Transferability of Natural Language Inference to Biomedical Question Answering

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Abstract. Biomedical question answering (QA) is a challenging problem due to the scarcity of data and the requirement of domain expertise. Growing interests of using pre-trained language models with transfer learning address the issue to some extent. Recently, learning linguistic knowledge of entailment in sentence pairs enhances the performance in general domain QA by leveraging such transferability between the two tasks. In this paper, we focus on facilitating the transferability by unifying the experimental setup from natural language inference (NLI) to biomedical QA. We observe that transferring from entailment data shows effective performance on Yes/No (+5.59%), Factoid (+0.53%), List (+13.58%) type questions compared to previous challenge reports (BioASQ 7B Phase B). We also observe that our method generally performs well in the 8th BioASQ Challenge (Phase B). For sequential transfer learning, the order of how tasks are fine-tuned is important. In factoid- and list-type questions, we thoroughly analyze an intrinsic limitation of the extractive QA setting when these questions are converted to the same format of the Stanford Question Answering Dataset (SQuAD).

Keywords: Transfer Learning · Domain Adaptation · Natural Language Inference · Biomedical Question Answering

1 Introduction

Biomedical question answering (QA) is a challenging problem due to the limited amount of data and the requirement of domain expertise. Recent success thanks to transfer learning [19,31] address the issues by using pre-trained language models [13,26] and further fine-tuning on a target task [2,4,7,20,32,36]. In spite of performance gains from transfer learning, results are still short of the upper bound in biomedical QA. Sequential transfer learning has been introduced as an improvement of transfer learning in order to further push performance closer to the upper bound [2,20,36]. For example, fine-tuning from large

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scale SQuAD dataset [28] to the much smaller BioASQ dataset [33] guarantees performance compared to leveraging the BioASQ dataset solely. In the general domain, training on the linguistic knowledge of entailment between sentence pairs shows effectiveness when deployed as the first step in sequential transfer learning pipeline [4,11,27,34,35]. Thus, in this paper, we try to exploit the task of NLI [1,10] to enhance the performance of biomedical QA. We find that the performance improves when the objective function of the fine-tuned task becomes similar to the downstream task. We also investigate that adapting NLI to biomedical QA confronts the obstacle of task discrepancy. Task discrepancy refers to the several differences between fine-tuned tasks such as distribution of context length, objective function and domain shift.

Specifically, between NLI and biomedical QA, we focus on reducing the discrepancy of context length to boost the performance of sequential transfer learning. In order to resolve the discrepancy, we unify the distribution of context length among fine-tuned tasks. We reorganize the SQuAD context into a single sentence containing the ground truth answer spans [23]. Fine-tuning on a unified distribution achieves speed improvements 52.95% on training and 25% on inference in BioASQ with comparable results. Finally, we introduce an intrinsic limitation of the extractive QA setting regarding answerability when the BioASQ dataset is converted to the same format as the SQuAD dataset.

Our contributions are as follows:

(i) Leveraging a NLI dataset as a fine-tuning procedure is meaningful to the Yes/No, Factoid and List type questions in BioASQ.

(ii) We demonstrate that a simple variation in the experimental setup can aid the transferability of NLI to biomedical QA.

(iii) In Factoid and List type questions, we introduce an intrinsic limitation of the extractive QA setting, when the BioASQ data is converted to the SQuAD format.

2 Related Works

Transfer Learning Transfer learning, also known as domain adaptation, refers to the situation in which the transfer of knowledge learned in a previous task improves learning in the following task. In various fields including image processing or natural language processing (NLP), many studies have shown the effectiveness of transfer learning based on deep neural networks [15,22,24,31,37]. More recently, especially in NLP, pre-trained language models such as ELMo [26] and BERT [13] lead most of NLP problems concerning transfer learning [4,11,13,18,19,21,25]. In a specific domain, unsupervised pre-training has also been introduced for biomedical contextualized representations [9,10,20]. Among them, BioBERT [20] is fine-tuned on biomedical corpora (e.g., PubMed and PubMed Central) using BERT and various tasks exploit BioBERT on the biomedical or clinical domain [8,9,10,17,25,36].
Transferability of Natural Language Understanding From the perspective of QA, the authors of [2] used the transfer of knowledge from a large open-domain SQuAD dataset to the target BioASQ dataset in order to handle the issue of scarcity. In [20,36], the authors adopted sequential transfer learning (e.g., BioBERT-SQuAD-BioASQ) to boost the performance of biomedical QA. Meanwhile, from the NLI point of view, multiple datasets corresponding to the general domain have emerged [1,10,28,35] and recently domain-specific data (e.g., biomedical) have also appeared [25,30]. In [4], the authors investigate that fine-tuning with MultiNLI [1] enhances the performance of target tasks consistently in all GLUE benchmarks [35]. Our work is more related to [12] where the authors suggest that transfer learning from NLI to diverse yes or no type QA tasks surely improves the performance in the general domain. Furthermore, the authors of [34] extensively experiment with the combination of question answering, text classification/regression, and sequence labeling with the constraint of data size. In this paper, we further facilitate the linguistic knowledge of the MultiNLI (MNLI) dataset to improve the performance of biomedical QA.

3 Methods

In this section, we outline our problem setup for the downstream task. Our training details are described in Appendix A. We formally explain our framework to learn biomedical entity representations with BioBERT. Then we describe how to proceed with sequential fine-tuning according to each biomedical question type of the BioASQ Challenge. The intention of our method is to facilitate the transferability of NLI to the BioASQ.

3.1 Problem Setup

We convert the BioASQ dataset to the SQuAD dataset format. In detail, instances in the BioASQ dataset are composed of a question (Q), human-annotated answers (A), and the relevant contexts (C) (also called snippets). Although the span of an answer is not suggested, we first find the exact spans in the contexts based on the human-annotated answers for factoid and list types. In this case, we enumerate all the combinations of Q-C-A triplets only when the answer exact matches the context with confidence in precise spans. For Yes/No type, yes and no answers cannot exactly match the context, thus we fine-tune a task-specific binary classifier to predict the answer.

3.2 Overall Architecture

The input sequence \( X \) consists of the concatenation of the BERT [CLS] token and the Q and C, with [SEP] tokens in between. This is denoted as \( X = \{[CLS] \parallel Q \parallel [SEP] \parallel C \parallel [SEP]\} \) where \( \parallel \) refers to the concatenation of tensors. The hidden representation vector for the \( i^{th} \) input token is denoted as \( h_i \in \mathbb{R}^H \) with the hidden size \( H \). Finally, we fine-tune the hidden vectors which are fed into softmax or binary classifier corresponding to each question type.
Yes/No Type  We compute the yes probability $P_{yes}$ by projecting a linear transformation matrix $M \in \mathbb{R}^{1 \times H}$ to transform the hidden representation of [CLS] token $C \in \mathbb{R}^{H}$. The sigmoid function is used for binary classification. The yes probability is calculated as follows.

$$P_{yes} = \frac{1}{1 + e^{-C \cdot M^\top}}$$  \hfill (1)

The binary cross entropy loss is utilized between yes probability $P_{yes}$ and its corresponding ground truth answer $a_{yes}$. Our total loss is computed as below.

$$Loss = -(a_{yes} \log P_{yes} + (1 - a_{yes}) \log(1 - P_{yes}))$$  \hfill (2)

Factoid & List type  We compute the start and end vector through one linear transformation matrix $M \in \mathbb{R}^{2 \times H}$ at hidden representation vectors. Let us denote a predicted $i^{th}, j^{th}$ answer tokens as start and end. The probability of $(P_{start}^i, P_{end}^j)$ can be calculated as follows,

$$P_i = \frac{e^{h_i \cdot M^\top}}{\sum_{i=1}^{s} e^{h_i \cdot M^\top}}, \quad P_j = \frac{e^{h_j \cdot M^\top}}{\sum_{i=1}^{s} e^{h_i \cdot M^\top}}$$  \hfill (3)

where $s$ denotes the sequence length of BioBERT and $\cdot$ refers to the dot-product. Our objective function is the negative log-likelihood for the predicted answer with the ground truth answer position. Computed start and end position loss are as below:

$$Loss_{start} = -\frac{1}{N} \sum_{n=1}^{N} \log P_{a_s}^{\text{start},n}, \quad Loss_{end} = -\frac{1}{N} \sum_{n=1}^{N} \log P_{a_e}^{\text{end},n}$$  \hfill (4)

3.3 Transferability through domains and tasks

Yes/No Type  Learning to classify entailment can enhance a model’s ability in the general domain for yes or no type QA \cite{12}. Following this finding, we think that the classification ability could be extended to the yes and no type of biomedical QA. Thus, we adopt the NLI task to solve biomedical yes or no type QA. We leverage the MNLI dataset because it is widely used and has enough data with multiple genres. For our learning sequence, we fine-tune BioBERT on the MNLI dataset to learn the linguistic knowledge of entailment between hypothesis and premise sentence pairs. We compose a sequence of transfer learning as BioBERT-MNLI-BioASQ. However, replacing the binary classifier to compute $P_{yes}$ with final layer of MNLI task shows no improvement in BioASQ performances. For this reason, we add a simple binary classifier on top of BioBERT to be fine-tuned. Furthermore, the distributions of context length in MNLI and snippet of Yes/No type in BioASQ are similar. Therefore, we skip the unifying of context length distribution in yes and no type.
Factoid & List Type To bridge the gap between different tasks, the order of sequential transfer learning is important. We investigate that the performance gain appears when the objective function of the fine-tuned task becomes similar to the downstream task in Table 5. Thus, we build our base learning sequence as BioBERT-MNLI-SQuAD-BioASQ rather than switching the order of intermediate tasks such as BioBERT-SQuAD-MNLI-BioASQ. In order to resolve the discrepancy of context length, we give a little variation to the original experimental setting. As suggested in [23], we reorganize the distribution of context length in the SQuAD dataset similar to the MNLI context and BioASQ snippet dataset. We aim to develop an extractive QA setup that is scalable to minimal context rather than using irrelevant sentences in full abstract [36]. Therefore, we extract a sentence containing the ground truth answer span and set as a total paragraph to construct a minimal context. As a result, we reduce the difference by unifying the distribution of context length in our sequential transfer learning. Due to the converted distribution of context length, we achieve speed improvements on training and inference in factoid and list type questions while achieving comparable results.

4 Experiments

4.1 Datasets

Our datasets are based on the pre-processed version provided by [1, 28, 36]. For the extractive QA setting, we convert all types of the BioASQ dataset (i.e., Yes/No, Factoid and List) into the same format as the SQuAD dataset. In [36], the authors suggested three pre-processing strategies and we utilize two of the three strategies: Snippet-as-is and Full-Abstract. We modify the previous data with a new criterion of including white space before and after each biomedical entity. This new criterion has shown to enhance the distinguishing of biomedical named entities. The statistics of the revised dataset are listed in Table 8. We have made the modified version of the BioASQ dataset publicly available.

For the unified experimental setting, we remove approximately 5K training instances in SQuAD dataset due to the missing cases of a string match between context and answer spans.

4.2 Experimental Results

In Table 1, we compare our results with last year’s BioASQ Challenge Task 7B (Phase B) scores [5–7, 14, 29, 36]. In comparison with the best results in the previous challenge, we observe that transferring from MNLI shows significant performance gain on the Yes/No (+5.59%), Factoid (+0.53%) and List (+13.58%) types.

First, the Yes/No type results of our method are shown in Table 2. We observe that using SQuAD as an intermediate fine-tuning procedure enhances

https://github.com/dmis-lab/bioasq8b
Table 1. BioASQ 7B Phase B challenge results and our results. We use dash (-) if the paper doesn’t suggest results corresponding to each question type. All scores are averaged of best score when batch results are reported in paper. **Bold** denotes the best score in each column.

| Reference System                  | Yes/No (Macro F1) | Factoid (MRR) | List (F1) |
|----------------------------------|-------------------|---------------|-----------|
| Dimitriadis & Tsoumakas [14]    | 0.5541            | -             | -         |
| Hosein et al., [7]              | -                 | 0.4562        | -         |
| Oita et al., [5]                | 0.4831            | -             | -         |
| Resta et al., [29]              | 0.7873            | -             | -         |
| Telukuntla et al., [6]          | 0.4486            | 0.4751        | 0.2002    |
| Yoon et al., [36]               | 0.7169            | 0.5116        | 0.4061    |
| **Ours**                        | **0.8432**        | **0.5163**    | **0.5419**|

Table 2. Yes/No type question experiments. Evaluation metrics are accuracy (Accuracy), f1 score of yes type (Yes F1), f1 score of no type (No F1) and macro f1 score of yes and no type (Macro F1). **Bold** denotes the best score of the columns in each task.

| # of Task | Sequence of Transfer Learning | Evaluation Metric |
|-----------|------------------------------|-------------------|
| 6B Test   | BioBERT-SQuAD-BioASQ         | 0.8518 0.9004 0.6896 0.7950 |
|           | BioBERT-MNLI-BioASQ          | **0.8857** **0.9212** **0.7798** **0.8505** |
| 7B Test   | BioBERT-SQuAD-BioASQ         | 0.8595 0.8990 0.7344 0.8167 |
|           | BioBERT-MNLI-BioASQ          | **0.8945** **0.9275** **0.7588** **0.8432** |

When leveraging the MNLI dataset in the factoid and list types, we have to consider the discrepancy of context lengths. The results are shown in Table 3 In the original setting, the SQuAD dataset is trained with full documents and the snippet is utilized in learning the BioASQ dataset. There are no performance gains in 6B test dataset. However, we observe that the performance enhances as the size of the training dataset increases as shown in the 7B test dataset. In the document setting, we respectively leverage the whole paragraph and full abstract of the SQuAD and BioASQ dataset. We investigate that this setting
Context Length Discrepancy

| # of Task | Setting | Sequence of Transfer Learning | Factoid (%) | List (%) |
|-----------|---------|-------------------------------|-------------|---------|
|           |         |                               | SAcc | LAcc | MRR | Prec | Recall | F1   |
| 6B Test   | Original | BioBERT-SQuAD-BioASQ          | 39.80  | 57.82 | 47.22 | 45.02 | 47.69  | 42.34 |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | 38.80  | 61.34 | 47.47 | 46.60 | 47.01  | 42.44 |
|           | Document| BioBERT-SQuAD-BioASQ          | 39.71  | 56.37 | 45.81 | 46.81 | 40.26  | 39.63 |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | 39.71  | 55.10 | 45.77 | 46.26 | 39.23  | 38.13 |
|           | Snippet | BioBERT-SQuAD-BioASQ          | 38.23  | 57.34 | 46.24 | **48.24** | 46.86  | **42.83** |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | **41.41** | 57.40 | **48.05** | 46.01 | 45.95  | 42.75 |
| 7B Test   | Original | BioBERT-SQuAD-BioASQ          | 41.95  | 58.30 | 48.66 | 61.32 | 52.83  | 52.36 |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | 42.22  | 61.06 | 49.85 | **61.46** | **54.02** | **54.19** |
|           | Document| BioBERT-SQuAD-BioASQ          | 44.46  | 57.98 | 50.02 | 58.30 | 39.19  | 43.89 |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | 43.34  | 58.13 | 49.21 | 61.01 | 41.82  | 45.78 |
|           | Snippet | BioBERT-SQuAD-BioASQ          | 40.79  | 58.93 | 48.27 | 60.08 | 53.96  | 53.18 |
|           |         | BioBERT-MNLI-SQuAD-BioASQ     | **45.10** | **62.45** | **51.63** | 60.92 | 53.12  | 53.01 |

Table 3. Experiments of Context Length Discrepancy. Factoid evaluation metrics are strict accuracy (SAcc), lenient accuracy (LAcc) and mean reciprocal rank (MRR). List evaluation metrics are precision (Prec), recall (Recall) and score of macro f1 (F1). Original indicates training in full document in SQuAD and using snippet in BioASQ. Document recurs to train in full document in SQuAD and use full abstract in BioASQ. Snippet denotes to train in a unified distribution of minimal context. All scores are averaged of 5 batch results. **Bold** denotes the best score of the columns in each task.

shows lower performance than the original setting due to the expansion of context. In other words, the search space to find the answer has been expanded in the full abstract rather than using the human annotated dataset (i.e., snippet). Nevertheless, in 7B test dataset, the performance enhances exceptionally for the factoid type when fine-tuned on the SQuAD dataset.

For the snippet setting, we unify the distributions of context length in the extractive QA tasks. By extracting a sentence which contains the ground truth answer span, we observe improvement in 6B & 7B test dataset. For list type questions, we need further analyses to reduce the context length difference in future work. For example, instead of producing one answer in an intermediate task such as SQuAD, we could modify the model to yield multiple answers.

5 Analysis

Order of Sequential Transfer Learning The BioASQ Challenge Task 8B (phase B) results are shown in Table 4. Each team can submit their systems up to 5 times with different combinations of strategies. The 8B ground truth answers are not available to manually evaluate our suggested methods. Thus, we report the uploaded scores in leaderboard.

4 http://participants-area.bioasq.org/results/8b/phaseB/
In this analysis, we explore the order of sequential transfer learning and the results are shown in Table 5. For the factoid type of questions, we investigate that leveraging the MNLI dataset shows consistent improvement. On the other hand, in list type questions, the performance improves when the objective function of fine-tuned tasks are related to the BioASQ objective function. In other words, fine-tuning on the SQuAD dataset needs to be trained after the MNLI dataset.

**Limitation of the Extractive QA Setting** So far, the problem setup has been done under the extractive QA setting. We transform factoid and list type questions into the same format as the SQuAD dataset. We sample examples from the BioASQ Challenge Task 7B (Phase B) test dataset which are unanswerable. Table 6 shows the unanswerable rate in all batches of 7B test datasets only for factoid and list type questions. We calculate this rate as a criterion of *Ground Truth Answer cannot be exactly match in Human Annotated Corpus (Snippet)*. The criteria subsumes the cases of no exact match, lowercase match, additional phrase added, and different type of white space between exact answer and snippet. In Table 7, there is a clear upper bound to solve the biomedical questions in the BioASQ under the extractive QA setting. The limitations brought about when sampling the examples only exist in the BioASQ Task 7B (Phase B) test dataset, but we doubt that this unanswerable ratio also applies to the entire train dataset. Therefore, we have to consider clarifying the limitation when we use the extractive QA setting in the future. In the process of problem setup, we hope our analysis provides a better way to establish it.
Order Importance

| # of Task | Sequence of Transfer Learning | Factoid (%) | List (%) |
|-----------|------------------------------|-------------|----------|
|           |                             | SAcc LAcc MRR Prec Recall F1 |          |
| 6B Test   | BioBERT-SQuAD-BioASQ        | 39.80 57.82 47.22 45.02 **47.69** 42.34 |          |
|           | BioBERT-SQuAD-MNLI-BioASQ   | **41.15** 57.95 47.29 46.18 44.56 40.98 |          |
|           | BioBERT-MNLI-SQuAD-BioASQ   | 38.80 **61.34** 47.42 **46.60** 47.01 **42.44** |          |
| 7B Test   | BioBERT-SQuAD-BioASQ        | 41.95 58.30 48.66 61.32 52.83 52.36 |          |
|           | BioBERT-SQuAD-MNLI-BioASQ   | **43.31** 58.69 49.24 60.77 50.74 50.72 |          |
|           | BioBERT-MNLI-SQuAD-BioASQ   | 42.22 **61.06** 49.85 **61.46** 54.62 54.19 |          |

Table 5. Experiments of the order importance in sequential transfer learning. Factoid evaluation metrics are strict accuracy (SAcc), lenient accuracy (LAcc) and mean reciprocal rank (MRR). List evaluation metrics are precision (Prec), recall (Recall) and score of macro f1 (F1). **Bold** denotes the best score of the columns in each task.

| Type | 7B Batch1 | 7B Batch2 | 7B Batch3 | 7B Batch4 | 7B Batch5 | 7B Total |
|------|-----------|-----------|-----------|-----------|-----------|----------|
| Factoid | 0.359 (14/39) | 0.120 (3/25) | 0.310 (9/29) | 0.118 (4/34) | 0.229 (8/35) | 0.216 (35/162) |
| List   | 0.083 (1/12) | 0.235 (4/17) | 0.200 (5/25) | 0.136 (3/22) | 0.500 (6/12) | 0.204 (18/88) |

Table 6. Statistics of Unanswerable rate in the extractive QA setting. The cases of *Ground Truth Answer cannot be exactly match in Human Annotated Corpus (Snippet)*. The unanswerable rate is related to the upper-bound.

6 Conclusion

In our work, we use natural language inference (NLI) as a first step of fine-tuning for biomedical question answering (QA). Learning linguistic knowledge of entailment in sentence pairs enhances the performance in biomedical QA. We empirically demonstrate that leveraging NLI enhances the performance in the BioASQ Challenge. In this process, sequential transfer learning needs to be consider the order of sequence while training. Furthermore, we unify the distributions of context length to mitigate the discrepancy between NLI and biomedical QA. Finally, when converting the BioASQ dataset into SQuAD format, we analyze an intrinsic limitation of human annotation that an answer does not exactly match the context.

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Limitation of Supervised Setting

| Type     | ID - Question - Context - Answer |
|----------|----------------------------------|
| Factoid  | ID: 5c531d8f7ebd6e231000017     |
|          | Question: What causes Bathing suit Ichthyosis (BSI)? |
|          | Ground Truth Answer: **transglutaminase-1 gene (TGM1) mutations** |
|          | Context: Bathing suit ichthyosis (BSI) is an uncommon phenotype classified as a minor variant of autosomal recessive congenital ichthyosis (ARCI). OBJECTIVES: We report a case of BSI in a 3-year-old Tunisian girl with a novel **mutation of the transglutaminase 1 gene (TGM1)** |

| List     | ID: 5c5214207cbb68231000003     |
|          | Question: List potential reasons regarding why potentially important genes are ignored |
|          | Ground Truth Answer: **Identifiable chemical properties, Identifiable physical properties, Identifiable biological properties, Knowledge about homologous genes from model organisms** |
|          | Context: Here, we demonstrate that these differences in attention can be explained, to a large extent, exclusively from a small set of **identifiable chemical, physical, and biological properties** of genes. Together with knowledge about homologous genes from model organisms, these features allow us to accurately predict the number of publications on individual human genes, the year of their first report, the levels of funding awarded by the National Institutes of Health (NIH), and the development of drugs against disease-associated genes. |

**Table 7.** Limitation of the extractive QA setting in BioASQ dataset. We sample examples of factoid and list type questions from 7B test dataset. Context recurs to the snippet which is human annotation suggested by organizer. **Bold** and **underline** denotes no exact match and exact match in lowercase respectively.

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A Training Details

| Type       | Data Strategy | 6B  | 7B  | 8B  | Train | Test | Train | Test | Train | Test |
|------------|---------------|-----|-----|-----|-------|------|-------|------|-------|------|
| Yes/No Snippet-as-is | 9,421 | 127 | 10,560 | 140 | 11,531 | 152 |
| Full-Abstract     | 7,911 | 9,403 | 10,147 |
| Factoid Appended-Snippet | 5,953 | 161 | 7,179 | 162 | 7,896 | 151 |
| Snippet-as-is      | 3,512 | 4,231 | 4,759 |
| Full-Abstract     | 14,008 | 15,719 | 16,879 |
| List Appended-Snippet | 10,878 | 81 | 12,184 | 88 | 13,251 | 75 |
| Snippet-as-is      | 6,922 | 7,865 | 8,676 |

Table 8. Statistics of transferred dataset (MNLI & SQuAD) and target dataset (BioASQ).

We use BioBERT as learning biomedical entity representation. We utilize a single NVIDIA Titan RTX (24GB) GPU to fine-tune the sequence of transfer...
learning. In MNLI task, we use hyperparameters suggested by Hugging Face.\(^5\)

For fine-tuning, we select the batch size as 12, 24 and a learning rate is within range 1e-6 to 9e-6. In post-processing, we use the abbreviation resolution module called Ab3P\(^6\) to remove the same answer appearance with a different form.

\(^5\) https://github.com/huggingface/transformers/tree/master/examples/text-classification

\(^6\) https://github.com/ncbi-nlp/Ab3P