

Overview of the MEDIQA-Sum Task at ImageCLEF 2023: Summarization and Classification of Doctor-Patient Conversations*

Wen-wai Yim^{1,*}, Asma Ben Abacha¹, Griffin Adams², Neal Snider³ and Meliha Yetisgen⁴

¹Microsoft Health AI, Redmond, 98052, USA

²Columbia University, New York, 10027 USA

³Nuance Communications, Burlington, 01803 USA

⁴University of Washington, Seattle, 98109 USA

Abstract

This paper presents the overview of the MEDIQA-Sum task at ImageCLEF 2023. MEDIQA-Sum 2023 includes three subtasks, in which a doctor-patient dialogue source is given, and participants were tasked with (A) dialogue2topic classification, e.g. classifying the conversation into one of twenty section header categories, (B) dialogue2note snippet generation, e.g. generating clinical note section text additionally given the clinical section header, and (C) dialogue2note full note summarization, e.g. generating a full clinical note. Twelve teams participated with a total of 48 runs. The best teams achieved 0.8 Accuracy on topic classification (subtask A) and ROUGE-1 scores of 0.43 and 0.49 F1, for subtasks B and C, respectively.

Keywords

Dialogue Summarization, Clinical Note Generation, Natural Language Generation, Doctor-patient Conversations

1. Introduction

To date, large language models (LLM) pre-trained with massive amounts of data have led to surprisingly large out-of-the-box gains across all sectors of machine learning. This is true in tasks that these models were not trained for, e.g. classification tasks, complex tasks that require special syntax and domain knowledge, e.g. generating code based on the functional description, and even creative tasks, e.g. generating original poems given a subject prompt. One specific area to test such technology is the problem of clinical note generation from doctor-patient conversations. As LLM are built to generate, this is a very natural task; on the other hand, note creation in the health care space is a critical ubiquitous burdensome task for health-care professionals[1].

Note generation from doctor-patient conversations is a daily occurrence accompanying a doctor-patient encounter. The clinical note, like meeting notes, highlight important discussion

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*Corresponding author.

✉ yimwenwai@microsoft.com (W. Yim); abenabacha@microsoft.com (A. Ben Abacha);

griffin.adams@columbia.edu (G. Adams); neal.snider@nuance.com (N. Snider); melihay@uw.edu (M. Yetisgen)



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points, relevant history and future planned tests and treatments. While clinical notes are generated natively, doctor-patient conversations are not routinely recorded. Therefore acquisition and testing of such datasets present a prohibitive hurdle[2]. Other domain challenges which increase the difficulty of the task include (a) the existence of clinical note format varieties, as well as their semi-structured technical writing, conditioned on provider preferences, specialties, and institutions[1]; (b) the high diversity and topic spread of the doctor-patient conversation, depending on regional practices, socioeconomic origin, speech characteristics, and meeting discussion preferences; and (c) the length of the generated notes, which are often longer than the typical generation tasks.

To investigate the state-of-the-art performances in this space, we have conducted the MEDIQA-Sum 2023 task as part of IMAGECLEF 2023[3], a pilot task for multi-modal summarization. In the tradition of MEDIQA tasks that began in 2019[4]—hosting various tasks related to clinical language inference, consumer health question answering entailment and retrieval ranking, as well as clinical findings and consumer health question-answering summarization—this year’s edition tackles a summarization task that spans clinical dialogue as a source and the clinical note as the target. An overlapping dataset was part of the related ACL 2023 ClinicalNLP challenge MEDIQA-Chat 2023[5].

In the following sections, we introduce the tasks, describe the evaluation, present the participating teams’ results, as well as provide some insight on future directions.

2. Task Description

The MEDIQA-Sum 2023 overall task comprises three sub-tasks: (A) dialogue2topic (section header) classification, (B) dialogue2note summarization given the target section header, and (C) full-encounter dialogue2note summarization. Although it’s possible to perform each task in series, with one model or data being utilized for the next, each task could be participated in independently.

2.1. Subtask A - Section Header Topic Classification

In speech language processing, text classification is often used for categorizing dialogue acts, domains, and intents as for dialogue systems[6, 7, 8]; as well as for topic clustering for further speech language processing[9, 10]. We pose the task of dialogue text topic classification as a means of identifying whether the clinical information relevant in a dialogue relates to certain parts of the clinical note. Such a task can be viewed as one step in a multi-step processing of a long dialogue (e.g. clustering similar information) or may be used to get classification information for a short dialogue. Although we simplify the task here so that each dialogue snippet is one of several headers, in real conversations, the same snippets of text may pertain to multiple sections or may be included in different overlapping relevant text windows. Previous work in the area includes the classification of patient dialogue encounters at a sentence level to SOAP format or other categories[11, 12]. Meanwhile the task of clinical section header identification is a well-studied task in clinical NLP[13, 14, 15].

In this subtask, section headers were one of the following 20: Family History/Social History (fam/sochx), History of Present Illness (genhx), Past Medical History (pastmedicalhx), Chief

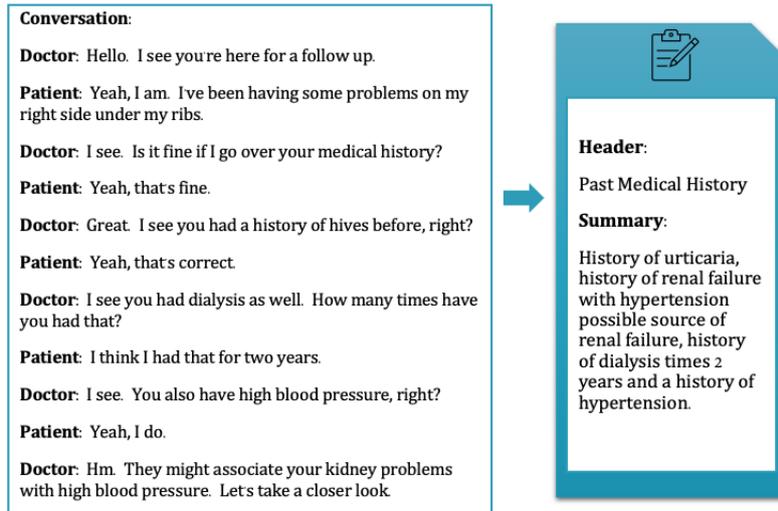


Figure 1: In Subtask A, short doctor-patient conversation can be categorized to a relevant section header. In Subtask B, The same conversation and a given section header can be used to generate a short clinical text snippet (example from the MTS-Dialog dataset).

Complaint [cc], Past Surgical History (pastsurgical), allergy, Review of Systems (ros), medications, assessment, exam, diagnosis, disposition, plan, Emergency Department Course (edcourse), immunizations, imaging, Gynecologic History (gynhx), procedures, other_history, and labs. An example of this problem is shown in Figure 1, where the header is the target output.

2.2. Subtask B - Short Dialogue2Note Summarization

Dialogue summarization encompasses variety of tasks, including spoken conversation and text chatting. Typical English open domain datasets are related to news headline summarization[16, 17]. Related dialogue summarization datasets include MedDialog[18], a dataset of online medical chats and their final treatment summaries, and SAMSUM dataset, a corpus of chat dialogues with manually created summaries[19]. Dialogue2note generation from doctor-patient conversations for short dialogue has been the subject of previous work[20], however their datasets are not open to the public. As shown in Figure 1, here available input includes the dialogue as well as the relevant section header from a short dialogue and the target output is the summary. Specifying the desired header as input is a realistic scenario, as the same dialogue snippet may be relevant to several sections; moreover, different note sections may require different language patterns.

Subtask A and B use the same test set. After Subtask A was closed, the gold standard section header was released so that it would be available as input to Subtask B.

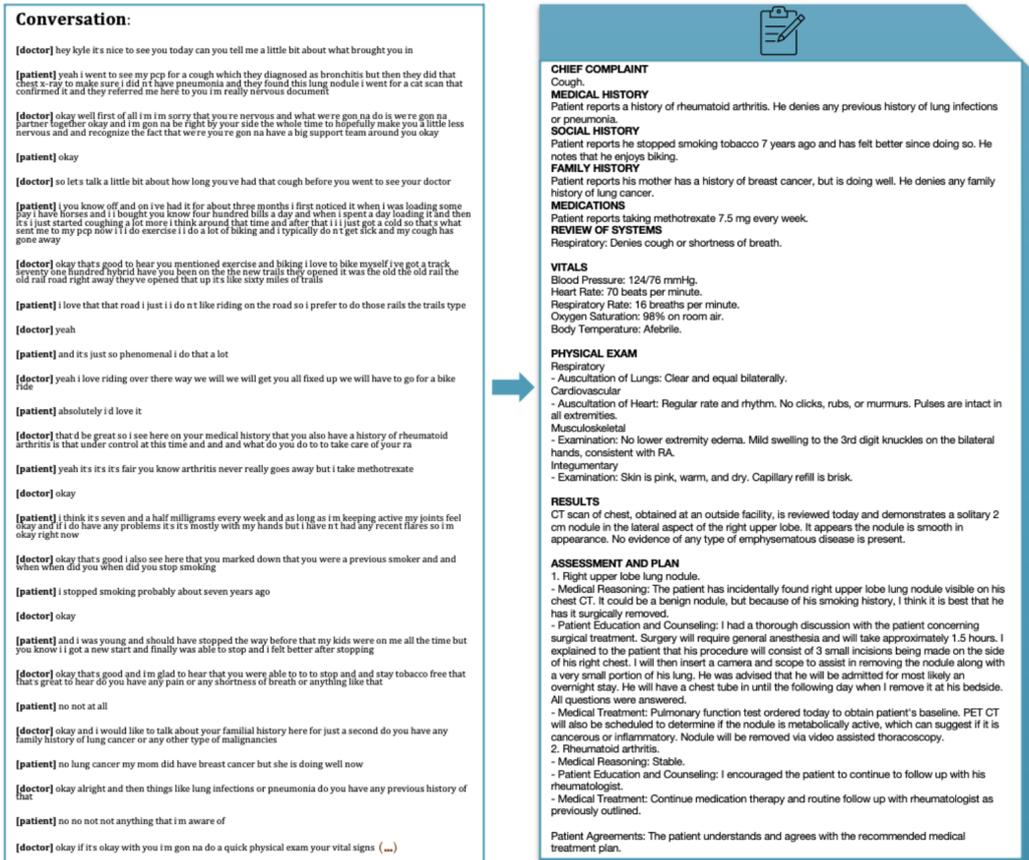


Figure 2: Task B: summarize each doctor-patient conversation to generate a full note with all relevant sections (example from the ACI-Bench dataset).

2.3. Subtask C - Full Dialogue2Note Summarization

In the full encounter summarization subtask, Subtask C, the objective is to generate a complete clinical note for each doctor-patient conversation, as shown in Figure 2. A similar task to this is the meeting summarization task, which includes long dialogues of multiple speakers as well as technical, at times semi-structured meeting notes[21, 22]. One challenge in this space is the long-document nature of notes. Similar issues arise in PubMed and arXiv scientific paper summarization, as well as BigPatent, BillSum, and GovReport summarizations[23, 24]. Previous works summarizing full doctor-patient conversations[25, 26] have not focused on full note generation and evaluation, rather splits full note generation targets into smaller note parts rather than the creation of the full note.

3. Dataset

The 2023 MEDIQA-Sum challenge includes data from two collections: MTS-Dialog[27] and ACI-BENCH[28]. Subtasks A and B consisted of 1,201 pairs of conversations and associated

section headers and contents; 100 examples in validation, and 200 pairs in test. Subtask C includes full encounters with 67 examples in training, 20 in validation, and 40 in test.

The train and validation set for all subtasks were featured in the MEDIQA-Chat 2023 task[5]; however with different test sets.

4. Evaluation Methodology

Subtask A topic classification was evaluated using accuracy. The subtask B snippet summarization was evaluated using the mean of BLEURT, BERTscore(microsoft/deberta- xlarge-mnli), and ROUGE-1; metrics found to be correlated to human evaluation in several independent health summarization datasets [29]. Full-encounter summarization in Subtask C used two metrics: (1) a full-note ROUGE-1 score and (2) an equally weighted division-based (subjective, objective_exam, objective_results, assessment_and_plan) aggregate score of the BLEURT, BERTscore, and ROUGE-1 metric[28].

Code repositories were required at submission. This was done to encourage high quality submissions as well as encourage participants to release code after the challenge. The organizers checked outputs of code against submitted runs and documented each team’s code replicability status as defined here:

1. Code runs and exactly reproduces
2. Code runs with minor differences
3. Results unstable due to non-deterministic components (e.g., generative API calls)
4. Results unstable
5. Code does not run under our configurations

We provided feedback on the shared codes and their outputs/errors to the participants.

5. Results and Discussion

Overall 12 teams participated with a total of 48 runs. Subtask A included 23 valid submissions among 11 teams. Subtask B included 16 submissions among 7 teams. Subtask C included 9 submissions among 4 teams. At most three runs were allowed per team in each subtask. With the exception of 1 team, all teams participated in Subtask A. Four teams participated in two subtasks. Three teams participated in all three subtasks. Table 1 shows the full breakdown.

Table 1

MEDIQA-Sum 2023: Participating teams, number of runs (with a limit of three runs/task), submitted codes, and working notes papers.

	team	affiliation	subtask	runs	code	paper
1	Cadence	Cadence Solutions, USA	A	1	2	[30]
2	ds4dh	University of Geneva, Switzerland	A	1	1	
3	HuskyScribe	University of Washington, USA	A,B,C	4	5,1,1	[31]
4	MLRG-JBTTM	Sri Sivasubramaniya Nadar College of Engineering, India	A	3	1	[32]
5	PULSAR	ASUS AICS / University of Manchester, Singapore, UK	B,C	5	1	[33]
6	SKKU-DSAIL	Department of Applied Artificial Intelligence, Sungkyunkwan University, South Korea	A,B	2	1	
7	SSNdhanyadiviyakavitha	Sri Sivasubramaniya Nadar College of Engineering, India	A	3	1	[34]
8	SSNSheerinKavitha	Sri Sivasubramaniya Nadar College of Engineering, India	A,B	6	5	[35]
9	StellEllaStars	University of Michigan , USA	A	3	1	[36]
10	SuryaKiran	Optum, India	A,B	4	1	[37]
11	Tredence	Tredence Inc, India	A,B,C	7	1	[38]
12	uetcorn	University of Engineering and Technology, VNUH, Vietnam	A,B,C	9	1	[39]

Table 2

Performance of the participating teams in the MEDIQA-Sum 2023 Subtask A on topic classification.

team	run	accuracy	rank	code_status
Cadence	run1	0.820	1	2
HuskyScribe	run1	0.815	2	5
Tredence	run2	0.800	3	1
Tredence	run1	0.800	3	1
StellEllaStars	run1	0.765	5	1
Tredence	run3	0.755	6	1
SSNSheerinKavitha	run3	0.740	7	1
SSNSheerinKavitha	run2	0.735	8	1
SuryaKiran	run1	0.735	8	1
SSNdhanyadiviyakavitha	run1	0.720	10	1
ds4dh	run1	0.710	11	1
uetcorn	run3	0.710	11	1
SKKU-DSAIL	run1	0.700	13	1
StellEllaStars	run2	0.695	14	1
SSNdhanyadiviyakavitha	run2	0.680	15	1
StellEllaStars	run3	0.675	16	1
uetcorn	run1	0.670	17	1
MLRG-JBTTM	run1	0.665	18	1
SSNdhanyadiviyakavitha	run3	0.660	19	1
uetcorn	run2	0.625	20	1
MLRG-JBTTM	run2	0.570	21	1
MLRG-JBTTM	run3	0.565	22	1
SSNSheerinKavitha	run1	0.140	23	1

The best teams achieved 0.8 Accuracy on Subtask A topic classification (Table 2) and an aggregate score of 0.43 for Subtask B (Table 3). The top two systems for Subtask C achieved ROUGE-1 at 0.49 F1 (Table 4) and aggregated scores at 0.44 (Table 5).

Subtask A submissions included classic machine learning algorithms as well as neural network based models. Specifically, for each category:

classical models

- SVM/Logistic regression: MLRG-JBTTM, SSNdhanyadivyaKavitha, SSNSheerinKavitha, StellellaStars
- KNN: MLRG-JBTTM
- Random Forest: SSNdhanyadivyaKavitha

pretrained models

- CBOW (with custom network): StellellaStars
- general models (bert, roberta, t5, longformer, bart): SSNSheerinKavitha, HuskyScribe, SKKU-DSAIL
- biomedical models (bioroberta, clinicalbert, bioclinicalbert, biomedical-roberta, clinical-longformer pubmedbert, clinicalT5): HuskyScribe, StellellaStars, SuryaKiran, Tredence

Pre-processing steps for the classical models included stop word removal, lower-casing, TF-IDF, and lemmatization. Eight out of 23 submissions either used additional training data or adjusted data sampling. The top team, Cadence, used bart-large and additionally augmented the training set with data produced by GPT3.5[30]. The second best system by the HuskyScribe team[31], used a T5 large model and fine-tuned on the training data. The two tied third best system by Tredence used a Clinical-Longformer and Biomedical-ROBERTA[38].

Table 3

Performance of the participating teams in the MEDIQA-Sum 2023 Subtask B on dialogue2note summarization.

team	run	aggregate_score	rank	code_status
SuryaKiran	run3	0.573	1	1
PULSAR	run2	0.569	2	1
PULSAR	run1	0.565	3	1
Tredence	run1	0.559	4	1
SuryaKiran	run2	0.559	5	1
SuryaKiran	run1	0.550	6	1
PULSAR	run3	0.538	7	1
HuskyScribe	run1	0.529	8	1
Tredence	run2	0.508	9	1
uetcorn	run1	0.481	10	1
uetcorn	run2	0.480	11	1
uetcorn	run3	0.479	12	1
SKKU-DSAIL	run1	0.461	13	1
SSNSheerinKavitha	run1	0.419	14	5
SSNSheerinKavitha	run2	0.419	14	5
SSNSheerinKavitha	run3	0.279	16	5

Subtask B primarily consisted of pre-trained sequence-to-sequence models fine-tuned on the training and validation sets. Eight out of 16 submissions used the gold standard section headers

released from Subtask A. Teams used similar families of models as shown below.

pretrained model families

- T5: HuskyScribe, PULSAR, SSNSheerinKavitha, SuryaKiran
- bart: SKKU-DSAIL, Tredence, SSNSheerinKavitha, SuryaKiran, UETCorn
- llama: PULSAR

The SSNSheerinKavitha team also experimented with a rule-based extractive system by selecting dialogue sentences based on scores related to word frequencies. The UETCorn team experimented with a mixture of conditioned reading comprehension extraction, using hand-crafted section-specific queries with rule-based processing. The best performing system was an ensemble method by the SuryaKiran team fined-tuned several BioBART-V2-large LoRA models (fine-tuned on different training folds) with both the dialogue and section header as inputs[37]. The best summary was selected using a semantic similarity approach. The second and third ranked systems by PULSAR, used a FLAN-T5 model and a FLAN-T5 model additionally pre-trained using a MIMIC III note term extraction objective.

Table 4

Performance of the participating teams in the MEDIQA-Sum 2023 Subtask C on dialogue2note summarization, ranked by ROUGE1.

team	run	rouge1	rank	code_status
Tredence	run2	0.500	1	1
uetcorn	run2	0.498	2	1
uetcorn	run3	0.497	3	1
Tredence	run1	0.486	4	1
uetcorn	run1	0.485	5	1
HuskyScribe	run1	0.470	6	1
HuskyScribe	run2	0.318	7	1
PULSAR	run2	0.294	8	1
PULSAR	run1	0.276	9	1

Table 5

Performance of the participating teams in the MEDIQA-Sum 2023 Subtask C on dialogue2note summarization, ranked by aggregate score.

team	run	agg_score	rank	code_status
Tredence	run1	0.455	1	1
Tredence	run2	0.454	2	1
uetcorn	run3	0.444	3	1
uetcorn	run2	0.443	4	1
uetcorn	run1	0.441	5	1
HuskyScribe	run1	0.413	6	1
HuskyScribe	run2	0.396	7	1
PULSAR	run2	0.305	8	1
PULSAR	run1	0.247	9	1

Subtask C featured a diverse set of systems that used creative means to circumvent a low-resource generation problem. Specifically, Uetcorn, HuskyScribe, and Tredence all divided the

problem into multiple parts. Firstly, relevant parts of the dialogue were grouped together as related to particular sections. Each team used a different method to achieve this; the UETCorn team identified relevant parts of dialogue for specific note section key points (e.g. “chief complaint” or “medications”), using a similarity function between dialogue sentences and a hand-crafted section-specific description; afterwards, several note generation strategies were used for each key point. HuskyScribe built a model classifying smaller dialogue exchanges into the same categories, while Tredence classified dialogues chunked by various window sizes. In the second step, grouped dialogue chunks were sent through a text generator to produce parts of the note. The use of pre-trained models such as BART/BioBART and FLAN-T5 for the generation was typical. The Uetcorn and Tredence team included some section/key-point specific questions as part of the generation input, e.g. (e.g. input: "question: {question} context: {conversation}", output: summary). The Uetcorn team also experimented with a reading comprehension answer extraction based on specially designed key point query (e.g. "names of medication used") and post-processing as in their Subtask B system. The HuskyScribe team additionally used Subtask A data to generate additional synthetic data for training. Finally, the completed note was assembled through concatenation and post-processing. Unlike the other three groups, the PULSAR team employed an end-to-end approach, experimenting with FLAN-T5 and llama models with additional data created using MTSamples data processed through GPT3.5.

6. Discussion and Conclusions

This year’s MEDIQA 2023 tasks, ACL ClinicalNLP MEDIQA-Chat Shared Tasks [5] and this ImageCLEF MEDIQA-Sum task, hosted similar problems on an overlapping dataset. A striking difference between the participants in this edition was that there were no GPT4 submissions. As GPT4 access requires a subscription, we can view the solutions from this evaluation lab as a whole to be constrained to only using open-source or free models and data.

In general, with the exception of the full-encounter task, scores in the two 2023 editions were comparable. Suggesting that many current off-the-self methods are still very competitive for classification and shorter generation tasks whereas longer generation may require more powerful and massive LLM. In MEDIQA-Chat Task A header generation scores were at 0.35-0.78 accuracy; the corresponding similar MEDIQA-Sum subtask A had a overlapping but larger range of 0.14-0.82 accuracy. The comparable MEDIQA-Sum subtask B was similar to MEDIQA-Chat subtask A snippet summarization with snippet summarization scores at a range of 0.37-0.58 aggregate score. In MEDIQA-Sum Subtask B snippet summarization, the scores were at 0.28-0.57 aggregate score; again with similar ranges. Finally the full-encounter task was MEDIQA-Chat in Task B, full-encounter generation ROUGE1 was at 0.28-0.61 and 0.21-0.65 for aggregate scoring. In this editions’ Subtask C, the ranges were at 0.28-0.50 ROUGE1 and 0.25-0.46 aggregate scoring; which were slightly lower than those in MEDIQA-Chat.

Classic meeting summarization systems have split the generation in several steps including topic identification, extractive summarization, and then abstractive summarization. In the MEDIQA-Sum challenges many of our systems followed this motif. Such a split may be the result of past models’ abilities to perform narrow tasks, as well as size constraints. With the latest LLM models as shown in MEDIQA-Chat, it is clear LLM can now perform the end-to-end

task competitively. However, recent work on GPT4 has shown that prompting for chain-of-thought reasoning, means multi-step generation may not be obsolete but may instead take a new form. We can track the progress of the field by continuing to benchmark on open datasets and shared tasks.

The results in the MEDIQA challenges are exciting, however there were limitations to this work. Although this is the largest source of both short and full-encounter dialogue2note generation datasets, the data here is relatively small and limited to a single institution with only a handful of content creators. There are many areas to further explore and expand. In terms of dataset expansion, we allude to at least three frontiers: (a) expanding to a larger content creation force which will enable more linguistic patterns and more transcript variations (including length); (b) incorporation of structured data as additional input (e.g. past labs and vitals) and output (e.g. orders); and (c) additional gold standard references, including multiple note references using the same note structure as well as additional gold standard summaries using a variety of note formats. For modeling, the challenges and learnings from our tasks point to needs in several exciting directions of research including increased attention to long-text and medical natural language generation evaluation methods, as well as studying performance of multi-modal generation and partial-inputs generation. We hope that these shared tasks are the small beginnings that will inspire further widespread study into automatic clinical note generation; and that these efforts can be translated into integrated technologies that may improve the quality and outcomes for both doctors and patients.

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