

Research Article

Generative Adversarial Networks Using Name Entity Recognition Model Using Clinical Health Records

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Abstract— Recently, there has been increased attention in the Clinical Named Entity Recognition research area within Medical Records (MR). As much clinical-related information exists in structured and unstructured textual data, Named Entity Recognition technology helps extract different types of patient data. The widespread use of MR has sparked interest in utilizing technology, especially in Biomedical Named Entity Recognition, which faces challenges due to various entities such as medications, genes, diseases, and proteins. Recently, advanced NLP technology has shown outstanding performance through pre-training textual encoders. The encoding of input data is pivotal to the effectiveness of neural sequence labeling models, as they are essential for generating the morphological data. This paper focuses on a variant of the deep neural network model to improve the proposed method. This analysis tackles the challenge of Biomedical Named Entity Recognition by employing Generative adversarial networks that integrate biological data analysis. Numerical sequences are converted into word embedding models. The creation of embeddings based on input is facilitated by pre-trained word embeddings such as GloVe. The model efficiency achieves an improved accuracy of 97.74%.

Keywords— Generative adversarial networks, Deep neural network, word embedding, Name entity recognition.

1. Introduction

The number of biomedical texts is rapidly increasing day by day. By combining the output data from Named Entity Recognition systems, NLP applications such as entity analysis, question answering, clustering, syntactic analysis, and co-reference resolution have become more complex problems. NER allows us to generate entity classes and extract the necessary data. An essential goal of the (Bio-NER) study is to recognize and extract biological textual data, such as protein sequence and gens data, along with the semantic classes that correlate to them, such as medical conditions, therapies, or clinical trials. BNER enables examining patient data, early disease identification, and risk analysis using medical entities [1]. Many approaches have been embraced by the biomedical natural language processing techniques that have been developed. These approaches include dictionaries, rules, statistical techniques, deep neural networks, and machine learning (ML) algorithms. By combining biological corpus data and improved hyperparameters with a deep network model (DNM), this study tackles the challenging task of Biomedical Named Entity Recognition [2]. A [3] surveyed two different types of entities, such as Arabic language-name Entity Recognition and English-based Named Entity Recognition methods from different language models,

which help to identify ANER. The manual creation of rules based on named entities and syntax in human language is a significant component of rule-based approaches.

They suggested [4] a transformer learning technique to improve the model using DL when the features are extracted. The Transformer learning model increases the network capability, generating a sequence-based model. The attention mechanism was first found successful in machine translation [5]. Because of its superior performance in neural network topologies, it later started to be widely applied in many other areas of natural language processing. Attention mechanism models can use information weights to weigh the significance of various information elements, accentuate important information, reduce irrelevant details, and pinpoint essential features that impact the model's overall performance by examining the context. It assigns each word weight to textual data inputs according to the original weights of attention given to every word, as the name implies. The Attention mechanism was initially used for the NER task by [6] with great success. Following that, many academics started using this strategy to complete NER assignments.

It is limited to the specific domains defined by the laws and calls for specialist knowledge. Statistical-based techniques

have used probabilistic models to get outstanding outcomes for NER tasks, such as conditional random field, RNN, CNN, etc. ML techniques utilize statistical methods that quantify the probability distribution to categorize, extract, and detect different named entity tags. Researchers frequently used generative models to improve their methods' performance. Many feature sets determine how ML techniques work in NER systems. Choosing features wisely and recognizing long-term connections between entities is difficult. NLP models are increasingly used in the biomedical and clinical domains because the manual abstraction is time-consuming, costly, prone to errors, and non-scalable. Entity Recognition is a fundamental component of all NLP systems that extract complete information about bio-medical analysis. In medical analysis, NER recognizes the sentences that refer to each named entity, such as illnesses, medications, diagnostic tests, and other entities. Machine learning and combining optimization methods are mainly focused on the NER domain. Most researchers are working on deep learning models. However, NER is challenging because named things in the biomedical sector have complicated structures, such as clinical and pharmacological entities.

Our work innovatively uses a deep learning approach to identify named entities while utilizing an advanced feature extraction strategy. Our method uses recently developed techniques like deep neural learning in many NLP applications presented in real life. At the top of the network, Bio-NER employs a Generative adversarial network as the primary objective of the proposed model. This study used a word embedding model for the NER problem to train the different types of medical entities.

The main contribution of the work.

- A novel-based neural network approach for the NER model. The proposed method gives better performance of the recently developed models.
- At the top of the network, GAN is the primary building block of our model. Furthermore, our word vectors have previously been initialized by training in BERT and word embeddings.
- The proposed GAN architecture to investigate the effects of every word and character level based on an embedding model related to medical NER tasks.
- The main feature block used in English words for biological named entity classification is word embedding and BERT.

The manuscript is arranged in the following sections: 1 introductory section. Section 2 relates work in the field of NER—proposed work Model in section 3. The methodology of the research work is in section 4. Result and analysis of the work section 5. Concludes the paper with future work in section 6.

2. Literature Survey

These systems are easily adjustable and updated, assuming a large dataset is provided. Researchers have created systems that combine rule-based and ML-based approaches for

autonomous rule upgrading and performance optimization, as demonstrated by [7]. For many NLP tasks, textual data and medical entities are based on transformers to identify the biomedical NER tasks. The BERT-based model for multiple types of entities in Biomedical Text Mining (Bio-BERT) was introduced by [8]. PubMed Central full-text papers and PubMed abstracts were used to train this transformer. A new domain and language cannot be directly used with the different feature sets for a particular NER solution. Because a hidden recurrent unit in recurrent neural networks operates to perform timely steps based on the model type, RNNs can accommodate sequences of different lengths [9]. Some researchers [10,11] have combined rule-based and ML methods to create systems for autonomous rule upgrading and performance optimization techniques and deep learning models. In contrast to general domains, bio-medical analysis is an interdisciplinary project integrating research areas and multiple disciplines, including biology and medicine. It has a large body of scientific literature that documents essential data, including gene expressions, clinical studies, and drug treatments. Written for domain experts, information extraction usually demands a greater domain-specific understanding. Zhang et al. [12] proposed a model for NER-based techniques to improve the best feature extraction methods based on pre-trained models. The recurrent Neural Network model is used to identify the multiple factors like sub-words, letters, and unique words to extract the NER model.

Named entity recognition is a method for extracting biological and clinical concepts from the literature by precisely indicating the necessary information based on the attributes of the targeted name entities. The NER process is based on a word embedding model that transforms words. Fan et al. [13] provide a particular deep neural network model to improve the different characters using a word embedding model. The transformer systems' capacity to generalize sufficiently and produce competitive outcomes when trained in a different language has been examined in earlier research. Sun and Yang [14] evaluated the Pharma CoNER dataset's usefulness for the BERT model and Bio-BERT (without training in Spanish data). Their findings also demonstrated the existing systems' effectiveness in zero-shot transfer.

Since BERT's introduction, natural language processing has advanced significantly and performed well across various workloads. In biomedical analysis, BERT is mainly used as a pre-trained model to represent each gene language translation biological sequence analysis and medical corpus, developed in response to the rise of diverse specialized domains. However, Bio-BERT's application is typically limited by its vast number of parameters and high resource requirements when used in real-world scenarios. Hakala and Pyysalo [15] demonstrated a method that produced an F1 score of 87 in the tested dataset on the Pharma CoNER data by employing BERT for the Spanish biological system of name entity recognition without additional training. Dash et al. [16] proposed neural network-based bio-clinical data to identify the different entities and sequence labeling data used. They also compared three different datasets with a proposed model

to existing techniques. Garcia et al. [17] introduced a Generative Pretrained Transformers model for the Spanish electronic health records and entity identification. This model performs a systematic solution and improves the accuracy and algorithm performance. Srinivasarao and Sharaff [18] developed an optimization model to detect the different aspects of targeted and untargeted emotion detection models. Landolsi et al. [19] used a BERT and embedding both to extract the sequence of features from a manually annotated dataset. Ahmad et al. [20] systematically review electronic-based health data to detect the different types of entity recognition tasks. They also suggested multiple domains of research in the NER domain. Bhattacharya et al. [18] introduced a new framework combining transfer learning and asymmetric tri-training models to detect the NER tasks. They also provided a good solution.

Bhattacharya et al. [21] performed a novel solution based on a neural network model to detect the automatically based online question-answering system. Hu and Ma et al. [22] evaluations produced before 2020 did not highlight the employment of cutting-edge models or explain numerous potential difficulties in clinical NLP, even though recent evaluations have discussed DL and ML-based techniques. Likewise, more information about validating the model or the assessment matrix is needed.

3. Propose Model

This section shows our advanced pre-trained neural network model for the NER tasks based on the word embedding technique and BERT for transformation data and Generative adversarial networks. Figure 1 shows the general diagram of the NER task using the Generative adversarial networks model.

3.1 pre-processing: In text analysis, pre-processing is the most important task because we need to clean the data using NLP models. Normal pre-processing has many available approaches, but we used only three methods: tokenization, part-of-speech tagging, and stop-word removal.

- **Tokenization:** It is stated that the lengthy paragraphs are text chunks that are divided into tokens or phrases. These can also be broken down into words. Let's look at an example of a tokenized sentence: "several receptor mutants revealed." The tokenization process breaks the sentence since it contains the words "several, receptor, mutants, revealed."
- **Stop Words Removal:** Many words that lack a precise meaning when examined using pattern analysis can be found in texts. For instance. Words like "the," "are," "is," "of," "was," and so forth are considered stop/useless words since they are not helpful in the context of knowledge discovery.
- **Speech component (POS):** With POS tagging, a word's grammatical category will be assigned so that its meaning in the sentence may be ascertained. Conventional speech components include verbs, nouns, conjunctions, adverbs, etc. POS taggers take a word

sequence as input and produce a list of tuples. Each word, in this instance, is linked to its corresponding tags.

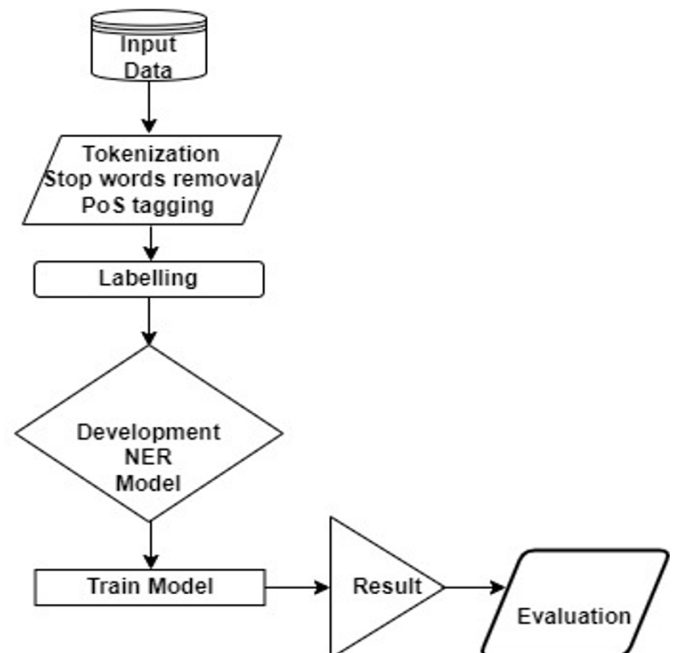


Figure 1. Proposed named-entity recognition using GAN

3.2 Word embedding method

The main functions the word embedding model's representation layer aims to provide will be utilized in constructing the suggested English NER tasks. The features have a significant value and influence on the system's adequate working conditions. Previously, features were extracted manually while following complex guidelines that might not apply to other domains. In contemporary, cutting-edge NLP projects, deep neural networks are usually employed to build distributed words that preserve the nuances of words' syntax and semantics meanings. Semantically represented, the words will have a related word-to-vector form, and the word will have a different vector representation in space. This approach is always used for word-distributed embeddings.

The objectives include a pre-trained model that does not require labelled data and a standard architecture that can be used in multiple scenarios. The relevant words, sub-words, and word positions moving based on embeddings are included in creating the word vector format of a specific token value. Bidirectional Encoder Representations from Transformers are used in addition to embedding words from Language Models (ELMO). ELMO model was used to extract the features and word convolutions.

4. Methodology

We first quickly go over the GANs' formulation in this part. In Section 4.1, we then introduce the GANs and their advantages.

4.1 Generative Adversarial Networks

The discriminator function D and generator function G are trained simultaneously by the GAN model as part of their

learning process. G aims to discover the distribution of P_G across the given data X. G begins by taking the number of samples of the input variables y from a Gaussian distribution function parameters are $p_z(y)$. A differentiable network is then used to map the input variables z to the data space G (z; θ_g). Conversely, D is a classifier D (x; θ_d) that seeks to identify if an image comes from G or training and testing data. The following formula can be used to express the minimum objective for GANs:

$$\frac{\min \text{Max}}{G} V_{GEN}(D, G) = \epsilon_x \sim P_{data}(x) [\log D(x)] + \epsilon_z \sim p_z [\log (1 - D)(G(z))] \quad (1)$$

The main functions the representation layer aims to provide will be utilized in constructing the suggested English NER tasks. Adversarial networks introduced by [23] proposed that the model be used to determine the minimum and maximum game between the generator of the different discriminators. The network aims to maximize the probability of training and testing values in word distributions with the high-low quality of the network. In recent years, one of the most notable developments in machine learning has been the emergence of GANs.

GAN models have shown effectiveness in areas where previous models were ineffective while significantly improving performance in other contexts. This section will thoroughly examine the key fields in which GAN designs have been implemented. Although a significant portion of current research has focused on using GANs to create unique synthesized data and simulate different data distributions, this section will examine the broader applications.

4.2 LSGAN

Normal GANs treat the discriminator as a classifier to perform different operations like cross-entropy, random state and loss function, etc. This loss function will result in the issue of gradients for the sample data on the right side of the decision-making process and their boundary, which is still distant from the actual data while updating the generator. We suggest using Least Squares Generative Adversarial Networks to solve this issue. Assume that the discriminator will employ the a-b coding scheme, in which a and b represent fictitious and actual data labels. Afterward, the following definition can be used for LSGAN objective functions:

$$\frac{\min}{D} V_{LSGAN}(D) = \frac{1}{2} \epsilon_x \sim (x) [(D(x) - b)^2] + \frac{1}{2} \epsilon_z \sim p_z [(D(G(z)) - a)^2] \quad (2)$$

Where c represents the value G wants D to accept as accurate given fake information.

There are two ways in which LSGANs are advantageous. First, LSGANs punish samples that are correctly classified but lie far on the correct side of the decision-making process, unlike ordinary GANs, which cause essentially no loss for those samples. The discriminator's parameters—the decision boundary—are fixed when we update the generator. Consequently, the generator will produce samples closer to the decision boundary due to the penalization. However, for

GAN learning to be successful, the decision boundary needs to span the manifold of accurate data. The learning process will get saturated otherwise. As a result, the sample values generated are brought to the decision values and closer to the actual data manifold. Second, when updating the generator, punishing the samples far from the decision boundary can produce more gradients, solving the issue of disappearing gradients. As a result, LSGAN performance during learning is more stable. some researchers [24] developed a new hybrid-based protocol in the network.

4.3 Parameters Selection

Satisfying $d-a = 1$ and $b-c = 2$ so that minimizing values of the function at Equation 2 minimizes Pearson χ^2 divergence between $p_d + p_g$ and $2p_g$ is one way to find the values of a, b, c, and d, and we get the number of objective functions used in this approach. Figure 2 represents generative adversarial network architecture. This network contains three layers, each working based on the input data it will be performing.

$$\frac{\min}{D} V_{LSGAN}(D) = \frac{1}{2} \epsilon_x \sim p_{data}(x) [(D(x) - 1)^2] + \frac{1}{2} \epsilon_z \sim p_z(z) [(D(G(z)) + 1)^2] \quad (3)$$

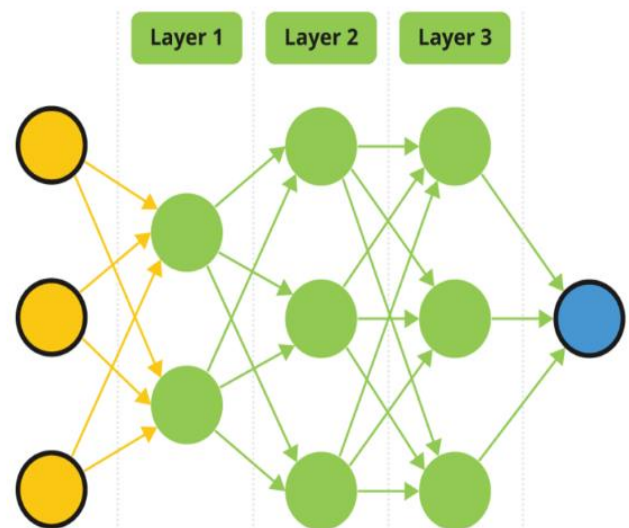


Figure 2. Generative adversarial network architecture

5. Experimental setup

We used extensive hyperparameter settings in conjunction with data from a biological set to train a deep neural network method using different evaluation matrices to assess our neural network model. Using the open-source Keras package, our suggested deep learning-based NER task was built using a Python program. We also utilized TensorFlow and Deep learning with better performance of Python libraries. It is employed to comprehend enhanced deep-learning methodologies.

Our study revealed a cutting-edge biological name entity identification and detection method. The proposed method used in this research is a current neural network methodology, which minimizes standard machine learning approaches' feature engineering methods. The performance of the proposed method compared with other state-of-the-art

techniques shows that our model has demonstrated exceptional results and delivered significant accuracy when incorporating word embedding approaches. Our research will support the identification of intricate biological words despite many obstacles. Here are some of the main barriers that biomedical NER must overcome. Accurately storing and retrieving crucial information from clinical documentation will grow more difficult as the volume of medical data increases. Table 1: GNA hyperparameters for the tested optimization model.

Table 1. GNA hyperparameters for the tested optimization model

Hyper Parameter	Testing Values
Layers	3
Functions	ELU, Linear, Tanh
Number of Epoches	1 to 100
Learning Rate	0.5 to 0.95
Loss	Wasserstein Loss, Binary cross entropy

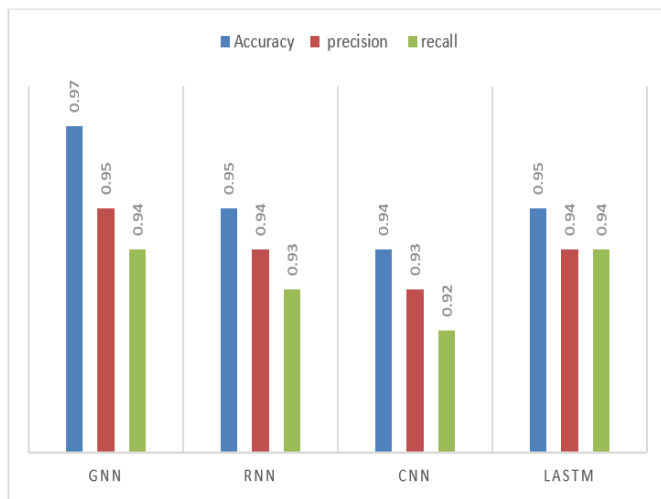


Figure 3. Clinical-named entity recognition using different matrix

The complex Bio-NER system's effectiveness is gauged using different matrices like accuracy, precision, and recall values. This matrix is compared with RNN, CNN, and LSTM models. This proposed model is compared with different state-of-the-art techniques. The proposed model performed better after comparing it with existing models and had good results. Finally, the proposed model achieved the highest accuracy value of 0.97% using bio-medical data analysis. Figure 3 shows the performance of different methods using different matrix comparisons. A finely proposed model gives better performance than other state-of-the-art models. Table 2 represents dataset names and the training and testing phase of the sentence collection of the model.

Table 2. Dataset used for the GAN model

Phase	BC2GM	NCBI
Training	21,742	25,972
Testing	25,716	29,293

The training and validation accuracy curves are crucial tools for assessing the efficacy of a machine-learning model. Figure 4 shows the training versus validation accuracy curve that GAN obtained. The training's accuracy began at a lesser value of 0.32 at the beginning and rose progressively to a

stunning 0.99 after the training time. This increasing trend shows that GAN can continuously enhance its classification performance by efficiently learning from the training data.

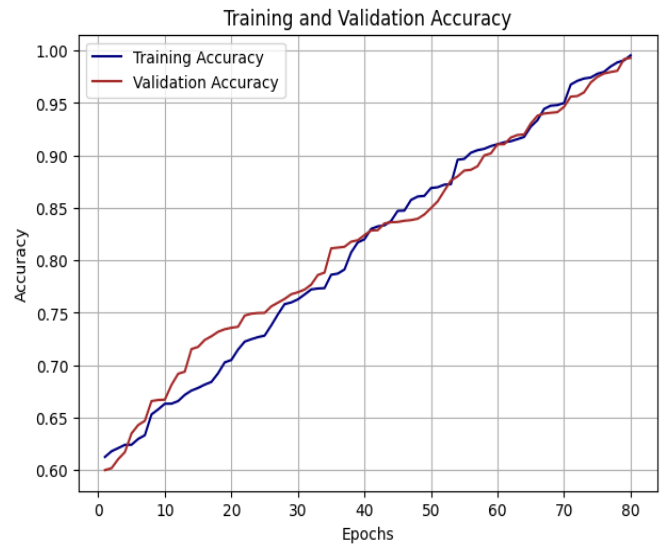


Figure 4. Validation of the accuracy of the 80 epochs

Figure 5 shows the training versus validation loss map. The training loss began at a more excellent value of 1.32 at the beginning of the training session and gradually dropped, ending at a minimal value of 0.09 at the conclusion. The declining trend suggests that the model minimizes the discrepancy between the anticipated and actual values by effectively learning from the training data. On the other hand, the validation loss, which had a slightly lower initial value of 1.28, eventually reached 0.22 after following a similar downward course that included some swings. Despite occasional variations, the validation loss significantly decreases over epochs, indicating that GAN generalizes well to previously unseen data. The durability and efficiency of GAN in the job at hand are demonstrated by the convergence of both training and validation losses towards shallow values, suggesting the network's capacity to minimize errors and reliably classify leukemia subtypes from peripheral blood smear pictures.

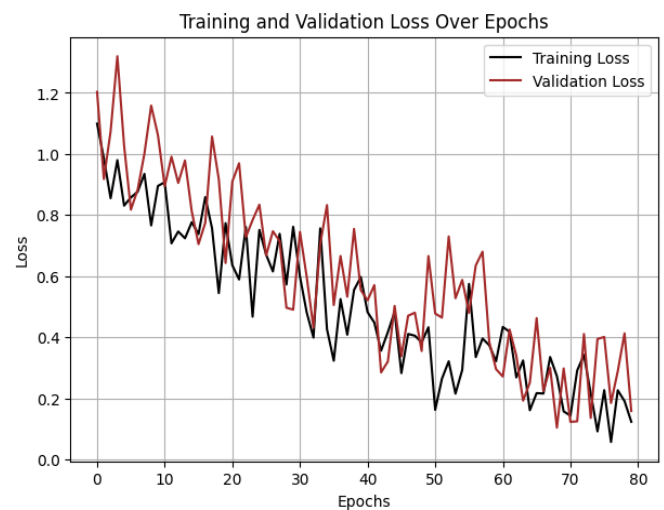


Figure 5. Loss function using the number of epochs

5.1. Performance analysis

Bio-NER is complex because several crucial elements influence the NER system's performance, including language, domain knowledge, and entity factors. In addition, it can be challenging to transfer the Bio-NER model using different types of entities. Our goal was to improve the performance of gene and entity values using deep learning models and effectively perform entity class classification using pre-trained models. Because the datasets are complex, we only displayed the performance metrics for a few and two different datasets, BC2GM and JNLPBA datasets; we have achieved better results using the NCBI dataset and have good, efficient results.

The suggested method generates an NER task, which has been transformed into a classification issue for evaluation. Following the classification of the various entities, the performance is evaluated using multiple classification metrics, including accuracy, precision, and recall. The calculation of three different matrices and formalisms are presented below in equation (4-6).

It is challenging to complete the NER task because it contains large textual data, and the different genres, domains, and entity types all affect its success or failure. Because of its unique nature, NER is challenging to transfer from one domain to another. We performed supervised approaches to the medical domain; an annotated large corpus data is necessary to categorize different name entities to discover the testing data.

$$Accuracy = \frac{\text{Number of messages Classified}}{\text{Total Number of messages}} \quad (4)$$

$$Precision = \frac{TP}{TP+FP} \quad (5)$$

$$Recall = \frac{TP}{TP+FN} \quad (6)$$

Table 3: Limitations of the existing works

Reference No.	Method	Limitations
Gong et al.[1]	Rule-based mode	No standard comparison
Dash et al. [2]	ELMO and BERT	Hyder parameter is not considered
Giorgi et al. [7]	Transfer learning and DNN	A small number of label dataset
Lee et al. [8]	Bio-BERT	Very low accuracy achieved
Zhang et al. [12]	global feature extraction	Only finance domain
Our Model	GAN	Better performance

Character embeddings are used to convert each token into a meaningful representation. This is followed by implementing a max-pool layer, a character embedding word vectorization approach. This word representation is transferred as the input to the GAN model. These models change the input data to get the best-recognized character-level and word-level embeddings, and they also help address the Vocabulary

problem for many NLP applications. Table 3 explains a few chosen articles' research constraints and literature analysis.

6. Conclusion

This paper describes two well-known word embeddings and the BERT model: Generative Adversarial Networks instead of vocabularies or big gazetteers. Mainly, we have improved the system performance based on advanced learning models using unlabeled datasets. We evaluate the performance of gene and entity values by integrating the ELMO model, which contains different layers. Our Model mitigates out-of-vocabulary concerns by modeling different rare-m—morphological forms of medical terminology to utilize this research work. Our results are better than those of other existing methods when comparing accuracy values. We evaluated the effectiveness of the model performance on the available data. One potential avenue for future research is to assess the effects of the ELMO model and BERT-based embedding by combining nested entity detection and categorization processes. We want to add more features to enhance the Model's overall functionality. Identifying entity relations as a possible area of investigation was another goal. Stacked GAN layers can learn context more efficiently. Thus, we will consider them in the future. In the future scope, the analysis of manually annotating corpora will be a challenging and labor-intensive operation; we will investigate the feasibility of using other feature-enhanced techniques to improve the proposed Model. Consequently, it will benefit the biomedical research field.

Data Availability

The data supporting this study's findings are available on request from the corresponding author.

Conflict of Interest

The authors declare no potential conflict of interest.

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Authors' Contributions

All Authors contribute equally to the development and presentation of this manuscript.

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