Large language models in biomedical natural language processing: benchmarks, baselines, and recommendations

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Abstract

Biomedical literature is growing rapidly, making it challenging to curate and extract knowledge manually. Biomedical natural language processing (BioNLP) techniques that can automatically extract information from biomedical literature help alleviate this burden. Recently, large Language Models (LLMs), such as GPT-3 and GPT-4, have gained significant attention for their impressive performance. However, their effectiveness in BioNLP tasks and impact on method development and downstream users remain understudied. This pilot study (1) establishes the baseline performance of GPT-3 and GPT-4 at both zero-shot and one-shot settings in eight BioNLP datasets across four representative tasks: named entity recognition, relation extraction, multi-label document classification, and semantic similarity and reasoning, (2) examines the errors produced by the LLMs and categorized the errors into three types: missingness, inconsistencies, and unwanted artificial content, and (3) provides suggestions for using LLMs in BioNLP applications.

Overall, GPT-4 achieved a macro-average accuracy of 0.6834 whereas GPT-3.5 had a substantially lower performance with a macro-average of 0.4965 at the zero-shot or one-shot setting. In comparison, the fine-tuned PubMedBERT model achieved a macro-average accuracy from 0.6852 to 0.8195 based on a combination of 18 hyperparameters. While the performance of GPT-4 is impressive, it only reached the lower bound of the results of PubMedBERT overall. However, GPT-4 outperforms PubMedBERT in biomedical question answering by 17%, showing that it excels at capturing semantic similarity and reasoning and has the potential to be applied to similar tasks. Despite its promising results, the missingness and inconsistencies produced by GPTs are prevalent – for instance, 14 out of 200 output samples in question answering have missing answers; 94 out of 200 output samples have four inconsistent formats in extracting protein-protein interactions. The results lead to three primary recommendations: (1) fine-tuning biomedical pretrained language models continues to be a prominent choice especially for tasks involving information extraction and classification; LLMs demonstrate encouraging performance especially in biomedical semantic similarity and reasoning tasks, even when applied in zero-shot or one-shot settings, (2) adapting both data and evaluation paradigms is key to the successful application of LLMs in BioNLP, and (3) addressing errors, missingness, and inconsistencies is critical to minimizing the risks of LLMs in biomedical and clinical applications. We make the datasets, baselines, and results publicly available to the community via https://github.com/qingyuqc/gpt_bionlp_benchmark for reproducibility and benchmarking.

Introduction

Biomedical literature presents direct obstacles to curation, interpretation, and knowledge discovery due to its vast volume and domain-specific challenges. PubMed alone sees an increase of approximately 5,000 articles every day, totaling over 35 million [1]. In specialized fields such as COVID-19, roughly 10,000 dedicated articles are added each month, bringing the total to around 0.35 million [2]. In addition to volume, the biomedical domain also poses challenges with ambiguous language. For example, a single entity such as Long COVID can be referred to using 763 different terms [3]. Additionally, the same term can describe different entities, as seen with the term AP2 which can refer to a gene, a chemical, or a cell line [4]. Beyond entities, identifying novel biomedical relations and capturing semantics in biomedical literature present further challenges [5, 6]

To overcome these challenges, biomedical natural language processing (BioNLP) techniques are utilized to assist with manual curation, interpretation, and knowledge discovery. Biomedical language models are considered the backbone of BioNLP methods; they leverage massive amounts of biomedical literature and capture biomedical semantic representations in an unsupervised or self-supervised manner. Biomedical language models have evolved from (1) non-contextual models (e.g., BioWordVec and BioSentVec) that use fully-connected neural networks [4, 7, 8], to (2) masked language models such as the biomedical bidirectional encoder representations from transformers (BERT) family (e.g., BioBERT and PubMedBERT) [9-11] using the encoder from the transformer architecture, and (3) to generative language models (e.g., BioGPT and BioMedLM) using generative pre-trained transformer (GPT) models [12, 13]. Studies have demonstrated that BioNLP applications built on top of biomedical language models achieve state-of-the-art performance in various BioNLP applications [10, 14], and have been successfully employed in PubMed-scale downstream applications such as biomedical sentence search [15] and COVID-19 literature mining [2].

Recently, the latest generative pre-trained transformer models, including GPT-3 and, more notably, GPT-4, have made significant strides and garnered considerable attention from society. A key characteristic of these models is the exponential growth of their parameters, with GPT-3 and GPT-4 featuring 175 billion and estimated 170 trillion parameters [16], respectively in contrast to GPT-2, which has 1.75 billion parameters. Models of this magnitude are commonly referred to as Large Language Models (LLMs) [17]. The launch of ChatGPT – a chatbot built from GPT-3 and GPT-4 – has marked a milestone in generative artificial intelligence. It has demonstrated strong capabilities in the tasks that its predecessors fail to do; for instance, GPT-4 passed over 20 academic and professional exams including the Uniform Bar Exam, SAT Evidence-Based Reading & Writing, and Medical Knowledge Self-Assessment Program [18]. The remarkable advancements have sparked extensive discussions among society, with excitement and concerns alike.

As is evident from the capabilities of LLMs, it is crucial to assess their effectiveness in BioNLP tasks and comprehend their impact on BioNLP method development and downstream users. However, to date, only a limited number of studies have conducted such analyses on biomedical literature, with a focus primarily on specific BioNLP applications such as biomedical relation extraction [19] and reasoning [20], or have solely evaluated GPT-3, which is not the best representative of LLMs [21]. Furthermore, these studies lack a thorough error analysis and recommendations. Arguably, understanding the limitations

and errors of LLMs in BioNLP applications and providing recommendations to BioNLP downstream users, including developers, researchers, and healthcare professionals, is more critical than a quantitative evaluation.

In this pilot study, we conducted extensive evaluations of LLMs in BioNLP applications and examined their limitations and errors. We began by evaluating GPT-3 and GPT-4 on eight BioNLP datasets across four applications: (1) named entity recognition, (2) relation extraction, (3) multi-label document classification, and (4) semantic similarity and reasoning. We then compared these models to the fine-tuned PubMedBERT, which served as a strong baseline. Next, we conducted a manual examination of the outputs generated by GPT-3 and GPT-4, and categorized the errors into three types: missingness, inconsistencies, and unwanted artificial content. The results and analysis lead to three recommendations:

- (1) Fine-tuning biomedical pretrained language models continues to be a prominent choice especially for tasks involving information extraction and classification; LLMs demonstrate encouraging performance especially in biomedical semantic similarity and reasoning tasks, even when applied in zero-shot or one-shot settings. The results demonstrate LLMs excel at capturing semantic similarity and reasoning and has the potential to be applied to similar tasks. In contrast, pre-trained biomedical language models remain state-of-the-art in most BioNLP applications and it should be considered as a strong baseline at the very minimum.
- (2) Adapting both data and evaluation paradigms is key to the successful application of LLMs in BioNLP. The current evaluation setting in BioNLP is tailored to supervised methods and may not be fair to LLMs. Additionally, datasets for tasks where LLMs excel (such as biomedical semantic similarity and reasoning) are limited in the biomedical domain.
- (3) Addressing errors, missingness, and inconsistencies is critical to minimizing the risks of LLMs in biomedical and clinical applications. We encourage a community effort to find better solutions to minimize these cases.

We believe that the findings of this study will be beneficial for BioNLP downstream users and also aid in further enhancing the performance of LLMs in BioNLP applications. To ensure reproducibility and enable benchmarking, we have made the relevant data, models, and results publicly accessible through https://github.com/qingyu-qc/gpt bionlp benchmark.

Data and methods

Table 1. Evaluation datasets, metrics, and distributions of the samples.

| Dataset | Metric | Samples | | |
|---------------------------|---------------------|------------------------------------|-----------------------|--|
| Named entity recogniti | - | | | |
| BC5CDR-chemical | Entity-level F1 | Instances with entities | 180 | |
| | · | Instances without entities | 20 | |
| | | Total | 200 with 317 entities | |
| NCBI-disease | Entity-level F1 | Instances with entities | 180 | |
| | | Instances without entities | 20 | |
| | | Total | 200 with 328 entities | |
| Relation extraction | | | | |
| ChemProt | Macro F1 | CPR:3 | 45 | |
| | | CPR:4 | 88 | |
| | | CPR:5 | 11 | |
| | | CPR:6 | 13 | |
| | | CPR:9 | 23 | |
| | | false | 20 | |
| | | Total | 200 | |
| DDI2013 | Macro F1 | DDI-advise | 33 | |
| | | DDI-effect | 69 | |
| | | DDI-mechanism | 60 | |
| | | DDI-int | 18 | |
| | | DDI-false | 20 | |
| | | Total | 200 | |
| Multi-label classificatio | n | | | |
| HoC | Label-wise macro F1 | Activating invasion and | 34 | |
| | | metastasis | 12 | |
| | | Avoiding immune destruction | 12 | |
| | | Cellular energetics | 15 | |
| | | Enabling replicative immortality | 13 | |
| | | Evading growth suppressors | 27 | |
| | | Genomic instability and mutation | 42 | |
| | | Inducing angiogenesis | 17 | |
| | | Resisting cell death | 53 | |
| | | Sustaining proliferative signaling | 57 | |
| | | Tumor promoting inflammation | 30 | |
| | | Total | 200 with 300 labels | |
| | | | | |

| LitCovid | Label-wise macro F1 | Diagnosis | 46 | |
|-----------------------|---------------------|----------------------|---------------------------|--|
| | | Epidemic Forecasting | 14 | |
| | | Mechanism | 38 | |
| | | Prevention | 87 | |
| | | Transmission | 17 | |
| | | Treatment | 67 200 with 286 labels | |
| | | Total | | |
| Semantic similarity a | and reasoning | | | |
| BIOSSES | Pearson correlation | Total | 20 | |
| PubMedQA | Macro F1 | Yes | 101 | |
| | | No | 71 | |
| | | Maybe | 28 | |
| | | Total | 200 | |

Evaluation datasets

Table 1 presents a summary of the evaluation datasets, metrics, and distributions of randomly selected test samples. We performed a quantitative evaluation of the models on eight datasets from four BioNLP applications, which are BC5CDR-chemical and NCBI-disease for Named Entity Recognition, ChemProt and DDI2013 for relation extraction, HoC and LitCovid for multi-label document classification, and BIOSSES and PubMedQA for semantic similarity and reasoning. These datasets have been widely used in benchmarking biomedical text mining challenges [22-24] and evaluating biomedical language models [9-11, 14]. We used their training, validation, and testing set prepared by the existing studies [9-11]. As the cost of GPT-4 is high (for instance, applying GPT-4 on the full testing set of ChemProt costs more than a thousand dollars), we randomly sampled 200 instances from the testing set per dataset except BIOSSES whose testing set has only 20 instances in total. The sampled datasets are also publicly available in the repository. A detailed description is below.

Named entity recognition. Named entity recognition is a task that involves identifying entities of interest from free text. As mentioned, biomedical entities can be described in various ways, and resolving the ambiguities is crucial [25]. Named entity recognition is typically a sequence labeling task, where each token is classified into a specific entity type. BC5CDR-chemical [26] and NCBI-disease [27] are manually annotated named entity recognition datasets for chemicals and diseases mentioned in biomedical literature, respectively. For each dataset, we randomly sampled 180 sentences with entities and 20 sentences without entities from its testing set. The exact match (that is, the predicted tokens must have the same text spans as the gold standard) F1-score was used to quantify the model performance.

Relation extraction. Relation extraction involves identifying the relationships between entities, which is important for drug repurposing and knowledge discovery [28]. Relation extraction is typically a multiclass classification problem, where a sentence or passage is given with identified entities and the goal is to classify the relation type between them. ChemProt [22] and DDI2013 [29] are manually curated relation extraction datasets for protein-protein iterations and disease-disease iterations from biomedical literature, respectively. Similarly, we randomly sampled 180 instances with actual relation

types and 20 negative instances. Macro F1-score was used to quantify the model performance, which considers different relation types equally.

Multi-label document classification. Multi-label document classification identifies semantic categories at the document-level. The semantic categories are effective for grasping the main topics and searching for relevant literature in the biomedical domain [30]. Unlike multi-class classification, which assigns only one label to an instance, multi-label classification can assign up to N labels to an instance. HoC [31] and LitCovid [23] are manually annotated multi-label document classification datasets for hallmarks of cancer (10 labels) and COVID-19 topics (7 labels), respectively. We sampled 200 instances, with an enrichment for minor labels to ensure there were enough instances for informative statistical analysis. The model performance was quantified using macro F1-score.

Semantic similarity and reasoning. Semantic similarity measures the relevance between two pieces of text, such as a query and a document, for information retrieval. In some cases, such as question-answering, it may also involve reasoning to generate an answer. These techniques are particularly useful for biomedical evidence attribution and question-answering [32]. BIOSSES [33] and PubMedQA [34] are manually annotated datasets for sentence similarity and question answering, respectively. We used the entire testing set of BIOSSES (20 instances in total) and randomly sampled 200 instances from the testing set of PubMedQA. Note that Accuracy is the official evaluation metric of PubMedQA; however, in the specific context of our study, we observed that Accuracy may be biased when a model only predicts the majority of answer categories. Therefore, we used macro-F1 instead.

Methods

Pretrained biomedical bidirectional encoder representations from transformers

We used the pre-trained biomedical BERT [35] as a baseline. As a representative, we selected PubMedBERT [14] – the BERT model that was trained from scratch on PubMed literature and achieved robust performance in a range of BioNLP benchmarks [36-38].

Table 2. Hyperparameter values for fine-tuning BERT models.

| Hyperparameters | Values |
|-----------------|-----------------------|
| Learning rate | 1e-05, 3e-5, and 5e-5 |
| Sequence length | 128, 256, and 512 |
| Batch size | 16 and 32 |
| Dropout rate | 0.1 |

Fine-tuning PubMedBERT. We fine-tuned PubMedBERT using the training and validation set prepared by the existing studies [9-11]. Table 2 demonstrates the hyperparameter values – consisting of a total of 18 combinations. Those values are derived from the original PubMedBERT study [14]. For each dataset, we fine-tuned the model using those 18 combinations, selected the model achieving the best loss in the validation set for evaluation, and reported the minimum, median, and max performance.

Large language models

We evaluated GPT-3.5 and GPT-4 as LLM representatives. Those two models have been regularly updated; for reproducibility, we used the snapshots GPT-3.5-turbo-0301 and GPT-4-0314.

Prompts. Figure 1 shows an example prompt for relation extraction in ChemProt. We designed the prompt consistently across different tasks such that it contains (1) task descriptions (e.g., classifying relations), (2) input specifications (e.g., a sentence with labeled entities), (3) output specifications (e.g., the relation type), (4) task guidance (e.g., detailed descriptions on relation types), and (5) example demonstrations if an example is provided. The prompts used for the datasets are also publicly available for reproducibility and benchmarking.

Zero- and one-shot. We comparatively evaluated the zero-shot and one-shot learning performance. For one-shot, we randomly selected an instance from the training set. Figure 1 shows the example demonstration for the one-shot learning. Due to the high cost of GPT-4, we limited the analysis to zero-and one-shot learning. In addition, we evaluated the performance of three- and five-shot learning on selected datasets for further analysis.

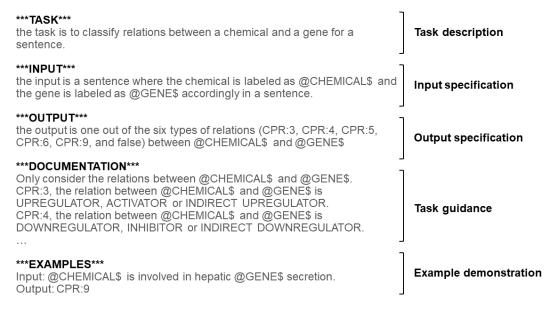


Figure 1. A prompt example for biomedical relation extraction.

Table 3. Evaluation results.

| | Fine-tuned PubMedBERT | | GPT-3.5 | | GPT-4 | | |
|------------------------|-----------------------|--------|---------|-----------|----------|-----------|----------|
| | Min | Median | Max | Zero-shot | One-shot | Zero-shot | One-shot |
| Named entity recogn | ition | | | | | | |
| BC5CDR-chemical | 0.9028 | 0.9230 | 0.9350 | 0.2925 | 0.1803 | 0.7443 | 0.8207 |
| NCBI-disease | 0.8336 | 0.8766 | 0.8986 | 0.2405 | 0.1273 | 0.5673 | 0.4837 |
| Relation extraction | | | | | | | |
| ChemProt | 0.6653 | 0.7184 | 0.7832 | 0.5743 | 0.6191 | 0.6618 | 0.6543 |
| DDI2013 | 0.6673 | 0.7624 | 0.8023 | 0.3349 | 0.3440 | 0.6325 | 0.6558 |
| Multi-label classifica | tion | | | | | | |
| HoC | 0.6991 | 0.8398 | 0.8915 | 0.6572 | 0.6932 | 0.7474 | 0.7402 |
| LitCovid | 0.8024 | 0.8692 | 0.8724 | 0.6390 | 0.6531 | 0.6746 | 0.6839 |
| Semantic similarity a | nd reasonin | ng | | | | | |
| PubMedQA | 0.2237 | 0.3014 | 0.3676 | 0.3553 | 0.3011 | 0.4374 | 0.5361 |
| BIOSSES | 0.6870 | 0.8400 | 0.9332 | 0.8786 | 0.9194 | 0.8832 | 0.8922 |
| Overall performance | | | | | | | |
| Average accuracy | 0.6852 | 0.7664 | 0.8195 | 0.4965 | 0.4797 | 0.6685 | 0.6834 |
| Average rank | - | - | 1.1250 | 4.6250 | 4.0000 | 2.6250 | 2.3750 |

Results and discussion

Overall performance

Table 3 shows a comprehensive overview of the model evaluation results on the eight datasets, including macro-average accuracies and rankings. Overall, fine-tuned PubMedBERT achieved the highest performance, with macro-average accuracies ranging from 0.6852 to 0.8195, ranking in the first place. GPT-4 one-shot learning obtained the second-highest macro-average accuracy of 0.6834, an impressive result given that the model was in the general domain and only received one instance. However, the accuracy only reached the lower bound of the results obtained by fine-tuned PubMedBERT. Specifically, GPT-4 outperformed PubMedBERT in one dataset (PubMedQA; 0.5361 vs. 0.3676), had comparable performance in one dataset (BIOSSES; 0.8922 vs. 0.9332), and underperformed in the remaining six datasets by a significant margin, ranging from approximately 10% (ChemProt; 0.6618 vs. 0.7832) to almost 40% (NCBI-disease; 0.4837 vs. 0.8986). The robust performance of GPT-4 on PubMedQA and BIOSSES suggests that it excels at capturing semantic similarity and reasoning, but it demonstrates poor to moderate performance in other applications, such as extraction and classification.

GPT-3.5 vs GPT-4

The macro-averaged accuracy of GPT-4 is significantly higher than that of GPT-3.5 under both zero-shot (0.6834 vs 0.4797) and one-shot settings (0.6685 vs 0.4965). GPT-4 consistently outperformed GPT-3.5 in seven out of eight datasets, except for BIOSSES, where it had only a 2% lower accuracy.

Poor performance in named entity recognition

The results show that GPT models, especially GPT-3.5, had extremely poor performance in named entity recognition compared to other tasks. We manually examined 20 samples and categorized the erroneous predictions into three types: (1) wrong entities, where the predicted entities are incorrect, (2) boundary issues, where the predicted entities are correct but with different text spans than the gold standard, and (3) missing entities, where the true entities are not predicted. Figure 2 shows the results for both GPT-3.5 and GPT-4. The most striking difference is that GPT-3.5 had five times more missing entities than GPT-4 under both zero-shot (43 vs. 8) and one-shot settings (49 vs. 9). This is the main bottleneck of GPT-3.5 in named entity recognition. It also shows that one-shot is more effective for the other two error types (for instance, one-shot reduced the number of wrong entity extractions from 12 to 4) but not for missing entities.

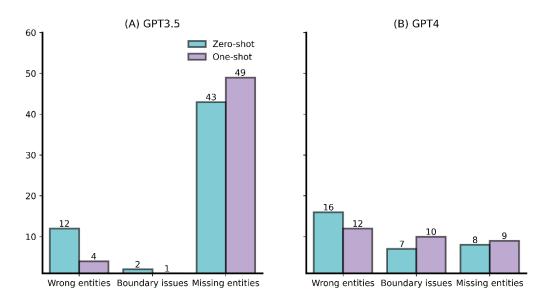


Figure 2. Error analysis on 20 samples of the LLMs predictions on named entity recognition. Wrong entities: the predicted entities are incorrect. Boundary issues: the predicted entities are correct but with different text spans of the gold standard; Missing entities: the true entities are not predicted

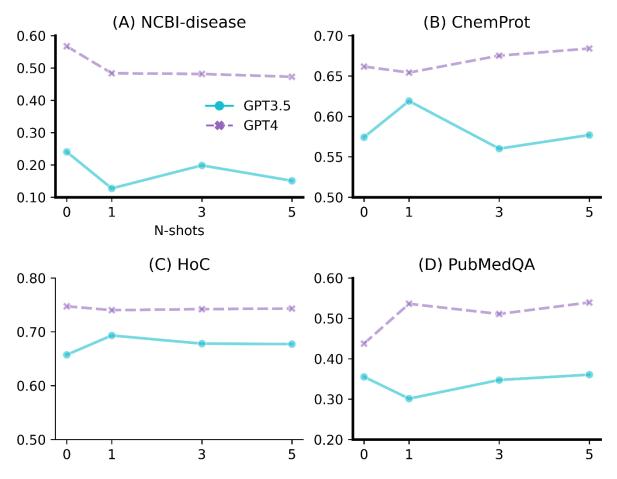


Figure 3. Performance of the number of demonstrations (training examples) in LLMs. Note that the y-axis has different ranges.

Zero-shot vs one-shot

Overall, one-shot learning outperformed zero-shot learning in both GPT-3.5 and GPT-4, with the macro-averaged rankings of 4 vs 4.65 and 2.37 vs 2.62, respectively. However, this trend is not consistent across all datasets. One-shot learning performed better in five out of eight datasets for both models, but in named entity recognition, the performance of one-shot learning was 10% lower. As mentioned earlier, Figure 2 demonstrates that one-shot learning is effective in reducing wrong entity extractions and entities with boundary issues, but it does not improve the detection of missing entities.

We further questioned whether providing more examples would be more effective and assessed the performance of three-shot and five-shot performance in selected datasets (again, due to associated cost). To maintain consistency with one-shot learning, we randomly sampled the examples from the training set. The results, shown in Figure 3, indicate that increasing the number of demonstrations does not necessarily improve performance. While increasing the number of demonstrations slightly improved performance for ChemProt and PubMedQA, the improvement was not linear. For HoC, the performance hardly varied, especially for GPT-4. Surprisingly, for NCBI-disease, more demonstrations actually decreased the performance. This could be because the demonstrations were randomly selected and may not have been the best representatives of the dataset. Alternatively, it could indicate that GPT models have reached their performance limit on these datasets using the current evaluation setting.

These findings motivate further assessment of prompting engineering and learning curves of GPT in BioNLP applications.

Table 4. A taxonomy of errors and inconsistencies generated by LLMs in addition to incorrect predictions.

| Types | Example |
|-----------------------------------|---|
| 1. Missing output | GPT-4 zero-shot on PubMedQA |
| | Required output: yes, maybe, or no |
| | Actual output: Are prophylactic antibiotics necessary for |
| | totally implantable venous access device placement by |
| | interventional radiologists? |
| 2. Inconsistent output | |
| 2.1 Inconsistent semantic output | GPT-3.5 zero-shot on PubMedQA |
| | Output 1: Maybe. The study shows that the curves of body |
| | mass index differed among birth cohorts, with more |
| | recent cohorts being more overweight as children but |
| | thinner as young women. However, the study does not |
| | provide a direct answer to whether overweight children |
| | necessarily become overweight adults. |
| | Output 2: Does the Barthel index alone provide sufficient |
| | information about the long term outcome of |
| | stroke? Maybe. |
| 2.2 Inconsistent syntactic output | GPT-3.5 one-shot on Chemprot |
| | Output1: CPR:9 |
| | Output2: A: CPR:9 |
| | Output3: CPR:9. |
| | Output4: Example-2 A: CPR:9 |
| 3. Artificial output | GPT-4 zero-shot on LitCovid |
| | Required output: up to seven labels from Case Report, |
| | Diagnosis, Epidemic Forecasting, Mechanism, Prevention, |
| | Transmission, Treatment |
| | Actual output: Telemedicine |

A taxonomy of problematic outputs by LLMs beyond inaccuracy

Importantly, apart from inaccurate predictions, we also noticed a considerable number of missing and inconsistent outputs from LLMs that require thorough manual examination and post-processing. In Table 4, we have summarized the taxonomy of such cases based on our manual review. Below, we explain each of the categories in detail.

Missing output. In this case, LLMs do not provide the output as requested. For instance, in PubMedQA, when asked to produce an answer from yes, no, or maybe, the model produced a paraphrased question instead. We found that 14 out of 200 samples from GPT-4 zero-shot had missing outputs.

Inconsistent output. In this case, LLMs indeed provide an output as requested, but the output is inconsistent across different instances. We further divided this category into **inconsistent semantic**

output and **inconsistent syntactic output**. Inconsistent semantic output is where LLMs provide explanations and paraphrases in an inconsistent manner. For example, in the QA example, LLMs may provide explanations or paraphrased questions in addition to the requested output. We found that 32 out of 200 samples from GPT-4 zero-shot fell under this category. In contrast, inconsistent syntactic output is where the outputs are in different syntactic structures. As shown in Table 4, for a relation type, the model may answer in different ways. We found that 94 out of 200 samples from GPT-3.5 one-shot provided answers in four different ways.

Artificial output. In this case, LLMs generate unexpected artificial outputs. For example, in LitCovid's multi-label classification, the model was explicitly asked to provide up to seven predefined labels, but it produced a new label instead. We only found one such case from GPT-4 zero-shot. However, it is still concerned about the potential harms that unexpected output from LLMs can cause.

Recommendations

Finally, the results and discussions lead to the following recommendations:

Fine-tuning biomedical pretrained language models continues to be a prominent choice especially for tasks involving information extraction and classification; LLMs demonstrate encouraging performance especially in biomedical semantic similarity and reasoning tasks, even when applied in zero-shot or one-shot settings. The performance of GPT-4 — while impressive — still falls by a large margin except for biomedical semantic similarity and reasoning applications. In contrast, the results demonstrate that pre-trained biomedical language models remain state-of-the-art in most BioNLP applications. Therefore, we recommend fine-tuning a pre-trained biomedical language model as the default choice for a downstream application, as it should be a strong baseline at the very minimum.

Adapting both data and evaluation paradigms is the key to applying LLMs in BioNLP. The poor performance in traditional BioNLP applications, especially named entity recognition, motivates revisiting the data and method paradigm for LLMs. The current BioNLP datasets and evaluation paradigms may not fit LLMs. Arguably, the current evaluation setting in BioNLP is tailored to supervised methods and is not fair for LLMs. The datasets for the tasks where LLMs excel are also limited in the biomedical domain.

Addressing errors, missingness, and inconsistencies produced by LLMs is critical. The prevalence of errors, missingness, and inconsistencies generated by LLMs is of concern, and we argue that they must be addressed for deployment. We encourage a community effort for better solutions to minimize those cases in biomedical and clinical applications.

Limitations and future work

This pilot study possesses several limitations that should be acknowledged. Firstly, in order to establish a baseline performance, we employed a uniform prompt template for all tasks and exclusively used zero-and one-shot learning strategies. However, employing more advanced task-based prompt engineering techniques may potentially enhance the performance of LLMs even further. In addition, the evaluation conducted in this study was limited to samples rather than the complete testing sets due to the associated costs of using GPT-4. We made the samples representative but the findings may still not fully represent the LLMs' performance on the entire dataset. Lastly, it is worth noting that the current

evaluation focused solely on GPT-3 and GPT-4. Our future work will encompass the evaluation of other LLMs as well, broadening the scope of the study.

Acknowledgment

This study is supported by the following National Institutes of Health grants: R01AG078154, 1K99LM01402, and the Intramural Research Program of the National Library of Medicine (NLM).

Conflict of Interest

Dr. Hua Xu and Dr. Jingcheng Du have research-related financial interests in Melax Technologies Inc.

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