the number of trainable blocks to 6 for SICK-R (consisting of 4,500 training instances), as presented in the bottom half of...
Back translation. Inspired by the work of Yu et al. (2019), we make use of machine translation tools to perform back translation (BT). Here, we choose Chinese as the pivot language as it is linguistically distant to English and supported by mature commercial translation solutions. That is, we first translate from English to Chinese and then back to English. We use Google Translate to translate each sentence in a sentence pair from English to Chinese, and Baidu Translation to translate back to English. For example, for the original sentence negative for cough and stridor, the backtranslated result is bad for coughing and wheezing. We apply this to each sentence pair, doubling the amount of training data.

5 Experiments

5.1 Experimental Setup

We evaluate the effectiveness of SR and BT on N2C2-STS with four baseline models: BERT_{base} (Devlin et al., 2019) and BERT_{clinical} (Alsentzer et al., 2019), both using CLS-pooling and consisting of 12 layers; ConvBERT_{base}, based on BERT_{base} with hierarchical convolution and fine-tuning over the last 4 layers (consistent with our findings of the best model configuration in Section 3); and ConvBERT_{STS-B}, where we take ConvBERT_{base} and fine-tune first over STS-B, before N2C2-STS.

We split the training partition of N2C2-STS into 1,233 (train) and 409 (dev) instances, and report results on the test set (412 instances).

5.2 Results

Experimental results are presented in Table 2. We see clear benefits of the two proposed data augmentation methods, consistently boosting performance across all categories, with BT providing larger gains than SR. This is likely caused by the rather naïve implementation of SR, resulting in unnatural segment sequences. A possible fix to this is to further filter out such irregular statements with a language model pre-trained on clinical corpora. We leave this for future work.

It is impressive that the best-performing configuration ConvBERT_{STS-B} + BT is capable of achieving comparable results with the state-of-the-art IBM-N2C2, an approach heavily reliant on external, domain-specific resources, and an ensemble of multiple pre-trained language models.

Table 2: Pearson $r$ and Spearman $\rho$ on N2C2-STS for models with and without segment reordering (“SR”) and back translation (“BT”).

| Model                   | $r$  | $\rho$ |
|------------------------|------|--------|
| IBM-N2C2               | 90.1 | —      |
| BERT_{base}            | 86.7 | 81.9   |
| + SR                   | 87.1 | 80.8   |
| + BT                   | 87.2 | 81.7   |
| BERT_{clinical}        | 86.1 | 81.4   |
| + SR                   | 87.4 | 82.7   |
| + BT                   | 88.6 | 82.4   |
| Conv1dBERT_{base}     | 87.7 | 80.7   |
| + SR                   | 88.0 | 81.4   |
| + BT                   | 88.1 | 82.2   |
| Conv1dBERT_{STS-B}    | 87.9 | 82.5   |
| + SR                   | 88.6 | 83.1   |
| + BT                   | 89.4 | 83.0   |

We additionally conduct a cross-domain experiment on BIOSSES (Soğancıoğlu et al., 2017), a biomedical literature STS dataset comprising 100 sentence pairs derived from the Text Analysis Conference Biomedical Summarization task with scores ranging from 0 (complete unrelatedness) to 4 (exact equivalence). Specifically, baseline model Pooling BERT_{base} and proposed ConvBERT_{STS-B} + BT are both fine-tuned on N2C2-STS, and then applied with no further training to BIOSSES. Despite the increase in task difficulty, the proposed method demonstrates strong generalisability, outperforming the baseline by an absolute gain of 2.4 and 3.9 to 85.42/82.83 ($r/\rho$).

6 Conclusions

In this paper, we have presented an empirical study of the impact of a number of model design choices on a BERT-based approach to clinical STS. We have demonstrated that the proposed hierarchical convolution mechanism outperforms a number of alternative conventional pooling methods. Also, we have investigated parameter fine-tuning strategies with varying degrees of flexibility, and identified the optimal number of trainable transformer blocks, thereby preventing over-tuning. Lastly, we have verified the utility of two data augmentation methods on clinical STS. It may be interesting to see the impact of leveraging target languages other than Chinese in BT, which we leave for future work.
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