Large Language Models are Few-Shot Clinical Information Extractors

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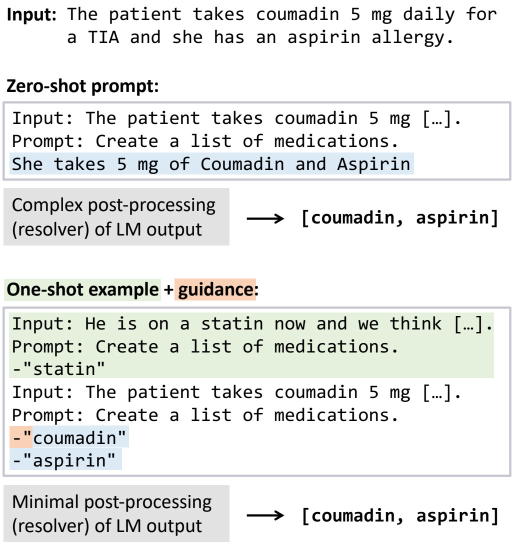
Abstract

A long-running goal of the clinical NLP community is the extraction of important variables trapped in clinical notes. However, roadblocks have included dataset shift from the general domain and a lack of public clinical corpora and annotations. In this work, we show that *large language models*, such as InstructGPT (Ouyang et al., 2022), perform well at zero- and few-shot information extraction from clinical text despite not being trained specifically for the clinical domain. Whereas text classification and generation performance have already been studied extensively in such models, here we additionally demonstrate how to leverage them to tackle a diverse set of NLP tasks which require more structured outputs, including span identification, token-level sequence classification, and relation extraction. Further, due to the dearth of available data to evaluate these systems, we introduce new datasets for benchmarking few-shot clinical information extraction based on a manual re-annotation of the CASI dataset (Moon et al., 2014) for new tasks[1]. On the clinical extraction tasks we studied, the GPT-3 systems significantly outperform existing zero- and few-shot baselines.


Input:
Zero-shot prompt:
Complex post-processing (resolver) of LM output
One-shot example + guidance:
Minimal post-processing (resolver) of LM output

```
Input: The patient takes coumadin 5 mg daily for
       a TIA and she has an aspirin allergy.
```

Zero-shot prompt:

```
Input: The patient takes coumadin 5 mg […].
Prompt: Create a list of medications.
She takes 5 mg of Coumadin and Aspirin
```

→ [coumadin, aspirin]

One-shot example + guidance:

```
Input: He is on a statin now and we think […].
Prompt: Create a list of medications.
-"statin"
Input: The patient takes coumadin 5 mg […].
Prompt: Create a list of medications.
-"coumadin"
-"aspirin"
```

→ [coumadin, aspirin]

Figure 1: Illustration of our approach using a one-shot example (green) and guidance (brown) to create a more structured LM output (blue). This significantly reduces the necessary post-processing effort of a resolver (gray).

1 Introduction

Clinical text contains a large amount of valuable information that is not captured by the structured data fields in electronic health records (Zweigenbaum et al., 2007; Wang et al., 2018). However, there are significant challenges to *clinical information extraction*. Because clinical text contains irregularities such as ambiguous jargon and nonstandard phrasal structure, most off-the-shelf NLP tools perform poorly, and clinical text annotation requires domain expertise (Zheng et al., 2011). Further, due to the sensitive nature of clinical text, public corpora are rare and restrictively licensed. As a result, clinical NLP datasets tend to be small and splintered across institutions (Xia and Yetisgen-Yildiz, 2012). To overcome these issues, practitioners often incorporate task-specific domain knowledge and regular expressions, even in modern deep learning pipelines, but these solutions can be brittle (Luo et al., 2020; Skreta et al., 2021; Chapman et al., 2001; Irvin et al., 2019; Johnson et al., 2019; Chauhan et al., 2020). Modern systems that do not use some combination of these elements are generally limited to areas where labels are generated as a byproduct of normal clinical practice, such as ICD code prediction (Zhang et al., 2020) and mortality prediction (Si and Roberts, 2019).

In this work, we benchmark how large language models (LLMs) such as GPT-3 (Brown et al., 2020; Ouyang et al., 2022) perform at clinical NLP tasks. This takes the form of three contributions:

- We introduce *three new annotated datasets* for benchmarking few-shot clinical information extraction methods, as many shared clinical corpora

[1] https://huggingface.co/datasets/mitclinicalml/clinical-ie

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Task	Description	Example Text	Answer	Data
Clinical sense disambiguation	Given a note and an abbreviation, expand the abbreviation (classification)	*[...] was sent to IR for thrombolysis. Post IR, ultrasound showed that [...]*	Interventional radiology	41 acronyms from 18,164 notes from CASI (Moon et al., 2014) and 8912 notes from MIMIC (Adams et al., 2020)
Biomedical evidence extraction	Given an abstract, list interventions (multi-span identification/generation)	*[...] paliperidone extended- release tablets and [...] with risperidone [...]*	-paliperidone extended-release tablets -risperidone	187 abstracts (token-level) and 20 newly annotated abstracts (arm identification) from EBM-NLP (Nye et al., 2018)
Coreference resolution	Given a note and a pronoun, identify the antecedent (span identification)	*[...] Did develop some tremors, however. These were well managed [...]*	some tremors	105 newly annotated examples from CASI (Moon et al., 2014) with one pronoun-antecedent pair each
Medication status extraction	Given a note, extract medications and their status, e.g. active (NER + classification)	*[...] have recommended Citrucel [...] discontinue the Colace. [...]*	-Citrucel: *active* -Colace: *discontinued*	105 newly annotated examples from CASI (Moon et al., 2014) with 340 medication-status pairs
Medication attribute extraction	Given a note, extract medications and 5 attributes, e.g. dosage, reason (NER + relation extraction)	*[...] she was taking 325 mg of aspirin per day for three years for a TIA. [...]*	aspirin: {dose: 325 mg, freq: per day, duration: three years, reason: TIA}	105 newly annotated examples from CASI (Moon et al., 2014) with 313 medications and 533 attributes

Table 1: Overview of the five tasks studied in this work and the datasets that were used.

(Murphy et al., 2010; Henry et al., 2020; Johnson et al., 2016) have data use agreements that prevent their use with LLM APIs such as OpenAI's. The datasets were generated by re-annotating the dataset from Moon et al. (2014) for new tasks.

- We show that GPT-3 performs well in clinical NLP over a set of diverse tasks (see Table 1), despite not being trained specifically for the domain. By replacing the complex hand-curated domain knowledge with the natural-language output of an LLM, the engineering effort required to solve a particular extraction task can be greatly reduced.
- While LLMs have been primarily evaluated at classification and generation tasks, our tasks involve a greater variety of expected output structures, such as relation extraction (see last three rows of Table 1). We therefore introduce *guided prompt design* to steer the LLM towards an easy-to-structure output and *resolvers* to map from the LLM outputs to the structured label space; see Figure 1.

2 Related Work

2.1 Prompt-Based Learning

In prompt-based learning (also known as in-context learning), a pretrained language model is adapted to different tasks via priming on natural language prompts—pieces of text that are combined with an input and then fed to the language model to produce an output for that task.

This paradigm has been successful for few-shot and zero-shot learning at many general-domain tasks (Brown et al., 2020; Liu et al., 2021; Wei et al., 2021; Sanh et al., 2021). More recently, large language models such as T0 and InstructGPT have re-configured their training objectives to explicitly encourage the model to perform well at such prompts (Sanh et al., 2021; Ouyang et al., 2022).

While prompt-based learning can be extended straightforwardly to classification tasks (e.g., multiple choice), more complex tasks require creativity in their implementation (Mishra et al., 2021). For example, coreference resolution is often re-framed as classification, asking which of two antecedents a pronoun refers to (Sanh et al., 2021) or whether a candidate antecedent is correct (Yang et al., 2022). This approach requires a list of antecedent candidates, which requires an additional component (e.g. a noun phrase generator) or many—potentially expensive—queries. Span classification and named entity recognition have been similarly reframed. For example, given a candidate entity X and full model access, the entity type can be predicted via an argmax over the possible types Y of the probability of statements like "X is a Y entity" (Cui et al., 2021). Alternatively, if only a single entity is being queried for a given input, prompting can be as simple as "What is the location"(Liu et al., 2022a); however, clinical NLP often concerns itself with extraction of multiple concepts. To extract multiple spans simultaneously, Li et al. (2019b) and Li et al. (2019a) use techniques from machine reading comprehension, relying on access to the underlying model and labeled data for training the extraction layer. While InstructGPT (Ouyang et al., 2022) has $\sim 2\%$ or $\leq 1k$ extraction examples in its training, the LLM output is never converted to a structured form, and extraction examples are only evaluated qualitatively for improvement over other models. That is, only results for classification and generation tasks are quantified.

2.2 Pretrained LMs for Clinical NLP

Clinical text differs significantly from text typically utilized in general NLP, both in syntax and vocabulary (Wu et al., 2020). As a result, the clinical NLP subcommunity often trains domain-specific models on clinical corpora following advances in language modeling from the broader NLP community. For example, clinical neural word embeddings were trained following word2vec (Mikolov et al., 2013; Wu et al., 2015; Roberts, 2016). More recently, following BERT, many clinical and biomedical variations swiftly followed including ClinicalBERT, SciBERT, BioBERT, and PubMedBERT (Devlin et al., 2018; Alsentzer et al., 2019; Ammar et al., 2018; Lee et al., 2020; Gu et al., 2021). However, in several applications, researchers observed the performance gains to be marginal to none over classical methods such as logistic regression (Chen et al., 2020; Krishna et al., 2021). Additionally, previous work has so far been unable to achieve competitive results on *biomedical* NLP tasks using domain-agnostic LLMs like GPT-3 (Moradi et al., 2021; Gutiérrez et al., 2022).

3 Methods

3.1 Predicting Structured Outputs with LLMs

In this work, we assume only query access to a large language model (i.e., no gradients, no log probabilities).

Suppose we have a set of n examples $(\{x_i, a_i\})_{i=1}^n$, where x_i is the input text as a string, a_i is (optional) side information as a string (e.g., which acronym to disambiguate). The outputs $y_i \in \mathbb{O}$ are unobserved (i.e., to be predicted). The output space $\mathbb{O}$ is defined per task. For example, for a binary sequence labeling task, if we let $|x_i|$ be the number of tokens in x_i, $\mathbb{O}$ is $\{0, 1\}^{|x_i|}$.

Prompt-based learning requires the specification of a prompt template to be applied on the input. In this work, we handcraft our prompt templates using a set of 5 validation examples per task. Let $p_j(x, a)$ be the result of filling prompt template j with inputs x and a, and further let $f(p_j(x, a)) \in \Sigma^\star$ be the string output by an LLM on input $p_j(x, a)$. The next step involves mapping the LLM generation from $\Sigma^\star$ to the structured label space $\mathbb{O}$. For example, in classification, the *verbalizer* defines a mapping between the LLM output space $\Sigma^\star$ and the discrete set of labels $\mathbb{O} = \{1, \ldots, L\}$ using a dictionary of token/label pairs (Schick and Schütze, 2021). However, for our structured tasks of interest, the label space $\mathbb{O}$ is more complex, and more complicated functions are needed to map to an element of $\mathbb{O}$. We define the *resolver* R as a function $R(x, a, f(p_1(x, a)))$ that maps the combined input and LLM output to the task-specific output space $\mathbb{O}$. For example, suppose the output space $\mathbb{O}$ is a *list* of strings. Then the resolver needs to turn each output $f(p_j(x, a))$ into a list (perhaps by choosing spans of text from inside of $f(p_j(x, a))$). For example, for medication extraction we might have:

$$
\begin{aligned}
&x = \textit{“switched Advil for Tylenol”}, a = \textit{“N/A”},\\
&p_1(x, a) = \textit{“Note: switched Advil for Tylenol.”}\\
&\qquad\qquad\quad \textit{Task: List medications.”}\\
&f(p_1(x, a)) = \textit{“Tylenol and Advil”}\\
&R(x, a, f(p_1(x, a))) = [\texttt{“Tylenol”}, \texttt{“Advil”}]
\end{aligned}
$$

We refer to the output from the resolver as Resolved GPT-3, or **GPT-3 + R**, for short. Throughout, when comparing resolvers, we place in parentheses the lines of code (LOC) in the resolver, as a proxy for complexity (defined as human effort, not runtime). The required complexity of the resolver depends largely on the cleanliness of the prompt output, and by extension the prompt itself. We introduce *guided prompt design* to simplify the resolver required for complex output. As seen in Figure 1, this consists of (i) a one-shot example with an output in the desired structured format (which could be incorrect content-wise), and (ii) guiding the model to use the same format. Specific constructions are found in Sections 6 and 7.

3.2 Dataset Annotation

In the short-term, research on clinical extraction via prompting may rely on sending data to external APIs. Since data use agreements on many existing annotated clinical datasets prohibit such activity, there is a dearth of benchmarks for the community to build on. The de-identified Clinical Acronym Sense Inventory (CASI) dataset is therefore a valuable resource, as it is “publicly available to support the research of the greater NLP and biomedical and health informatics community" (Moon et al., 2014). CASI contains snippets of clinical notes across specialties in four University of Minnesota-affiliated hospitals. While CASI was originally annotated for acronym disambiguation, we created three new annotated datasets from existing snippets of the CASI dataset. Annotation was performed by two of the authors who have background in both clinical NLP and medicine. For each task, a set of examples was jointly annotated to establish an annotation schema, each annotator then independently labeled the same set of 105 examples using PRAnCER software (Levy et al., 2021), and the two sets were then merged via joint manual adjudication.

In the following sections, we show how to build simple resolvers for five clinical NLP tasks. We find that resolvers for guided prompts are much easier to write than resolvers for un-guided prompts. The implicit structured imposed by the prompt guidance means that resolvers for a guided prompt can be less than 10 LOC. On the tasks below, we find that GPT-3 + R matches or exceeds strong few-shot, zero-shot, and even supervised baselines.

4 Clinical Sense Disambiguation

Overview. Clinical notes are rife with overloaded jargon and abbreviations. `Pt` can mean patient, prothrombin time, physical therapy, or posterior tibial (Weeber et al., 2001; Shilo and Shilo, 2018). This ambiguity impacts the utility of notes for patients, clinicians, and algorithms (Kuhn, 2007; Mowery et al., 2016). In this section, we first evaluate clinical sense disambiguation on the CASI dataset directly and then transfer a model distilled via weak supervision to another dataset.

Dataset 1. The Clinical Acronym Sense Inventory dataset consists of 500 text examples for each of 75 acronyms (Moon et al., 2014). Due to noise in the dataset (e.g. duplications), it is common to filter to a subset of the dataset; we follow the filtering from Adams et al. (2020), leading to a subset of 18,164 examples and 41 acronyms for evaluation. Similar to other works, we treat the task as multiple-choice.

Dataset 2. We additionally use a reverse substitution dataset (Adams et al., 2020) generated over the MIMIC-III Critical Care Database (Johnson et al., 2016). In *reverse substitution*, labeled data is generated from unlabeled text by replacing expansions (e.g. *physical therapy*) with their acronyms (*PT*) and using the original expansion as the label. We evaluate on their 8912 test examples over the same 41 acronyms as the CASI subset. Since we cannot query *GPT-3* on this dataset, we distill and transfer a model trained on the outputs from Dataset 1.

Prompting + Resolver. We used *GPT-3 edit* (using engine *text-davinci-edit-001*) with greedy decoding (temperature = 0). For each example, we provided the full clinical snippet and appended the single instruction `Expand the abbreviation:{abbr}`. Since we did *not* provide the LLM with the answer choices, the form of the output string could still differ slightly from all the candidate answers (e.g. editing "RA" to "right atria" when "right atrium" was expected). In the resolver, we choose the answer choice with the highest contiguous character overlap with the LLM generated output.

Model Distillation via Weak Supervision. Direct deployment of large language models can be difficult due to model size and data privacy. To remedy these issues, we follow several recent works (Lang et al., 2022a; Smith et al., 2022; Wang et al., 2021) and show that we can instead view the LLM + resolver system as a *labeler* rather than as a *classifier*, and that this can even boost performance. In particular, we use outputs of this system on CASI as weak supervision (e.g., Ratner et al., 2017) to train a smaller, task-specific model. Here we fine-tune PubMedBERT (Gu et al., 2021) and follow Lang et al. (2022a); details and hyperparameters are found in the appendix.

Baselines. We compare the performance of our approach to other zero-shot language modeling methods: (i) Latent Meaning Cells (LMC), a deep latent variable model from Adams et al. (2020) which is pre-trained on millions of notes from MIMIC, (ii) ELMo pre-trained on the same dataset (Peters et al., 2018), and (iii) Clinical BioBERT (Alsentzer et al., 2019). Numbers for these three baselines are taken from Adams et al. (2020); for all three, they choose the answer choice with the most similar representation to the contextual representation of the acronym. We also show performance for random guessing and choosing the most common answer choice per acronym (since the expansions of many acronyms follow a long-tailed distribution).

Evaluation. Accuracy and macro F1 are calculated per acronym and averaged over all acronyms (see left of Table 2). On CASI, GPT-3 edit + R alone already clearly outperforms the LMC model on both metrics, and the addition of weak supervision with PubMedBERT further boosts this performance. On the MIMIC Reverse Substitution dataset, despite

Algorithm	CASI Acc.	CASI Macro F1	MIMIC Accuracy	MIMIC Macro F1
Random	0.31	0.23	0.32	0.28
Most Common	0.79	0.28	0.51	0.23
BERT (from Adams et al. (2020))	0.42	0.23	0.40	0.33
ELMo (from Adams et al. (2020))	0.55	0.38	0.58	0.53
LMC (from Adams et al. (2020))	0.71	0.51	0.74	**0.69**
GPT-3 edit + R: 0-shot	0.86	0.69	*	*
GPT-3 edit + R: 0-shot + distillation	**0.90**	**0.76**	**0.78**	**0.69**

Table 2: **Clinical sense disambiguation.** Accuracy and macro F1 for zero-shot language modeling approaches on a subset of the Clinical Acronym Sense Inventory (CASI) data set (Moon et al., 2014) and the MIMIC Reverse substitution dataset (Adams et al., 2020). GPT-3 is not run on MIMIC due to the data use agreement. To evaluate on MIMIC we distill GPT-3 + R into a smaller model by treating the outputs as weak supervision and following Lang et al. (2022b) "+ distillation", then evaluate the smaller model on MIMIC as well.

being transferred to a new domain, our weakly-supervised PubMedBERT model performs similarly to LMC (Adams et al., 2020), which was pre-trained specifically on the MIMIC distribution. This indicates we can use GPT-3 edit + R to label a public dataset, distill its labels into a smaller task-specific model, and then transfer that model to a private dataset to obtain competitive performance. Since the CASI dataset is publicly accessible, one possible caveat is that the dataset could have been in the language model's training data; to investigate further (see Section C.1), we prompt the LLM on acronyms *not in the original annotations*.

5 Biomedical Evidence Extraction

Task Overview. Evidence-based medicine (EBM) involves synthesizing findings from across clinical research studies, but the current rapid clip of research makes it nearly impossible to keep up with all studies (Sackett, 1997; Bastian et al., 2010). Therefore, automated approaches for parsing clinical abstracts could aid the adoption of EBM (Verbeke et al., 2012; Nye et al., 2018). Here, we focus on extracting interventions and controls (which we will refer to just as Intervention), where the underlying goal is to identify the distinct arms of a clinical trial (Nye et al., 2018). Token-level classification is often used as a proxy for this goal, but distilling identified spans into distinct interventions is non-trivial and often requires significant domain knowledge. Prior work on arm identification has attempted to use coreference resolution (Ferracane et al., 2016) and to identify of pairs of spans with redundant information (Nye et al., 2018).

Dataset. We assess intervention identification from the angles of (i) the token classification proxy task and (ii) the underlying task of arm identification. For (i), we use the token-level annotations provided in version 2 of the dataset from Nye et al. (2018) and evaluate on the 187 test abstracts provided. The average Cohen's κ was only 0.59 on this set. For (ii), the two annotators from Section 3.2 manually derived a list of the intervention-control arms for 20 abstracts in the test set, with perfect agreement.

Prompting + Resolvers. We use a single prompt with InstructGPT (engine *text-davinci-002*) and greedy decoding. The resolver for the token-labeling task removes noisy tokens (stop words) from the LLM output, maps remaining tokens in the output to the original input and labels those as 1, and merges fractured spans. The full process can be found in Appendix C.2. For the arm identification task, resolving simply involved splitting the output string on new lines.

Comparison. We compare to supervised approaches that train on the 4800 labeled training examples from Nye et al. (2018). PubMedBERT with an additional classification layer (LSTM or CRF) achieves close to state-of-the-art performance on the full task (Gu et al., 2021). Since prior works report numbers combined over multiple classes, we re-run training on only the Intervention label using PubMedBERT-CRF. We also include the best supervised baseline from Nye et al. (2018), an LSTM-CRF over word and character-level embeddings.

Token-level results (Proxy Task). We first evaluate sequence labeling precision at the token-level (F1 in Table 3). Resolved GPT-3 performs respectably compared to supervised deep baselines, but underperforms on these token-level metrics. Many error modes occur due to particularities of the schema, e.g. including extra details (like dosing schedule or route of administration) and only in-

Algorithm	Token-level F1	Abstract-level Accuracy
PubMedBERT-CRF (sup)	**0.69**	0.35
LSTM-CRF (sup)	0.65	*
GPT-3 + R: 0-shot	0.61	**0.85**

Table 3: **Biomedical Evidence Extraction**. Test F1 scores on the binary token-level sequence labeling problem for Intervention identification (Nye et al., 2018), and abstract-level accuracy at arm identification. The supervised baselines were trained on 4,800 abstracts.

cluding an acronym or its expansion, but not both. A clarifying example can be found in Section C.2.

Arm Identification Results. To measure arm identification accuracy, we evaluated whether the number of arms was accurate and manually checked whether the main differentiator of each intervention arm was captured, similar to Ferracane et al. (2016). For the PubMedBERT baseline, in order to distill the identified spans to a list of arms, we assume (i) oracle splitting of spans into arms (given a span describing multiple arms, we can correctly split the span) and (ii) near-oracle coreference resolution (given multiple spans describing the same arm, we can correctly merge). Resolved GPT-3 successfully identified the correct number and content of the arms in 17 of the 20 examples. The three examples it missed were also missed by PubMedBERT. Assuming oracle splitting and coreference (a nontrivial task), PubMedBERT would still have issues with 10 further examples. Details of the evaluation and error modes are in Section C.2.

6 Coreference Resolution

Task Overview. Coreference resolution involves grouping noun phrases that refer to the same underlying entity (e.g. a person, a medical concept), and it is considered particularly important for clinically accurate information retrieval and summarization (Zheng et al., 2011). For example, when surfacing past medical history, it is critical to correctly parse pronouns to understand whether the history describes the patient or a family member.

Dataset Description. In clinical NLP, coreference resolution has been largely evaluated on the 2011 i2b2/VA challenge, which consists of thousands of coreference *chains* (Uzuner et al., 2012). Due to i2b2's data use agreement, the two annotators annotated a new dataset using CASI snippets, with 5 coreference pairs for prompt design and 100 pairs for evaluation (Moon et al., 2014). We prioritized difficult examples by focusing on pronoun coreference, where the input is a pronoun, the output its antecedent, and no tokens overlap between the two. More details are in Section B.2.

Algorithm	Recall	Precision
Toshniwal et al. (2020, 2021)	0.73	0.60
GPT-3 + R (50 LOC): 0-shot	**0.78**	0.58
GPT-3 + R (1 LOC): 1-shot (incorrect)	$0.76_{.02}$	$\mathbf{0.78}_{.04}$
GPT-3 + R (1 LOC): 1-shot (correct)	$0.75_{.04}$	$0.77_{.04}$

Table 4: **Coreference Resolution**. Macro unigram recall and unigram precision of methods on our newly annotated task using CASI (Moon et al., 2014). The end-to-end baseline was trained on three non-clinical coreference resolution datasets and transferred to this new setting. 1-shot results are averaged over 5 prompts.

Prompting and Resolvers. We used the 5 examples for prompt design with InstructGPT (engine *text-davinci-002*) and greedy decoding (temperature = 0). We use a guided 1-shot prompt, where we provide an example input and begin a formatted response: "{pronoun} refers to". For 1-shot, we experiment with both correct (the true noun phrase) and incorrect answers (a random incorrect noun phrase preceding the pronoun) in the example input to tease apart the effect of the example answer versus the example formatting. To clarify that effect, we average over results from 5 different 1-shot examples. We also compare to an *unguided* zero-shot prompt, which simply appends "What does {pronoun} ... refer to?" to the input. The zero-shot resolver involves mapping tokens back to the input due to potential paraphrases; the one-shot resolver involves only the removal of a single quotation mark, making the guided prompt easier to resolve. Section A.3 contains more detail on the prompts.

Comparison. We compare to deep end-to-end coreference resolution, as it has been shown to perform well (Lee et al., 2017). In particular, we compare to the *longdoc* model from (Toshniwal et al., 2020), which trained on multiple coreference datasets in order to generalize to new settings.

Results. We evaluated via macro unigram recall (% of label's unigrams in the resolved output) and unigram precision (% of unigrams in the resolved output in the label) (Table 4). We tokenized using Stanza (Qi et al., 2020) for these metrics. While the *longdoc* baseline trained on thousands of non-clinical coreference examples performed considerably well already, it is outperformed by Resolved GPT-3. We found the 1-shot example mostly con-

Algorithm	Recall	Precision
ScispaCy (Neumann et al., 2019)	0.73	0.67
GPT-3 + R (32 LOC) (0-Shot)	0.87	0.83
GPT-3 + R (8 LOC) (1-Shot)	$\mathbf{0.90}_{.01}$	$\mathbf{0.92}_{.01}$

Table 5: **Medication extraction.** Micro recall and precision for medication extraction on our self-annotated dataset.

Algorithm	Conditional Accuracy	Conditional Macro F1
T-Few (20-shot)	0.86	0.57
GPT-3 + R (32 LOC) (0-Shot)	0.85	0.69
GPT-3 + R (8 LOC) (1-shot)	$\mathbf{0.89}_{.01}$	$0.62_{.04}$
GPT-3 + R (8 LOC) (1-shot) + added classes	$0.88_{.02}$	$\mathbf{0.71}_{.03}$
GPT-3 + R (8 LOC) (1-shot) with shuffled classes	$0.88_{.01}$	$0.66_{.03}$

Table 6: **Medication status classification.** Conditional accuracy and macro F1-score for Identification of medication status *active*, *discontinued*, and *neither*.

strains the LLM output to quoting (rather than paraphrasing); without guidance, the LLM may output e.g., “The antecedent is unclear." Further, the accuracy of the 1-shot example was irrelevant to the performance, an observation previously reported in the classification setting, now seen for span extraction (Min et al., 2022).

7 Medication Extraction

The recognition of clinical concept mentions (problems, treatments, etc.), their modifiers (e.g., negation), and relations (e.g., dosage) is a fundamental building block in clinical NLP (Jiang et al., 2011). Here we examine the extraction of medication concepts with two different schemas.

7.1 Recognition + Status Classification

Here we extract a list of medications and label each with a status modifier: active, discontinued, or neither (e.g. allergy or proposed medication).

Dataset description. We created new annotations for medication and status on top of CASI Moon et al. (2014). The examples were enriched for changeover in treatment. For 105 randomly selected snippets, the annotators extracted all medications mentioned and classified its status with one of the 3 labels. Further details are in Appendix B.3. Unlike in Section 7.2, all mentions corresponding to the same medication are collapsed.

Prompting and Resolver. We again used 5 examples for prompt design with InstructGPT (engine *text-davinci-002*) and greedy decoding. Our prompt asked the model to simultaneously output the list of medications and the status of each. We evaluate the prompt in an unguided zero-shot manner and in a guided one-shot manner. Further, to clarify the effect of the 1-shot example on modifier accuracy, we examine how status classification performance changes if we (i) artificially augment the 1-shot example so all three status classes are observed, and (ii) whether the statuses need to be correct, or just present. We averaged over 5 different 1-shot inputs to clarify these effects; each 1-shot example contained between 3 and 8 medications. We describe the resolvers for the zero- and one-shot cases in detail in Section C.4; the former involved several regular expressions, and the latter required only a few short lines.

Comparison. We used a rule-based method as a medication extraction baseline, since historically they perform well (Sohn et al., 2014). To this end, we leveraged the Python library ScispaCy with the `en_core_sci_sm` package for entity recognition (Neumann et al., 2019, details in Appendix C.4).[2] For medication status classification, we compare to `T-Few` (Liu et al., 2022b), a few shot LLM method fine-tuned on a set of additional snippets we labeled from the same distribution (20 snippets containing 60 medication statuses). This method predicts the status, *given the token indices for each medication.*

Results. Table 5 shows micro recall and precision for medication extraction; we count a prediction as correct if the predicted string exactly matches one. Overall, Resolved GPT-3 outperforms the ScispaCy linkage baseline consistently by a considerable margin. The addition of the 1-shot example greatly improves precision, since in the 0-shot case, some GPT-3 outputs included extraneous extractions (e.g. a procedure). Typical failure modes of the baseline include incorrect recognition of overloaded abbreviations and missing vendor-specific drug names. Table 6 shows *conditional* accuracy on medication status classification. For an apples-to-apples comparison, we conditioned on the subset of medications found by all GPT-3 methods (241/340) and evaluated T-few on that subset as well. We find that if the rarer *Neither* class wasn’t demonstrated

[2] We do not use a supervised baseline trained on the i2b2 2009 challenge data (as in Section 7.2) because their schema purposefully excluded medications in the *Neither* category.

Subtask	Algorithm	Medication	Dosage	Route	Frequency	Reason	Duration
Token-level	PubMedBERT + CRF (Sup.)	0.82	0.92	0.77	0.76	0.35	**0.57**
	GPT-3 + R: 1-shot	**0.85**	0.92	**0.87**	**0.91**	**0.38**	0.52
Phrase-level	PubMedBERT + CRF (Sup.)	0.73	0.78	0.71	0.41	**0.22**	**0.30**
	GPT-3 + R: 1-shot	**0.75**	**0.82**	**0.81**	**0.87**	0.21	0.25
Relation Extraction	PubMedBERT + CRF + Shi and Lin (2019) (Sup.)	*	0.67	**0.65**	0.36	0.19	**0.21**
	GPT-3 + R: 1-shot	*	**0.80**	0.63	**0.60**	**0.34**	0.16

Table 7: **Medication attribute extraction.** F1 scores on our newly annotated medication extraction dataset. The baselines are trained using supervised learning on i2b2 (Uzuner et al., 2010), then transferred to the test domain. *Relation Extraction* additionally requires the model to match modifiers (dosage, route, etc.) to the medication span. Baseline end-to-end relation extraction performance suffers due to errors cascading from the extraction step.

in the 1-shot example, it was unlikely to be output, depressing the F1 score; including all classes in the 1-shot prompt appears more important than necessarily having the correct labels.

7.2 Recognition + Relation Extraction

Dataset description. The annotators created a second new dataset for medication extraction from the snippets from Moon et al. (2014). The annotators closely followed the schema from the 2009 i2b2 medication challenge (Uzuner et al., 2010), with small deviations explained in Appendix B.4. For 105 randomly selected snippets, the annotators labeled mentions of medications, dosages, routes, frequencies, reasons, and durations, if available, and their correspondences. We examine the task from three different framings: a token-level annotation task, a phrase-level annotation task, and end-to-end relation extraction. For the example phrase "Tylenol twice daily", the desired output for the tasks would be: *[Med, Frequency, Frequency]*, *[B-Med, B-Frequency, I-Frequency]*, and *Medication: "Tylenol", Frequency: "twice daily".*, respectively.

Prompting and Resolver. We again used 5 examples for prompt design with InstructGPT (engine *text-davinci-002*) and greedy decoding (temperature = 0). We use a different guided 1-shot prompt (containing 7 entities each) for each of the three framings outlined above; these can be found in Appendix A. The resolvers for all were short.

Comparison. For token and phrase-level classification, we used a PubMedBERT model topped with a CRF layer. For end-to-end relation extraction, we first used the token-level baseline to extract entity spans, then used the technique from Shi and Lin (2019) to classify whether each pair of entities was related. We then postprocessed these pairwise outputs to match modifiers to their medications. For all the three tasks, since we followed the 2009 i2b2 medication extraction annotation guidelines, we fine-tuned the baselines with labeled data from i2b2 (10 fully annotated notes with 154 medication mentions, which we postprocess into smaller annotated chunks) and directly evaluated them on our datasets. (Uzuner et al., 2010). Appendix C.5 contains more detail for the baselines and evaluation.

Results. Table 7 shows that the 1-shot GPT-3+R outperforms the i2b2-supervised baseline across all task framings. The baseline end-to-end relation extraction performance suffers due to cascading extraction errors, as the longest token in the medication name had to be matched. GPT-3+R struggles with the *duration* and *reason* entities; however, it has been previously found that there is often large disagreement (F1 estimated 0.2–0.5) in inter-annotator agreement for these two entities, since they tend to be longer with ambiguous boundaries.

8 Conclusion

In this work, we introduced new annotated datasets to show that (i) large language models have great promise at diverse clinical extraction tasks and (ii) we can guide generations to map to complex output spaces with only light post-processing. We also demonstrated how weak supervision over the system's outputs can be used to train smaller, task-specific models that are more deployable. The scope of clinical NLP extends past what we studied here, and important next steps involve experimenting with LLMs such as OPT (Zhang et al., 2022) for which we can run inference locally, enabling evaluation on existing benchmarks and fine-tuning. Another important direction involves leveraging the outputs from several prompts (e.g. 1-shot prompts with different examples) to learn to determine when GPT-3 is uncertain; this increased reliability will be vital given the high-stakes in clinical information extraction. Taken as a whole, our work indicates a new paradigm for clinical information extraction—one that can scale to the lofty goals of clinical NLP.

Limitations

While large language models show great promise at clinical information extraction, there are clear limitations to their use. First, it is still difficult to guide a LLM to match an exact schema—clinical annotation guidelines are often multiple pages. We found that even when the Resolved GPT-3 outputs were impressive qualitatively, they did not always match at the token-level. For example, in tagging durations, one Resolved GPT-3 output was "X weeks" instead of "for X weeks". While this particular omission is trivial, it highlights the difficulty of communicating nuanced guidelines.

Second, we found a bias in GPT-3 towards outputting a non-trivial answer even where none exists. For example, for medication extraction the prompt we ended up using was, "Create a bulleted list of which medications are mentioned and whether they are active, discontinued, or neither." However, prior to this we had experimented with two separate prompts: "Create a bulleted list of *active* medications, if any." and "Create a bulleted list of *discontinued* medications, if any." If there was one active and one discontinued medication, the respective LLM outputs would be correct. However, if there were two active medications and none discontinued, the LLM primed with the discontinuation prompt tended to try to find an output and usually resorted to listing one or more active medications. Therefore, it is important to craft prompts or tasks that avoid this pitfall. For example, this could be achieved via (i) chaining multiple prompts, e.g., first asking if a certain entity type exists in the input, before asking for a list (Li et al., 2019b; Wu et al., 2022) or (ii) using an output structure like the sequence tagging approach.

Finally, because of the data use restrictions on most existing clinical datasets, which prohibit publicly sharing the data (e.g., to the GPT-3 APIs), all tasks except for biomedical evidence extraction were derived from the publicly-available CASI dataset (Moon et al., 2014). While we show the promise of transferring to a new setting in Section 4, it would be ideal to have been able to directly evaluate on multiple hospital systems at multiple points throughout time. Clinical text in CASI was drawn from notes from several hospitals and a diverse set of specialties, but is by no means representative of all clinical text. For example, the CASI paper states that the notes were "primarily verbally dictated and transcribed," but this practice is not universal. Further, as is unfortunately common in clinical NLP, we only tested in English, leaving testing the ability of LLMs to operate in different languages to future work (Névéol et al., 2018).

Ethics Statement

The datasets introduced in this paper involved only new annotations on top of existing, publicly available clinical text. Dataset annotation was conducted by two authors of the paper, and therefore there are no associated concerns, e.g. regarding compensation. As discussed in limitations, we believe these new annotated datasets serve as a starting point for the evaluation of LLMs on clinical text, but we concede that conclusions about specific performance cannot be ported to other languages, hospital systems, or temporal settings (as clinical text is quite subject to dataset shift).

If large language models were to be integrated into clinical extraction pipelines, as presented in this paper, there are large potential benefits. Clinical text is being created at a scale far too large for manual annotation, and as a result, cohorts for clinical study are largely small and hand-curated. Automatic structuring of clinical variables would help catalyze research that may be prohibitively expensive otherwise – allowing for study of rarer or less funded diseases as well as the analysis of real-world evidence for subpopulations that may not be observed in clinical trials. However, due to the high-stakes setting, it is imperative that the performance of such a system is evaluated in the same environment it will be used in, and that the performance numbers are stratified by cohorts of note (e.g. racial, socioeconomic, patient comorbidities, disease stage, site of care, author's clinical role and seniority); such variables were not available in the data we used here.

In this work, we accessed the GPT-3 model using the OpenAI API alone. However, we acknowledge that even the inference cost is still nontrivial (see Appendix D). We presented in Section 4 a paradigm of using weak supervision to distill a much smaller model, using pseudolabels learned from GPT-3, and we encourage such work to mitigate the environmental impact of deployment.

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References

Griffin Adams, Mert Ketenci, Shreyas Bhave, Adler J. Perotte, and Noémie Elhadad. 2020. Zero-shot clinical acronym expansion via latent meaning cells. In *Machine Learning for Health Workshop, ML4H@NeurIPS 2020, Virtual Event, 11 December 2020*, volume 136 of *Proceedings of Machine Learning Research*, pages 12–40. PMLR.

Emily Alsentzer, John R Murphy, Willie Boag, Wei-Hung Weng, Di Jin, Tristan Naumann, and Matthew McDermott. 2019. Publicly available clinical bert embeddings. *arXiv preprint arXiv:1904.03323*.

Waleed Ammar, Dirk Groeneveld, Chandra Bhagavatula, Iz Beltagy, Miles Crawford, Doug Downey, Jason Dunkelberger, Ahmed Elgohary, Sergey Feldman, Vu Ha, et al. 2018. Construction of the literature graph in semantic scholar. *arXiv preprint arXiv:1805.02262*.

Hilda Bastian, Paul Glasziou, and Iain Chalmers. 2010. Seventy-five trials and eleven systematic reviews a day: how will we ever keep up? *PLoS medicine*, 7(9):e1000326.

Olivier Bodenreider. 2004. The unified medical language system (umls): integrating biomedical terminology. *Nucleic acids research*, 32(suppl_1):D267–D270.

Tom Brown, Benjamin Mann, Nick Ryder, Melanie Subbiah, Jared D Kaplan, Prafulla Dhariwal, Arvind Neelakantan, Pranav Shyam, Girish Sastry, Amanda Askell, et al. 2020. Language models are few-shot learners. *Advances in neural information processing systems*, 33:1877–1901.

Wendy W Chapman, Will Bridewell, Paul Hanbury, Gregory F Cooper, and Bruce G Buchanan. 2001. A simple algorithm for identifying negated findings and diseases in discharge summaries. *Journal of biomedical informatics*, 34(5):301–310.

Geeticka Chauhan, Ruizhi Liao, William Wells, Jacob Andreas, Xin Wang, Seth Berkowitz, Steven Horng, Peter Szolovits, and Polina Golland. 2020. Joint modeling of chest radiographs and radiology reports for pulmonary edema assessment. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pages 529–539. Springer.

Irene Y Chen, Emily Alsentzer, Hyesun Park, Richard Thomas, Babina Gosangi, Rahul Gujrathi, and Bharti Khurana. 2020. Intimate partner violence and injury prediction from radiology reports. In *BIOCOMPUTING 2021: Proceedings of the Pacific Symposium*, pages 55–66. World Scientific.

Leyang Cui, Yu Wu, Jian Liu, Sen Yang, and Yue Zhang. 2021. Template-based named entity recognition using bart. *arXiv preprint arXiv:2106.01760*.

Jacob Devlin, Ming-Wei Chang, Kenton Lee, and Kristina Toutanova. 2018. Bert: Pre-training of deep bidirectional transformers for language understanding. *arXiv preprint arXiv:1810.04805*.

Elisa Ferracane, Iain Marshall, Byron C Wallace, and Katrin Erk. 2016. Leveraging coreference to identify arms in medical abstracts: An experimental study. In *Proceedings of the Seventh International Workshop on Health Text Mining and Information Analysis*, pages 86–95.

Yu Gu, Robert Tinn, Hao Cheng, Michael Lucas, Naoto Usuyama, Xiaodong Liu, Tristan Naumann, Jianfeng Gao, and Hoifung Poon. 2021. Domain-specific language model pretraining for biomedical natural language processing. *ACM Transactions on Computing for Healthcare (HEALTH)*, 3(1):1–23.

Bernal Jiménez Gutiérrez, Nikolas McNeal, Clay Washington, You Chen, Lang Li, Huan Sun, and Yu Su. 2022. Thinking about gpt-3 in-context learning for biomedical ie? think again. *arXiv preprint arXiv:2203.08410*.

Sam Henry, Kevin Buchan, Michele Filannino, Amber Stubbs, and Ozlem Uzuner. 2020. 2018 n2c2 shared task on adverse drug events and medication extraction in electronic health records. *Journal of the American Medical Informatics Association*, 27(1):3–12.

Or Honovich, Uri Shaham, Samuel R Bowman, and Omer Levy. 2022. Instruction induction: From few examples to natural language task descriptions. *arXiv preprint arXiv:2205.10782*.

Jeremy Irvin, Pranav Rajpurkar, Michael Ko, Yifan Yu, Silviana Ciurea-Ilcus, Chris Chute, Henrik Marklund, Behzad Haghgoo, Robyn Ball, Katie Shpanskaya, et al. 2019. Chexpert: A large chest radiograph dataset with uncertainty labels and expert comparison. In *Proceedings of the AAAI conference on artificial intelligence*, volume 33, pages 590–597.

Min Jiang, Yukun Chen, Mei Liu, S Trent Rosenbloom, Subramani Mani, Joshua C Denny, and Hua Xu. 2011.

A study of machine-learning-based approaches to extract clinical entities and their assertions from discharge summaries. *Journal of the American Medical Informatics Association*, 18(5):601–606.

Alistair EW Johnson, Tom J Pollard, Seth J Berkowitz, Nathaniel R Greenbaum, Matthew P Lungren, Chih-ying Deng, Roger G Mark, and Steven Horng. 2019. Mimic-cxr, a de-identified publicly available database of chest radiographs with free-text reports. *Scientific data*, 6(1):1–8.

Alistair EW Johnson, Tom J Pollard, Lu Shen, Li-wei H Lehman, Mengling Feng, Mohammad Ghassemi, Benjamin Moody, Peter Szolovits, Leo Anthony Celi, and Roger G Mark. 2016. Mimic-iii, a freely accessible critical care database. *Scientific data*, 3(1):1–9.

Kundan Krishna, Amy Pavel, Benjamin Schloss, Jeffrey P Bigham, and Zachary C Lipton. 2021. Extracting structured data from physician-patient conversations by predicting noteworthy utterances. In *Explainable AI in Healthcare and Medicine*, pages 155–169. Springer.

Ivy Fenton Kuhn. 2007. Abbreviations and acronyms in healthcare: when shorter isn't sweeter. *Pediatric nursing*, 33(5).

Hunter Lang, Monica Agrawal, Yoon Kim, and David Sontag. 2022a. Co-training improves prompt-based learning for large language models. *arXiv preprint arXiv:2202.00828*.

Hunter Lang, Aravindan Vijayaraghavan, and David Sontag. 2022b. Training subset selection for weak supervision. *arXiv preprint arXiv:2206.02914*.

Jinhyuk Lee, Wonjin Yoon, Sungdong Kim, Donghyeon Kim, Sunkyu Kim, Chan Ho So, and Jaewoo Kang. 2020. Biobert: a pre-trained biomedical language representation model for biomedical text mining. *Bioinformatics*, 36(4):1234–1240.

Kenton Lee, Luheng He, Mike Lewis, and Luke Zettlemoyer. 2017. End-to-end neural coreference resolution. *arXiv preprint arXiv:1707.07045*.

Ariel Levy, Monica Agrawal, Arvind Satyanarayan, and David Sontag. 2021. Assessing the impact of automated suggestions on decision making: Domain experts mediate model errors but take less initiative. In *Proceedings of the 2021 CHI Conference on Human Factors in Computing Systems*, pages 1–13.

Xiaoya Li, Jingrong Feng, Yuxian Meng, Qinghong Han, Fei Wu, and Jiwei Li. 2019a. A unified mrc framework for named entity recognition. *arXiv preprint arXiv:1910.11476*.

Xiaoya Li, Fan Yin, Zijun Sun, Xiayu Li, Arianna Yuan, Duo Chai, Mingxin Zhou, and Jiwei Li. 2019b. Entity-relation extraction as multi-turn question answering. *arXiv preprint arXiv:1905.05529*.

Andy T Liu, Wei Xiao, Henghui Zhu, Dejiao Zhang, Shang-Wen Li, and Andrew Arnold. 2022a. Qaner: Prompting question answering models for few-shot named entity recognition. *arXiv preprint arXiv:2203.01543*.

Haokun Liu, Derek Tam, Mohammed Muqeeth, Jay Mohta, Tenghao Huang, Mohit Bansal, and Colin Raffel. 2022b. Few-shot parameter-efficient fine-tuning is better and cheaper than in-context learning. *arXiv preprint arXiv:2205.05638*.

Pengfei Liu, Weizhe Yuan, Jinlan Fu, Zhengbao Jiang, Hiroaki Hayashi, and Graham Neubig. 2021. Pre-train, prompt, and predict: A systematic survey of prompting methods in natural language processing. *arXiv preprint arXiv:2107.13586*.

Ilya Loshchilov and Frank Hutter. 2018. Decoupled weight decay regularization. In *International Conference on Learning Representations*.

Yen-Fu Luo, Sam Henry, Yanshan Wang, Feichen Shen, Ozlem Uzuner, and Anna Rumshisky. 2020. The 2019 n2c2/umass lowell shared task on clinical concept normalization. *Journal of the American Medical Informatics Association*, 27(10):1529–e1.

Tomas Mikolov, Ilya Sutskever, Kai Chen, Greg S Corrado, and Jeff Dean. 2013. Distributed representations of words and phrases and their compositionality. *Advances in neural information processing systems*, 26.

Sewon Min, Xinxi Lyu, Ari Holtzman, Mikel Artetxe, Mike Lewis, Hannaneh Hajishirzi, and Luke Zettlemoyer. 2022. Rethinking the role of demonstrations: What makes in-context learning work? *arXiv preprint arXiv:2202.12837*.

Swaroop Mishra, Daniel Khashabi, Chitta Baral, Yejin Choi, and Hannaneh Hajishirzi. 2021. Reframing instructional prompts to gptk's language. *arXiv preprint arXiv:2109.07830*.

Sungrim Moon, Serguei Pakhomov, Nathan Liu, James O Ryan, and Genevieve B Melton. 2014. A sense inventory for clinical abbreviations and acronyms created using clinical notes and medical dictionary resources. *Journal of the American Medical Informatics Association*, 21(2):299–307.

Milad Moradi, Kathrin Blagec, Florian Haberl, and Matthias Samwald. 2021. Gpt-3 models are poor few-shot learners in the biomedical domain. *arXiv preprint arXiv:2109.02555*.

Danielle L Mowery, Brett R South, Lee Christensen, Jianwei Leng, Laura-Maria Peltonen, Sanna Salanterä, Hanna Suominen, David Martinez, Sumithra Velupillai, Noémie Elhadad, et al. 2016. Normalizing acronyms and abbreviations to aid patient understanding of clinical texts: Share/clef ehealth challenge 2013, task 2. *Journal of biomedical semantics*, 7(1):1–13.

Shawn N Murphy, Griffin Weber, Michael Mendis, Vivian Gainer, Henry C Chueh, Susanne Churchill, and Isaac Kohane. 2010. Serving the enterprise and beyond with informatics for integrating biology and the bedside (i2b2). *Journal of the American Medical Informatics Association*, 17(2):124–130.

Mark Neumann, Daniel King, Iz Beltagy, and Waleed Ammar. 2019. ScispaCy: Fast and Robust Models for Biomedical Natural Language Processing. In *Proceedings of the 18th BioNLP Workshop and Shared Task*, pages 319–327, Florence, Italy. Association for Computational Linguistics.

Aurélie Névéol, Hercules Dalianis, Sumithra Velupillai, Guergana Savova, and Pierre Zweigenbaum. 2018. Clinical natural language processing in languages other than english: opportunities and challenges. *Journal of biomedical semantics*, 9(1):1–13.

Benjamin Nye, Junyi Jessy Li, Roma Patel, Yinfei Yang, Iain J Marshall, Ani Nenkova, and Byron C Wallace. 2018. A corpus with multi-level annotations of patients, interventions and outcomes to support language processing for medical literature. In *Proceedings of the conference. Association for Computational Linguistics. Meeting*, volume 2018, page 197. NIH Public Access.

Long Ouyang, Jeff Wu, Xu Jiang, Diogo Almeida, Carroll L Wainwright, Pamela Mishkin, Chong Zhang, Sandhini Agarwal, Katarina Slama, Alex Ray, et al. 2022. Training language models to follow instructions with human feedback. *arXiv preprint arXiv:2203.02155*.

Matthew E. Peters, Mark Neumann, Mohit Iyyer, Matt Gardner, Christopher Clark, Kenton Lee, and Luke Zettlemoyer. 2018. Deep contextualized word representations. In *Proceedings of the 2018 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies, Volume 1 (Long Papers)*, pages 2227–2237, New Orleans, Louisiana. Association for Computational Linguistics.

Peng Qi, Yuhao Zhang, Yuhui Zhang, Jason Bolton, and Christopher D Manning. 2020. Stanza: A python natural language processing toolkit for many human languages. In *Proceedings of the 58th Annual Meeting of the Association for Computational Linguistics: System Demonstrations*, pages 101–108.

Alexander Ratner, Stephen H Bach, Henry Ehrenberg, Jason Fries, Sen Wu, and Christopher Ré. 2017. Snorkel: Rapid training data creation with weak supervision. In *Proceedings of the VLDB Endowment. International Conference on Very Large Data Bases*, volume 11, page 269. NIH Public Access.

Kirk Roberts. 2016. Assessing the corpus size vs. similarity trade-off for word embeddings in clinical nlp. In *Proceedings of the Clinical Natural Language Processing Workshop (ClinicalNLP)*, pages 54–63.

David L Sackett. 1997. Evidence-based medicine. In *Seminars in perinatology*, volume 21, pages 3–5. Elsevier.

Victor Sanh, Albert Webson, Colin Raffel, Stephen H Bach, Lintang Sutawika, Zaid Alyafeai, Antoine Chaffin, Arnaud Stiegler, Teven Le Scao, Arun Raja, et al. 2021. Multitask prompted training enables zero-shot task generalization. *arXiv preprint arXiv:2110.08207*.

Timo Schick and Hinrich Schütze. 2021. Exploiting cloze-questions for few-shot text classification and natural language inference. In *Proceedings of the 16th Conference of the European Chapter of the Association for Computational Linguistics: Main Volume*, pages 255–269.

Peng Shi and Jimmy Lin. 2019. Simple bert models for relation extraction and semantic role labeling. *arXiv preprint arXiv:1904.05255*.

Lotan Shilo and Gila Shilo. 2018. Analysis of abbreviations used by residents in admission notes and discharge summaries. *QJM: An International Journal of Medicine*, 111(3):179–183.

Yuqi Si and Kirk Roberts. 2019. Deep patient representation of clinical notes via multi-task learning for mortality prediction. *AMIA Summits on Translational Science Proceedings*, 2019:779.

Marta Skreta, Aryan Arbabi, Jixuan Wang, Erik Drysdale, Jacob Kelly, Devin Singh, and Michael Brudno. 2021. Automatically disambiguating medical acronyms with ontology-aware deep learning. *Nature communications*, 12(1):1–10.

Ryan Smith, Jason A Fries, Braden Hancock, and Stephen H Bach. 2022. Language models in the loop: Incorporating prompting into weak supervision. *arXiv preprint arXiv:2205.02318*.

Sunghwan Sohn, Cheryl Clark, Scott R Halgrim, Sean P Murphy, Christopher G Chute, and Hongfang Liu. 2014. Medxn: an open source medication extraction and normalization tool for clinical text. *Journal of the American Medical Informatics Association*, 21(5):858–865.

Shubham Toshniwal, Sam Wiseman, Allyson Ettinger, Karen Livescu, and Kevin Gimpel. 2020. Learning to ignore: Long document coreference with bounded memory neural networks. *arXiv preprint arXiv:2010.02807*.

Shubham Toshniwal, Patrick Xia, Sam Wiseman, Karen Livescu, and Kevin Gimpel. 2021. On generalization in coreference resolution. *arXiv preprint arXiv:2109.09667*.

Ozlem Uzuner, Andreea Bodnari, Shuying Shen, Tyler Forbush, John Pestian, and Brett R South. 2012. Evaluating the state of the art in coreference resolution for electronic medical records. *Journal of the American Medical Informatics Association*, 19(5):786–791.

Özlem Uzuner, Imre Solti, and Eithon Cadag. 2010. Extracting medication information from clinical text. *Journal of the American Medical Informatics Association*, 17(5):514–518.

Mathias Verbeke, Vincent Van Asch, Roser Morante, Paolo Frasconi, Walter Daelemans, and Luc De Raedt. 2012. A statistical relational learning approach to identifying evidence based medicine categories. In *Proceedings of the 2012 Joint Conference on Empirical Methods in Natural Language Processing and Computational Natural Language Learning*, pages 579–589.

Shuohang Wang, Yang Liu, Yichong Xu, Chenguang Zhu, and Michael Zeng. 2021. Want to reduce labeling cost? gpt-3 can help. In *Findings of the Association for Computational Linguistics: EMNLP 2021*, pages 4195–4205.

Yanshan Wang, Liwei Wang, Majid Rastegar-Mojarad, Sungrim Moon, Feichen Shen, Naveed Afzal, Sijia Liu, Yuqun Zeng, Saeed Mehrabi, Sunghwan Sohn, et al. 2018. Clinical information extraction applications: a literature review. *Journal of biomedical informatics*, 77:34–49.

Marc Weeber, James G Mork, and Alan R Aronson. 2001. Developing a test collection for biomedical word sense disambiguation. In *Proceedings of the AMIA Symposium*, page 746. American Medical Informatics Association.

Jason Wei, Maarten Bosma, Vincent Y. Zhao, Kelvin Guu, Adams Wei Yu, Brian Lester, Nan Du, Andrew M. Dai, and Quoc V. Le. 2021. Finetuned language models are zero-shot learners. *arXiv:2109.01652*.

Thomas Wolf, Lysandre Debut, Victor Sanh, Julien Chaumond, Clement Delangue, Anthony Moi, Pierric Cistac, Tim Rault, Rémi Louf, Morgan Funtowicz, et al. 2019. Huggingface's transformers: State-of-the-art natural language processing. *arXiv preprint arXiv:1910.03771*.

Stephen Wu, Kirk Roberts, Surabhi Datta, Jingcheng Du, Zongcheng Ji, Yuqi Si, Sarvesh Soni, Qiong Wang, Qiang Wei, Yang Xiang, et al. 2020. Deep learning in clinical natural language processing: a methodical review. *Journal of the American Medical Informatics Association*, 27(3):457–470.

Tongshuang Wu, Michael Terry, and Carrie Jun Cai. 2022. Ai chains: Transparent and controllable human-ai interaction by chaining large language model prompts. In *CHI Conference on Human Factors in Computing Systems*, pages 1–22.

Yonghui Wu, Jun Xu, Yaoyun Zhang, and Hua Xu. 2015. Clinical abbreviation disambiguation using neural word embeddings. In *Proceedings of BioNLP 15*, pages 171–176.

Fei Xia and Meliha Yetisgen-Yildiz. 2012. Clinical corpus annotation: challenges and strategies. In *Proceedings of the Third Workshop on Building and Evaluating Resources for Biomedical Text Mining (BioTxtM'2012) in conjunction with the International Conference on Language Resources and Evaluation (LREC), Istanbul, Turkey*.

Xiaohan Yang, Eduardo Peynetti, Vasco Meerman, and Chris Tanner. 2022. What gpt knows about who is who. *arXiv preprint arXiv:2205.07407*.

Jieyu Zhang, Yue Yu, Yinghao Li, Yujing Wang, Yaming Yang, Mao Yang, and Alexander Ratner. 2021. Wrench: A comprehensive benchmark for weak supervision. In *Thirty-fifth Conference on Neural Information Processing Systems Datasets and Benchmarks Track (Round 2)*.

Susan Zhang, Stephen Roller, Naman Goyal, Mikel Artetxe, Moya Chen, Shuohui Chen, Christopher Dewan, Mona Diab, Xian Li, Xi Victoria Lin, et al. 2022. Opt: Open pre-trained transformer language models. *arXiv preprint arXiv:2205.01068*.

Zachariah Zhang, Jingshu Liu, and Narges Razavian. 2020. Bert-xml: Large scale automated icd coding using bert pretraining. *arXiv preprint arXiv:2006.03685*.

Jiaping Zheng, Wendy W Chapman, Rebecca S Crowley, and Guergana K Savova. 2011. Coreference resolution: A review of general methodologies and applications in the clinical domain. *Journal of biomedical informatics*, 44(6):1113–1122.

Pierre Zweigenbaum, Dina Demner-Fushman, Hong Yu, and Kevin B Cohen. 2007. Frontiers of biomedical text mining: current progress. *Briefings in bioinformatics*, 8(5):358–375.

A Prompts and Sample GPT-3 Outputs

We present examples for each task alongside their corresponding prompts to illustrate different prompting strategies used for each task.

A.1 Clinical Sense Disambiguation

For clinical sense disambiguation we used GPT-3 edit mode which edits the input text rather than continuing it.

Example 1

GPT-3 edit input:

```
GENERAL: Patient is sedated on vent. HEENT:
Normocephalic, atraumatic. Pupils are sluggish
but reactive and equal bilaterally. NECK: Supple.
No lymphadenopathy. No JVD. CARDIAC: Regular rate
and rhythm. No murmurs. LUNGS: CTA, intubated.
ABDOMEN: Obese, nontender, positive bowel sounds.
EXTREMITIES: Positive pulses, positive edema.
SKIN: Chronic changes pretibial area bilaterally.
```

GPT-3 edit prompt:

```
Expand the abbreviation: CTA
```

GPT-3 edit output:

```
GENERAL: Patient is sedated on vent. HEENT:
Normocephalic, atraumatic. Pupils are sluggish
but reactive and equal bilaterally. NECK: Supple.
No lymphadenopathy. No JVD. CARDIAC: Regular rate
and rhythm. No murmurs. LUNGS: Clear to
auscultation, intubated. ABDOMEN: Obese,
nontender, positive bowel sounds. EXTREMITIES:
Positive pulses, positive edema. SKIN: Chronic
changes pretibial area bilaterally.
```

Example 2

GPT-3 edit input:

```
2. Severe hypertension. 3. Severe mitral
regurgitation. 4. Osteoporosis. PROCEDURES: 1.
Coronary angiography and hemodynamic evaluation
with right heart catheterization. Right heart
catheterization shows right atrial pressure of 1,
right ventricular pressure of 47/11, PA pressure
of 48/16, with a pulmonary capillary wedge
pressure of 29, with a large B-wave confirmed
with a wedge saturation of 95
```

GPT-3 edit prompt:

```
Expand the abbreviation: PA
```

GPT-3 edit output:

```
2. Severe hypertension. 3. Severe mitral
regurgitation. 4. Osteoporosis. PROCEDURES: 1.
Coronary angiography and hemodynamic evaluation
with right heart catheterization. Right heart
catheterization shows right atrial pressure of 1,
right ventricular pressure of 47/11, pulmonary
artery pressure of 48/16, with a pulmonary
capillary wedge pressure of 29, with a large
B-wave confirmed with a wedge saturation of 95%.
```

A.2 Biomedical Evidence Extraction

For biomedical evidence extraction we used GPT-3 Davinci. The generated output is shown in blue.

Example 1

GPT-3 Davinci:

Assessment of acute bronchodilator effects from specific airway resistance changes in stable COPD patients.
BACKGROUND In COPD patients, reversibility is currently evaluated from the changes of forced expiratory volume at 1s (ΔFEV1) and forced vital capacity (ΔFVC). By lowering peripheral airway smooth muscle tone, bronchodilators should decrease dynamic hyperinflation, gas trapping, and possibly dyspnea at rest. Hence, we hypothesize that specific airway resistance changes (ΔsRAW) should better characterize the acute response to bronchodilators.
METHODS On two days, 60 COPD patients underwent dyspnea evaluation (VAS score) and pulmonary function testing at baseline and one hour after placebo or 300μg indacaterol administration.
RESULTS Spirographic and ΔsRAW-based criteria identified as responders 24 and 45 patients, respectively. ΔsRAW correlated with changes of intrathoracic gas volume (ΔITGV) (r=0.61; p<0.001), residual volume (ΔRV) (r=0.60; p<0.001), ΔFVC (r=0.44; p=0.001), and ΔVAS (r=0.73; p<0.001), while ΔFEV1 correlated only with ΔFVC (r=0.34; p=0.008). Significant differences in terms of ΔITGV (p=0.002), ΔRV (p=0.023), and ΔVAS (p<0.001) occurred only if patients were stratified according to ΔsRAW.
[...]

Create a bulleted list of the arms in this trial.

- Placebo
- Indacaterol (300 μg)

Example 2

GPT-3 Davinci:

Serum biochemical characteristics of Beluga, Huso huso (L.), in response to blood sampling after clove powder solution exposure.
In order to investigate the effect of anesthesia on serum parameters, Beluga, Huso huso (L.) were blood-sampled immediately without anesthesia (control) or subjected to following anesthesia procedure: 40, 120, and 240 s exposure to 3,000, 700, and 500 mg l^{-1} clove solution, respectively. Blood samples were collected after these periods, when fish were immobile and reached stage 4 anesthesia. Results showed that cortisol and glucose levels were significantly high in 700 and 500 but not 3,000 mg l^{-1} group compared to control. Serum lactate levels were significantly high in 500 mg l^{-1} group compared to control group. Lactate levels were not significantly differed between control, 3,000, and 700 mg l^{-1} groups. There were no significant differences in serum levels of cholesterol, total protein, lactate dehydrogenase, aspartate aminotransferase, alanine aminotransferase, Na^{+}, Cl^{-}, K^{+}, and Ca^{2+}. Results suggest that rapid anesthesia with higher dose is better than slow anesthesia with lower dose for blood sampling in Beluga.

Create a bulleted list of the arms in this trial.

- Control
- 3,000 mg l^{-1} clove solution
- 700 mg l^{-1} clove solution
- 500 mg l^{-1} clove solution

A.3 Coreference Resolution

Example 1: Zero-shot unguided

GPT-3 Davinci:

```
[...] Her current regimen for her MS is Rebif
Monday, Wednesday, and Friday and 1 gram of
methylprednisolone p.o. every month. This had
been working previously; however, she feels that
her symptoms return before her next dose of
methylprednisolone is due.

What does "This" in the sentence "This had been
working previously; however, she feels that her
symptoms return before her next dose of
methylprednisolone is due." refer to?

The sentence is unclear, but it seems to be
referring to the Rebif regimen.
```

Example 1: One-shot guided (incorrect)

```
[...] ASSESSMENT  PLAN: The patient has no
physical evidence of progression of disease. It
is somewhat worrisome that her CEA is up, but
will be keep watching that to see if it is just
within a normal swing for her. [...]

What does "that" in the sentence "It is somewhat
worrisome that her CEA is up, but will be keep
watching that to see if it is just within a
normal swing for her." refer to?

"that" refers to "progression of disease"

[...] Her current regimen for her MS is Rebif
Monday, Wednesday, and Friday and 1 gram of
methylprednisolone p.o. every month. This had
been working previously; however, she feels that
her symptoms return before her next dose of
methylprednisolone is due.

What does "This" in the sentence "This had been
working previously; however, she feels that her
symptoms return before her next dose of
methylprednisolone is due." refer to?

"This" refers to "her current regimen for her MS"
```

Example 1: One-shot guided (correct)

```
[...] ASSESSMENT  PLAN: The patient has no
physical evidence of progression of disease. It
is somewhat worrisome that her CEA is up, but
will be keep watching that to see if it is just
within a normal swing for her. [...]

What does "that" in the sentence "It is somewhat
worrisome that her CEA is up, but will be keep
watching that to see if it is just within a
normal swing for her." refer to?

"that" refers to "her CEA"

[...] Her current regimen for her MS is Rebif
Monday, Wednesday, and Friday and 1 gram of
methylprednisolone p.o. every month. This had
been working previously; however, she feels that
her symptoms return before her next dose of
methylprednisolone is due.

What does "This" in the sentence "This had been
working previously; however, she feels that her
symptoms return before her next dose of
methylprednisolone is due." refer to?

"This" refers to "her current regimen for her MS"
```

A.4 Medication Status Extraction

Example 1: Zero-shot guided

```
[...] home dose of Kadian as this is her
long-acting medication and DC the continuous
Dilaudid given IV. 5. Urinary tract infection
with Klebsiella and E. coli, both sensitive to
Levaquin. Since this was diagnosed Foley has been
DC'd. For now would continue Levaquin and recheck
urinalysis.

Create a bulleted list of which medications are
mentioned and whether they are active,
discontinued, or neither.

-"Kadian" (active)
-"Dilaudid" (discontinued)
-"Levaquin" (active)
```

Example 1: One-shot guided (incorrect)

```
[...] start her on Ativan 1 mg p.o. q. 8 hours
and use Ativan 1 mg IV q. 4 hours p.r.n. for
agitation. I will also start her on Inderal LA 60
mg p.o. q.d. for essential tremors. She does not
want to take Celexa, and I will put her back on
Lexapro 2 mg p.o. q.d. I will discontinue
Esmolol.

Create a bulleted list of which medications [...]

-"Ativan" (discontinued)
-"Inderal LA" (active)
-"Celexa" (neither)
-"Lexapro" (active)
-"Esmolol" (active)

[...] home dose of Kadian as this is her
long-acting medication and DC the continuous
Dilaudid given IV. 5. Urinary tract infection
with Klebsiella and E. coli, both sensitive to
Levaquin. Since this was diagnosed Foley has been
DC'd. For now would continue Levaquin and recheck
urinalysis.

Create a bulleted list of which medications [...]

-"Kadian" (active)
-"Dilaudid" (discontinued)
-"Levaquin" (active)
```

Example 1: One-shot guided (correct)

```
[...] start her on Ativan 1 mg p.o. q. 8 hours
and use Ativan 1 mg IV q. 4 hours p.r.n. for
agitation. I will also start her on Inderal LA 60
mg p.o. q.d. for essential tremors. She does not
want to take Celexa, and I will put her back on
Lexapro 2 mg p.o. q.d.

Create a bulleted list of which medications [...]

-"Ativan" (active)
-"Inderal LA" (active)
-"Lexapro" (active)
-"Celexa" (neither)

[...] home dose of Kadian as this is her
long-acting medication and DC the continuous
Dilaudid given IV. 5. Urinary tract infection
with Klebsiella and E. coli, both sensitive to
Levaquin. Since this was diagnosed Foley has been
DC'd. For now would continue Levaquin and recheck
urinalysis.

Create a bulleted list of which medications [...]

-"Kadian" (discontinued)
-"Dilaudid" (discontinued)
-"Levaquin" (discontinued)
```

A.5 Medication Attribute Extraction

Example 1: Token-level

```
<One-shot-example>

Label the tokens: medication, dosage, route,
frequency, duration, reason, or none. Ignore
allergies.

<One-shot-labels>

Input: 8. Albuterol 2 puffs every 4-6 hours as
needed. HOSPITAL COURSE: This is an 80-year-old
female who was hospitalized about 2 months ago
for chronic obstructive pulmonary disease
exacerbation. At that time she was put on
prednisone and antibiotics and seemed to get
better. However, she was put on Augmentin ES and
continued to have difficulty tasting food and
felt that food tasted very salty. She had no
appetite and she has continued to lose weight
over the last 2 months.

Label the tokens: medication, dosage, route,
frequency, duration, reason, or none. Ignore
allergies.

-”8”: none
-”.”: none
-”Albuterol”: medication
-”2”: dosage
-”puffs”: dosage
-”every”: frequency
-”4-6”: frequency
-”hours”: frequency
-”as”: none
-”needed”: none
-”.”: none
-”HOSPITAL”: none
-”COURSE”: none
-”This”: none
-”is”: none
-”an”: none
-”80-year-old”: none
-”female”: none
-”who”: none
-”was”: none
-”hospitalized”: none
-”about”: duration
-”2”: duration
-”months”: duration
-”ago”: duration
-”for”: reason
-”chronic”: reason
-”obstructive”: reason
-”pulmonary”: reason
-”disease”: reason
-”exacerbation”: reason
-”.”: none
-”At”: none
-”that”: none
-”time”: none
-”she”: none
-”was”: none
-”put”: none
-”on”: none
-”prednisone”: medication
[...]
```

Example 1: Phrase-level

```
<One-shot-example>

Label the tokens: medication, dosage, route,
frequency, duration, reason, or none. Ignore
allergies.

<One-shot-labels>

Input: 8. Albuterol 2 puffs every 4-6 hours as
needed. HOSPITAL COURSE: This is an 80-year-old
female who was hospitalized about 2 months ago
for chronic obstructive pulmonary disease
exacerbation. At that time she was put on
prednisone and antibiotics and seemed to get
better. However, she was put on Augmentin ES and
continued to have difficulty tasting food and
felt that food tasted very salty. She had no
appetite and she has continued to lose weight
over the last 2 months.

Label the tokens: medication, dosage, route,
frequency, duration, reason, or none. Chunk the
same entity together. Ignore allergies.

-”8”: none
-”.”: none
-”Albuterol”: medication
-”2 puffs”: dosage
-”every 4-6 hours”: frequency
-”as needed”: duration
-”.”: none
-”HOSPITAL COURSE”: none
-”This”: none
-”is”: none
-”an”: none
-”80-year-old”: none
-”female”: none
-”who”: none
-”was”: none
-”hospitalized”: none
-”about”: none
-”2 months”: duration
-”ago”: none
-”for”: none
-”chronic”: none
-”obstructive”: none
-”pulmonary”: none
-”disease”: reason
-”exacerbation”: none
-”.”: none
-”At”: none
-”that”: none
-”time”: none
-”she”: none
-”was”: none
-”put”: none
-”on”: none
-”prednisone”: medication
[...]
```

Example 1: Relation Extraction

```
 <One-shot-example>

Label the tokens: medication, dosage, route,
frequency, duration, reason, or none. Ignore
allergies.

<One-shot-labels>

Input: 8. Albuterol 2 puffs every 4-6 hours as
needed. HOSPITAL COURSE: This is an 80-year-old
female who was hospitalized about 2 months ago
for chronic obstructive pulmonary disease
exacerbation. At that time she was put on
prednisone and antibiotics and seemed to get
better. However, she was put on Augmentin ES and
continued to have difficulty tasting food and
felt that food tasted very salty. She had no
appetite and she has continued to lose weight
over the last 2 months.

Label medications, ignoring allergies. Include
dosage, route, frequency, duration, reason, if
available.

-"medication: "Albuterol", dosage: "2 puffs",
frequency: "every 4-6 hours", duration: "as
needed"
-medication: "prednisone", duration: "2 months"
-medication: "antibiotics", duration: "2 months"
-medication: "Augmentin ES", duration: "2 months"
```

B Annotation Process

A screenshot of the annotation process can be seen in Figure 2.

B.1 Biomedical Evidence Extraction

For arm identification 20 out of 187 abstracts from the test set of Nye et al. (2018) were randomly selected. Both annotators separately identified the study arms in each abstract. They included all characteristics of a arm that were necessary for differentiation (Ferracane et al., 2016). For example, we would not require the route of administration for a drug (e.g. “oral" in *oral X*) unless another arm contained the the same drug in a different formal (e.g. *X nasal spray*). There was full consensus between annotators for the identified numbers of arms. A single abstract was replaced due to its ambiguity.

B.2 Coreference Resolution

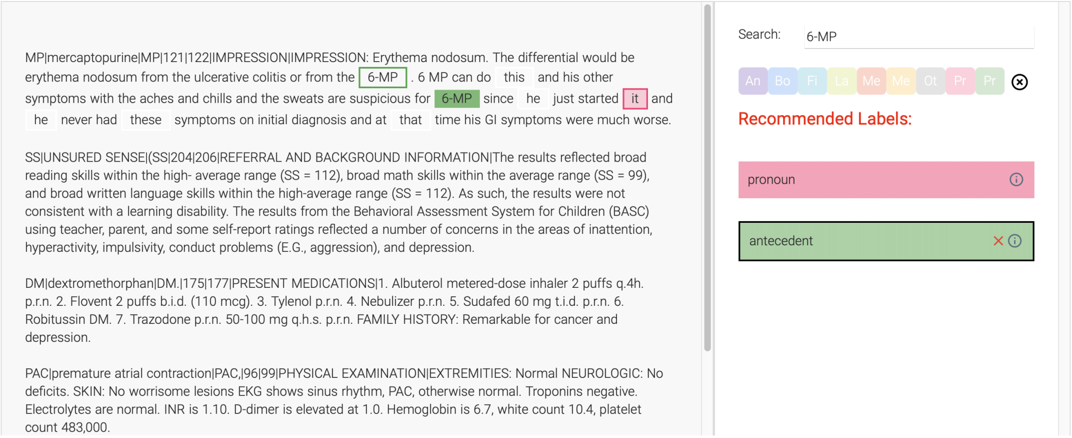
Annotators labeled 105 snippets from the CASI dataset with pronouns and their corresponding noun phrase antecedent (Moon et al., 2014). The antecedent was annotated as the entire noun phrase (barring any dependent clauses); in cases where two antecedents were available, both were labeled. For the purposes of evaluation, we chose the antecedent with the highest overlap to each model's output. To ensure nontrivial examples, the annotators excluded all examples of personal pronouns (e.g. “he”, “she”) if another person (and possible antecedent) had not yet been mentioned in the snippet.

B.3 Medication Status Extraction

We wanted to create a dataset of challenging examples containing a changeover in treatment. From a sample, only ~5% of CASI snippets contained such examples. To increase the density of these examples, speeding up annotation, clinical notes were filtered with the following search terms: *discont*, *adverse*, *side effect*, *switch*, and *dosage*, leading to 1445 snippets. We excluded snippets that were purely medication lists, requiring at least some narrative part to be present. For 105 randomly selected snippets, the annotators first extracted all medications. Guidelines excluded medication categories (e.g. “ACE-inhibitor”) if they referred to more specific drug names mentioned elsewhere (even if partially cut off in the snippet). For instance, only the antibiotic Levaquin was labeled in: “It is probably reasonable to treat with antibiotics [...]. I would agree with Levaquin alone [...]”. Guidelines also excluded electrolytes and intravenous fluids as well as route and dosage information. In a second step, medication were assigned to one of three categories: *active*, *discontinued*, and *neither*. Discontinued medications also contain medications that are temporarily on hold. The category *neither* was assigned to all remaining medications (e.g. allergies, potential medications).

B.4 Medication Attribute Extraction

For medication attribute extraction, we also labeled 105 examples from CASI (Moon et al., 2014). Annotation guideline were adopted from the 2009 i2b2 medication extraction challenge (Uzuner et al., 2010) with slight modifications. We allowed medication attributes to have multiple spans. Also, we grouped together different names of the same drug (e.g. “Tylenol” and “Tylenol PM”) for the purpose of relation extraction. After annotation of the data, we create three versions of the dataset: token-level, phrase-level, and relation-level. For the first, we split all word in the example and assigned them their respective label or *none* if they were not part of a label (see token-level example in A.5. For phrase-level, we kept consecutive words with the same label grouped together as phrases (see phrase-level example in A.5. The relation level just contained the extracted medication and their attributes (see relation extraction example in A.5. We note that medication lists were downsampled in the creation of the dataset, since the 2009 i2b2 challenge had found performance on narrative text was far lower than on medication lists.



MP|mercaptopurine|MP|121|122|IMPRESSION|IMPRESSION: Erythema nodosum. The differential would be erythema nodosum from the ulcerative colitis or from the 6-MP . 6 MP can do this and his other symptoms with the aches and chills and the sweats are suspicious for 6-MP since he just started it and he never had these symptoms on initial diagnosis and at that time his GI symptoms were much worse.

SS|UNSURED SENSE|(SS|204|206|REFERRAL AND BACKGROUND INFORMATION|The results reflected broad reading skills within the high- average range (SS = 112), broad math skills within the average range (SS = 99), and broad written language skills within the high-average range (SS = 112). As such, the results were not consistent with a learning disability. The results from the Behavioral Assessment System for Children (BASC) using teacher, parent, and some self-report ratings reflected a number of concerns in the areas of inattention, hyperactivity, impulsivity, conduct problems (E.G., aggression), and depression.

DM|dextromethorphan|DM.|175|177|PRESENT MEDICATIONS|1. Albuterol metered-dose inhaler 2 puffs q.4h. p.r.n. 2. Flovent 2 puffs b.i.d. (110 mcg). 3. Tylenol p.r.n. 4. Nebulizer p.r.n. 5. Sudafed 60 mg t.i.d. p.r.n. 6. Robitussin DM. 7. Trazodone p.r.n. 50-100 mg q.h.s. p.r.n. FAMILY HISTORY: Remarkable for cancer and depression.

PAC|premature atrial contraction|PAC,|96|99|PHYSICAL EXAMINATION|EXTREMITIES: Normal NEUROLOGIC: No deficits. SKIN: No worrisome lesions EKG shows sinus rhythm, PAC, otherwise normal. Troponins negative. Electrolytes are normal. INR is 1.10. D-dimer is elevated at 1.0. Hemoglobin is 6.7, white count 10.4, platelet count 483,000.

Search: 6-MP

Figure 2: Platform used for annotation of the three new labeled datasets, shown for the coreference resolution annotation task.

C Additional Experimental details

Across all datasets, similar to Honovich et al. (2022), we assume the latest generation of models on the OpenAI API is the set of InstructGPT models from Ouyang et al. (2022).

C.1 Clinical Sense Disambiguation

How do we know CASI is not in the LLM training set? Since the CASI dataset is publicly accessible from the Internet and on Github, one potential pitfall is that the dataset may have been in the language models' training data. While this is also true of other common NLP benchmarks, we attempted to confirm results were not merely an artifact. To do so, we annotated 50 distinct acronyms that occurred in sentences in the CASI dataset that were *not* included in the original annotations. While this set of acronyms is easier (e.g., they many only have a single clinical expansion), this allows us to check that GPT-3 is not simply pattern matching to potential past training data. In the set of 50, we find *GPT-3 edit* correctly expanded 47 (94%). In 2 of these cases, the acronym was in fact a typo (SMIV instead of SIMV, AVG instead of ABG), and the correct expansion was given regardless. Of the 3 that were incorrect, one was in fact incorrect, one was of unspecified meaning to the annotator, and one had 2/3 of the words correct in the expansion.

Resolver Details

Weak Supervision For weak supervision, we only consider the 97% of the dataset where the overlap with an answer choice was at least 5 characters as candidates for pseudolabels. Following prior work (Lang et al., 2022a,b), we additionally used a technique called the *cut statistic* to select a high-quality subset of the weakly labeled data to reduce the noise in the training process. We selected a subset of size 75% to decrease noise while still choosing a large enough set to ensure all acronyms were seen during training. We fine-tuned a PubMedBERT (Gu et al., 2021) model, a BERT variant that was pretrained on biomedical abstracts and full-text articles from PubMed, using learning rate 1e-5, weight decay 0.01, the AdamW optimizer (Loshchilov and Hutter, 2018), and batch size 4, using the `BERTForMultipleChoice` functionality in HuggingFace Transformers (Wolf et al., 2019).

C.2 Biomedical Evidence Extraction

Baseline Training Details We trained for 10,000 steps using the AdamW optimizer, learning rate 2e-5, batch size 32, and weight decay 1e-6, inheriting these hyperparameters from Zhang et al. (2021). These were the best-performing hyperparameters across the set reported in Zhang et al. (2021, Table 10, "BERT-CRF").

Resolver Details To evaluate on the original token-level labels we tokenize the GPT-3 output and remove bullet points, numbers, stop words, and the words "treatment", "control", and "group" which GPT-3 often appended for clarification (e.g. "- Placebo (Control group)"). Then, any token in the input that is found in the remaining GPT-3 output is labeled with a 1, and others with a 0. Since our procedure may have interrupted valid spans, we fill in any 0's between 1's as well as acronyms within parentheses. These steps transform the LLM output strings l_i to a binary labeling of the full input.

Example of Token-level Error Modes As an example describing token-level error modes of GPT-3, consider the output, the resolved output, and the gold label for a study with two arms below.

GPT-3 output

- Inhaled fluticasone
- Placebo

Resolved GPT-3 output:

Inhaled fluticasone reduces [...] double-blind, placebo-controlled study [...] inhaled fluticasone [...] or placebo. Large-scale [...] of inhaled steroid therapy on [...]

Gold-label (token-level):

Inhaled fluticasone reduces [...] double-blind, placebo-controlled study [...] inhaled fluticasone [...] or placebo. Large-scale [...] of inhaled steroid therapy on [...]

GPT-3 correctly identifies both study arms. However, the resolved output, which simply labels the token sequence of the identified arms in the original input, disagrees with the gold labels for several tokens. For example, the output includes the route, "inhaled", which isn't kept in the annotation schema, dinging precision. Further, the output excludes "placebo-controlled" (given "placebo" is included), dinging recall. Therefore, despite qualitatively capturing the arms of this trial, there was a middling F1-score of 0.70 for this example. This serves to underline why token-level metrics can be misleading as to true performance towards the underlying goal.

Oracle Details We assumed oracle splitting and oracle coreference resolution in order to distill the token-level labels to a list for the PubMedBERT baselines. As an example of oracle splitting, PubMedBERT assigned a 1 to the span *"40, 120, and 240 s exposure to 3,000, 700, and 500mg l^1 clove solution;"* this span in fact contains three different arms, and we assume it can be perfectly split, since the required information is theoretically present in the identified span. As an example of oracle coreference resolution, consider this example with two arms: *capecitabine and oxaliplatin plus radiotherapy (Cap-Oxa-CRT)* and *concurrent capecitabine and radiotherapy (Cap-CRT)*. The spans recognized by PubMedBERT include "adjuvant concurrent chemotherapy", "capecitabine-based concurrent chemotherapy", "postoperative CRT of capecitabine with or without oxaliplatin", "concurrent capecitabine and radiotherapy (Cap-CRT)" and "capecitabine and oxaliplatin plus radiotherapy (Cap-Oxa-CRT)." To be generous to the baseline, we assumed those 5 spans *could* possibly be reduced to the two arms with oracle coreference resolution. No oracle splitting or coreference resolution was conducted for Resolved GPT-3.

Analysis of Error Modes for Arm Identification Resolved GPT-3 successfully identified the correct number and content of the arms in 17 of the 20 examples. The three examples it missed were also missed by PubMedBERT. In one case with two arms, both methods included a procedure as a separate third arm; in reality, the procedure occurred for both arms and was not the intervention itself. In the second case, the prompt output did not elaborate on the treatment group sufficiently, and in the final case, it fully misparsed. Assuming the oracle splitting and coreference, PubMedBERT would still have issues with 10 further examples: two again included a common procedure as a third arm, four were missing control arms, one was missing a treatment arm, two arms required further domain knowledge to consolidate (e.g., that Ramipril is an ACE inhibitory therapy), and another required properly consolidating a therapy with no overlapping tokens.

C.3 Coreference Resolution

Baseline Details We benchmark using a transformer-based model trained jointly on three large coreference datasets (Toshniwal et al., 2021) that can be found on the HuggingFace model hub (`shtoshni/longformer_coreference_joint`).

Resolvers The resolver for the 0-shot unguided prompt was 50 LOC, or 973 tokens in the Codex tokenizer. In contrast, the 1-shot guided prompt required only stripping a final quotation mark, period, or space, which required 20 tokens per the Codex tokenizer.

C.4 Medication + Status Extraction

Resolver details For an unguided prompt, to map the GPT-3 output string to a list of medication strings, the first step is to break the output string up into substrings by parsing the "bulleted list" output by GPT-3, which we do with regular expressions. The output strings for this prompt followed several different formats, making this step slightly more involved than in previous cases. The two basic formats were a newline-separated list and a comma-separated list of medication names. The modifiers were also expressed in different ways: some outputs were *{Medication}: {Status}*, while others were *{Medication} ({Status})*. A few examples instead grouped the medications by status, so the output was *Active: {medication1}, {medication2}, Discontinued: {medication3}*. Examples of these outputs can be found in Appendix A.4. Despite this variation, we output a list by simply replacing newlines with commas to reduce to the comma-separated case, and then applying two regular expressions to extract the medication names and modifiers from the list.

The previous steps turn the LLM output strings into lists of strings. The next step in the resolver is to *denoise* the individual strings in each list by first stripping dosage and route information (e.g., "10 mg" or "patch") and then performing input-consistency checking by removing tokens that do not appear in the input. Finally, strings that, after the prior denoising steps, only consist of stop words or primarily consist of punctuation and whitespace, are removed from the prediction lists. This required 32 lines of code, and 946 tokens in a byte-pair encoding. In contrast, with a 1-shot prompt, output could be simply split on the bullets, and the status extracted from parentheses, requiring 8 lines of code and 165 tokens in a byte-pair encoding.

Medication Extraction Baseline For normalization, all entities were linked to the UMLS via the default string overlap functionality of ScispaCy (Bodenreider, 2004). We filtered the resulting UMLS concepts by their semantic types and only kept concepts of the types *Antibiotic*, *Clinical Drug*, *Pharmacologic Substance*, and *Vitamin*. Finally, the baseline predictions are run through the same denoising steps as the GPT-3 predictions to ensure a fair comparison.

Status Classification: T-Few We use T-Few (Liu et al., 2022b) for medication status classification using 20 additional annotated examples as the few-shot training set. We used a single prompt:

```
In the clinical note below, what is the status of
the medication Albuterol?

Albuterol 2 puffs every 4-6 hours as needed.
HOSPITAL COURSE: This is an 80-year-old female
who was hospitalized about 2 months ago for
chronic obstructive pulmonary disease
exacerbation. At that time she was put on
prednisone and antibiotics and seemed to get
better. However, she was put on Augmentin ES and
continued to have difficulty tasting food and
felt that food tasted very salty. She had no
appetite and she has continued to lose weight
over the last 2 months.
```

For the answer choices, we used `Discontinued`, `Active`, and `Neither`. We did not use IA$^{(3)}$ pretraining, but otherwise directly followed the T-Few recipe (i.e., we used the default values for all hyperparameters including batch size, learning rate, number of steps, length normalization, etc.). We used the T0-11B model.

C.5 Medication + Relation Extraction

Resolver The resolver for the first two tasks iterates over the lines in the GPT-3 output and grabs both the text span and the label; the text span is mapped to tokenized space, and all labels not in the label space (e.g. "Instructions") are mapped to *None*. For phrase-level labeling, a single additional step is conducted to map the labels to BIO format. For the relation extraction task, the resolver additionally assumes all entities mentioned in a line correspond to the medication on that line.

Sequence Tagging baseline We model extraction and labeling of medication + modifier (dosage, frequency, route, duration, reason) as a sequence tagging task. We use the `B/I/O` encoding for the label space, adding tags to the `B` and `I` labels indicating the type of entity. For training data, we split the 10 notes from the 2009 i2b2 challenge into shorter contexts using an off-the-shelf sentence segmenter, and merged split contexts of less than 30 tokens into the previous context. This results in 176 training contexts for the PubMedBERT + CRF model. As with Biomedical Evidence Extraction, we search for hyperparameters over the search space reported in Zhang et al. (2021, Table 10, "BERT-CRF"). The final model is chosen based on validation F1 score on a randomly selected validation set of 10% of the training data (i.e., 18 contexts).

Relation Extraction Baseline We use the model from Shi and Lin (2019) for relation extraction on top of PubMedBERT. For training data, we again use the 2009 i2b2 challenge set, but since the goal is to associate modifiers with individual medications, we split up the 10 long notes into rolling chunks around each medication mention. For each ground-truth medication entity, we create a context including the 30 tokens before and after that entity. We extended these windows to be on an `O` label so that entities are not split across contexts. We use a binary label space, since each modifier type (dosage, route, etc.) determines the relation type: the relevant task is to classify whether each pair of (medication, modifier) entities in a span is associated. We create one positive sample for each truly related (medication, modifier) pair. For each context, we add a negative sample for each (medication, modifier) pair that is not related. This results in 1416 examples (many of which have largely overlapping context, but a different pair of entities) for training the relation extraction model.

Task	Cost/Token	Tokens/Example	# of Examples	Experimental Settings	Estimated Cost
Clinical sense disambiguation	$0 (free in *edit* beta mode)	100	105	1	$0
Biomedical evidence extraction	$0.00006	500	187	1	$6
Coreference resolution	$0.00006	300	105	11	$21
Medication status extraction	$0.00006	300	105	16	$30
Medication attribute extraction	$0.00006	600	105	3	$12

Table 8: Estimate of cost of running the experiments included in this work

D Experimental Cost

At time of experimentation the cost of experiments included in this work were under $100. A breakdown of the upper bound of API costs can be found in the table below and is based on OpenAI API pricing in spring 2022. All estimates of tokens/example are rough upper bounds; some experimental settings were cheaper.