Fine Tuning QnA Chatbot Enhanced with RAG using FAISS Vector Database for Drugs Domain

Deep Learning / LC01 / 5th Semester

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Chapter 1: Introduction

1.1 Background

Access to accurate drug information is very essential for patients, healthcare students, and in public generally. However, searching through all drugs monograph and medical documents can be very complex and time-consuming. While traditional chatbots often just rely on predefined rules or limited datasets, making them inflexible and incapable of handling diverse user questions.

Retrieval-Augmented Generation is a modern approach that combines LLMs with a vector-based retrieval system to improve their accuracy, relevance, and grounding for factual information. In our project, we use FLAN-T5-base, a Seq2seq(encoder decoder) model, which is well-known for their strong instruction-following capabilities. However, models like FLAN-T5 are limited by their internal parameters and can't store all the knowledge on the domain. So, we integrate FAISS Vector Database to store document embeddings that allows the system to retrieve relevant information before generating a response.

By integrating FLAN-T5 with FAISS, the system becomes more accurate, less prone to hallucination, and increases their capabilities for grounding answers based on real documents.

1.2 Problem Statement

Access to accurate and trustworthy medication information remains a significant challenge for the general public these days. Many existing chatbot systems rely on only generative language models which may produce responses that are incomplete, outdated, or just factually incorrect, especially in the medical domain. This limitation poses serious risks, as inaccurate drug-related information can negatively impact on anyone.

Furthermore, traditional chatbot architecture often lacks mechanisms to explicitly ground their responses in authoritative medical sources. Without retrieval-based support, these systems are prone to hallucination answers and struggle to provide consistent, context-aware answers to diverse medication-related questions such as meds dosage, side effects, warnings, and usage instructions. Another challenge lies in the effective utilization of domain-specific datasets, while curated medical QA datasets such as MedInfo2019 and MedQuAD exist, they often suffer from issues such as incomplete answers or inconsistent format. This makes it difficult to build a robust and reliable medical question-answering system using a single dataset.

Therefore, there is a need for a medical chatbot system that can combine supervised fine-tuning on high-quality QA datasets with real-time retrieval of authoritative medical information. Such a system should be capable of generating accurate, context-aware, and trustworthy responses while minimizing hallucination and maintaining scalability.

1.3 Objectives

The main objective of this project include:
-   Building a drug QnA chatbot with FLAN-T5 as the generator

-   implementing a FAISS-based retrieval pipeline to provide factual grounding
-   Evaluating the effectiveness of RAG in reducing wrong answers

1.4 Significance

The benefits of our projects are:
-   Retrieval-Augmented Generation integration with FAISS vector database significantly improves the factual reliability for generated answers
-   Use of FLAN-T5-base enables effective natural language understanding and controlled answer generation.
-   Contributes on healthcare information access.
-   Provides a reproducible framework for building domain-specific QA models by combining a fine-tuned generative model with a retrieval mechanism.

Chapter 2: Related Works

2.1. Seq2Seq (Encoder–Decoder) Models

FLAN-T5-base is built on the sequence to sequence architecture which includes encoder and decoder.

1. Encoder

    Processes the entire input sequence at once and operates bidirectionally while capturing full context.

2. Decoder

    Generates the output sequence one token at a time, and uses both previous tokens and the encoder's representation of the input.

Seq2seq is ideal for RAG for their performance on question answering, highly controllable and conditionable on external context

2.2. Retrieval-Augmented Generation(RAG)

Three main components of Retrieval-Augmented Generation:

1. Embedding Model

   Converts text into dense vectors and captures semantic meaning of documents.

2. FAISS Vector Database

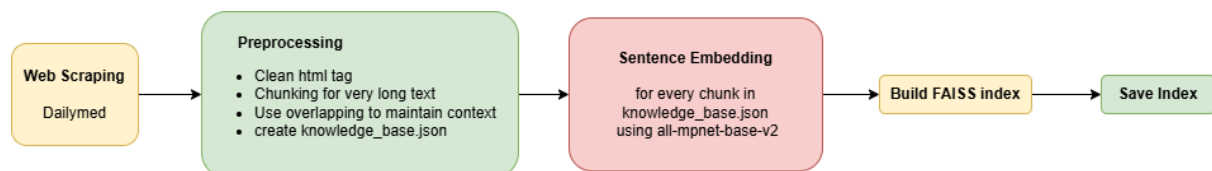   Stores the embedding vectors, performs fast similarity search, and finds the most relevant document.

3. FLAN-T5 Generator

Receives the retrieved context from FAISS, generates grounded also factual answers, and reduces hallucinations significantly.

Chapter 3: Methodology
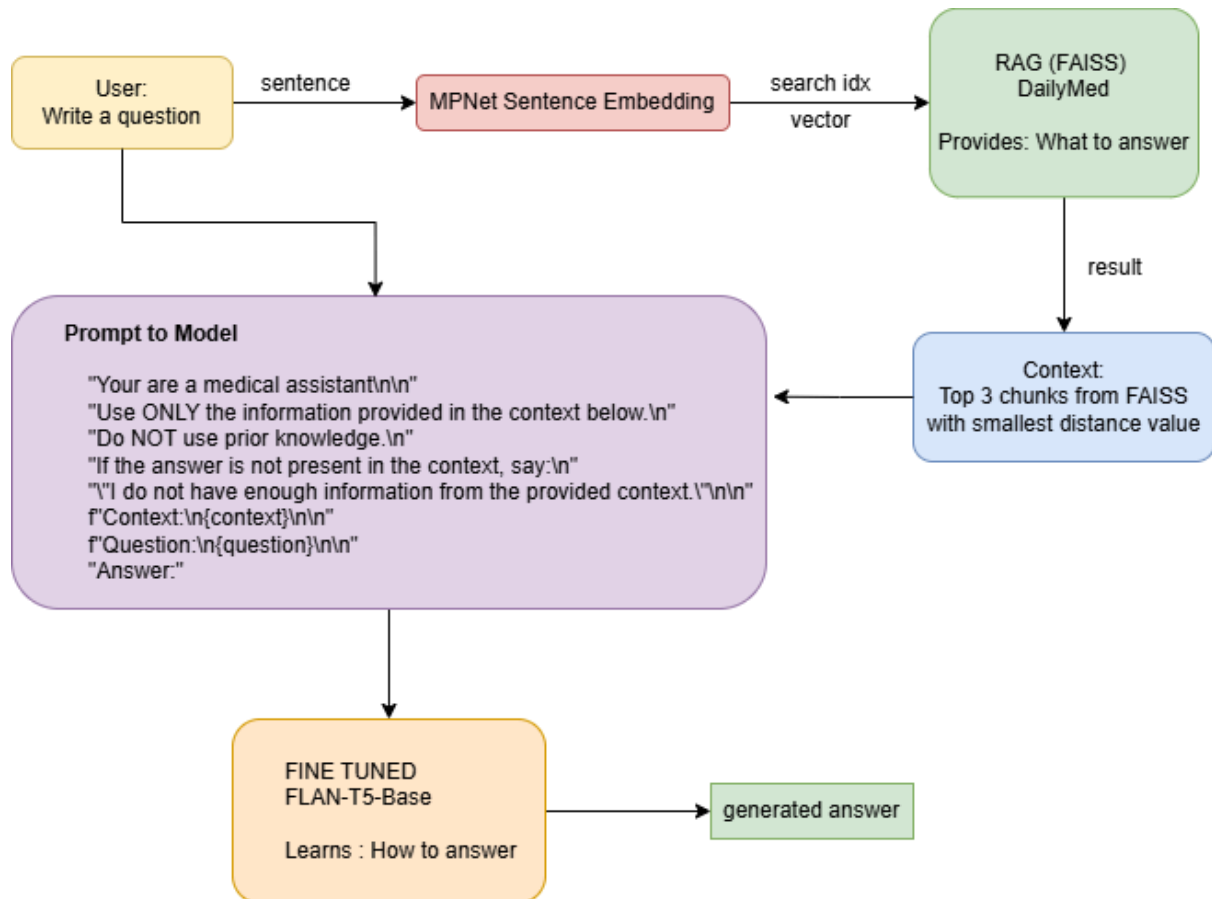
3.1. Dataset Collection

3.1.1 DailyMed (for RAG)
Source: DailyMed Website
(https://dailymed.nlm.nih.gov/dailymed/)

This study utilizes DailyMed as the primary data source for constructing the knowledge base used in the Retrieval-Augmented Generation(RAG) framework. DailyMed is an official service provided by the U.S National Library of Medicine (NLM) that offers free, reliable, and up-to-date information on marketed pharmaceutical products in the United

States. The data available on DailyMed is derived from Structured Product Labeling (SPL) documents submitted by drug manufactures and approved by the U.S Food and Drug Administration(FDA).

In order to collect drug related information, this project leverages the publicly available DailyMed Application Programming Interfaces (APIs). Data retrieval is performed programmatically by submitting requests based on the drug name specified by the user. The first API endpoint used in the data collection process is:
https://dailymed.nlm.nih.gov/dailymed/services/v1/drugname/{drug_name}/human/spls.json
This endpoint returns a JSON response containing metadata related to the queried drug, including the product title, unique identifier (setid), and the publication date of the labeling information. The setid serves as a unique reference to a specific SPL document.

Subsequently, the retrieved setid is used as a query parameter for the second API endpoint:https://dailymed.nlm.nih.gov/dailymed/services/v2/spls/{setid}.xml
This endpoint provides the complete Structured Product Labeling (SPL) document in XML format. The XML data contains detailed and authoritative drug information, such as indications, dosage and administration, contraindications, warnings, and adverse effects.

The collected SPL documents are then processed and stored as a knowledge base for the RAG system. By relying on DailyMed as the data source, the model is ensured to generate responses grounded in factual, authoritative, and trustworthy medical information, thereby reducing the risk of misinformation in drug-related question answering.

3.1.1. MedlinePlus Drug Information Dataset (for fine-tuning)
Sources:
HuggingFace MedQuAD dataset
(https://huggingface.co/datasets/lavita/MedQuAD/tree/main/data)

This is a large dataset on Medical Question Answering, that provides many document sources of medical information. This project only uses the MPlusDrugs document source that is suitable to fine tune the chatbot model. The question type on MPlusDrugs documents typically includes
- Indication
- Usage
- Precautions
- Dietary
- Severe reaction
- Contraindications, and many else

Unfortunately, for the answer column it turns out to be empty, so later on the preprocessing step, this project will use the document url that points to medlineplus website and scrape the answer from this website (https://medlineplus.gov/druginformation.html).

Purpose in the system:

This dataset is used as the fine tuning dataset because it is provided with a question and answer that later can be processed to adjust the fine tuning format of the Flan-T5 model. The answer will fine tune the model to learn the styling answer to the drug domain.

3.1.2. MedInfo2019 QA Medication Dataset (for fine-tuning)

Source:

(https://github.com/abachaa/Medication_QA_MedInfo2019/blob/master/MedInfo2019-QA-Medications.xlsx)

This dataset provides data in the format of question and answer about drug related information that come from different sources. There are many question type in this dataset, some of them are:
- Information
- Dose
- Usage
- Side effects
- Indication
- Interaction

Purpose in the system:

This dataset is used as the fine tuning dataset because it is provided with a question and answer that later can be processed to adjust the fine tuning format of the Flan-T5 model. The answer will fine tune the model to learn the styling answer to the drug domain.

3.2. Data Preprocessing

The data preprocessing stage consists of two datasets: MedInfo2019 and MedQuAD. Each dataset required different preparation steps being used for fine-tuning and evaluation.

3.2.1. MedInfo2019 Dataset Preprocessing

The MedInfo2019 dataset contains medication-related question-answer pairs   in   excel format. Csv file was obtained by cloning the public github repo from:

(https://github.com/abachaa/Medication_QA_MedInfo2019/)

By loading the csv file into a structured DataFrame, cleaned unnecessary whitespace, HTML characters, and formatting inconsistencies, then ensuring that each row contained a valid question and answers, the data will be clean and loaded. Then doing Standardization into Seq2seq format and Marking for final the dataset merge.

3.2.2. MedQuAD Dataset Preprocessing

the MedQuAD dataset was originally retrieved from:

(https://huggingface.co/datasets/lavita/MedQuAD/tree/main/data)

The dataset required extensive processing, especially for extraction drug-domain question answer pairs and filling the missing answers fields. firstly convert the dataset from parquet to

csv format, filtering the drug domain by only selecting rows with "document_source == MPlusDrugs", Handling missing answers:

- extracting the fields such as document_url, question, and question_type
- Fix the outdated MedlinePlus URLs
- Web scraping for the answers
- After the missing answers were handled, we exported the completed dataset and saved it as mplusdrugs_with_answer.csv then splitting the train and test dataset into 80% training and 20% testing.

3.2.3. Final Dataset Assembly

the purpose is now to create the final training and evaluation sets:

1. Merge Sources
   both the full MedInfo2019 dataset and MedQuAD MPlusDrugs training subset which is 80% of it.
2. Remove Duplicate Questions
   Duplicate entries were detected using the exact question text matching, so only unique question-answer pairs will be trained.
3. JSON Formatting
   the final training set will be exported into train.json with the following structure will be like:

   ```
   [
        {
         "instruction": "<question text>",
         ""output":"<answer text>"
        },
   ]
   ```

3.3 Model Architecture

3.3.1 FLAN-T5-Base
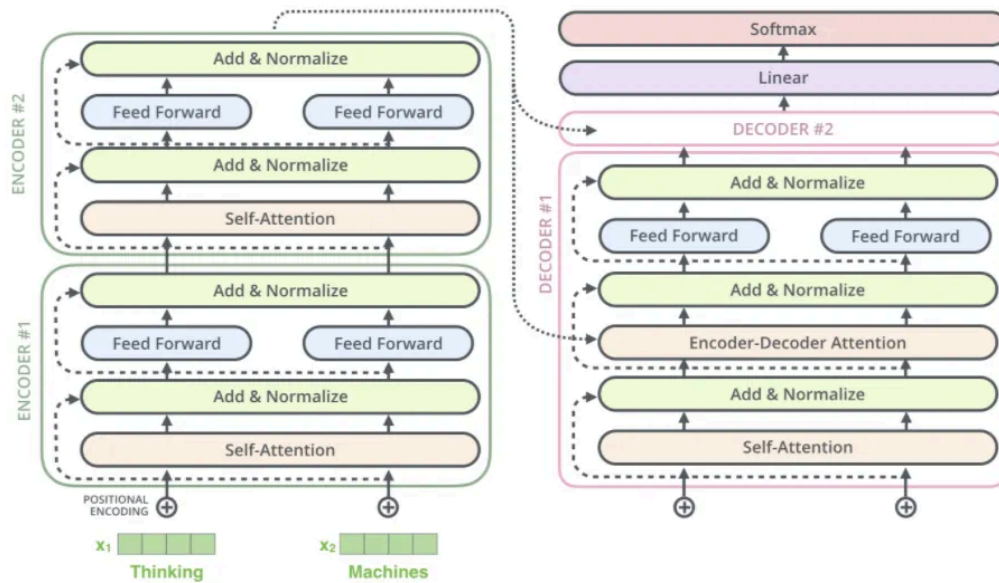
FLAN-T5 is a language model based on the Transformer architecture that was built upon the Text-to-Text Transfer Transformer (T5) concept. T5 uses an encoder-decoder , where the encoder block processes and understands the contextual representation of input text, while the decoder block generates output text autoregressively by utilizing a cross-attention mechanism on the encoder's output. One of T5 characteristics is its text-to-text approach, meaning that all NLP tasks including question answering, classification, and summarization are formulated as a mapping from input text to output text. Additionally, T5 uses relative positional encoding unlike another transformer model that uses absolute positional encoding.

FLAN-T5 retains the T5 architecture without structural changes to its layer or attention mechanism, but it enhances its performance through a process called instruction fine-tuning. In this stage, the pre-trained T5 model is further trained on FLAN dataset, which consist of various NLP tasks formatted as natural language instruction and expected outputs. The goal of this instruction fine tuning is to teach the model to better understand and execute explicit instructions provided in text form.

This is the reason for this project using FLAN-T5-base to fine tune on the available question answer dataset. Because the FLAN-T5 model is already pre-trained on the question answer dataset in the format of instruction and our dataset can be easily formatted to instruction and expected output. Also the ability of FLAN T5 base following instruction, we expect the model will obey the instruction for not answering drug questions without enough drug context from retrieval.

3.3.2 all-mpnet-base-v2
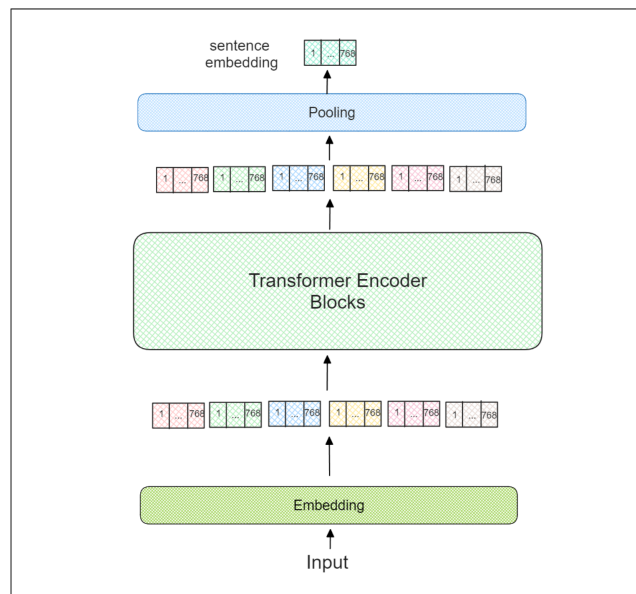
The knowledge base scraped from the DailyMed website must be embedded to produce vector representations that can later be retrieved using queries through a FAISS vector database. Traditional embedding models such as Word2Vec are limited to capturing context at the word level and are not well suited for representing long-form textual content. In contrast, MPNet (Masked and Permuted Language Model) is a sentence embedding model that employs a Transformer-based architecture as its backbone.

MPNet combines the strengths of Masked Language Modeling (MLM), as used in BERT, and Permuted Language Modeling (PLM), as introduced in XLNet, while addressing the limitations of both approaches. Although BERT is well known for its bidirectional contextual modeling, allowing a token to be predicted based on both its left and right context. It relies on MLM, where randomly masked tokens are predicted independently. This independence assumption prevents the model from leveraging dependencies among masked tokens, even though predicting one token could provide useful information for predicting subsequent masked tokens. On the other hand, XLNet's autoregressive, permutation-based training enables richer contextual modeling but sacrifices absolute positional information, which is essential for understanding sentence structure and word order.

MPNet overcomes these limitations by integrating PLM with a two-stream self-attention mechanism. This design allows the model to capture dependencies between predicted tokens while simultaneously preserving access to the full positional information of the input sequence. Trained on approximately one billion text pairs, the all-mpnet-base-v2 model maps variable-length textual inputs into a fixed 768-dimensional dense vector space. These embeddings form the core data representation within the FAISS vector database, enabling efficient semantic retrieval and clustering through vector similarity measures such as cosine similarity.

The knowledge base data that consists of drug names, categories, section titles, and detailed content text, comprises relatively long textual sequences. Therefore, MPNet, with its fixed 768-dimensional embedding space and strong sentence-level semantic modeling capabilities, is particularly well suited for embedding this type of data.

3.4 Training Setup

Model Configuration:
- Base model: Google FLAN-T5-base
- Architecture: seq2seq (Encoder-Decoder)

Device: GPU RTX 4060 vram 8GB (CUDA)

LoRA Configuration:
- LoRA Rank : 8
- LoRA Scaling Factor : 32
- LoRA Dropout: 0.05

Data Split:
- Training: 80% (3449 samples)
- Testing: 20% (699 samples)

Training Configuration:
- Epoch: 5
- Batch size: 8
- Gradient Accumulation Step: 2
- Per device train batch size: 4
- Learning rate: 0.0001
- Max length: 256
- Warmup ratio: 0.03

3.5 Evaluation Metrics

Metrics for Fine Tuning the Flan-T5-base model: Rouge-1, Rouge-2, Rouge-l, Blue, and F1
Evaluation of FAISS retriever quality is done by using Recall@K

Chapter 4: Implementation & Result

4.1 Implementation

After building the FAISS vector database and fine-tuning the FLAN-T5 Base model, the trained components were integrated into the chatbot application. Due to the use of Parameter-Efficient Fine-Tuning (PEFT) with Low-Rank Adaptation (LoRA), the fine-tuning process does not modify or overwrite the original pretrained model parameters. Instead, only a small set of task-specific adapter weights is learned and stored.

As a result, the saved model directory contains only the LoRA adapter files, including the adapter weights and configuration, along with the tokenizer files. The original FLAN-T5 Base model parameters are not duplicated in order to reduce storage requirements and improve deployment efficiency.

During the implementation phase, the chatbot model is loaded using a two-step process. First, the pretrained FLAN-T5 Base model is loaded either from the local cache or a local directory. Second, the LoRA adapter weights obtained from the fine-tuning stage are attached to the base model to reconstruct the complete fine-tuned model. This approach enables the chatbot to retain the general language understanding capabilities of FLAN-T5 while incorporating domain-specific knowledge related to drug question answering.

4.2 Fine tuning Flan-T5-base results

Epoch	Training Loss	Validation Loss	Rouge1	Rouge2	Rougel	Bleu	F1
1	4.030700	3.559692	0.110115	0.015623	0.099892	0.008779	0.041341
2	3.735000	3.256807	0.158803	0.053070	0.147189	0.038538	0.060716
3	3.579000	3.121470	0.252317	0.144494	0.234268	0.097129	0.137150
4	3.508200	3.060488	0.302213	0.193377	0.277246	0.130816	0.181346
5	3.456300	3.042266	0.304649	0.194534	0.278225	0.133254	0.182185

The FLAN-T5 Base model was successfully fine-tuned on an instruction-output dataset using a parameter-efficient-fine-tuning (PEFT) approach with LoRA, where only approximately 0.36% of the model parameters (884.746 out of 248 million) were updated during training. The model was trained for five epochs using 3.449 training samples and evaluated on 699 evaluation samples, with performance assessed at the end of each epoch.
The training results show a steady decrease in training loss from 4.03 in the first epoch to 3.46 in the final epoch, alongside a reduction in validation loss from 3.56 to 3.04, indicating that the model progressively learned the instruction-following patterns without exhibiting significant overfitting. In addition, text generation quality metrics demonstrated consistent improvement, with ROUGE-1 increasing from 0.11 to 0.30, ROUGE-2 from 0.02 to 0.19, and ROUGE-L from 0.10 to 0.28, reflecting better content alignment and structural similarity between generated responses and reference answers.

Despite these improvements, the obtained BLEU score and F1-score remain relatively low, reaching 0.133 and 0.182, respectively, in the final epoch. This outcome is expected in the context of open-ended generative question answering, particularly in the drug information domain, where a single question can admit multiple valid answers that differ lexically while remaining semantically equivalent. BLEU and token-level F1 metrics rely heavily on exact word overlap and token order, making them less effective at capturing semantic similarity in free-form text generation. Consequently, lower BLEU and F1 scores do not necessarily indicate poor model performance but rather highlight the limitations of token-matching-based evaluation metrics for generative QA tasks. In this setting, the consistent improvement in ROUGE metrics, together with qualitative inspection of generated responses, provides a more representative assessment of the model's ability to produce relevant, informative, and contextually appropriate answers for a drug information chatbot.

4.3 Result of FAISS retriever evaluation:

- Recall@1 : 0.625
  Meaning:
  From 100 query to the FAISS vector database, 62- 63 query is successfully found with a minimum of 1 correct chunk in the top 1 chunk retrieved from FAISS vector database.
- Recall@3: 0.675
  Meaning:
  From 100 query to the FAISS vector database, 67- 68 query is successfully found with a minimum of 1 correct chunk in the top 3 chunk retrieved from FAISS vector database.
- Recall@5: 0.675
  Meaning:
  From 100 query to the FAISS vector database, 67- 68 query is successfully found with a minimum of 1 correct chunk in the top 3 chunk retrieved from FAISS vector database.

Chapter 5: Discussion & Limitation

The experimental results demonstrate that integrating FAISS-based retrieval with FLAN-T5-base is significant in improving the reliability of medication-related question answering. The RAG-enhanced system consistently generated answers that were grounded in authoritative MedlinePlus drug information, which effectively reduced the occurrence of unsupported or fabricated content commonly observed in standalone generative models. Then, the Seq2Seq encoder-decoder architecture of FLAN-T5 enabled the model to fully process the retrieved documents before generating responses, allowing better contextual understanding and alignment between the question and the supporting information. This observation is consistent with prior chatbot studies that emphasize the importance of contextual comprehension in NLP-based conversational systems. In addition, stratified evaluation across different question_type categories like dosage, side effects, and warnings, showed stable performance, indicating that the model generalized well across a wide range of medication-related inquiries.

Limitation:

- Long or complex drug interaction questions occasionally produced partial answers.
- The system is not designed to replace professional medical consultation.
- Performance depends heavily on the quality of retrieved documents.

Nevertheless, compared to traditional chatbot architectures discussed in, the proposed system demonstrates a more flexible and knowledge-grounded approach.

Chapter 6 : Conclusion & Future Work

This study presents a drug question-answering chatbot that integrates FLAN-T5-base, a Seq2Seq transformer model, with Retrieval-Augmented Generation using FAISS Vector Database. The combination of supervised fine-tuning on medication QA data and document retrieval from MedlinePlus enables the system to generate more accurate, relevant, and trustworthy responses compared to traditional chatbot approaches.

The experimental results confirm that RAG is an effective strategy for mitigating hallucination and improving factual consistency in medical chatbot systems. Future work may explore larger language models, improved evaluation metrics, and real-time updating of medical knowledge sources.

References

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Dataset:

A. Ben Abacha, Y. Mrabet, M. Sharp, T. Goodwin, S. E. Shooshan, and D. Demner-Fushman, "Bridging the gap between consumers' medication questions and trusted answers," *MEDINFO 2019*, 2019.

A. Ben Abacha and D. Demner-Fushman, "A question-entailment approach to question answering," *BMC Bioinformatics*, vol. 20, no. 1, pp. 511:1-511:23, 2019. [Online].

Available: https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-019-3119-4

Appendix

1. Team Contributions

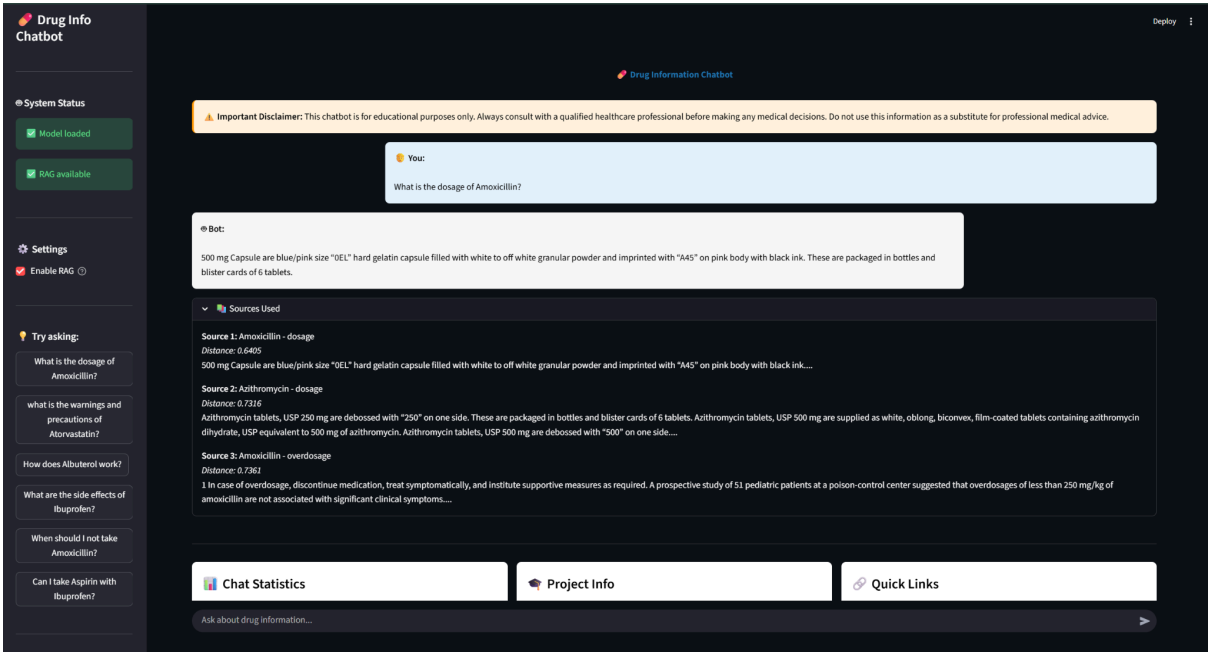| Task	PIC	Task Description
Find Dataset	Stephen, Yoseph	Yoseph: searching for drug domain dataset from various sources like kaggle, huggingface, github, and mendeley. Also doing the web scraping Stephen: searching for drug domain dataset from various sources
EDA	Yoseph	Melakukan EDA
Preprocessing	Yoseph	Melakukan Preprocessing
Model Creation	Yoseph	Melakukan fine tuning
Model Evaluation	Yoseph	Melakukan evaluation pada model fine tune dan kualitas retriever
Create App	Yoseph	Mengintegrasikan chatbot yang terdisi dari model dan rag ke dalam streamlit menjadi aplikasi yang bisa dipakai pengguna
Final Report	Stephen, Yoseph	Menyusun final report
Presentation	Stephen, Yoseph	Menyusun slide presentasi

2. Supporting Documents

No	Document	Link
1.	Github Repo	https://github.com/yosephyusanto/FinalProject-DeepLearning
3.	Demo Video	https://youtu.be/evrFux7Xfxk
4.	Presentation Slide	https://www.canva.com/design/DAG7ehGveow/aJXaijP

3. Screenshots and Code Snippets