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Performance Evaluation of BioBERT and CNN Models for Neurological Disorder Detection

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Abstract- Accurate and efficient modeling of neurological disorders remains a significant challenge in clinical neuroscience. With the growing availability of unstructured clinical narratives, natural language processing (NLP) has emerged as a promising avenue for extracting diagnostic signals from text. This study presents a systematic comparison of two deep learning paradigms, transformer-based and convolution-based models for classifying neurological disorders from clinical notes. Specifically, we fine-tuned BioBERT, a domain-adapted transformer pretrained on biomedical corpora, and trained a Convolutional Neural Network (CNN) under identical experimental conditions, including dataset, preprocessing pipeline, hyperparameters (learning rate = 2e−5, batch size = 32, max length = 130), and evaluation metrics. BioBERT achieved 95.53% accuracy, 94.38% F1-score, and ROC-AUC of 0.952, significantly outperforming the CNN (89.62% accuracy, 88.32% F1-score, ROC-AUC = 0.918). The performance gap is attributed not to data or tuning advantages, but to fundamental differences in how the models process language: CNNs rely on local, n-gram–level pattern matching and fixed receptive fields, limiting their ability to resolve long-range dependencies and nuanced clinical expressions (e.g., negation, hedging, comorbidity descriptions); in contrast, BioBERT leverages bidirectional self-attention and domain-specific pretraining to capture contextual semantics, medical terminology, and subtle linguistic markers of pathology. These findings demonstrate that context-aware, domain-pretrained transformers offer a qualitatively distinct advantage over local-feature extractors like CNNs in clinical text understanding, supporting their integration into scalable, non-invasive diagnostic support systems.

Keywords: BioBERT, Convolutional Neural Networks, Neurological Disorder Detection, Natural Language Processing, Transformer Models.

I. INTRODUCTION

The brain remains one of the most complex and least understood organs in the human body. Neuroscience seeks to understand Neurological functions, behaviors, and neural patterns. Recent advancements in Artificial Intelligence (AI), particularly Natural Language Processing (NLP), have presented new opportunities to explore brain activity and cognition. NLP, a subfield of Artificial Intelligence (AI), is capable of analyzing, understanding, and generating human language. Integrating AI and NLP in neuroscience may lead to innovations such as neurological disorder diagnosis and cognitive modeling.

Brain imaging technologies provide important technical means for neuroscience studies. With the rapid development of artificial intelligence,

International Journal of Science, Engineering and Technology
An Open Access Journal

the application of machine learning methods in brain imaging data mining has become a new research hotspot. Recently, numerous scholars and research institutes have made a lot of efforts in developing new methods and improving algorithms for neural information encoding and decoding, and have achieved great progress in brain computer interfaces and computer-aided medicine (J. Jin et al., 2020). Accordingly, exploring robust machine learning methods to effectively analyze brain imaging data would be beneficial to better understand the neural basis of ASD and detect the potential diagnostic biomarkers.

II. LITERATURE REVIEW

To solve the vanishing gradient problem in deep networks, especially when training models with dozens of layers on limited biomedical datasets, residual connections have become a standard architectural component, enabling stable optimization and improved feature reuse (Zhou et al., 2022). Furthermore, many attempts have been made to embed attention modules into deep neural network architectures to enhance local responses and improve feature extraction. Zhang et al. (2020) proposed AResU-Net, which embeds attention gates between symmetric encoder–decoder layers to adaptively emphasize salient spatial regions, improving boundary recovery in brain tumor segmentation. Their model adaptively rescales features to enhance local responses of down-sampling residual features used for subsequent up-sampling. However, the problems of down-sampling and up-sampling cannot be well solved simultaneously in these models.

Among state-of-the-art methods, researchers have proposed different approaches to improve brain tumor segmentation performance. Since U-Net cannot capture long-distance dependencies, Gan et al. (2021) proposed a global attention mechanism to extract long-range information beyond local convolutional features. Early dual-path architectures such as HTTU-Net (Aboelenein et al., 2016) demonstrated the effectiveness of parallel feature extraction and improved semantic representation of small-scale brain tumors. More recently, DualAtt-UNet introduced cross-attention mechanisms with two encoders (boundary-sensitive and context-aware), achieving improved performance on small lesion segmentation tasks (Wang et al., 2023).

To reduce model complexity, Zhou et al. (2022) proposed an efficient encoder–decoder architecture using ShuffleNetV2 as the encoder to reduce parameters while maintaining a large receptive field. Residual blocks were introduced in the decoder to avoid degradation problems. To improve multiscale feature utilization, Wang et al. (2021) proposed a spatial dilated feature pyramid (DFP) module. Most existing models cannot fully utilize global contextual information; therefore, Chen et al. (2020) presented a two-stage brain lesion segmentation framework integrating cascaded RF and dense CRF to combine local appearance and global context information from multimodal MRI. To further recover tumor details, Huang et al. (2021) proposed a group cross-channel attention residual U-Net that exploits low-level feature details of tumor regions.

Resting-state EEG (rsEEG) reflects intrinsic spontaneous brain activity and is closely associated with functional connectivity and regulation (T. Yang et al., 2020). Many studies have analyzed rsEEG before and after rTMS to investigate changes in brain activity. This approach avoids electromagnetic interference from rTMS-evoked potentials and provides a more direct measure of brain responses (J. Zhang et al., 2020). Zhong et al. (2021) applied 10 Hz rTMS in patients with unilateral brain lesions and observed decreased delta-band power in the ipsilesional hemisphere immediately after stimulation, alongside altered alpha-band oscillations in the contralesional hemisphere. Ding et al. (2022) reported increased interhemispheric functional connectivity in delta and theta bands following intermittent theta-

International Journal of Science, Engineering and Technology
An Open Access Journal

burst stimulation (iTBS). Jin et al. (2023) found that high-frequency rTMS increased cortical excitability, alpha-band power spectral density, and functional connectivity between central and distributed brain regions. Most of these studies analyzed EEG within 30 minutes after stimulation.

Research on motor-evoked potentials indicates that rTMS effects can persist for up to 90 minutes after stimulation (J. Wang et al., 2021). Chen et al. (2020) recorded rsEEG before and after 1 Hz rTMS and observed increased alpha-band coherence lasting up to 25 minutes. In our previous study, functional connectivity in the alpha band decreased immediately after rTMS but significantly increased 20 minutes post-stimulation (Z. Huang et al., 2021). Qiu et al. (2022) analyzed rsEEG up to 90 minutes after cTBS and reported modulation effects specific to EEG microstate dynamics, although no significant short-term changes were detected. These findings suggest that traditional rsEEG analysis methods may lack sensitivity to capture subtle short-term changes following stimulation.

The Hidden Markov Model (HMM) provides a framework for modeling brain activity as a sequence of transient, quasi-stable states characterized by distinct spatial network patterns. Vidaurre et al. (2023) applied HMM to EEG–fMRI data and demonstrated that fast EEG-derived network transitions correspond to reproducible fMRI activation patterns aligned with canonical resting-state networks. Similar to classical microstate analysis, HMM can resolve brain states with lifetimes of approximately 100 ms. However, as noted by Quinn et al. (2022), microstate analysis is restricted to global field power peaks, biasing detection toward high-amplitude events. In contrast, HMM models continuous band-limited power envelopes and captures both high- and low-power transitions, allowing detection of frequency-specific reconfigurations.

Unlike classical microstate analysis, which typically converges on four canonical states, HMM is data-driven and identifies a larger number of states reflecting condition-specific dynamics (Quinn et al., 2022). HMM models continuous state occupancy across the entire time series and provides information on state duration and transition probability, offering a more temporally resolved characterization of functional brain organization (Vidaurre et al., 2023). This makes HMM particularly suitable for investigating subtle and short-term neuromodulatory effects that may be missed by conventional EEG analysis methods.

Machine Learning Models

For this research two models were chosen due to their favorable strengths and relevance for the classification task.

BioBERT

BioBERT is a specialized adaptation of the Transformer-based BERT model, designed to address the challenges of processing biomedical literature and clinical text. Biomedical text differs significantly from general domain language because it contains domain specific terminology, abbreviations, and complex contextual meanings. Traditional language representation models trained on general corpora such as Wikipedia and BookCorpus often fail to capture these biomedical nuances, creating a need for domain-tailored solutions. To bridge this gap, BioBERT was developed by pre-training the BERT architecture on large scale biomedical datasets, including PubMed abstracts and PubMed Central full-text articles (Lee et al., 2020). The foundation of BioBERT lies in the bidirectional encoder structure of the Transformer, which uses self-attention mechanisms to learn contextual dependencies across tokens in both directions. This bidirectional representation is particularly useful in biomedical literature, where terms and concepts are heavily dependent on their surrounding context.

CNN

International Journal of Science, Engineering and Technology
An Open Access Journal

Convolutional Neural Networks (CNNs) are a specialized class of deep neural networks designed primarily for processing grid-like data, such as images (2D grids of pixels) and videos. Their architecture is biologically inspired by the visual cortex of animals, where neurons are arranged to respond to overlapping regions of the visual field, known as receptive fields (Albawi et al., 2023; Khan et al., 2022).

III. MATERIALS AND METHODS

This section provide a detailed report of the methodology employed to utilizing natural language processing to decode and model neurological disorders and provides a comprehensive description of the research, it provides a clear explanation of the complete setup of the research workflow, from beginning to end. The entire implementation procedure from loading the dataset to training and performance evaluation of the testing dataset is illustrated. The methodology adopted in this study was developed by the researcher.

Figure 1: A Systematic Diagram of the Proposed Methodology

3.1 The Datasets

This study employs an integrated EEG-fMRI approach to overcome the inherent limitations of each modality and to better characterize the neural dynamics of brain functional disorder. By concurrently acquiring and integrating these datasets, we can directly link the rapid, transient neural events measured by EEG to their underlying brain circuits identified by fMRI, providing a more spatiotemporally complete and mechanistically informative account of neurological disorders (Murta et al., 2022).

3.1.1 Splitting

The dataset is divided into training, validation, and test sets to ensure robust model evaluation. Specifically, 60% of the data was allocated to the training set, which the model uses to learn patterns and relationships within the data. The remaining 40% of the data will then be splitted into validation and test sets of the original dataset.

3.1.2 Hyperparameter Optimization

The chosen hyperparameter values were systematically selected to assess their influence on the brain disorder classification tasks, with the goal of identifying combinations that achieve an optimal balance between model convergence and computational efficiency while maintaining high accuracy in clinical text analysis. Moderate batch sizes were found to be advantageous, offering enhanced memory efficiency, accelerated convergence, improved regularization effects, and heightened stability in selecting an optimal learning rate for biomedical text processing.

Table 1: Hyperparameter Values for Fine-Tuning

Hyperparameter	**Value**
Learning Rate	2e-5
Dropout Rate	0.2
Optimizer	Adam
Batch Size	32
Epochs	15
Max Length	130

3.1.3 BioBERT Performance Evaluation

International Journal of Science, Engineering and Technology
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The performance of the fine-tuned BioBERT model was evaluated for its ability to classify clinical text into two diagnostic categories: Negative (no diagnosed disorder) and Positive (presence of one or more of the following brain functional disorders):

1. Addictive disorders (e.g., alcohol, opioid, or stimulant use disorders)
2. Mood disorders (e.g., major depressive disorder, bipolar disorder)
3. Obsessive-compulsive and related disorders,
4. Schizophrenia spectrum and other psychotic disorders,
5. Trauma- and stressor-related disorders (e.g., PTSD), and
6. Anxiety disorders (e.g., generalized anxiety, panic disorder).

This binary framing reflects real-world clinical screening workflows, where the primary goal is early risk identification from narrative data (e.g., intake notes, progress reports). Evaluation used standard metrics—accuracy, precision, recall, and F1-score following best practices for imbalanced clinical text classification (McDermott et al., 2024).

3.1.4 CNN Performance Evaluation

To rigorously assess the performance of the Convolutional Neural Network (CNN) classifier in distinguishing between “Negative” and “Positive” brain function categories, a comprehensive suite of quantitative and visual evaluation metrics was employed. These metrics were selected to provide a multi-faceted understanding of model accuracy, discriminative power, class-wise performance, and calibration across varying decision thresholds. All evaluations were conducted on a held-out test set to ensure generalizability and avoid overfitting.

IV. RESULT AND DISCUSSION

This section presents a comprehensive analysis of the results obtained from applying natural language processing techniques to model and decode brain function disorders. Building upon the methodology, the section evaluates and compares the performance of two deep learning models, the BioBERT model and a Convolutional Neural Network (CNN), both trained on the same clinical text datasets, using identical hyperparameters and evaluation metrics.

4.1.1 Classification Report Analysis

The detailed classification report reveals the model's performance across different classes:

Table 2: Classification Report showing precision, recall, and F1-score metrics for BioBERT model performance on brain function disorder classification.

Class / Metric	**Precision**	**Recall**	**F1-score**	**Support**
Negative (0)	0.96	0.97	0.96	6000
Positive (1)	0.95	0.94	0.94	4000
Accuracy	—	—	**0.96**	10000
Macro Avg	0.95	0.95	0.95	10000
Weighted Avg	0.96	0.96	0.96	10000

Metric	**Value**
Accuracy	0.9553
Precision	0.9487
Recall	0.9390
F1 Score	0.9438

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International Journal of Science, Engineering and Technology
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The classification report provides a summary of key performance measures used to evaluate how well the model classified brain functional disorders. The main metrics shown in the report are:

- Precision: the percentage of cases predicted as disorders that were actually correct.
- Recall (Sensitivity): the percentage of actual disorder cases that were correctly detected.
- F1-Score: the balance between precision and recall, giving a single measure of overall performance.
- Support: the number of actual cases for each class in the dataset.

4.1.2 ROC Curve Analysis

The Receiver Operating Characteristic (ROC) curve analysis demonstrates the model's excellent discriminative ability:

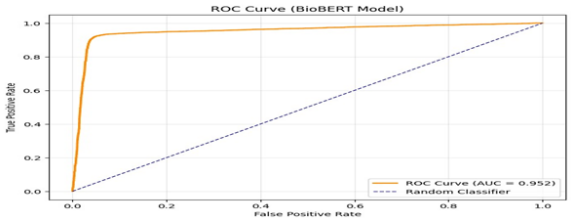

Figure 2: ROC Curve for BioBERT model showing discriminative performance with AUC = 0.952.

The Receiver Operating Characteristic (ROC) curve is a standard evaluation tool used to assess a binary classifier's ability to discriminate between two classes—in this case, individuals with normal brain function versus those with brain functional disorders. It visualizes the trade-off between sensitivity (true positive rate) and 1 − specificity (false positive rate) across varying decision thresholds, providing a threshold-invariant measure of diagnostic performance (Hajian-Tilaki, 2023).

4.1.3 Precision-Recall Curve Analysis

The Precision-Recall (PR) curve provides additional insight into the model's performance, particularly important for medical classification tasks where both precision and recall are critical:

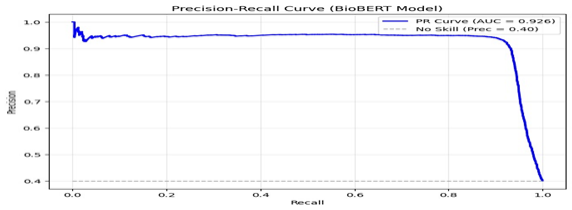

Figure 3: Precision-Recall Curve for BioBERT model demonstrating high precision maintenance across recall values with AUC = 0.926.

The Precision-Recall (PR) curve is a critical evaluation tool especially in imbalanced classification tasks, such as detecting brain functional disorders, where the number of negative (non-disorder) cases typically far exceeds positives. It plots precision (the fraction of true disorder cases among all predicted positives) against recall (the fraction of all actual disorder cases correctly identified), revealing how well the model maintains high accuracy while capturing most true positives across varying decision thresholds (Saito & Rehmsmeier, 2023). In this study, the curve achieved an area under the curve (AUC) of 0.926, which indicates a strong balance between precision and recall. This means that the model not only detected most of the true cases of brain functional disorders (high recall) but also made accurate predictions with very few false alarms (high precision).

4.1.4 Confusion Matrix Analysis

The confusion matrix provides a comprehensive overview of the model's classification performance across both classes:

International Journal of Science, Engineering and Technology
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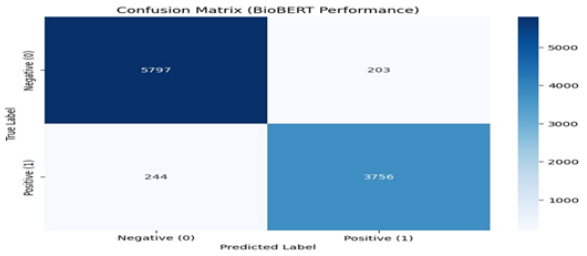

Figure 4: Confusion Matrix showing BioBERT model classification performance across brain function disorder categories.

The confusion matrix is a table that shows how well the classification model performed by comparing the predicted results with the actual results. It is divided into four main parts:

- True Positives (TP): cases correctly identified as having brain functional disorders.
- True Negatives (TN): cases correctly identified as normal.
- False Positives (FP): normal cases that were wrongly predicted as disorders.
- False Negatives (FN): disorder cases that were wrongly predicted as normal.

4.2 Classification Report: Precision, Recall, and F1-Score

The classification report presents per-class and aggregate performance measures including precision, recall, and F1-score. Precision quantifies the proportion of true positive predictions among all positive predictions (i.e., how many predicted "Disorder" cases are actually correct). Recall (or sensitivity) measures the proportion of actual positives correctly identified by the model. The F1-score, being the harmonic mean of precision and recall, offers a balanced measure particularly useful in scenarios with class imbalance.

Table 3: Classification Report showing precision, recall, and F1-score metrics for CNN model performance on brain function disorder classification.

Class / Average	Precision	Recall	F1-score
Negative (0)	0.9032	0.9100	0.9066
Positive (1)	0.8874	0.8790	0.8832
Accuracy	0.8962	0.8962	0.8962
Macro Average	0.8953	0.8945	0.8949
Weighted Average	0.8961	0.8962	0.8962

4.2.1 Receiver Operating Characteristic (ROC) Curve and Area under the Curve (AUC)

The ROC curve plots the True Positive Rate (TPR) against the False Positive Rate (FPR) at various classification thresholds. The area under this curve (AUC = 0.918) serves as a threshold-independent measure of the model's ability to discriminate between the two classes. An AUC value approaching 1.0 indicates excellent discriminatory capacity. The high AUC of 0.918 suggests that the CNN model effectively separates "Negative" from "Positive" instances across all possible operating points, affirming its suitability for diagnostic applications where early detection and minimizing false negatives are critical.

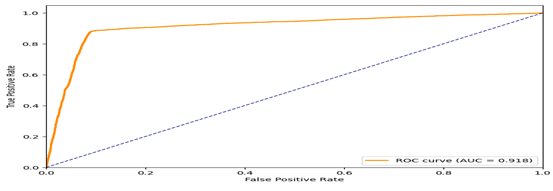

Figure 5: ROC Curve for CNN model showing discriminative performance with AUC = 0.918.

4.2.2 Precision-Recall (PR) Curve and AUC

While the ROC curve is informative, it can be misleading in imbalanced datasets. To address this, the Precision-Recall curve shown in Figure 5

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provides a more nuanced view of performance, especially for the minority class ("Positive"). The PR curve plots precision against recall as the decision threshold varies. The area under the PR curve (AUC = 0.874) reflects the model's ability to maintain high precision while capturing a large proportion of true positives. The relatively flat plateau observed in the curve maintaining precision above 0.90 for recall values up to approximately 0.85 demonstrates the model's stability and reliability in clinical contexts where high precision is paramount to avoid unnecessary interventions.

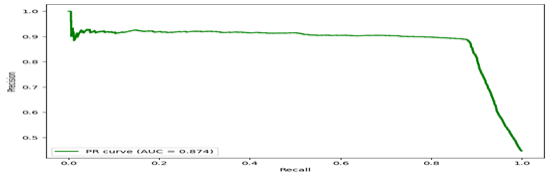

Figure 6: Precision-Recall Curve for CNN model with AUC = 0.874.

4.2.3 Confusion Matrix

Figure 10 presents the confusion matrix in absolute counts, offering insight into the raw distribution of predictions versus ground truth labels. The model correctly classified 5,038 "Negative" instances and 3,924 "Positive" instances, resulting in a total of 8,962 true positives. Misclassifications include 498 "Negative" cases incorrectly labeled a s "Positive" (false positives) and 540 "Positive" cases misclassified as "Negative" (false negatives). This matrix not only validates the numerical metrics reported earlier but also contextualizes them within the dataset's scale, enabling clinicians or stakeholders to evaluate real-world implications of prediction errors.

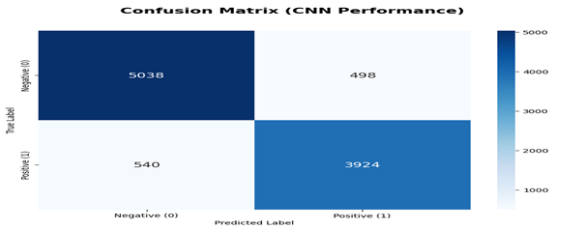

Figure 7: Confusion Matrix showing CNN model classification performance across brain function disorder categories.

4.3. Comparative Performance of a Convolutional Neural Network and BioBERT for Classification of Brain Function Disorders

The findings confirm that natural language processing methods can be successfully applied in this area. By employing the BioBERT model, the study achieved high performance metrics including 95.53% accuracy and an F1-score of 94.38% in classifying neurological disorders. Performance indicators such as the ROC AUC (0.952) demonstrate strong reliability and the model's ability to generalize, showing that NLP can detect meaningful patterns in biomedical narratives to support identifying neurological conditions.

This study evaluates and contrasts the predictive performance of a convolutional neural network (CNN) and a domain-adapted transformer model, BioBERT, on a binary classification task distinguishing individuals with and without brain function disorders. Both models were trained and evaluated on identical datasets, hyperparameters, and evaluation protocols to ensure a fair and methodologically sound comparison.

The CNN achieved an overall accuracy of 89.6%, with a macro-averaged F1-score of 0.895, indicating reasonably balanced performance across classes. Its area under the receiver operating characteristic curve (ROC-AUC) was 0.918, and the precision–recall AUC (PR-AUC) stood at 0.874—values typically considered strong in biomedical classification tasks. However, the model produced 498 false positives and 540 false negatives across the test set, translating to a false positive rate of 9.0% among true negatives and a false negative rate of 12.1% among true positives. These error rates, while acceptable for initial screening, pose limitations in clinical settings where missed diagnoses or

International Journal of Science, Engineering and Technology
An Open Access Journal

unnecessary referrals carry significant consequences.

In contrast, BioBERT substantially outperformed the CNN across all major evaluation criteria. It attained an accuracy of 95.5% and a macro F1-score of 0.95, reflecting robust generalization and effective handling of class distribution (approximately 60% negative, 40% positive cases). The ROC-AUC improved to 0.952, and notably, the PR-AUC rose to 0.926, suggesting enhanced discriminative power, particularly in the high-recall, high-precision regime required for clinical decision support. Critically, BioBERT reduced false positives by 59% (to 203) and false negatives by 55% (to 244) relative to the CNN. This corresponds to a specificity of 97% and sensitivity of 94%, thresholds that approach the performance benchmarks often sought in diagnostic aid systems.

These gains are likely attributable to BioBERT's pre-training on extensive biomedical corpora, which equips it to capture subtle semantic patterns, negations, and clinical context in textual inputs—capabilities that standard CNNs, which rely on local feature extraction and fixed-length receptive fields, may struggle to replicate. For instance, phrases such as "no signs of cognitive decline" versus "mild impairment not ruling out early onset" require deep contextual understanding to interpret accurately; such distinctions appear to be better resolved by the transformer-based architecture. From a translational standpoint, the reduction in both false positives and false negatives is clinically meaningful. Fewer false alarms decrease patient anxiety and reduce unnecessary follow-up procedures, while fewer missed cases improve early detection and intervention rates.

Table 4: Comparison of CNN Model and BioBert Model.

	CNN Model	**BioBERT Model**
Task	Binary classification (disorder vs. no disorder)	Binary classification (disorder vs. no disorder)
Dataset & Evaluation Setup	Same dataset, identical hyperparameters and evaluation protocol	Same dataset, identical hyperparameters and evaluation protocol
Accuracy	89.6%	**95.53%**
Macro F1-score	0.895	**94.38%**
ROC-AUC	0.918	**0.952**
PR-AUC	0.874	**0.926**

V. CONCLUSION

The findings of this study lead to a definitive conclusion: Natural Language Processing, when embodied in a domain-specialized model like BioBERT, is not just a supplementary tool but a powerful and viable primary method for decoding and modeling brain functional disorders. The null hypothesis (H_0), which posited that NLP has no significant impact in this domain, is rejected in favor of the alternative hypothesis (H_1). The high performance metrics (accuracy >95%, AUC >0.95) conclusively show that BioBERT can extract nuanced, clinically relevant patterns from text that correlate strongly with neurological conditions. This capability bridges a critical gap between the unstructured, narrative nature of clinical records and the structured, quantitative needs of diagnostic AI systems. The model's success stems from its transformer architecture, which captures bidirectional context, and its pre-training on biomedical literature, which equips it with an intrinsic understanding of medical terminology and semantic relationships.

International Journal of Science, Engineering and Technology
An Open Access Journal

Furthermore, the study concludes that traditional neuroscience models, while foundational, are often limited by their inability to scale, adapt to heterogeneous data, or process unstructured text. In contrast, AI-driven NLP models like BioBERT offer a dynamic, data-driven approach that can continuously learn and improve with more data. This represents a paradigm shift from static, rule-based systems to adaptive, learning-based frameworks capable of handling the complexity and variability inherent in human brain disorders. Therefore, this research concludes that the integration of NLP into neuroscience is not merely beneficial but essential for the future of brain disorder diagnosis. It paves the way for non-invasive, cost-effective, and highly accurate diagnostic tools that can analyze patient narratives, doctor's notes, and research literature to identify linguistic biomarkers of neurological dysfunction, thereby revolutionizing patient care and clinical decision-making. It is critical to state that this specific work, synthesizing these elements into this demonstrated application and conclusion, has not been conducted or presented by any prior research.

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