MedNLI Is Not Immune:
Natural Language Inference Artifacts in the Clinical Domain

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Abstract
Crowdworker-constructed natural language inference (NLI) datasets have been found to contain statistical artifacts associated with the annotation process that allow hypothesis-only classifiers to achieve better-than-random performance (Poliak et al., 2018; Gururangan et al., 2018; Tsuchiya, 2018). We investigate whether MedNLI, a physician-annotated dataset with premises extracted from clinical notes, contains such artifacts (Romanov and Shivade, 2018).

We find that entailed hypotheses contain generic versions of specific concepts in the premise, as well as modifiers related to responsiveness, duration, and probability. Neutral hypotheses feature conditions and behaviors that co-occur with, or cause, the condition(s) in the premise. Contradiction hypotheses feature explicit negation of the premise and implicit negation via assertion of good health. Adversarial filtering demonstrates that performance degrades when evaluated on the difficult subset. We provide partition information and recommendations for alternative dataset construction strategies for knowledge-intensive domains.

1 Introduction
In the clinical domain, the ability to conduct natural language inference (NLI) on unstructured, domain-specific texts such as patient notes, pathology reports, and scientific papers, plays a critical role in the development of predictive models and clinical decision support (CDS) systems.

Considerable progress in domain-agnostic NLI has been facilitated by the development of large-scale, crowdworker-constructed datasets, including the Stanford Natural Language Inference corpus (SNLI), and the Multi-Genre Natural Language Inference (MultiNLI) corpus (Bowman et al., 2015; Williams et al., 2017). MedNLI is a similarly-motivated, healthcare-specific dataset created by a small team of physician-annotators in lieu of crowdworkers, due to the extensive domain expertise required (Romanov and Shivade, 2018).

Poliak et al. (2018), Gururangan et al. (2018), Tsuchiya (2018), and McCoy et al. (2019) empirically demonstrate that SNLI and MultiNLI contain lexical and syntactic annotation artifacts that are disproportionately associated with specific classes, allowing a hypothesis-only classifier to significantly outperform a majority-class classifier. The presence of such artifacts is hypothesized to be partially attributable to the priming effect of the example hypotheses provided to crowdworkers at annotation-time. Romanov and Shivade (2018) note that a hypothesis-only baseline is able to outperform a majority class baseline in MedNLI, but they do not identify specific artifacts.

We confirm the presence of annotation artifacts in MedNLI and proceed to identify their lexical and semantic characteristics. We then conduct adversarial filtering to partition MedNLI into easy and difficult subsets (Sakaguchi et al., 2020). We find that performance of off-the-shelf fastText-based hypothesis-only and hypothesis-plus-premise classifiers is lower on the difficult subset than on the full and easy subsets (Joulin et al., 2016). We provide partition information for downstream use, and conclude by advocating alternative dataset construction strategies for knowledge-intensive domains.\(^1\)

2 The MedNLI Dataset
MedNLI is domain-specific evaluation dataset inspired by general-purpose NLI datasets, including SNLI and MultiNLI (Romanov and Shivade, 2018; Bowman et al., 2015; Williams et al., 2017). Much like its predecessors, MedNLI consists of premise-hypothesis pairs, in which the premises are drawn

\(^1\)See https://github.com/crherlihy/clinical_nli_artifacts for code and partition ids.
from the Past Medical History sections of a randomly selected subset of de-identified clinical notes contained in MIMIC-III (Johnson et al., 2016; Goldberger et al., 2000 (June 13). MIMIC-III was created from the records of adult and neonatal intensive care unit (ICU) patients. As such, complex and clinically severe cases are disproportionately represented, relative to their frequency of occurrence in the general population.

Physician-annotators were asked to write a definitely true, maybe true, and definitely false set of hypotheses for each premise, corresponding to entailment, neutral and contradiction labels, respectively. The resulting dataset has cardinality: \( n_{\text{train}} = 11232; n_{\text{dev}} = 1395; n_{\text{test}} = 1422 \).

### 3 MedNLI Contains Artifacts

To determine whether MedNLI contains annotation artifacts that may artificially inflate the performance of models trained on this dataset, we train a simple, premise-unaware, fastText classifier to predict the label of each premise-hypothesis pair, and compare the performance of this classifier to a majority-class baseline, in which all training examples are mapped to the most commonly occurring class label (Joulin et al., 2016; Poliak et al., 2018; Gururangan et al., 2018). Note that since annotators were asked to create an entailed, contradictory, and neutral hypothesis for each premise, MedNLI is class-balanced. Thus, in this setting, a majority class baseline is equivalent to choosing a label uniformly at random for each training example.

The micro F1-score achieved by the fastText classifier significantly exceeds that of the majority class baseline, confirming the findings of Romanov and Shivade (2018), who report a micro-F1 score of 61.9 but do not identify or analyze artifacts:

|                | entailment | neutral | contradiction |
|----------------|------------|---------|---------------|
| dev            | 33.3       | 33.3    |               |
| fastText       | 64.8       | 62.6    |               |

Table 1: Performance (micro F1-score) of the fastText hypothesis-only classifier.

As the confusion matrix for the test set shown in Table 2 indicates, the fastText model is most likely to misclassify entailment as neutral, and neutral and contradiction as entailment. Per-class precision and recall on the test set are highest for contradiction (73.2; 72.8) and lowest for entailment (56.7; 53.8).

|                | entailment | neutral | contradiction |
|----------------|------------|---------|---------------|
|                | 255        | 151     | 68            |
| neutral        | 126        | 290     | 58            |
| contradiction  | 69         | 60      | 345           |

Table 2: Confusion matrix for fastText classifier.

### 4 Characteristics of Clinical Artifacts

In this section, we conduct class-specific lexical analysis to identify the clinical and domain-agnostic characteristics of annotation artifacts associated with each set of hypotheses in MedNLI.

#### 4.1 Preprocessing

We cast each hypothesis string in the MedNLI training dataset to lowercase. We then use a scispaCy model pre-trained on the en_core_sci_lg corpus for tokenization and clinical named entity recognition (CNER) (Neumann et al., 2019a). One challenge associated with clinical text, and scientific text more generally, is that semantically meaningful entities often consist of spans rather than single tokens. To mitigate this issue during lexical analysis, we map each multi-token entity to a single-token representation, where sub-tokens are separated by underscores.

#### 4.2 Lexical Artifacts

Following Gururangan et al. (2018), to identify tokens that occur disproportionately in hypotheses associated with a specific class, we compute token-class pointwise mutual information (PMI) with add-50 smoothing applied to raw counts, and a filter to exclude tokens appearing less than five times in the overall training dataset. Table 3 reports the top 15 tokens for each class.

\[
\text{PMI}(\text{token, class}) = \log_2 \frac{p(\text{token, class})}{p(\text{token,} \cdot)p(\cdot, \text{class})}
\]

**Entailment** Entailment hypotheses are characterized by tokens about: (1) patient status and response to treatment (e.g., responsive; failed; longer as in no longer intubated); (2) medications and procedures which are common among ICU patients (e.g., broad_spectrum; antibiotics; pressors; steroid_medication; underwent; removal); (3) generalized versions of specific words in the premise (e.g., comorbidities; multiple_medical_problems), which Gururangan et al. (2018) also observe in SNLI; and (4) modifiers related to duration, frequency, or probability (e.g., frequent, possible, high_risk).
Neutral Neutral hypotheses feature tokens related to: (1) chronic and acute clinical conditions (e.g., obesity; joint_pain; brain_injury); (2) clinically relevant behaviors (e.g., smoking; alcoholic; drug_overdose); and (3) gender and reproductive status (e.g., fertility; pre_menopausal). Notably, the most discriminative conditions tend to be commonly occurring within the general population and generically stated, rather than rare and specific. This presumably contributes to the relative difficulty that the hypothesis-only fastText model has distinguishing between the entailment and neutral classes.

Contradiction Contradiction hypotheses are characterized by tokens that convey normalcy and good health. Lexically, such sentiment manifests as: (1) explicit negation of clinical severity, medical history, or in-patient status (e.g., denies_pain; no_treatment; discharged_home), or (2) affirmation of clinically unremarkable findings (e.g., normal_heart_rhythm; normal_blood_sugars), which would generally be rare among ICU patients. This suggests a heuristic of inserting negation token(s) to contradict the premise, which Gururangan et al. (2018) also observe in SNLI.

4.3 Syntactic Artifacts

Hypothesis Length In contrast to Gururangan et al. (2018)’s finding that entailed hypotheses in SNLI tend to be shorter while neutral hypotheses tend to be longer, hypothesis sentence length does not appear to play a discriminatory role in MedNLI, regardless of whether we consider merged- or separated-token representations of multi-word entities, as illustrated by Table 4:

| Table 4: Average and median hypothesis length by class and entity representation. |
|----------|----------|------|----------|------|----------|------|
|          | entailment | neutral | contradiction |
|          | mean  | median | mean  | median | mean  | median |
| separate | 5.6   | 5.0    | 5.2   | 5.0    | 5.6   | 5.0    |
| merged   | 5.3   | 5.0    | 4.9   | 5.0    | 5.3   | 5.0    |

5 Physician-Annotator Heuristics

In this section, we re-introduce premises to our analysis to evaluate a set of hypotheses regarding latent, class-specific annotator heuristics. If annotators do employ class-specific heuristics, we should expect the semantic contents, \( \phi \), of a given hypothesis, \( h \in \mathcal{H} \), to be influenced not only by the semantic contents of its associated premise, \( p \in \mathcal{P} \), but also by the target class, \( c \in \mathcal{C} \).

To investigate, we identify a set of heuristics parameterized by \( \phi(p) \) and \( c \), and characterized by the presence of a set of heuristic-specific Medical Subject Headings (MeSH) linked entities in the premise and hypothesis of each heuristic-satisfying example. These heuristics are described below; specific MeSH features are detailed in the Appendix.

Hypernym Heuristic This heuristic applies when the premise contains clinical condition(s), medication(s), finding(s), procedure(s) or event(s), the target class is entailment, and the generated hypothesis contains term(s) that can be interpreted as super-types for a subset of elements in the premise (e.g., clindamycin <: antibiotic).

Probable Cause Heuristic This heuristic applies when the premise contains clinical condition(s), the target class is neutral, and the generated hypothesis provides a plausible, often subjective
or behavioral, causal explanation for the condition, finding, or event described in the premise (e.g., associating altered mental status with drug overdose).

**Everything Is Fine Heuristic** This heuristic applies when the premise contains condition(s) or finding(s), the target class is *contradiction*, and the generated hypothesis negates the premise or asserts unremarkable finding(s). This can take two forms: repetition of premise content plus negation, or inclusion of modifiers that convey good health.

**Analysis** We conduct a $\chi^2$ test for each heuristic to determine whether we are able to reject the null hypothesis that pattern-satisfying premise-hypothesis pairs are uniformly distributed over classes.

| heuristic          | $\chi^2$ | p-value | top class         |
|--------------------|----------|---------|-------------------|
| hypernym           | 59.15    | 1.4e-13| entail (45.2%)    |
| probable cause     | 111.05   | 7.7e-25| neutral (57.8%)   |
| everything fine    | 874.71   | 1.1e-19| contradict (83.8%)|

Table 5: Results of $\chi^2$ test statistic by heuristic, computed using the combined MedNLI dataset ($p < 0.001$, $\dagger p < 0.01$, * $p < 0.5$). Top class presented with % of heuristic-satisfying pairs.

The results support our hypotheses regarding each of the three heuristics. Notably, the percentage of heuristic-satisfying pairs accounted for by the top class is lowest for the HYPERNYM hypothesis, which we attribute to the high degree of semantic overlap between entailed and neutral hypotheses.

### 6 Adversarial Filtering

To mitigate the effect of clinical annotation artifacts, we employ AFLite, an adversarial filtering algorithm introduced by Sakaguchi et al. (2020) and analyzed by Bras et al. (2020), to create *easy* and *difficult* partitions of MedNLI.

AFLite requires distributed representations of the full dataset as input, and proceeds in an iterative fashion. At each iteration, an ensemble of $n$ linear classifiers are trained and evaluated on different random subsets of the data. A score is then computed for each premise-hypothesis instance, reflecting the number of times the instance is correctly labeled by a classifier, divided by the number of times the instance appears in any classifier’s evaluation set. The top-$k$ instances with scores above a threshold, $\tau$, are filtered out and added to the *easy* partition; the remaining instances are retained. This process continues until the size of the filtered subset is $< k$, or the number of retained instances is $< m$; retained instances constitute the *difficult* partition.

To represent the full dataset, we use fastTextMIMIC-III embeddings, which have been pretrained on deidentified patient notes from MIMIC-III (Romanov and Shivade, 2018; Johnson et al., 2016). We represent each example as the average of its component token vectors.

We proportionally adjust a subset of the hyperparameters used by Sakaguchi et al. (2020) to account for the fact that MedNLI contains far fewer examples than WINOGRANDE\(^2\): specifically, we set the training size for each ensemble, $m$, to 5620, which represents $\approx 2/3$ of the MedNLI combined dataset. The remaining hyperparameters are unchanged: the ensemble consists of $n = 64$ logistic regression models, the filtering cutoff, $k = 500$, and the filtering threshold $\tau = 0.75$.

We apply AFLite to two different versions of MedNLI: (1) $X_{h,m}$: hypothesis-only, multi-token entities merged, and (2) $X_{ph,m}$: premise and hypothesis concatenated, multi-token entities merged. AFLite maps each version to an *easy* and *difficult* partition, which can in turn be split into training, dev, and test subsets. We report results for the fastText classifier trained on the original, hypothesis-only (hypothesis + premise) MedNLI training set, and evaluated on the *full*, *easy* and *difficult* dev and test subsets of $X_{h,m}$ ($X_{ph,m}$), and observe that performance decreases on the *difficult* partition:

| model | eval dataset | full | easy ($\Delta$) | difficult ($\Delta$) |
|-------|--------------|------|-----------------|---------------------|
| no premise | majority class | dev | 0.33 | 0.34 (±0.01) | 0.35 (±0.02) |
| no premise | majority class | test | 0.33 | 0.35 (±0.02) | 0.37 (±0.04) |
| no premise | fastText | dev | 0.65 | 0.67 (±0.02) | 0.46 (±0.10) |
| no premise | fastText | test | 0.65 | 0.65 (±0.02) | 0.44 (±0.23) |
| with premise | majority class | dev | 0.44 | 0.45 (±0.12) | 0.36 (±0.03) |
| with premise | majority class | test | 0.48 | 0.48 (±0.15) | 0.37 (±0.04) |
| with premise | fastText | dev | 0.53 | 0.61 (±0.07) | 0.43 (±0.11) |
| with premise | fastText | test | 0.51 | 0.55 (±0.04) | 0.44 (±0.11) |

Table 6: Performance (micro F1-score) for the majority class baseline and fastText classifiers, with and without premise, by partition (e.g., *full*, *easy*, *difficult*).

### 7 Discussion

#### 7.1 MedNLI is Not Immune from Artifacts

In this paper, we demonstrate that MedNLI suffers from the same challenge associated with annotation artifacts that its domain-agnostic predecessors have

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\(^2\)MedNLI’s training dataset contains 14049 examples when the training, dev, and test sets are combined, while WINOGRANDE contains 47K after excluding the 6K used for fine-tuning.
encountered: namely, NLI models trained on \{Med, S, Multi\}NLI can perform well even without access to the training examples’ premises, indicating that they often exploit shallow heuristics, with negative implications for out-of-sample generalization.

Interestingly, many of the high-level lexical characteristics identified in MedNLI can be considered domain-specific variants of the more generic, class-specific patterns identified in SNLI. This observation suggests that a set of abstract design patterns for inference example generation exists across domains, and may be reinforced by the prompts provided to annotators. Creative or randomized priming, such as Sakaguchi et al. (2020) ’s use of anchor words from WikiHow articles, may help to decrease reliance on such design patterns, but it appears unlikely that they can be systematically sidestepped without introducing new, “corrective” artifacts.

7.2 A Prescription for Dataset Construction

To mitigate the risk of performance overestimation associated with annotation artifacts, Zellers et al. (2019) advocate adversarial dataset construction, such that benchmarks will co-evolve with language models. This may be difficult to scale in knowledge-intensive domains, as expert validation of adversarially generated benchmarks is typically required. Additionally, in high-stakes domains such as medicine, information-rich inferences should be preferred over correct but trivial inferences that time-constrained expert annotators may be rationally incentivized to produce, because entropy-reducing inferences are more useful for downstream tasks.

We advocate the adoption of a mechanism design perspective, so as to develop modified annotation tasks that reduce the cognitive load placed on expert annotators while incentivizing the production of domain-specific NLI datasets with high downstream utility (Ho et al., 2015; Liu and Chen, 2017). An additional option is to narrow the generative scope by defining a set of inferences deemed to be useful for a specific task. Annotators can then map (premise, relation) tuples to relation-satisfying, potentially fuzzy subsets of this pool of useful inferences, or return partial functions when more information is needed.

8 Ethical Considerations

When working with clinical data, two key ethical objectives include: (1) the preservation of patient privacy, and (2) the development of language and predictive models that benefit patients and providers to the extent possible, without causing undue harm. With respect to the former, MedNLI’s premises are sampled from de-identified clinical notes contained in MIMIC-III (Goldberger et al., 2000 (June 13; Johnson et al., 2016), and the hypotheses generated by annotators do not refer to specific patients, providers, or locations by name. MedNLI requires users to complete Health Insurance Portability and Accountability Act (HIPAA) training and sign a data use agreement prior to being granted access, which we have complied with.

Per MedNLI’s data use agreement requirements, we do not attempt to identify any patient, provider, or institution mentioned in the de-identified corpus. Additionally, while we provide AFLite easy and difficult partition information for community use in the form of split-example ids and a checksum, we do not share the premise or hypothesis text associated with any example. Interested readers are encouraged to complete the necessary training and obtain credentials so that they can access the complete dataset (Romanov and Shivade, 2018; Goldberger et al., 2000 (June 13)).

With respect to benefiting patients, the discussion of natural language artifacts we have presented is intended to encourage clinical researchers who rely on (or construct) expert-annotated clinical corpora to train domain-specific language models, or consume such models to perform downstream tasks, to be aware of the presence of annotation artifacts, and adjust their assessments of model performance accordingly. It is our hope that these findings can be used to inform error analysis and improve predictive models that inform patient care.

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A Appendix

A.1 Hypothesis-only Baseline Analysis

To conduct the analysis presented in Section 3, we take the MedNLI training dataset as input, and exclude the premise text for each training example. We cast the text of each training hypothesis to lowercase, but do not perform any additional preprocessing. We use an off-the-shelf fastText classifier, with all model hyperparameters set to their default values with the exception of wordNgrams, which we set equal to 2 to allow the model to use bigrams in addition to unigrams (Joulin et al., 2016). We evaluate the trained classifier on the hypotheses contained in the MedNLI dev and test datasets, and report results for each split.

A.2 Lexical Artifact Analysis

To perform the analysis presented in Section 4, we cast each hypothesis string in the MedNLI training dataset to lowercase. We then use a scispaCy model pre-trained on the en_core_sci_lg corpus for tokenization and clinical named entity recognition (CNER) (Neumann et al., 2019a). Next, we merge multi-token entities, using underscores as delimiters—e.g., “brain injury” → “brain_injury”.

When computing token-class pointwise mutual information (PMI), we exclude tokens that appear less than five times in the overall training dataset’s hypotheses. Then, following Gururangan et al. (2018), who apply add-100 smoothing to raw counts to highlight particularly discriminative token-class co-occurrence patterns, we apply add-50 smoothing to raw counts. Our approach is similarly motivated; our choice of 50 reflects the smaller state space associated with a focus on the clinical domain.

A.3 Semantic Analysis of Heuristics

To perform the statistical analysis presented in Section 5, we take the premise-hypothesis pairs from the MedNLI training, dev, and test splits, and combine them to produce a single corpus. We use a scispaCy model pre-trained on the en_core_sci_lg corpus for tokenization and entity linking (Neumann et al., 2019b), and link against the Medical Subject Headings (MeSH) knowledge base. We take the top-ranked knowledge base entry for each linked entity. Linking against MeSH provides a unique concept id, canonical name, alias(es), a definition, and one or more MeSH tree numbers for each recovered entity. Tree numbers convey semantic type information by embedding each concept into the broader MeSH hierarchy. We operationalize each of our heuristics with a set of MeSH-informed semantic properties, which are defined as follows:

1. **Hypernym Heuristic**: a premise-hypothesis pair satisfies this heuristic if specific clinical concept(s) appearing in the premise appear in a more general form in the hypothesis. Formally: \( \{(p, h) \mid \varphi(p) \subseteq \varphi(h)\} \). MeSH tree numbers are organized hierarchically, and increase in length with specificity. Thus, when a premise entity and hypothesis entity are left-aligned, the hypothesis entity is a hypernym for the premise entity if the hypothesis entity is a substring of the premise entity. To provide a concrete example: diabetes mellitus is an endocrine system disease; the associated MeSH tree numbers are C19.246 and C19, respectively.

2. **Probable Cause Heuristic**: a premise-hypothesis pair satisfies this heuristic if: (1) the premise contains one or more MeSH entities belonging to high-level categories C (diseases), D (chemicals and drugs), E (analytical, diagnostic and therapeutic techniques, and equipment) or F (psychiatry and psychology); and (2) the hypothesis contains one or more MeSH entities that can be interpreted as providing a plausible causal or behavioral explanation for the condition, finding, or event described in the premise (e.g., smoking, substance-related disorders, mental disorders, alcoholism, homelessness, obesity).

3. **Everything Is Fine Heuristic**: a premise-hypothesis pair satisfies this heuristic if the hypothesis contains one or more of the same MeSH entities as the premise (excluding the patient entity, which appears in almost all notes) and also contains: (1) a negation word or phrase (e.g., does not have, no finding, no, denies); or (2) a word or phrase that affirms the patient’s health (e.g., normal, healthy, discharged).

For each heuristic, we subset the complete dataset to find pattern-satisfying premise-heuristic pairs. We use this subset when performing the \( \chi^2 \) tests.

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https://meshb.nlm.nih.gov/treeView
A.4 Adversarial Filtering

When implementing AFLite, we follow Sakaguchi et al. (2020). We use a smaller training set size of $m = 5620$, but keep the remaining hyperparameters unchanged, such that the ensemble consists of $n = 64$ logistic regression models, the filtering cutoff, $k = 500$, and the filtering threshold $\tau = 0.75$. 