Extracting Structured Data from Physician-Patient Conversations
By Predicting Noteworthy Utterances

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Abstract. Despite diverse efforts to mine various modalities of medical data, the conversations between physicians and patients at the time of care remain an untapped source of insights. In this paper, we leverage this data to extract structured information that might assist physicians with post-visit documentation in electronic health records, potentially lightening the clerical burden. In this exploratory study, we describe a new dataset consisting of conversation transcripts, post-visit summaries, corresponding supporting evidence (in the transcript), and structured labels. We focus on the tasks of recognizing relevant diagnoses and abnormalities in the review of organ systems (RoS). One methodological challenge is that the conversations are long (around 1500 words), making it difficult for modern deep-learning models to use them as input. To address this challenge, we extract noteworthy utterances—parts of the conversation likely to be cited as evidence supporting some summary sentence. We find that by first filtering for (predicted) noteworthy utterances, we can significantly boost predictive performance for recognizing both diagnoses and RoS abnormalities.

Introduction

Medical institutions collect vast amounts of patient data in Electronic Health Records (EHRs), including family history, past surgeries, medications and more. Such EHR data helps physicians recall past visits, assess the trajectory of a patient’s condition over time, and access crucial information (e.g., drug allergies) in emergency scenarios. However, entering data in the EHR can be a tedious and time consuming for physicians. For every hour of visiting patients, physicians spend around 45 minutes on EHR documentation [21], and often need to complete documentation outside of work hours, a significant contributor to burnout [8]. Physicians spend much of the EHR documentation time recalling and manually entering information discussed with the patient (e.g., reported symptoms). While transcribing physician-patient discussions could aid EHR documentation, such conversations are long (10 minutes / 1500 words in our dataset) and difficult to read due to redundancies and disfluencies typical of conversation.

To mitigate the burden of EHR documentation, we leverage transcribed physician-patient conversations to automatically extract structured data. As an initial investigation,
we explore two prediction tasks using the physician-patient conversation as input: relevant diagnosis prediction, and organ system abnormality prediction. In the first task, we extract the set of diagnosis mentioned in the conversations that are relevant to the chief complaint of the patient (i.e. the purpose of the visit), omitting irrelevant diagnosis. For instance, a patient’s diagnosis of hypercholestremia (high cholesterol) may be relevant if his visit is for hypertension but not relevant if the visit is for common cold. For the second task, we recognize the organ systems for which the patient reported an abnormal symptom during a review. For instance, a patient whose chief complaint is diabetes might report fatigue (symptom) indicating a musculoskeletal (system) abnormality. Taken together, the diagnosis and symptomatic organ systems can provide a high-level overview of patient status to aid physicians in post-visit EHR documentation.

We formulate our tasks as multilabel classification and evaluate task performance for a medical-entity-based string-matching baseline, traditional learning approaches (e.g., logistic regression), and state-of-the-art neural approaches (e.g., BERT). One challenge is that conversations are long, containing information irrelevant to our tasks (e.g., small talk). A crucial finding is that a filtering-based approach to pre-select important parts of the conversation (we call them “noteworthy” utterances/sentences) before feeding them into a classification model significantly improves the performance of our models, increasing micro-averaged F1 scores by 10 points for diagnosis prediction and 5 points for RoS abnormality prediction. We compare different ways of extracting noteworthy sentences, such as using a medical entity tagger and training a model to predict such utterances, using annotations present in our dataset. An oracle approach using ground truth noteworthy sentences annotated in the dataset, boosts performance of the downstream classifiers significantly and, remarkably, we are able to realize a significant fraction of that gain by using our learned filters.

We find that using sentences that are specifically noteworthy with respect to medical diagnoses works best for the diagnosis prediction task. In contrast, for the RoS abnormality prediction task, the best performance is achieved when using sentences extracted by a medical entity tagger along with sentences predicted to be noteworthy with respect to review of systems.

Related Work

Prior work has focused on qualitative and quantitative evaluation of conversations between physicians and patients, which has been surveyed by [17]. Researchers have analyzed patients’ questions to characterize their effects on the quality of interaction[18], and tried to draw correlations between questioning style of physicians and the kind of information revealed by the patients [19]. Although research on extracting information from clinical conversations is scarce, there is significant work on extracting information from other forms of conversation such as summarizing email threads [14] and decisions in meetings [24].

Compared to patient-physician conversations, EHR data has been heavily leveraged for a variety of tasks, including event extraction [6], temporal prediction [3], and de-identification [5]. We point to [20] for an overview. Researchers have used patient admission notes to predict diagnoses [11]. Using content from certain specific sections of
the note improves performance of diagnosis extraction models when compared to using the entire note [4]. In our work too, making diagnosis predictions on a smaller part of conversations consisting of filtered noteworthy sentences leads to better model performance. Leveraging extracted symptoms from clinical notes using Metamap [2] medical ontology improves performance on diagnosis prediction [9]. This shows the usefulness of incorporating domain knowledge for diagnosis prediction, which we have also leveraged for our tasks by using a medical entity tagging system. Beyond diagnosis prediction, EHR data has been used to extract other information such as medications and lab tests [25], including fine-grained information like dosage and frequency of medicines and severity of diseases [10].

The systems in all of this work are based on clinical notes in the EHR, which are abundant in datasets. The research on information extraction from medical conversations is scarce likely owed in part to the paucity of datasets containing both medical conversations and annotations. Creating such a dataset is difficult due to the medical expertise that is required to annotate medical conversations with tags such as medical diagnoses and lab test results. One notable work in this area extracts symptoms from patient-physician conversations [16]. Their model takes as input snippets of 5 consecutive utterances and predicts whether the snippet has a symptom mentioned and experienced by the patient, using a recurrent neural network. In contrast, we make predictions of diagnoses and RoS abnormalities from an entire conversation using a variety of models including modern techniques from deep NLP, and introduce an approach to aid this by filtering out noteworthy sentences from the conversation.

Dataset

This paper addresses a dataset of human-transcribed physician-patient conversations. The dataset includes 2732 cardiologist visits, 2731 family medicine visits, 989 interventional cardiologist visits, and 410 internist visits. Each transcript consists of time-stamped utterances with speaker labels. A typical conversation consists of 200-250 utterances. The median utterance is short (Figure 1a), possibly due to the high frequency of back-chanelling (e.g., “umm-hmm”, “okay”, etc.). In total, each conversation contains around 1500 words (Figure 1b).

In our dataset, the transcribed conversations are coupled with corresponding structured text summaries and summary annotations. The structured text summaries (SOAP notes) are typically written by a physician to summarize a patient visit, and their annotations were constructed by expert clinical annotators who received task-specific training. The acronym SOAP in SOAP note stands for the four sections of the note: The (S)ubjective section contains a subjective accounting of the patient’s current symptoms, and a history of the present illness, and miscellaneous details. The (O)bjective section contains objective information such as results from lab tests, and observations from a physical examination. The (A)ssessment and (P)lan sections contain the inferences made by the physician, including the differential diagnosis, and the plan for treatment, including further tests, planned changes to the patient’s medications, other non-pharmaceutical therapeutics, and more.
In total, our dataset consists of 6862 datapoints (i.e., physician-patient conversation transcripts with corresponding annotated notes), which we have then divided into train and test sets with sizes 6270 and 592, respectively. To train our models, we set aside 500 points as a validation set for tuning hyperparameters. The number of datapoints and the splits are the same for both the tasks.

In our dataset, each line in a SOAP note is classified into one of 12 total subsections within one of the high-level Subjective, Objective, Assessment, or Plan sections. For example, subsections for the Subjective section include Subjective: Review Of Systems and Subjective: Past Medical History. Each line in a SOAP note appears alongside structured categorical or numerical metadata. For instance, a SOAP note line about medication (e.g., “Take Aspirin once a day.”) may be coupled with structured data for the medication name (e.g., “Aspirin”) and the dosage (e.g., “daily”). Each SOAP note line is also associated with the lines in the transcript that were used as evidence by the annotator create the line and its metadata. Each SOAP note line with its associated metadata, i.e., SOAP note entry, uses an average of 3.85 transcript lines as evidence (Figure 1c).

We take subsets of information from the dataset described above to design datasets for the relevant diagnosis prediction and review of systems abnormality prediction tasks.

**Relevant Diagnosis Prediction**

Given a physician-patient conversation, we aim to extract the mentioned past and present diagnoses of the patient that are relevant to the primary reason for the patient’s visit (called the Chief Complaint). For each conversation, we create a list of the Chief Complaint and related medical problems by using categorical tags associated with the following subsections of the SOAP note:

1. The Chief Complaint of the patient from Subjective: Chief Complaint the subsection of the SOAP note.
Table 1: Diagnoses and abnormal systems extracted from the train+validation split of the dataset with their number of occurrences

| Diagnosis                  | Frequency | System      | Frequency |
|----------------------------|-----------|-------------|-----------|
| hypertension               | 1573      | cardiovascular | 2245     |
| diabetes                   | 1423      | musculoskeletal | 1924     |
| atrial fibrillation        | 1335      | respiratory  | 1401     |
| hypercholesterolemia       | 1023      | gastrointestinal | 878      |
| heart failure              | 584       | skin        | 432      |
| myocardial infarction      | 386       | head        | 418      |
| arthritis                  | 288       | neurologic  | 385      |
| cardiomyopathy             | 273       |             |          |
| coronary arteriosclerosis  | 257       |             |          |
| heart disease              | 240       |             |          |
| chronic obstructive lung disease | 235 |             |          |
| dyspnea                    | 228       |             |          |
| asthma                     | 188       |             |          |
| sleep apnea                | 185       |             |          |
| depression                 | 148       |             |          |

2. All medical problems in the Subjective: Past Medical History subsection tagged with “HPI” (History of Present Illness) to signify that they are related to the Chief Complaint.

3. The medical problem tags present in the Assessment and Plan: Assessment subsection of the SOAP note.

We then simplified the medical problem tags by converting everything to lowercase, and removing elaborations given in parentheses. For example, we simplify “hypertension (moderate to severe)” to hypertension”. For each of the 20 most frequent tags retrieved after the previous simplifications, we searched among all medical problems and added the ones that had the original tag as a substring. For example, “systolic hypertension” was merged into “hypertension”. After following the above procedure on the training and validation set, we take the 15 most frequent medical problem tags (Table 1) and restrict the task to predicting whether each of these medical problems were diagnosed for a patient or not.

Review of Systems (RoS) Abnormality Prediction

Given a physician-patient conversation, we also predict the organ systems (e.g., respiratory system) for which the patient predicted a symptom (e.g., trouble breathing). During a patient’s visit, the physician conducts a Review of Systems (RoS), where the physician reviews organ systems and potential associated symptoms and asks if the patient is experiencing each symptom. In our dataset SOAP notes, the Subjective: Review of Systems subsection contains annotated observations from the RoS, each containing a system, symptom, and result. For instance, a system (e.g., “cardiovascular”), an associated symptom (e.g., “chest pain or discomfort”) and a result based on patient feedback
(e.g., “confirms”, “denies”). To reduce sparsity in the data for system/symptom pairs, we consider only systems and whether or not each system contained a confirmed symptom. We also consider only the set of 7 systems for which more than 5% of patients reported abnormalities, for prediction (Table 1).

Methods

We use a single suite of models for both tasks.

Input-agnostic baseline We establish the best value of each metric that can be achieved without using the input (i.e., an input-agnostic classifier). The behavior of the input-agnostic classifier depends on the metric. For example, to maximize accuracy, the classifier predicts the majority class (usually negative) for all diagnoses. On the other hand, to maximize F1 and recall, the classifier predicts the positive class for all diagnoses. To maximize AUC and precision-at-1, the classifier assigns probabilities to each diagnosis according to their prevalence rates. For a detailed description of multilabel performance metrics, we point to [12].

Medical-entity-matching baseline This baseline uses a traditional string-matching tool. For extracting relevant diagnoses, for each diagnosis, we check to see whether it is mentioned in the conversation. Since a diagnosis can be expressed in different ways, e.g., “myocardial infarction” has the same meaning as the common term “heart attack”, we use a system for tagging medical terms (QuickUMLS) that maps strings to medical entities with a unique ID. For example, “hypertension” and “high blood pressure” are both mapped to the same ID.

For predicting RoS abnormalities, our baseline predicts that the person has an abnormality in a system if any symptom related to the system is mentioned in the text as detected by QuickUMLS. The symptoms checked for each system are taken from the RoS tags in the dataset. For example, the cardiovascular system has symptoms like “chest pain or discomfort” and “palpitations, shortness of breath”.

Learning based methods We apply the following classical models: Logistic Regression, Support Vector Classifier, Multinomial Naive Bayes, Random Forest, and Gradient Boosting. We use bag-of-words representation of conversations with unigrams and bigrams with TF-IDF transform on the features.

We also applied state of the art neural methods on the problem. We classified diagnoses and RoS abnormalities as present or not using two BERT models with wordpiece [26] tokenization—one generic, pretrained BERT model, and one pretrained BERT model that is finetuned on clinical text [1]. Each of our BERT models are 12-layered with a hidden size of 768. The final hidden state of the [CLS] token is taken as the fixed-dimensional pooled representation of the input sequence. This is fed into a linear layer with sigmoid activation and output size equal to the number of prediction classes (15 for diagnosis prediction and 7 for the RoS abnormality prediction), thus giving us the probability for each class. Since the pretrained BERT models do not support
a sequence length of more than 512 tokens, we break up individual conversations into chunks of 512 tokens, pass the chunks independently through BERT, and mean-pool their [CLS] representations. Due to memory constraints, we only feed the first 2040 tokens of a conversation into the model.

**Hybrid models**

The long length of the input sequence makes the task difficult for the neural models. We tried a variety of strategies to pre-filter the contents of the conversation so that we only feed in sentences that are more relevant to the task. We call such sentences *noteworthy*. We have 3 ways for deciding if a sentence is noteworthy, which lead to 3 kinds of noteworthy sentences.

- **UMLS-noteworthy**: We designate a sentence as noteworthy if the QuickUMLS medical tagger finds an entity relevant to the task (e.g., a diagnosis or symptom) as defined in the medical-entity-matching baseline.
- **All-noteworthy**: We deem a sentence in the conversation noteworthy if it was used as evidence for any line in the annotated SOAP note. We train a classifier to predict the noteworthy sentences given a conversation.
- **Diagnosis/RoS-noteworthy**: Here, only those sentences that were used as evidence for an entry containing the ground truth tags (diagnosis/RoS abnormality) that we are trying to predict are deemed noteworthy.

In addition to trying out these individual filtering strategies, we also try their combinations as we shall discuss in the following section.

**Results and Discussion**

**Metrics**

We evaluate the performance of models using the following metrics: accuracy, area under the receiver-operator characteristics (AUC), F1 score, and precision-at-1. Because this is a 15-label multilabel classification task reporting aggregate scores across labels requires some care. For both F1 and AUC, we aggregate scores using both micro- and macro-averaging following the metrics for multilabel diagnosis prediction in [13]. Macro-averaging averages scores calculated separately on each label, while micro-averaging pools predictions across labels before calculating a single metric. We also compute precision-at-1 to capture the percentage of times that each model’s most confident prediction is correct (i.e., the frequency with which the most confidently predicted diagnosis actually applies).

**Results**

We evaluated the performance of all models aggregated across classes on the tasks of relevant diagnosis prediction (Table 2) and RoS abnormality prediction (Table 3). Predicting RoS abnormality proves to be a more difficult task than predicting relevant
Table 2: Aggregate results for the medical diagnosis prediction task. AN: predicted noteworthy utterances, DN: utterances predicted to be noteworthy specifically concerning a summary passage discussing diagnoses, F2K: UMLS-extracted noteworthy utterances with added top predicted AN/DN utterances to get K total utterances, M-: macro average, m-: micro average

| Model                              | Accuracy | M-AUC | M-F1  | m-AUC | m-F1  | Precision-at-1 |
|------------------------------------|----------|-------|-------|-------|-------|----------------|
| Input agnostic baseline            | 0.9189   | 0.5000| 0.1414| 0.7434| 0.3109| 0.2027         |
| UMLS Medical Entity Matching       | 0.9122   | 0.8147| 0.5121| 0.8420| 0.5833| 0.5034         |
| Logistic Regression                | 0.9417   | 0.8930| 0.2510| 0.9317| 0.5004| 0.6064         |
| LinearSVC                          | 0.9395   | 0.8959| 0.2113| 0.9354| 0.4603| 0.6199         |
| Multinomial NaiveBayes             | 0.9269   | 0.7171| 0.0615| 0.8296| 0.1938| 0.4848         |
| Random Forest                      | 0.9212   | 0.8868| 0.0155| 0.8795| 0.0541| 0.5304         |
| Gradient Boosting Classifier       | 0.9467   | 0.9181| 0.5024| 0.9447| 0.6514| 0.5861         |
| BERT                               | 0.9452   | 0.8953| 0.4413| 0.9365| 0.6009| 0.6199         |
| CLINICALBERT (CBERT)               | 0.9476   | 0.9040| 0.4573| 0.9413| 0.6029| 0.6300         |
| AN+CBERT                           | 0.9511   | 0.9222| 0.4853| 0.9532| 0.6561| 0.6470         |
| DN+CBERT                           | 0.9551   | 0.9342| 0.5655| 0.9616| 0.7029| **0.6621**     |
| UMLS+CBERT                         | 0.9519   | 0.8615| 0.5238| 0.9290| 0.6834| 0.6030         |
| UMLS-AN-CBERT                      | 0.9541   | 0.9261| 0.5317| 0.9588| 0.6803| **0.6621**     |
| UMLS-DN-CBERT                      | 0.9510   | 0.9359| 0.5210| 0.9593| 0.6641| 0.6368         |
| UMLS-F2K-AN+CBERT                  | **0.9554**| 0.9188| 0.5599| 0.9567| **0.7139**| 0.6487         |
| UMLS+F2K-DN+CBERT                  | 0.9535   | 0.9354| 0.5301| 0.9610| 0.6911| 0.6486         |
| (Oracle) AN+CBERT                  | 0.9509   | 0.9418| 0.5500| 0.9588| 0.6789| 0.6250         |
| (Oracle) DN+CBERT                  | 0.9767   | 0.9771| 0.7419| 0.9838| 0.8456| 0.7162         |

Diagnoses as reflected by the lower values achieved on all metrics. We hypothesize that this is because of the variety of symptoms that can be checked for each system. The cardiovascular system has 152 symptoms in our dataset, including ‘pain in the ribs’, ‘palpitations’, ‘increased heart rate’ and ‘chest ache’. A learning-based model would must learn to associate all of these symptoms with the cardiovascular system in addition to recognizing whether or not any given patient experiences the symptom.

For diagnosis prediction, medical-entity-matching baseline achieves better F1 scores than many of the classical models (Table 2). The high recall and low precision together demonstrate that if a diagnosis has been made for the patient, the diagnosis is often directly mentioned in the conversation but the converse is not true. Among the BERT-based models, we see a modest improvement in F1 and precision-at-1 when using ClinicalBERT instead of the common BERT. Using predicted noteworthy sentences from the transcript instead of all of the transcript generally yielded performance gains. For diagnosis prediction, models that only ingest predicted diagnosis-noteworthy sentences rather than all-noteworthy sentences perform the best for a majority of the metrics. For RoS abnormality prediction, the trend reverses and using predicted RoS-noteworthy sentences performs worse than using predicted all-noteworthy sentences from the transcript. If we train on oracle noteworthy sentences, we achieve a precision-at-1 of 0.72 for diagnosis prediction and 0.50 for RoS abnormality prediction. Note that the max-
| Model                               | Accuracy | M-AUC  | M-F1   | m-AUC  | m-F1   | Precision-at-1 |
|-------------------------------------|----------|--------|--------|--------|--------|----------------|
| Input agnostic baseline             | 0.8677   | 0.5000 | 0.2235 | 0.7024 | 0.3453 | 0.3040         |
| UMLS Medical Entity Matching        | 0.4532   | 0.7074 | 0.2797 | 0.7454 | 0.3079 | 0.3226         |
| Logistic Regression                 | 0.8819   | 0.8050 | 0.2102 | 0.8496 | 0.3506 | 0.3952         |
| LinearSVC                           | 0.8798   | 0.8093 | 0.1623 | 0.8516 | 0.3025 | 0.3986         |
| Multinomial NaiveBayes              | 0.8687   | 0.6183 | 0.0369 | 0.7383 | 0.0653 | 0.3818         |
| Gradient Boosting Classifier        | 0.8740   | 0.7949 | 0.2500 | 0.8405 | 0.3324 | 0.4020         |
| Random Forest                       | 0.8677   | 0.7210 | 0.0000 | 0.7670 | 0.0000 | 0.3412         |
| BERT                                | 0.8818   | 0.8240 | 0.3304 | 0.8620 | 0.4275 | 0.3986         |
| CLINICALBERT (CBERT)                | 0.8784   | 0.8305 | 0.3878 | 0.8667 | 0.4857 | 0.4003         |
| AN+CBERT                            | 0.8837   | 0.8491 | 0.3560 | 0.8801 | 0.4761 | 0.4274         |
| RN+CBERT                            | 0.8861   | 0.8391 | 0.3720 | 0.8788 | 0.4925 | 0.4054         |
| UMLS+CBERT                          | 0.8769   | 0.8036 | 0.3421 | 0.8464 | 0.4457 | 0.3902         |
| UMLS+AN+CBERT                       | 0.8868   | 0.8252 | 0.3039 | 0.8626 | 0.4515 | 0.4139         |
| UMLS+RN+CBERT                       | 0.8810   | 0.8390 | 0.3122 | 0.8745 | 0.4152 | 0.3902         |
| UMLS+F2K-AN+CBERT                   | 0.8834   | 0.8169 | 0.2385 | 0.8585 | 0.3894 | 0.4189         |
| UMLS+F2K-RN+CBERT                   | 0.8827   | 0.8595 | 0.3987 | 0.8895 | 0.5308 | 0.4291         |
| (Oracle) AN+CBERT                   | 0.8846   | 0.8535 | 0.3662 | 0.8841 | 0.5062 | 0.4375         |
| (Oracle) RN+CBERT                   | 0.9454   | 0.9595 | 0.7235 | 0.9703 | 0.7847 | 0.4966         |

Table 3: Aggregate results for the RoS abnormality prediction task. AN: predicted noteworthy utterances, RN: utterances predicted to be noteworthy specifically concerning a summary passage discussing review of systems, F2K: UMLS-extracted noteworthy utterances with added top predicted AN/RN utterances to get K total utterances, M-: macro average, m-: micro average

| Disease                        | Prevalence rate | Precision | Recall | F1    | Accuracy | AUC  | CP@1     |
|--------------------------------|-----------------|-----------|--------|-------|----------|------|----------|
| atrial fibrillation             | 0.2568          | 0.8667    | 0.9408 | 0.9022| 0.9476   | 0.9773| 0.3597   |
| hypertension                    | 0.2027          | 0.6667    | 0.4833 | 0.5604| 0.8463   | 0.8817| 0.0995   |
| diabetes                        | 0.1959          | 0.8411    | 0.7759 | 0.8072| 0.9274   | 0.9586| 0.1837   |
| hypercholesterolemia            | 0.1216          | 0.5694    | 0.5694 | 0.5694| 0.8953   | 0.9246| 0.0740   |
| heart failure                   | 0.1014          | 0.8049    | 0.5500 | 0.6535| 0.9409   | 0.9692| 0.0638   |
| myocardial infarction           | 0.0861          | 0.8571    | 0.8235 | 0.8400| 0.9730   | 0.9857| 0.0995   |
| coronary arteriosclerosis       | 0.0372          | 0.3846    | 0.2273 | 0.2857| 0.9578   | 0.8307| 0.0051   |
| chronic obstruct. lung disease  | 0.0372          | 0.7391    | 0.7727 | 0.7556| 0.9814   | 0.9665| 0.0281   |
| dyspnea                         | 0.0304          | 0.5000    | 0.0556 | 0.1000| 0.9696   | 0.9608| 0.0077   |
| depression                      | 0.0304          | 0.6471    | 0.6111 | 0.6286| 0.9780   | 0.9555| 0.0230   |
| asthma                          | 0.0287          | 0.8462    | 0.6471 | 0.7333| 0.9865   | 0.9951| 0.0230   |
| cardiomyopathy                  | 0.0236          | 0.7143    | 0.7143 | 0.7143| 0.9865   | 0.9779| 0.0128   |
| heart disease                   | 0.0236          | 0.0000    | 0.0000 | 0.0000| 0.9764   | 0.7058| 0.0026   |
| arthritis                       | 0.0220          | 0.3636    | 0.3077 | 0.3333| 0.9730   | 0.9843| 0.0128   |
| sleep apnea                     | 0.0186          | 0.6667    | 0.5455 | 0.6000| 0.9865   | 0.9937| 0.0051   |

Table 4: Performance of our best diagnosis prediction model (DN+CBERT) at predicting individual diagnoses. CP@1: contribution to precision-at-1, the fraction of times a disease was a correct top prediction
| System          | Prevalence rate | Precision | Recall | F1    | Accuracy | AUC    | CP@1 |
|-----------------|-----------------|-----------|--------|-------|----------|--------|------|
| cardiovascular  | 0.3041          | 0.5867    | 0.7333 | 0.6519| 0.7618   | 0.8475 | 0.5079|
| musculoskeletal | 0.2010          | 0.5893    | 0.5546 | 0.5714| 0.8328   | 0.8579 | 0.2402|
| respiratory     | 0.1571          | 0.5231    | 0.3656 | 0.4304| 0.8480   | 0.8639 | 0.1063|
| gastrointestinal| 0.0845          | 0.5217    | 0.4800 | 0.5000| 0.9189   | 0.8636 | 0.0669|
| head            | 0.0828          | 0.4412    | 0.3061 | 0.3614| 0.9105   | 0.9252 | 0.0591|
| neurologic      | 0.0574          | 0.0000    | 0.0000 | 0.0000| 0.9426   | 0.7864 | 0.0000|
| skin            | 0.0389          | 0.6667    | 0.1739 | 0.2759| 0.9645   | 0.8719 | 0.0197|

Table 5: Performance of our best RoS abnormality prediction model (UMLS+F2K-RN+CBERT) at predicting abnormalities in each system. CP@1: contribution to precision-at-1, the fraction of times an RoS abnormality was a correct top prediction.

Table 5: Performance of our best RoS abnormality prediction model (UMLS+F2K-RN+CBERT) at predicting abnormalities in each system. CP@1: contribution to precision-at-1, the fraction of times an RoS abnormality was a correct top prediction.
Fig. 2: Precision-at-1 at different thresholds of the diagnosis-noteworthy utterance classifier. Average number of noteworthy sentences extracted in parentheses at the binary prediction of each diagnosis/RoS abnormality (Table 4 and Table 5). We see that generally diagnoses that are more common are detected better. One exception is hypertension which has a low recall and precision despite affecting around 20% of the patients. The instances of hypertension that are not identified by our model show that it is rarely mentioned explicitly during conversation. Instead, it needs to be inferred by values of blood pressure readings and phrases like “that blood pressure seems to creep up a little bit”. This indirect way in which hypertension is mentioned possibly makes it harder to detect accurately. In contrast, atrial fibrillation is usually mentioned explicitly during conversation, which is why even the medical-entity-matching baseline achieves a high recall of 0.83 at predicting atrial fibrillation. The model has the worst performance for predicting heart disease. We think it is due to a combination of low frequency and the generic nature of the class. We found that the heart disease tag is used in miscellaneous situations like genetic defect, weakness in heart’s function, or pain related to stent placement.

We also calculate the contribution to precision-at-1 for each class for both tasks. This gives us a sense of how often a diagnosis/RoS abnormality becomes the model’s top prediction. We do not want a situation where only the most frequent diagnoses/RoS abnormalities are predicted with the highest probability and the rarer classes are never represented among the top predictions. We define the contribution to precision-at-1 for a class as the number of times it was a correct top prediction divided by the total number of correct top predictions made by the model. We see that for both tasks, contribution to precision-at-1 is roughly in proportion to the prevalence rate of each diagnosis (Table 4 and Table 5). This suggests that the model predicts even the rarer diagnoses with enough confidence for them to show up as top predictions.

Experimental details
The hyperparameters of each learning based model are determined by tuning over the validation set. All models except the neural network based ones are sourced from
The UMLS based tagging system is taken from [22]. The BERT-based models are trained in AllenNLP [7]. The vanilla BERT model is the bert-base-uncased model released by Google and the clinical BERT model is taken from [1].

The BERT models have a learning rate of 0.00002. We tuned the probability threshold for predicting noteworthy sentences. The optimal threshold was 0.4 for predicting all noteworthy sentences, 0.1 for predicting diagnosis-related noteworthy sentences, and 0.02 for predicting RoS-related noteworthy sentences. Among the FillUptoK predictors for diagnosis prediction, the one using AllNoteworthy sentences had $K = 50$ and the one using diagnosis-noteworthy sentences has $K = 15$. For the FillUptoK predictors used for RoS abnormality prediction, the one using all-noteworthy sentences had $K = 50$ and the predictor using RoS-noteworthy sentences had $K = 20$.

The noteworthy sentence extractors are logistic regression models trained, validated and tested on the same splits of the dataset as the other models. All models are L2-regularized with the regularization constant equal to 1. The AUC scores for the classifiers extracting all, diagnosis-related, and RoS-related noteworthy sentences are 0.6959, 0.6689 and 0.7789 respectively.

**Conclusion and Future Work**

This work is a preliminary investigation into the utility of medical conversations for drafting SOAP notes. Although we have only tried predicting diagnoses and review of systems, there are more tasks that can be attacked using the annotations in the dataset we used (e.g., medications, future appointments, lab tests etc). Our work shows that extracting noteworthy sentences improves the performance significantly. However, the performance of noteworthy sentence extractors leaves room for improvement, a promising direction for future work. Currently, we are only predicting the organ system that has a reported symptom and not the exact symptom that was reported by the patient. This was because the frequency of occurrence of each symptom was fairly low. In future work, we plan to explore models capable of performing better on the long tail in clinical prediction tasks.

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