A hybridized Deep Learning Model for bipolar and schizophrenia Disorder Detection

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Abstract: Psychiatric disease detection is an emerging interdisciplinary field that explores the complex neurobiological mechanisms underlying mental disorders. As the global burden of mental illness continues to rise, there is an urgent need for more precise diagnostic tools. Disorders such as schizophrenia and bipolar disorder affect a significant portion of the population and often present overlapping genetic and clinical features, making diagnosis particularly challenging. To address this, a deep learning-based framework is proposed to identify key gene biomarkers using gene expression data from the GEO (Gene Expression Omnibus) database. This model employs the kernel-applied Fisher score (KFScore) method for effective feature selection, followed by an ensemble approach combining the sine-cosine method with the Monarch Butterfly algorithm, referred to as SC-MBO, is applied to optimize the hyperparameters of the Convolutional Neural Network (CNN) to accurately classify and detect psychiatric conditions.

Keywords: Psychiatric disease; Kernal Fisher Score; Deep learning; significant biomarker; Convolutional neural network

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Introduction

The pharmacological treatment of schizophrenia and bipolar disorder carries notable risks, including: Motor symptoms: extrapyramidal reactions, tardive dyskinesia, akathisia. Endocrine, metabolic, and systemic issues: elevated prolactin, weight gain, hyperlipidaemia, hyperglycaemia/diabetes, hypothyroidism (especially with lithium), hepatic toxicity (e.g., valproate), and cognitive impairment. Other adverse events: sedation, orthostatic hypotension, anticholinergic effects, cardiac conduction abnormalities, seizures, and rare, serious syndromes like neuroleptic malignant syndrome, agranulocytosis, myocarditis, and acute pancreatitis [1]. The incidence and severity of these effects differ among medications—typical antipsychotics more often cause movement disorders, while atypical antipsychotics are more likely to cause metabolic and endocrine disturbances [2].

These risks heavily inform clinicians' treatment decisions and the individual risk–benefit analysis. Schizophrenia affects both genders similarly and manifests through hallucinations, delusions, cognitive disorganization, negative symptoms, and mood disturbances that disrupt daily functioning and relationships [3]. It is thought to arise from neurotransmission dysregulation, influenced by genetic and environmental factors in treating both schizophrenia and bipolar disorder, selecting medications that balance efficacy, safety, and patient adherence is critical. Psychosocial interventions like cognitive-behavioral therapy (CBT) also play a vital role in managing schizophrenia [4].

Bipolar disorder, affecting about 2% of people worldwide, is a significant psychiatric condition characterized by episodic mania and depression [5]. Genetic factors are prominent, and clinical differentiation from major depressive disorder can be challenging, often leading to misdiagnosis and suicidality [6] [7]. Symptoms include mood swings, irritability, anxiety, and sleep disturbances, with antipsychotics and mood stabilizers (e.g., lithium, valproate) commonly used in treatment.

The model development proceeds in two distinct phases:

Phase I employs a novel gene-ranking algorithm—Kernel Fisher Score (KFScore)—to identify the most informative genes.

Phase II introduces an ensemble metaheuristic—referred to as SC MBO—which integrates the Sine–Cosine algorithm with the Monarch Butterfly Optimization (MBO). This hybrid approach is used to fine-tune the hyperparameters of a convolutional neural network (CNN) and to perform robust classification based on the selected genetic markers.

Related work

To effectively distinguish between bipolar disorder and schizophrenia and identify key genomic biomarkers, researchers have developed a range of sophisticated classification models and feature-extraction strategies. Many studies leverage ensemble frameworks that integrate traditional machine learning with metaheuristic optimization techniques for feature selection and classifier tuning These ensemble approaches enhance gene–gene interaction insights and improve the performance of biomarker identification methods.

Chen et al. [8] utilize deep neural networks (DNNs) to differentiate schizophrenia from bipolar disorder based on genomic data. Mashayekhi Shams & Jabbari et al. [9] propose an end-to-end CNN–LSTM pipeline (15- and 16-layer architectures) for automated schizophrenia detection using imaging data. Keshavan et al. [10] develop a concise clinical scale that quantifies psychotic and affective symptom profiles across illness stages. Arribas et al. [11] apply independent component analysis (ICA) and default mode network (DMN) metrics to identify schizophrenia biomarkers. Karthik & Sudha [12] employ deep neural networks to predict bipolar disorder and schizophrenia. Fond et al. [13] apply CART decision trees for schizophrenia diagnosis. Trakaddis et al. [14] use gradient boosted trees with regularization to classify schizophrenia genomic profiles. Karrer et al. [15] integrate meta-analytic cognitive priors to forecast cognitive outcomes in schizophrenia. Talpalaru et al. [16] implement logistic regression, SVM, and random forests to predict schizophrenia symptom severity. Salvador et al. [17] employ Ridge Regression for schizophrenia classification.

While prior studies have focused on either deep learning or traditional machine learning, our work presents a direct comparison between these paradigms for classifying bipolar disorder and schizophrenia.

Moreover, we introduce a novel ensemble method—SC MBO CNN—that integrates a Kernel Fisher Score (KFScore) filter for feature extraction with SC MBO (Sine–Cosine + Monarch Butterfly Optimization) to fine-tune CNN hyperparameters. This hybrid model aims to enhance classification accuracy and aid clinicians in making more reliable diagnoses. The following section details our proposed model architecture in depth.

Proposed Hybridized Approach

This study presents a two-phase ensemble framework aimed at selecting key genomic features and classifying disease-related data:
Figure 1 illustrates the overall workflow of the KFScore driven SC MBO CNN pipeline. Below is a detailed breakdown of the proposed methodology:

1. Data Preprocessing & Partitioning
   The effectiveness of the proposed approach is verified using a dimensional a bipolar and schizophrenia dataset, sourced from NCBI GEO with the accession number GSE12649. Refer to Table 1 for detailed descriptions of the dataset.

   Table 1 The detailed elaboration of the dataset.

Data Availability	# Sample	# Feature	# Classes
Gene expression omnibus GSE12649 [18]	102 (33 bipolar disorder patients, 35 schizophrenia patients, 34 control samples)	22,283	2 (0 stands for Control, 1 stands for Case)

   Apply min–max normalization to the bipolar and schizophrenia datasets, then split the normalized data into training and testing subsets.
2. Feature Selection
   Use the Kernel Fisher Score (KFScore) filter to identify the most informative genetic features.
3. Model Training & Hyperparameter Optimization
   Feed the KFScore-selected genes into a CNN classifier. Simultaneously, employ the SC MBO metaheuristic—an ensemble of the Sine–Cosine algorithm and the Monarch Butterfly Optimization—to tune key hyperparameters (e.g., dropout rate, learning rate, batch size, network depth).
4. Evaluation
   Evaluate the trained KFScore SC MBO CNN model on the test set using the optimized feature subset, with classification accuracy serving as the primary performance metric.
5. Comparative Analysis

Benchmark the proposed method against standard machine learning classifiers to assess relative performance.

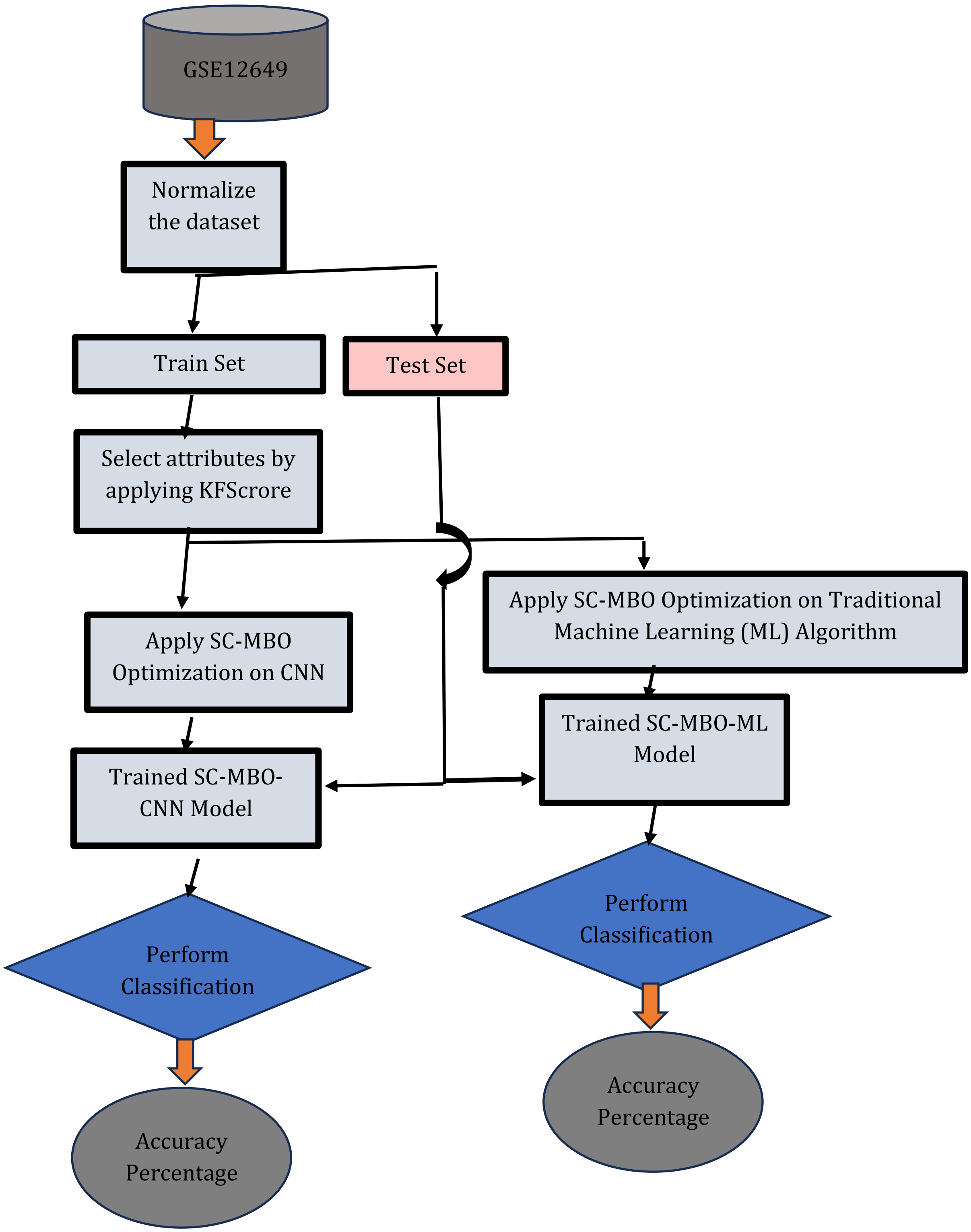

Figure 1. The overall description of the presented KFScore-SC-MBO-CNN strategy.

Conclusions

In this experimental research, we propose an ensemble deep learning framework tailored for the GSE12649 dataset. The proposed model is designed to achieve the following key objectives: (i) Initially, the KFScore algorithm is applied to identify the most relevant genomic features. A major advantage of using KFScore is its ability to eliminate irrelevant genes from the high-dimensional feature space by transforming the dataset through a kernel function. (ii) Subsequently, the SC-ensembled MBO (Modified Butterfly Optimization) algorithm is employed to fine-tune the CNN's random parameters. This optimization technique is notable for its lower computational cost and reduced execution time. The performance of the proposed approach is evaluated based on accuracy, the number of significant genes identified, sensitivity, specificity, and the ROC curve.

Please note- Not all articles will have similar conclusions mentioned as above. Review articles differ in the way they are written.

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