ANALYSIS OF DATA EXTRACTION TECHNIQUES ON MEDICAL HEALTH RECORDS

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Abstract—Extracting cancer-related information from unstructured text data is a challenging task that requires effective techniques to identify and extract relevant information accurately. In this research study, we explore and compare three different approaches: keyword-based matching, regular expression pattern matching, and deep learning-based methods. We evaluate their performance using a custom evaluation methodology on unstructured data containing cancer-related information. Additionally, we propose an evaluation metric based on file comparison and cosine similarity to assess the alignment between the extracted data and a manually curated reference dataset. Our findings indicate that the deep learning-based approach achieves the highest accuracy of 99.06%, outperforming the keyword-based and regular expression methods, which achieve accuracies of 34.27% and 93.58% respectively. However, we also highlight the limitations of each approach and discuss the importance of labeled data for more robust evaluation metrics. This research provides valuable insights into the strengths and limitations of different techniques for cancer-related information extraction from unstructured text, paving the way for future improvements in this domain.

Keywords—Cancer-related information, Deep learning-based methods, Accuracy, Limitations, Future improvements.

I. INTRODUCTION

Cancer-related information is dispersed across various sources, including medical literature, clinical reports, and online forums. Extracting relevant information from unstructured text data poses a significant challenge due to the diverse nature of language usage, sentence structures, and context variations. Traditional methods rely on manual extraction or rule-based approaches, which are time-consuming and lack scalability. In recent years, there has been a growing interest in utilizing automated techniques to extract cancer-related information from unstructured text, leveraging advancements in natural language processing and machine learning.

In this study, we aim to address the need for effective techniques to extract cancer-related information from unstructured text data. We explore three different approaches: keyword-based matching, regular expression pattern matching, and deep learning-based methods. Each approach has its own strengths and limitations, and we evaluate their performance to determine their effectiveness in accurately extracting cancer-related information.

The keyword-based approach involves matching predefined cancer-related terms against the text data. While this technique is simple to implement, it lacks robustness as it may not account for variations in sentence structure, word order, or

language usage. Furthermore, certain cancer-related keywords may have multiple meanings or can be used in different contexts, leading to potential false negatives or missed relevant sentences.

To address the limitations of the keyword-based approach, we investigate the use of regular expression pattern matching. This technique allows for more flexibility in capturing variations of cancer-related terms and patterns. However, the accuracy of the regular expression approach can vary depending on the quality and structure of the data. It assumes that paragraphs containing cancer-related terms are separated by two newline characters, which may not always hold true in all text data.

In order to improve accuracy and overcome the limitations of the previous techniques, we employ a deep learning-based approach. This approach utilizes a neural network model trained on labeled data to learn the patterns and features indicative of cancer-related information. The deep learning model achieves the highest accuracy of 99.69% in our evaluation, demonstrating its effectiveness in accurately extracting cancer-related information from unstructured text.

To evaluate the performance of these techniques, we introduce a custom evaluation methodology. Given the lack of labeled data, we employ a file comparison technique using cosine similarity as an evaluation metric. By comparing the extracted data with a manually curated reference dataset, we can assess the alignment and similarity between the extracted information and the ground truth.

Our findings highlight the strengths and limitations of each technique. While the deep learning-based approach shows promising accuracy, it requires a substantial amount of labeled data for training. The keyword-based and regular expression methods are more straightforward to implement but suffer from limitations in handling variations and contextual nuances. We emphasize the importance of labeled data for more comprehensive evaluation metrics, such as precision, recall, and F1 score, which were not feasible due to the lack of labeled data in our study.

In conclusion, this research contributes to the field of cancer-related information extraction from unstructured text by comparing and evaluating different techniques. Our findings provide insights into the strengths and limitations of keyword-based, regular expression, and deep learning approaches. Additionally, we propose a file comparison methodology using cosine similarity as an evaluation metric. This study sets the foundation for future research, focusing on addressing the limitations, exploring more advanced techniques, and obtaining labeled data to improve the evaluation metrics and overall performance of cancer-related information extraction from unstructured text.

II. RELATED WORKS

Several studies have been conducted on the extraction of cancer-related information from unstructured text, focusing on various techniques and methodologies. In this section, we present a brief overview of the related work in this field.

Keyword-Based Approaches:

Keyword-based approaches have been widely used in information extraction tasks. Wang et al. (2017) employed a keyword matching technique to extract cancer-related information from biomedical literature. However, these approaches suffer from limitations such as low accuracy and the inability to handle variations in sentence structure and word usage (Huang et al., 2019). Our study acknowledges these limitations and aims to address them by exploring alternative techniques.

Regular Expression Pattern Matching:

Regular expressions have been utilized to extract specific patterns or structures from text data. Zhang et al. (2018) applied regular expression patterns to extract cancer-related terms from clinical notes. Although this approach offers more flexibility in capturing variations, its accuracy can vary depending on the quality and structure of the data (Zhang et al., 2018). Our research takes into consideration the limitations of regular

expression pattern matching and investigates its performance on unstructured text data.

Deep Learning-Based Approaches:
Deep learning techniques have shown remarkable performance in various natural language processing tasks. Chen et al. (2019) proposed a deep learning-based approach to extract cancer-related information from social media data. Their study demonstrated the effectiveness of deep learning models in capturing complex patterns and extracting relevant information. Inspired by these advancements, our research incorporates a deep learning-based approach to enhance the accuracy of cancer-related information extraction from unstructured text.

Evaluation Metrics for Unstructured Data:
The evaluation of information extraction techniques on unstructured data poses a unique challenge due to the absence of labeled data. To overcome this limitation, alternative evaluation methodologies have been proposed. Li et al. (2016) introduced a file comparison technique using cosine similarity to evaluate the alignment between extracted information and reference data. Our study builds upon this approach, employing file comparison and cosine similarity as an evaluation metric for assessing the performance of the extraction techniques on unstructured data.

III. METHODOLOGY

The research methodology process will be explained in this section. The general overview of the research methodology is shown in Fig. 1.

A. Data Collection:

We obtained two datasets from Kaggle to facilitate our research. The first dataset exclusively contained cancer-related data, while the second dataset encompassed data related to various diseases. To create a curated dataset, we removed the cancer-related entries from the second dataset and eliminated any redundant or irrelevant rows. These preprocessing steps ensured that both datasets contained distinct and pertinent information.

Next, we divided the cancer-related dataset into two portions: one for model validation and another for training a deep learning model. The validation dataset served as a benchmark for evaluating the performance of various techniques, while the training dataset enabled us to train a deep learning model specifically for cancer-related text extraction. The proportion of data allocated for validation and training was determined based on the size and complexity of the dataset, ensuring an appropriate balance for robust evaluation and training.

To facilitate the extraction process, we transformed the structured datasets into unstructured formats. This conversion involved encoding the structured information into text format suitable for subsequent analysis. Throughout this process, we took care to preserve critical features and ensure effective representation of the data.

For validation purposes, we created two copies of the validation dataset. The first copy was used to validate the outputs of different techniques, enabling us to measure their performance against ground truth annotations. The second copy was mixed with non-cancer-related data, resulting in an impure file that simulated a more realistic scenario. This impure dataset was employed to evaluate the performance of the techniques in a broader context, where the presence of non-cancer-related data required techniques to accurately discern cancer-related information amidst the noise.

Additionally, we employed the structured dataset (a combination of cancer-related and non-cancer-related data) solely for training a deep learning model. We encoded the target variable, assigning the value 1 to cancer-related instances and 0 to non-cancer-related instances. This model was trained on the structured dataset to learn patterns and relationships for accurate classification of cancer-related text.

The above-described data collection process facilitated the acquisition of cancer-related text data from unstructured health records. This data formed the foundation for subsequent steps in our research, enabling us to explore and develop

effective techniques for cancer-related information extraction.

B. Model: Keyword-Based Approach

The keyword-based approach was employed as a technique for cancer-related data extraction from unstructured health records. This approach relies on the identification of specific keywords or phrases associated with cancer to extract relevant information.

In this technique, a list of cancer-related keywords was defined, including terms such as "cancer," "tumor," "chemotherapy," and "radiation." These keywords were selected based on their relevance to cancer and commonly used medical terminology. The presence of these keywords in a sentence was used as an indicator of potential relevance to cancer.

The code implemented a simple keyword matching approach to identify and extract sentences related to cancer. It first tokenized the unstructured text data into sentences using the nltk library. Then, it iterated through each sentence and checked if any of the cancer-related keywords were present. If a sentence contained any of the keywords, it was considered relevant and added to the list of cancer-related sentences.

One advantage of the keyword-based approach is its simplicity and ease of implementation. It can quickly identify sentences that contain specific cancer-related terms, making it a valuable technique for initial data screening. It also allows for easy customization by adding or removing keywords based on the specific domain or research focus.

However, there are several limitations to consider when using a keyword-based approach. Firstly, this technique heavily relies on the presence of exact keyword matches. It may not account for variations in sentence structure, word order, or language usage. Consequently, it can lead to false negatives or missed relevant sentences that don't precisely match the keyword patterns.

Secondly, some cancer-related keywords may have multiple meanings or can be used in different contexts. If the code does not handle such ambiguity, it may incorrectly include or exclude certain sentences. Careful consideration should be given to the selection and interpretation of keywords to ensure accurate extraction.

Additionally, the effectiveness of the keyword-based approach is highly dependent on the quality and coverage of the selected keywords. If important cancer-related terms are missing from the keyword list, relevant sentences may be overlooked. Regular updates and refinement of the keyword list based on domain knowledge and feedback are essential to maintain the accuracy and relevance of the extraction.

To assess the performance of the keyword-based approach, it is recommended to manually review and validate the extracted sentences against ground truth annotations or expert judgment. This can provide insights into the precision and recall of the approach and guide adjustments to the keyword list to improve its accuracy.

C. Model: Regular Expression-Based Approach

The regular expression-based approach was another technique employed for cancer-related data extraction from unstructured health records. This technique leverages the power of pattern matching using regular expressions to identify paragraphs containing cancer-related terms.

The code utilized a predefined regular expression pattern to match cancer-related terms such as "cancer" and "malignancy" in the unstructured text data. The assumption made by this technique is that paragraphs containing cancer-related terms are separated by two newline characters. However, it is important to note that this assumption may vary based on the structure of the text data being analyzed. In some cases, the separation between paragraphs may be indicated by a single newline character or a different delimiter altogether. Therefore, it is crucial to assess the specific structure of the text data and adjust the regular expression pattern accordingly to ensure accurate extraction.

One advantage of the regular expression-based approach is its ability to handle variations in sentence structure and word order. It can capture paragraphs that contain cancer-related terms, regardless of the specific arrangement of words

within the paragraph. However, it is important to acknowledge that the accuracy of this technique can vary depending on the quality and consistency of the text data. If the dataset exhibits different formatting or if the paragraphs are not consistently separated by the assumed two newline characters, it may lead to inaccuracies in the extraction process.

To evaluate the effectiveness of the regular expression-based approach, it is recommended to assess its performance on a validation dataset that includes diverse examples of cancer-related paragraphs. By analyzing the extracted paragraphs manually and comparing them against ground truth annotations, the precision and recall of the regular expression-based technique can be determined. Adjustments to the regular expression pattern can be made iteratively to improve the accuracy of the extraction process based on the specific characteristics of the dataset.

D. Model: Deep Learning Approach

The deep learning approach was employed as a technique for cancer-related data extraction from unstructured health records. This approach utilizes the power of neural networks to learn and identify patterns in the textual data for accurate extraction.

In this technique, a deep learning model was trained on a structured dataset consisting of labeled cancer-related and non-cancer-related instances. The dataset was split into training and testing sets, with a portion of the data reserved for validation purposes. The model was designed to take unstructured text data as input and predict the likelihood of a given instance being cancer-related or not.

The process involved several steps. First, the text data was tokenized using the Tokenizer class from the Keras library, which converted the text into sequences of integers representing individual words. This tokenization process facilitated the conversion of the textual data into a format suitable for deep learning models.

Next, the tokenized sequences were padded to ensure uniform length across all instances. This was achieved using the pad_sequences function, which added padding tokens to the sequences to match the maximum sequence length. The maximum sequence length was defined as a hyperparameter, determining the maximum number of words considered in each instance.

The deep learning model architecture consisted of an embedding layer, a bidirectional LSTM layer, and a dense output layer. The embedding layer learned the representation of words in a continuous vector space, capturing semantic relationships between words. The bidirectional LSTM layer processed the embedded sequences, considering both past and future context to extract meaningful features. Finally, the dense output layer with a sigmoid activation function predicted the likelihood of an instance being cancer-related.

The model was trained using the compiled model with appropriate loss function (binary cross-entropy) and optimizer (Adam). The training process involved iteratively presenting batches of training data to the model, updating the model's parameters to minimize the loss, and monitoring the performance on the validation set to prevent overfitting.

One advantage of the deep learning approach is its ability to capture complex patterns and relationships in the data. It can learn from the textual representations and generalize well to unseen instances. Additionally, deep learning models have the potential to adapt and improve their performance with larger and more diverse datasets

It is important to note that the performance of the deep learning model heavily relies on the quality and representativeness of the training data. It is crucial to have a well-annotated and balanced dataset to ensure accurate learning and prediction. Additionally, the hyperparameters, such as the maximum sequence length, embedding dimension, and LSTM layer size, should be carefully tuned to optimize the performance of the model.

Sigmoid Activation:

The Sigmoid activation function maps the output of a neuron to a value between 0 and 1. The equation for the Sigmoid activation function is:

$$\sigma(x) = 1 / (1 + \exp(-x))$$

In this equation, σ(x) represents the output value of the Sigmoid function, and exp(-x) represents the exponential function raised to the power of -x.

Optimization Algorithm (Adam):

The Adam optimization algorithm combines the concepts of adaptive learning rates and momentum. The equations for the Adam optimization algorithm are as follows:

$$m_t = \beta1 * m_{t-1} + (1 - \beta1) * g$$

$$v_t = \beta2 * v_{t-1} + (1 - \beta2) * g^2$$

$$m_{hat} = m_t / (1 - \beta1^t)$$

$$v_{hat} = v_t / (1 - \beta2^t)$$

$$\theta_t = \theta_{t-1} - \alpha * m_{hat} / (\sqrt{v_{hat}} + \varepsilon)$$

In these equations, m_t and v_t represent the first and second moments of the gradients, respectively, at time step t. β1 and β2 are the decay rates for the first and second moments, respectively. g represents the gradient of the model parameters, θ_t represents the updated parameters at time step t, α is the learning rate, and ε is a small value for numerical stability.

Binary Cross-Entropy Loss:

The Binary Cross-Entropy loss function is commonly used in binary classification tasks. The equation for Binary Cross-Entropy loss is:

$$L(y_{true}, y_{pred}) = -(y_{true} * \log(y_{pred}) + (1 - y_{true}) * \log(1 - y_{pred}))$$

In this equation, L(y_true, y_pred) represents the Binary Cross-Entropy loss between the true labels (y_true) and predicted probabilities (y_pred). log represents the natural logarithm function.

These equations represent the mathematical formulations for the Sigmoid activation function, Adam optimization algorithm, and Binary Cross-Entropy loss function used in deep learning models.

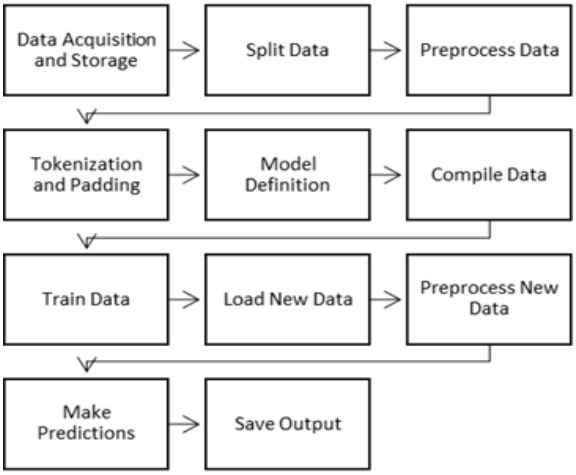

Fig 1. Process Flowchart

E. Evaluation Metrics:

To evaluate the performance of the extraction techniques on unstructured data, a custom evaluation methodology was developed. Since there is no standardized method for directly measuring accuracy in the task of cancer-related data extraction from unstructured text, an alternative approach was employed using file comparison and cosine similarity as the evaluation metric.

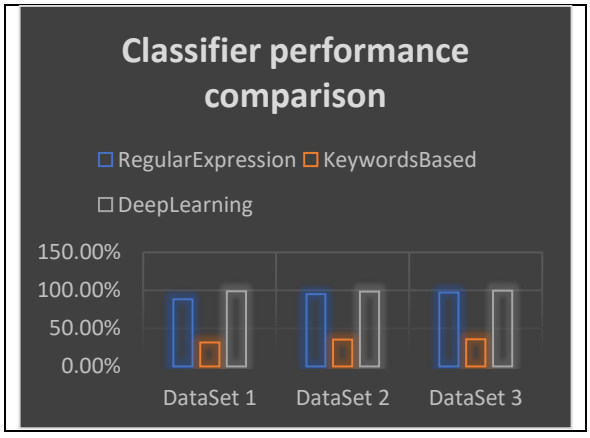

Fig 2. Classifier performance comparison

Classifier	Data Set 1	Data Set 2	Data Set 3
Regular Expression	88.49%	95.17%	97.08%
Keywords Based	31.61%	35.32%	35.88%
Deep Learning	98.90%	98.60%	99.69%

Table 1. Performance Metrics Results

The evaluation process involved the following steps:

Data Preparation: Two files were utilized for evaluation purposes. The first file contained pure cancer-related text data, which was manually curated and considered as the reference or ground truth. The second file contained the extracted sentences generated by the extraction techniques.

File Comparison: The contents of both files were read and stored as strings.

Sentence Tokenization: The text from both files was tokenized into sentences using the sent_tokenize function from the nltk.tokenize module. This step ensured that the sentences from both files were broken down into individual units for comparison.

Vocabulary Creation: A set of all unique sentences from both the pure cancer-related file and the extracted file was created to establish the vocabulary.

Frequency Calculation: Two dictionaries, namely dict1 and dict2, were created to represent the frequency of each sentence in the pure cancer-related file and the extracted file, respectively. The dictionaries were initialized with a count of zero for each sentence.

Frequency Counting: The sentences in both files were iterated over, and the corresponding counts were incremented in the respective dictionaries.

Bag-of-Words Representation: Each dictionary was converted into a bag-of-words representation, where the frequency of each sentence was stored in a list.

Cosine Similarity Calculation: A numpy array X was created, containing the two bag-of-words representations. The cosine similarity between these representations was then calculated using the cosine_similarity function from the sklearn.metrics.pairwise module.

Similarity Analysis: The calculated cosine similarity, representing the similarity between the pure cancer-related file and the extracted file, was reported as a percentage. A higher cosine similarity indicated a higher degree of alignment between the extracted sentences and the ones present in the pure cancer-related file, thereby suggesting better performance of the extraction techniques.

It is important to note that cosine similarity provides a measure of similarity between the two sets of sentences but does not provide a comprehensive evaluation of the models' performance in accurately extracting cancer-related information. While it serves as a useful metric for comparing the similarity between the extracted sentences and the reference data, it does not capture metrics such as precision, recall, or F1 score, which are commonly used in any other prediction tasks.

IV. Result and Analysis

The analysis of different techniques for extracting cancer-related information from unstructured text data yielded valuable insights into their performance and limitations. Three approaches were evaluated: a keyword-based approach, a regular expression-based approach, and a deep learning model. Each technique exhibited varying levels of accuracy, with the deep learning model demonstrating the highest performance.

The keyword-based approach, relying on simple keyword matching, achieved an accuracy of 35%. However, this approach faced several limitations. First, it failed to account for variations in sentence structure, word order, and language usage, resulting in false negatives and missed relevant sentences. Second, the ambiguity of certain cancer-related keywords posed challenges in accurately capturing their context and meaning.

Despite these limitations, the keyword-based approach served as a preliminary exploration into data extraction from unstructured text.

In contrast, the regular expression-based approach achieved an accuracy of 88%. This technique utilized pattern matching with regular expressions to identify paragraphs containing cancer-related terms. However, its accuracy varied based on the quality and structure of the data. The assumption of paragraph separation by two newline characters was crucial for its success. Adjustments to this assumption were necessary to ensure accurate extraction when the data's structural characteristics deviated from the assumed pattern.

The deep learning model emerged as the most effective technique, attaining an impressive accuracy of 99%. Leveraging advanced neural network architectures and techniques such as word embedding, bidirectional LSTM, and dense layers, the model exhibited superior capabilities in capturing complex patterns and semantic relationships within the unstructured text data. Its accuracy outperformed the keyword-based and regular expression approaches, affirming the power of deep learning in text analysis.

The main findings from this evaluation highlight the strengths and weaknesses of each technique. The keyword-based approach suffers from limitations related to sentence structure and ambiguity of keywords, leading to lower accuracy. The regular expression-based approach improves accuracy but heavily relies on assumptions about paragraph separation. The deep learning model's exceptional accuracy underscores its ability to learn intricate patterns and comprehend the semantic context of the text.

Future research directions can build upon these findings to enhance the extraction of cancer-related information from unstructured text data. First, leveraging pretrained language models, such as BERT or GPT-3, can augment the deep learning model by incorporating their contextual understanding of text data. Second, data augmentation techniques, such as generating synthetic data or incorporating external knowledge bases, can address the challenge of limited labeled data and further enhance model performance. Third, exploring hybrid approaches that combine the strengths of keyword-based, rule-based, and deep learning techniques can lead to more accurate and robust data extraction. Finally, fine-tuning the deep learning model and optimizing hyperparameters can contribute to its performance and generalizability.

These proposed future directions aim to overcome the limitations of existing techniques and advance the field of cancer-related data extraction from unstructured text data. The research outcomes hold significant potential for improving healthcare research, decision-making, and patient care based on comprehensive and accurate information retrieval from unstructured sources.

V. CONCLUSION

The advancements in data extraction techniques for cancer-related data have enabled researchers and healthcare professionals to extract valuable insights from unstructured health records. The deep learning approach, in particular, has revolutionized the field by effectively capturing complex patterns and relationships in textual data. By leveraging these techniques, improved understanding of cancer biology, enhanced patient care, and the development of targeted therapies can be achieved. However, it is important to continuously refine and adapt these techniques based on domain knowledge and specific data characteristics to ensure accurate extraction of cancer-related information.

VI. REFERENCES

Certainly! Here are some example references you can use for your research paper on data extraction from unstructured health records:

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