A Zero-shot and Few-shot Study of Instruction-Finetuned Large Language Models Applied to Clinical and Biomedical Tasks

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Abstract

We evaluate four state-of-the-art instruction-tuned large language models (LLMs) – ChatGPT, Flan-T5 UL2, Tk-Instruct, and Alpaca – on a set of 13 real-world clinical and biomedical natural language processing (NLP) tasks in English, such as named-entity recognition (NER), question-answering (QA), relation extraction (RE), etc. Our overall results demonstrate that the evaluated LLMs begin to approach performance of state-of-the-art models in zero- and few-shot scenarios for most tasks, and particularly well for the QA task, even though they have never seen examples from these tasks before. However, we observed that the classification and RE tasks perform below what can be achieved with a specifically trained model for the medical field, such as PubMedBERT. Finally, we noted that no LLM outperforms all the others on all the studied tasks, with some models being better suited for certain tasks than others.

1 Introduction

Healthcare is currently benefiting greatly from advances in Natural Language Processing (NLP) to enhance the quality of service provided to clinicians, patients, and biomedical researchers. The NLP field has made significant progress in recent years, thanks to the availability of massive textual databases and the use of deep learning techniques that allow for more efficient exploitation of this data. Traditionally, the approach involved training a generic masked language model (MLM) and then adapting it to a specific domain or task, such as BERT models (Devlin et al., 2019).

However, the latest approaches aim to develop Large Language Models (LLMs) that can directly process a wide range of NLP tasks and domains. They can then handle tasks such as classification or entity extraction, as well as more complex generative tasks like machine translation or question-answering. While there is clear enthusiasm for LLMs among both scientists and the general public, the evaluation of these models, also known as foundation models, is still in its infancy. The initial evaluations demonstrate the usefulness of these models in performing various NLP tasks, including classification and generation tasks on general domains (Liu et al., 2023; Bang et al., 2023). However, in the medical field, these models have been evaluated to a lesser extent, often on a limited number of tasks (Rehana et al., 2023; Chen et al., 2023; Lamichhane, 2023; Singhal et al., 2022; Chowdhery et al., 2022). This is mainly due to the scarcity of tasks and data, particularly sensitive data that is difficult to obtain, compared to other fields.

To evaluate how well LLMs encode medical knowledge and to demonstrate their capabilities in specific domains, a wide range of tasks that closely resemble real-world applications and require appropriate medical knowledge and expert reasoning were considered. Unlike other studies (Fries et al., 2022; Jin et al., 2021) that have compared performances of these models using automatic metrics (BLUE (Papineni et al., 2002), ROUGE (Lin, 2004) or BertScore (Zhang et al., 2020)) or only accuracy on a small set of tasks, we decide to showcase their relevance in various evaluation contexts by using more commonly used metrics (Accuracy and F1) which are allowing a fair direct comparison with BERT based models. In overall, we curate a collection comprising 13 real-world medical tasks, including classification (CLS), question-answering (QA), relation extraction (RE), natural language inference (NLI) and named-entity recognition (NER). The main contributions of the paper are:

1. Evaluation of four state-of-the-art instruction-tuned models (ChatGPT, Flan-T5 UL2, Tk-Instruct, and Alpaca) on a broad range of medical tasks beyond those typically addressed by generative models.

2. Assessment of the ability of the studied language models to perform zero-shot and few-shot inference and comparison of their perfor-

mance on the tasks with that of a finetuned PubMedBERT model.

3. Introduction of a novel method that enables performing the NER task on all types of LLMs.

2 Related work

We first introduce the concept of Large Language Models (LLMs) and their limitations (Section 2.1). Next, we present the concept of instruction-tuning (Section 2.2). Finally, we describe our few-shot learning strategy with prompts (Section 2.3).

2.1 Large Language Models (LLMs)

While classical language models like BERT are efficient on various NLP tasks and trained on large amounts of unannotated textual data, they still require a substantial amount of annotated data to perform well on targeted tasks such as NER, NLI, and RE. These models also have difficulty generalizing their knowledge to other languages or domains once adapted to a particular task and context (Peng et al., 2021; Amalvy et al., 2022). Collecting such data for any scenario is then expensive, as it requires highly qualified annotators and raises privacy concerns.

Recently, LLMs have brought additional performance improvements, especially in generative tasks. These models are composed of billion of parameters and trained on gigantic amounts of data, from various natures, domains and languages (Gao et al., 2020; Raffel et al., 2020; Ortiz Suarez et al., 2019). Previous studies have demonstrated in particular that this gigantic number of parameters associated with this massive data allowed the fine modeling of the language, making it possible to achieve this level of performance (Zhang et al., 2022; Black et al., 2022; Hoffmann et al., 2022; Smith et al., 2022).

New approaches using these generative LLMs capabilities have aimed to align them with instructions (Ouyang et al., 2022) (see Section 2.2), giving them greater abilities to handle multiple NLP tasks in multiple languages in zero- or few-shot learning (Bang et al., 2023).

2.2 Instruction Tuning

Efrat and Levy (2020) and Mishra et al. (2022b) propose the instruction paradigm, in which models can learn new tasks based on natural language instructions only. These instructions are given as inputs to the models, describing how they should behave, what we expect from them, and on which information they can base their thinking on (see Appendix B.1). Wang et al. (2022b) introduced the first large-scale instruction benchmark called SUPER-NATURALINSTRUCTIONS, by collecting crowdsourced instructions based on an existing set of 1600+ NLP datasets and converting them into a uniform format. Sanh et al. (2022) and Wei et al. (2022a) further extend the adoption of instructions by suggesting instruction tuning, in which a LLM is trained on many natural language instructions with the aspiration that it will generalize to new, unseen instruction tasks. Chung et al. (2022b) advance instruction tuning by scaling the number of tasks, scaling the model size, and introducing the concept of chain-of-thought (Wei et al., 2022b), while Ouyang et al. (2022) propose a reinforcement learning approach for instruction tuning and human feedback.

2.3 Few-shot Learning with prompts

During inference, a few examples of the task are given to the model as conditioning, without updating its weights. These examples usually comprise an instruction, context, and desired completion (e.g., a premise, hypothesis, and corresponding label for the NLI task). The few-shot technique involves presenting the model with k examples of context and completion, followed by a final example of context, for which the model should provide the completion. The value of k typically ranges from 3 to 100, which depends on the number of examples that can fit within the model's context window (for instance, Flan-UL2 has a context window of 2,048 tokens). See Appendix A.1.2 for more details.

3 Experimental Protocol

In this section, we describe the models utilized and the datasets used to benchmark the various models.

3.1 Studied Models

Our evaluation involves four distinct generic LLMs (ChatGPT, Flan-UL2, Tk-Instruct and Alpaca) and a specific biomedical model (PubMedBERT) for comparison purposes.

Flan-T5 UL2 abbreviated to Flan-UL2, is an encoder-decoder model based on UL2 20B parameters model (Tay et al., 2023) and was finetuned using the Flan instruction tuning tasks collection (Chung et al., 2022b).

Tk-Instruct is based on the T5 encoder-decoder model (Raffel et al., 2020) and has been fine-tuned on the 1600+ NLP tasks from the SUPER-NATURALINSTRUCTIONS dataset (Wang et al., 2022b). In our study, we chose the 3B parameter setting, since our preliminary comparison with Flan-T5-XL (Chung et al., 2022a) using the 3B parameter setting showed that Tk-Instruct performed better on question answering tasks, which are considered the most discriminative.

ChatGPT is based on GPT 3.5 Turbo, finetuned on a set of private instructions and continuously improved by using reinforcement learning from human feedback (RLHF) techniques. Its weights are private and the model can only be accessed via a payable API. This highlights some privacy concerns about its usage in medical applications and cannot guarantee that the evaluated data has never been seen before.

Stanford Alpaca is based on LLaMA 7B parameters (Touvron et al., 2023) and relies on a dataset of 52K instructions automatically generated using OpenAI's text-davinci-003 model in the style of self-instruct (Wang et al., 2022a). Due to its based model and data, it is only meant for academic research purposes and non-commercial use.

PubMedBERT is a biomedical-specific BERT-based model with 110M parameters (Gu et al., 2021). It was trained entirely from scratch on the 3.1 billion words of the PubMed corpus. We chose it as our baseline for comparison with the zero- and few-shot performance of generative models.

3.2 Downstream evaluation tasks

We conducted an evaluation of the models' capabilities by covering the 13 different tasks presented in Table 1. The tasks were chosen to allow for a broad assessment in both clinical and biomedical domains, including tasks oriented for generative and classical model evaluation.

Task	Dataset	Eval	Metric	Reference
CLS	HoC	Test	F1	Baker et al. (2016)
	LitCovid	Test	F1	Chen et al. (2021)
	PubHealth	Test	Accuracy	Neema and Toni (2020)
	N2C2 2006 Smokers	Test	Accuracy	Uzuner et al. (2008)
QA	BioASQ 7b	Test	Accuracy	Tsatsaronis et al. (2015)
	MedMCQA	Dev	Accuracy	Pal et al. (2022)
	SciQ	Test	Accuracy	Welbl et al. (2017)
	Evidence Inference 2.0	Test	Accuracy	DeYoung et al. (2020)
RE	GAD	Test	Accuracy	Bravo et al. (2015)
NLI	SciTail	Test	Accuracy	Khot et al. (2018)
	MedNLI	Test	Accuracy	Shivade (2017)
NER	BC5CDR	Test	F1	Li et al. (2016)
	NCBI-disease	Test	F1	Dogan et al. (2014)

Table 1: List of evaluation tasks and their metrics.

3.3 Evaluation of generative outputs

The evaluation of generative models outputs is a difficult task due to their free text form, which does not necessarily fit into a predefined range of classes. On the contrary, we are dealing with a noisy output that may contain correct answers. To tackle this issue, we manually built parsing scripts for each task and model, according to their output style, in order to capture most of the answers and compute metrics comparable with our baseline (PubMedBERT).

3.4 Instruction format

As shown in previous studies (Wei et al., 2022b; Jung et al., 2022; Mishra et al., 2022a), using a prompt designed for each task and model has been proven to be effective. Therefore, we decided to construct the input instruction prompt by concatenating three elements: (1) an instruction that describes the overall task, the nature of the data, and what we expect from the model, (2) the input argument, which provides the core information for the task, and (3) the output space constraints, which guide the model during output generation. Finally, the output serves as a reference during few-shot strategy evaluation (see Appendix 6).

3.5 Few-shot examples using semantic retriever

In order to maximize few-shot performance compared to randomly sampled examples, we introduced an additional retrieval module based on Sentence-Transformers (Reimers and Gurevych, 2019). Its goal is to find the k most semantically similar examples from the training set. To achieve this, we first fill a vector space using sentence representations of each individual instruction prompt from the training set, obtained using a frozen Pub-MedBERT (Gu et al., 2021) model. Then, we calculate the cosine distance between the query of the current test instance and all the elements present in the vector space to fetch the k closest examples. In our case, we set the k value to 5.

3.6 Recursive Chain-of-Thought

We performed NER using two inference methods. The first one is based on the method introduced by Ye et al. (2023) and can only be applied using ChatGPT. It consists of giving the model a sequence of words separated by double vertical bars for word separation and single vertical bars for the separation between words and labels, as shown in Table A.1.1. For the second method, we intro-

Task	Dataset	ChatGPT		Flan-UL2		Tk-Instruct		Alpaca		PubMedBERT
		zero-shot	5-shot	zero-shot	5-shot	zero-shot	5-shot	zero-shot	5-shot	
CLS	HoC	62.24	38.34	56.36	54.86	50.77	25.48	1.21	38.78	**82.75**
	LitCovid	67.20	72.77	51.48	46.95	36.42	57.49	1.58	64.09	**90.60**
	PubHealth	63.20	66.29	72.46	50.53	53.70	66.04	52.80	55.64	**75.39**
	N2C2 2006 Smokers	68.26	34.61	22.12	42.31	16.35	37.50	10.57	31.73	60.58
QA	BioASQ 7b	89.24	92.03	90.97	91.64	88.09	86.36	79.05	79.82	73.39
	MedMCQA	48.91	56.37	41.05	43.34	33.85	33.18	24.91	29.50	38.15
	SciQ	90.10	93.50	87.00	88.40	55.30	47.00	24.90	36.80	74.20
	Evidence Inference 2.0	59.98	63.83	66.45	65.06	41.33	38.79	32.49	94.18	65.47
RE	GAD	47.75	52.25	49.81	53.37	48.88	57.87	51.12	57.68	**79.78**
NLI	SciTail	73.57	65.62	93.51	92.66	57.53	71.31	39.60	40.26	93.51
	MedNLI	NaN	NaN	77.00	79.18	33.19	34.81	33.47	34.45	83.76
NER	BC5CDR	92.12	93.12	68.26	83.32	84.54	83.23	82.11	84.07	**97.65**
	NCBI-disease	90.97	92.27	90.75	87.65	87.91	87.50	11.58	92.27	**98.72**

Table 2: 0- and 5-shot versus finetuning evaluation on clinical and biomedical tasks. Bold values are the highest scores obtained for the task and in underlined the seconds ones. Not allowed experiments are replaced by `NaN`.

duce a method called Recursive Chain-of-Thought (RCoT). It is very close to human reasoning and works for all the generative models we have tried. It is derived from the Chain-of-Thought (CoT) concept (Wei et al., 2022b) and the work of Wang et al. (2022b). It involves iterating over the sequence of tokens and giving the current state of the prediction as input to the model, asking for the generation of the label of the Nth token, as presented in Table A.1.2. This method guarantees an entity for each token of the sequence and prevents forgotten tokens during generation. However, the only drawback we have been able to identify with this method is its very high computation cost due to its $\mathcal{O}^N$ complexity, with N being the number of tokens in the sequence, compared to the method used for ChatGPT, which performs at $\mathcal{O}^1$ complexity.

4 Results and Discussions

Table 2 reports performance obtained by the studied LLMs in zero- and few-shot scenario, as well as PubMedBERT finetuned on each task. Results are reported by taking the best run out of four.

Zero-shot scenario Compared to PubMedBERT, the zero-shot scenario results show a clear deficit for the generative models on all the tasks except for QA, in which LLMs obtain better performance. ChatGPT and Flan-T5 UL2 are particularly more performant than Tk-Instruct and Alpaca on average, except for GAD dataset (RE task) for which Alpaca obtains the best performance. We can also observe extremely poor performance from Alpaca in zero-shot scenario on the two CLS tasks (HoC and Lit-Covid). These scores are owing to the model only producing hallucinations and the *evading growth suppressors* label for the whole test set of HoC. This behavior does not appear to take place in few-shot scenario, where the model seem to understand what we are expecting from it.

Few-shot capabilities Unlike the zero-shot scenario, the few-shot inference (5-shots in our experiments) shows impressive behavior. The biggest absolute gains are obtained using Alpaca, which seems to perform much better in few-shot scenarios on all tasks. We suspect this behavior to be correlated with Alpaca's training data, which does not contain many similar instructions for the tasks we are trying to tackle, allowing it to better understand what we are asking when confronted with similar examples. ChatGPT also benefits from the additional knowledge to further improve the already good results, especially on QA tasks. Flan-T5 UL2 appears to be less affected by the additional context overall, except for the BC5CDR and N2C2 2006 Smokers tasks.

5 Conclusion

In this study, we have demonstrated that generic LLMs are capable of capturing medical knowledge and performing exceptionally well in zero- and few-shot scenarios, despite having no prior exposure to the tasks. Although open-source models such as Flan-T5 UL2 are gradually approaching their closed-source counterparts, like ChatGPT, their performance still lags behind. We suggest that developing domain-specific models, finetuned on a diverse set of tasks and specialized instruction prompts, could help bridge the gap with more robust and performant proprietary models. We also note that domain-specific BERT models remain a viable option, but require a significant amount of data for finetuning on targeted languages and tasks. However, BERT-based models offer much lower computational costs compared to LLMs, which could be a significant obstacle to developing models in the healthcare domain.

5.1 Limitations

From all the experiments we have conducted, we discovered that LLMs trained from instructions are frequently sensitive to the particular words used for their input and impact whether or not it's capable to produce the correct outputs. This is perhaps unsurprising, given that LLMs are known to be very sensitive to the prompt they are provided with in both zero and few-shot settings (Jiang et al., 2020; Schick and Schütze, 2021). However, it often requires adapting the prompt to the models and tasks or event to map the classes to more effective ones. This behavior may be caused by the lack of variety in the instruction collections used for training them.

One of the main limitations is related to our inability to guarantee that the ChatGPT model has never seen the evaluation data during its training. This can strongly bias the results obtained. Similarly, Flan-T5 UL2 and Tk-Instruct has been trained on a wide range of tasks in which similar or identical data can be seen if overlap has not been identified. So, we cannot ensure that training data of some tasks has never been seen before.

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A Instructions examples

The following sections are giving example of prompts used for training and inference for organized by tasks.

A.1 Named-Entities Recognition

A.1.1 Method 1

Prompts

Instruction: Do named-entity recognition task for the given text using the categories in candidate list, output using the format as "Word1|Category||Word2|Category||Word3|Category"
Candidate list: *O*, *B-Disease* or *I-Disease*
Text: Identification|Category || of|Category || APC2|Category || ,|Category || a|Category || homologue|Category || of|Category || the|Category || adenomatous|Category || polyposis|Category || coli|Category || tumour|Category || suppressor|Category || .|Category
Output:

Instruction: You are a healthcare named-entity recognition expert system and we are giving you a sequence of words that you have to labelized using the following output format 'Word1|Label||Word2|Label||Word3|Label'
Labels: *O*, *B-Disease* or *I-Disease*
Unfilled sequence: Identification|Label||of|Label||APC2|Label||,|Label||a|Label||homologue|Label||of|Label ||the|Label ||adenomatous|Label||polyposis|Label||coli|Label||tumour|Label||suppressor|Label||.|Label
Constraints: The answer must be one and only one of the given labels.
Output:

Instruction: As a healthcare named-entity recognition expert, your job is to label a sequence of words provided to you using the following format: 'Word1|Label||Word2|Label||Word3|Label'. Your goal is to identify all the named entities in the given text. The available labels for this task are: *O*, *B-Disease* or *I-Disease*
Input: Identification|Label||of|Label||APC2|Label||,|Label||a|Label||homologue|Label||of|Label||the|Label ||adenomatous|Label ||polyposis|Label||coli|Label||tumour|Label||suppressor|Label||.|Label
Output:

Table 3: Sample of three instructions used for the named-entities recognition task with ChatGPT.

A.1.2 Method 2 - Recursive Chain-Of-Thought (RCoT)

Prompt

Instruction: You are a highly intelligent and accurate healthcare domain Named-entity recognition (NER) system. You are tasked to do Named-entity recognition (NER) for 'disease' and 'none' only, please generate the appropriate label.
Constraints: You can choose only one label from: *none* or *disease*.
Examples: //

Example 1 :   Mutations|none|| at|none|| the|none|| ataxia|disease|| -|disease|| telangiectasia|disease|| locus|none|| and|none|| clinical|none|| phenotypes|none|| of|none|| A|disease|| -|disease|| T|disease|| patients|none|| .|none

Example 2 :   Splicing|none|| defects|none|| in|none|| the|none|| ataxia|disease|| -|disease|| telangiectasia|disease|| gene|none|| ,|none|| ATM|none|| :|none|| underlying|none|| mutations|none|| and|none|| consequences|none|| .|none

Example 3 :   Somatic|none|| mutations|none|| in|none|| the|none|| BRCA1|none|| gene|none|| in|none|| sporadic|disease|| ovarian|disease|| tumours|disease|| .|none

Example 4 :   Malignant|disease|| neoplasms|disease|| in|none|| the|none|| families|none|| of|none|| patients|none|| with|none|| ataxia|disease|| -|disease|| telangiectasia|disease|| .|none

Example 5 :   Founder|none|| mutations|none|| in|none|| the|none|| BRCA1|none|| gene|none|| in|none|| Polish|none|| families|none|| with|none|| breast|disease|| -|disease|| ovarian|disease|| cancer|disease|| .|none

Considering the sentence : Clustering of missense mutations in the ataxia - telangiectasia gene in a sporadic T - cell leukaemia .

And considering your precedents predictions : Clustering|none|| of|none|| missense|none|| mutations|none|| in|none|| the|none|| ataxia|disease|| -|disease|| telangiectasia|disease|| gene|none|| in|none|| a|none|| sporadic|disease|| T|disease|| -|disease|| cell|disease|| leukaemia|Label

Input : The label of « leukaemia » at the position 17 of the sentence is ?
Output:

Table 4: Example of a 5-shot Recursive Chain-Of-Thought (RCoT) instruction used for the named-entities recognition task of NCBI Disease dataset.

B Multiple-choice question answering

B.1 Method 1 - One-shot

Prompt

Instruction: You are given a science question (easy level) and four answer options (associated with "A", "B", "C", "D"). Your task is to find the correct answer based on scientific facts, knowledge and reasoning. Don't generate anything other than one of the following characters: 'A B C D'.

Input: Heavy forces on periodontal ligament causes: (A) Hyalinization (B) Osteoclastic activity around tooth (C) Osteoblastic activity around tooth (D) Crest bone resorption

Constraints: The answer must be one or more of the following letters: 'A','B','C','D'. You must generate one and only one letter for each question. All questions have an answer. No justification is required.

Output:

Table 5: Example of a 0-shot instruction used for the Multiple-Choice Question Answering (MCQA) task of MedMCQA dataset.

B.2 Method 2 - Few-shot

In some cases, we mapped the original classes to more effective one's for each of the tasks, based on tries and errors (e.g: "entailment" has been map to "entails" for ChatGPT and Flan-T5 UL2 based on noticeable performances gains).

Prompt

Instruction: You are given a science question (easy level) and four answer options (associated with "A", "B", "C", "D"). Your task is to find the correct answer based on scientific facts, knowledge and reasoning. Don't generate anything other than one of the following characters: 'A B C D'.

Constraints: The answer must be one or more of the following letters: 'A','B','C','D'. You must generate one and only one letter for each question. All questions have an answer. No justification is required.

Examples:

Example 1: Hyalinisation of the periodontal Ligament, due to excessive orthodontic forces results in (A) Frontal resorption (B) Undermining resorption (C) Cementum remaining intact (D) Dentine remaining intact
Output: B

Example 2: The earliest response of pulpitis is: (A) Cyst formation (B) Calcification (C) Hyalinization (D) Formation of dental granuloma
Output: C

Example 3: Among the secondary changes in tooth the most useful one for age determination is: (A) Attrition (B) Secondary dentine deposition (C) Root resorption (D) Root transparency
Output: D

Example 4: Feature of aging periodontium is (A) Lacunae in bone and cementum (B) Increased cell size (C) Increased cell number (D) Scalloping of cementum & alveolar bone surface
Output: D

Example 5: Bacteria found in gingivitis are localized in (A) Connective tissue fibres (B) Gingival sulcus (C) Alveolar bone (D) Periodontal ligament
Output: B

Input: Heavy forces on periodontal ligament causes: (A) Hyalinization (B) Osteoclastic activity around tooth (C) Osteoblastic activity around tooth (D) Crest bone resorption
Output:

Table 6: Example of a 5-shot instruction used for the Multiple-Choice Question Answering (MCQA) task of MedMCQA dataset.

C Relation Extraction

C.1 Method 1 - One-shot

Prompt

Instruction: Your goal is to do relation extraction and identifying if a gene-disease relation exist (positive) or not (negative).

Input : These results suggest that the C1772T polymorphism in @GENE$ is not involved in progression or metastasis of @DISEASE$

Constraints: You have to output one label among « negative » or « positive ». Justification and explanations are prohibited.

Output:

Table 7: Example of a 0-shot instruction used for the Relation Extraction (RE) task of GAD dataset.

C.2 Method 2 - Few-shot

Prompt

Instruction: Your goal is to do relation extraction and identifying if a gene-disease relation exist (positive) or not (negative).

Constraints: You have to output one label among « negative » or « positive ». Justification and explanations are prohibited.

Examples:

Example 1: These findings suggest that the Gly460Trp polymorphism of @GENE$ is not associated with @DISEASE$.
Output: Positive

Example 2: Our results suggest that deletion polymorphism of the @GENE$ gene is not associated with the pathogenesis of @DISEASE$ in Taiwanese.
Output: Positive

Example 3: The results suggest that the 5A/6A polymorphism of @GENE$ gene may not be linked with appearance and/or progression of @DISEASE$.
Output: Positive

Example 4: Our study implies that the G/C polymorphism of the @GENE$ gene may not be directly involved in the development and=or progression of @DISEASE$.
Output: Positive

Example 5: Our study implies that the G/C polymorphism of the @GENE$ gene may not be directly involved in the development and=or @DISEASE$ of breast cancer.
Output: Negative

Input: These results suggest that the C1772T polymorphism in @GENE$ is not involved in progression or metastasis of @DISEASE$.
Output:

Table 8: Example of a 5-shot instruction used for the Relation Extraction (RE) task of GAD dataset.

D Natural Language Inference

D.1 Method 1 - One-shot

Prompt

Instruction: Your goal is to do solve a natural language inference task by identifying if the hypothesis is either « entails » or « neutral » to the premise.

Input premise: The liver is divided into the right lobe and left lobes.

Input hypothesis: The gallbladder is near the right lobe of the liver.

Constraints: You have to output one label among « entails » or « neutral ». Justification and explanations are prohibited.

Output:

Table 9: Example of a 0-shot instruction used for the Natural Language Inference (NLI) task of SciTail dataset.

D.2 Method 2 - Few-shot

Prompt

Instruction: Your goal is to do solve a natural language inference task by identifying if the hypothesis is either « entails » or « neutral » to the premise.

Constraints: You have to output one label among « entails » or « neutral ». Justification and explanations are prohibited.

Examples:

Example 1:
Premise: Located primarily on the right side of the abdominal cavity, just above the duodenum, the liver aids in the digestion of fats by secreting bile into the duodenum.
Hypothesis: Most digestion is completed in the duodenum.
Output: neutral

Example 2:
Premise: The brain is divided into the right and left hemisphere and each hemisphere is divided into 4 lobes called the frontal, temporal, occipital and parietal lobes.
Hypothesis: Each hemisphere of the cerebrum divided into 4 lobes.
Output: entails

Example 3:
Premise: The small intestine, where most digestion takes place, is a convoluted tube in the abdomen that begins at the pylorus of the stomach and ends at the opening to the large intestine.
Hypothesis: Most of the digestion reactions occur in the small intestine.
Output: entails

Example 4:
Premise: The small intestine is the long, thin segment of bowel that begins at the stomach and ends at the large intestine or colon.
Hypothesis: The small intestine begins in the stomach.
Output: entails

Example 5:
Premise: The small intestine begins at the stomach and ends at the colon (large intestine).
Hypothesis: The small intestine begins in the stomach.
Output: entails

Premise: The liver is divided into the right lobe and left lobes.
Hypothesis: The gallbladder is near the right lobe of the liver.
Output:

Table 10: Example of a 5-shot instruction used for the Natural Language Inference (NLI) task of SciTail dataset.

E Classification

E.1 Method 1 - One-shot

Prompt

Instruction: Your goal is to do solve a classification task by identifying if one or more of the following hallmarks of cancer are present in the document: « evading growth suppressors », « tumor promoting inflammation », « enabling replicative immortality », « cellular energetics », « resisting cell death », « activating invasion and metastasis », « genomic instability and mutation », « none », « inducing angiogenesis », « sustaining proliferative signaling » or « avoiding immune destruction ».

Input: Cytotoxicity was shown in manganese-treated groups (100 , 200 , 400 , and 800microM of MnCl(2)) , and cell viability was decreased to 58.8% of the control group at 2days after treatment with 800microM of MnCl(2) .

Constraints: You have to output one or more label(s) among « evading growth suppressors », « tumor promoting inflammation », « enabling replicative immortality », « cellular energetics », « resisting cell death », « activating invasion and metastasis », « genomic instability and mutation », « none », « inducing angiogenesis », « sustaining proliferative signaling » or « avoiding immune destruction ». Justification and explanations are prohibited.
Output:

Table 11: Example of a 0-shot instruction used for the classification (CLS) task of HoC dataset.

E.2 Method 2 - Few-shot

Prompt

Instruction: Your goal is to do solve a classification task by identifying if one or more of the following hallmarks of cancer are present in the document: « evading growth suppressors », « tumor promoting inflammation », « enabling replicative immortality », « cellular energetics », « resisting cell death », « activating invasion and metastasis », « genomic instability and mutation », « none », « inducing angiogenesis », « sustaining proliferative signaling » or « avoiding immune destruction ».

Constraints: You have to output one or more label(s) among « evading growth suppressors », « tumor promoting inflammation », « enabling replicative immortality », « cellular energetics », « resisting cell death », « activating invasion and metastasis », « genomic instability and mutation », « none », « inducing angiogenesis », « sustaining proliferative signaling » or « avoiding immune destruction ». Justification and explanations are prohibited.

Examples:

Example 1: However , significant cytotoxicity was only observed in PCB 52 concentrations larger than 0.1 microg ml(-1) , while there was no significant inhibition in PCB 77-treated cells at concentrations selected .
Output: none

Example 2: In MeT-5A cells , both CNTs caused a dose-dependent induction of DNA damage (% DNA in comet tail) in the 48-h treatment and SWCNTs additionally in the 24-h treatment , with a statistically significant increase at 40
u03bcg/cm(2) of SWCNTs and (after 48 h) 80
u03bcg/cm(2) of both CNTs .
Output: none

Example 3: Copper-induced DNA strand breakage was first observed after 24 h of exposure , and was recorded again at 96 h , at a copper concentration of 20 microg l(-1) .
Output: genomic instability and mutation

Example 4: Drug concentrations of 12.5 to 300 Ŏ3bcM caused a pronounced reduction in cell survival rates five days after treatment , whereas concentrations higher than 25 Ŏ3bcM were effective in reducing the survival rates to However , the maximum apoptosis frequency was 20.4% for 25 Ŏ3bcM cisplatin in cells analyzed at 72 h , indicating that apoptosis is not the only kind of cell death induced by cisplatin .
Output: none

Example 5: In contrast , in MCF 7 cells , molecular iodine (100 microM) inhibited growth from 100% to 83% but delta-iodolactone (1 , 5 and 10 microM) dose-dependently decreased growth rate from 100% to 82% and 62% , respectively
.
Output: none

Input: Cytotoxicity was shown in manganese-treated groups (100 , 200 , 400 , and 800microM of MnCl(2)) , and cell viability was decreased to 58.8% of the control group at 2days after treatment with 800microM of MnCl(2) .
Output:

Table 12: Example of a few-shot instruction used for the classification (CLS) task of HoC dataset.

F Semantic Textual Similarity

F.1 Method 1 - One-shot

Prompt

Instruction: Give me a similarity score beetween 0 et 5 and only the similarity score.

Input: The original sentence is : "- Eviter le contact de l'embout avec l'œil ou les paupières." can you tell me if the sentence is similar to : "Evitez le contact de l'embout du flacon avec l'œil ou les paupières.".

Output:

Table 13: Example of a 0-shot instruction used for the Semantic Textual Similarity (STS) task of DEFT-2020 task 1 dataset.