RIGA at SMM4H-2024 Task 1: Enhancing ADE discovery with GPT-4

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Abstract

The following is a description of the RIGA team's submissions for the SMM4H-2024 Task 1: Extraction and normalization of adverse drug events (ADEs) in English tweets. Our approach focuses on utilizing Large Language Models (LLMs) to generate data that enhances the fine-tuning of classification and Named Entity Recognition (NER) models. Our solution significantly outperforms mean and median submissions of other teams. The efficacy of our ADE extraction from tweets is comparable to the current state-of-the-art solution, established as the task baseline. The code for our method is available on GitHub¹.

1 Introduction

The SMM4H-2024 Task 1, as outlined in the overview (Xu et al., 2024), challenged participants to extract and normalize ADEs to MedDRA high-level term identifiers (HLTIs).

Our submission aims to harness the capabilities of large language models (LLMs) to enhance performance. Additionally, we compare the performance of the off-the-shelf submission, which did not involve model training, with a fine-tuned model that combines the original input with the output generated by GPT.

2 Related work

The baseline system (Magge et al., 2021) utilizes a pipeline method for solving the task. The pipeline involves 3 components and are executed sequentially: (1) the ADE classifier for identifying tweets containing ADE mentions, (2) the ADE span extractor or named entity recognition (NER) for extracting ADE mentions, and (3) the ADE normalizer, which maps the extracted ADE mention to MedDRA HLT identifiers. In our submission we utilize the same pipeline components.

Dataset	Train	Dev	Test
Full	18185	965	11799
Contain ADEs	1239	65	N/A

Table 1: Dataset size distribution

The paper concentrates on integrating the GPT model generation with the original text. A comparable methodology was employed in SemEval-2023 (Mukans and Barzdins, 2023), where the task involved token classification with highly specific tags. To streamline the process, the RIGA team utilized GPT as a knowledge database for individuals, entities, food items, and other relevant entities mentioned in the text.

According to the LLM for Generative Information Retrieval Survey (Xu et al., 2023), our method can be classified as a form of data augmentation. Similar approaches have been independently employed in several studies (Amalvy et al., 2023; Chen and Feng, 2023; Li et al., 2023)

3 Data

In contrast to the previous version of the task, the new challenge in the most recent dataset lies in the inclusion of negative samples (falling outside MedDRA categories) in each data split.

As presented in Table 1, the data is highly imbalanced. The amount of tweets containing any ADE is 6.8% for train data split and 6.7% for dev data split.

4 Methodology

In order to address the issue of high data imbalance, our pipeline includes tweet classification as the initial step to filter out the majority of the tweets. Subsequently, for the filtered tweets, we conduct NER to extract the precise spans that contain an ADEs. In the final step, we generate a sentence embedding for the span and identify the nearest

¹https://github.com/emukans/smm4h2024-riga

Submission	F1-Norm	P-Norm	R-Norm	F1-NER	P-NER	R-NER	F1-Norm-Unseen
GPT few-shot	31.8	29.5	34.6	40.3	37.7	43.4	21.2
Custom + GPT	10.3	12.1	9	47.9	52.5	44.1	6.5
Baseline	43.9	39.3	49.8	48.1	43.1	54.3	32.3
Mean	28.264	29.244	33.388	32.672	35.625	34.032	20.936
Median	29.3	33.9	32.6	37.6	43.7	37.4	14.1

Table 2: The performance of our submissions

HLTIs using cosine similarity.

We used four Tesla v100 16GB GPUs, provided by our institution, for conducting these experiments.

4.1 Tweet classification

According to Table 1, more than 93% of the tweets do not contain any ADEs. To filter out these tweets, we developed a binary classification model to identify the presence of ADEs in the input tweets. This model is based on a language model fine-tuned from RoBERTa-large (Antypas et al., 2023; Liu et al., 2019).

Before the classification model fine-tuning, all tweets are preprocessed with GPT-4 Turbo (OpenAI et al., 2024) prompt engineering (Brown et al., 2020) to extract mentioned ADEs in the text. The generative model simply needs to mention all ADEs from the provided text in a free-form manner. The prompt used in our submission is detailed in Appendix A.

The GPT output is then concatenated with the original tweet in the following format and used as input to a binary classification model:

{tweet} <sep> {ADE extracted with GPT}.

4.2 ADE span extraction

All categorized tweets with ADEs are forwarded to the span extraction stage. We employ a BIOtagging schema with only three tags: B-ADE, I-ADE, and O.

In this stage, we also incorporate GPT output as additional context for downstream fine-tuning. The prompt utilized in our submission is detailed in Appendix B.

As shown in Table 2, the ADEs generated by GPT few-shot demonstrate strong performance in comparison to the mean and median scores. However, a notable limitation of GPT is its verbosity and propensity for hallucinations. Often, the generated spans contain verbs that contribute to coherent sentence structures but are not directly pertinent to ADEs. Furthermore, the model may generate text that deviates from the original text. For instance, it might produce ADE expressions that do not exactly match the words in the given tweet. This issue goes beyond minor discrepancies, such as differences in American and British spelling, and highlights a broader challenge in utilizing generative models for extracting ADEs from tweets. The foundational model's training datasets, like C4, which predominantly feature texts with American dialects, contribute to this bias (Dodge et al., 2021).

To fine-tune DeBERTaV3 for span extraction (He et al., 2021), we adopt a similar input structure as in the classification step. However, since tweets may contain multiple ADEs, we separate each ADE in the input using the sep token.

The output generated by the fine-tuned model Custom + GPT, using the following input format is less noisy compared to the original GPT results.

4.3 Span mapping to MedDRA HLTIs

In total, MedDRA contains 23,389 HLTIs, but the training and development data only contain 319 unique identifiers. This indicates that the majority of HLTIs are not present in our dataset.

Training a classifier to map the spans to the HLTIs using the provided data would be futile due to the high variety of HLTIs. Additionally, the test data includes unseen categories that the trained classifier would not be able to identify.

In our submission, we utilized an off-the-shelf solution by leveraging OpenAI's Embedding API. Initially, we computed an embedding representation for all MedDRA HLTIs, followed by doing the same for each ADE span. Subsequently, we identified the closest HLTIs by calculating the cosine similarity between the embeddings.

Unfortunately, we ran out of resources and time to achieve a higher F1-Norm score for the Custom + GPT model. Despite using the same approach as the GPT few-shot model, the Custom + GPT model's performance on F1-Norm suffered.

5 Results

In Table 2, we compare our solutions with the current state-of-the-art solution, which serves as a baseline for the task. The competition evaluates performance using two metrics: F1-Norm and F1-NER. Our primary focus was on the F1-NER metric, where the Custom + GPT model demonstrates performance comparable to the baseline and significantly higher than both the mean and median. The GPT few-shot submission also achieved results above both the mean and median for both metrics.

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A Classification prompt

For tweet classification we used the following prompt:

You will be provided with a tweet. Summarise it into a brief sentence and highlight already happened adverse drug events (ADE) if there are any related to drugs.

```
Format:
Summary: {text}
ADE: {text or null}
```

Tweet:

.....

{tweet}
"""

The model generates two lines in the output: "Summary" and "ADE." In our submission, we utilize only the "ADE" field. The intention behind the "Summary" field was to classify summarized tweets instead of the original text, potentially simplifying the task by producing summaries in a unified language and style. Unfortunately, this hypothesis did not hold. GPT likely omits important keywords common to many ADE-containing tweets, or the semantics of the generated text do not match the original tweet. It is probable that using a "rewrite" instruction instead of "summarize" would have been more effective.

B ADE extraction prompt

For mining text spans containing ADEs we used the following prompt:

```
You will be provided with a tweet.
Your task is to identify and highlight
any adverse drug events (ADEs) mentioned
in relation to drug use.
                               Only the
exact phrases describing the ADEs should
be outputted,
                without including
                                     any
additional context.
                       Each ADE should
be listed on a new line. If the same
ADE is mentioned multiple times, each
occurrence should be listed separately.
If multiple different ADEs are identified
within the same tweet, they should be
listed on separate lines. If no ADEs are
found, output "null".
Format:
SPAN: {text or null}
Samples:
Tweet:
.....
  user
if avelox has hurt your liver, avoid
tylenol always, as it further damages
liver,
        eat grapefruit unless taking
cardiac drugs
.....
SPAN: hurt your liver
Tweet:
......
losing it. could not remember the word
power strip. wonder which drug is doing
this memory lapse thing. my guess the
cymbalta. helps
,, ,, ,,
SPAN: not remember
SPAN: memory lapse
Tweet:
,,,,,,,
is adderall a performance enhancing drug
for mathletes?
,,,,,,,
SPAN: null
Tweet:
n n n
{tweet}
n n n
```

Since the most of tweets will be filtered out during the classification step, and token classification is more complex task, than sequence classification, the prompt contains more instructions and output samples.