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Machine Learning Applications in the Diagnosis and Classification of Schizophrenia

Zijia Li

Concord Academy, Concord, USA
Bellazj777@Gmail.com

Abstract. Schizophrenia is a severe mental disorder that significantly affects individuals' quality of life. Therefore, early detection and precise diagnosis are crucial for effective intervention. However, due to the complex pathophysiology of schizophrenia, traditional methods fail to perform accurate and efficient diagnosis. Machine learning (ML) has proven to be a useful tool for handling complex data and detecting subtle changes in the brain for early detection, addressing the current challenges in psychiatry. This paper explores different data types, such as EEG, MRI, fMRI, behavioral, and genetic data, and ML models for schizophrenia diagnosis by examining specific data processing, feature selection, and classification methods. Gaps and challenges in current models, including data biases and model explainability, are also addressed in later sections. EEG data trained with supervised and deep learning models achieved the highest classification accuracy out of all the data modalities and ML models. The studies also found that functional connectivity, behavioral data, specific genes, immune-based metabolites and cytokines are all important biomarkers of SZ. This review aims to provide insight into the application of ML in the diagnosis of schizophrenia, highlighting its potential for broader clinical use.

Keywords: Schizophrenia, Machine Learning, Diagnosis, Classification

1. Introduction

Schizophrenia (SZ) is a long-term mental health condition characterized by symptoms such as hallucinations, delusions, lack of motivation, and motor and cognitive impairment. Individuals with schizophrenia have an increased risk of premature mortality, with estimated average lifespans of 28.5 years after diagnosis [1]. Therefore, early detection and intervention of SZ are crucial to improving patients' long-term prognosis and overall life quality. Though the precise cause of SZ is unknown, research has shown that genetics, environment, and brain chemistry are all contributors to the onset of schizophrenia. Current diagnostic methods are limited to clinical evaluation, which is subjective and leads to misdiagnosis. Therefore, it is imperative to develop methods for the efficient and accurate diagnosis of schizophrenia.

Machine Learning (ML) is an approach that learns from data to make decisions without explicit programming, making it a good candidate for effective diagnosis and predictive modelling of mental conditions [2]. ML models for brain disease diagnosis are trained on large datasets of brain imaging data and other behavioral and genetic data, such as electroencephalogram (EEG), CT scans, and

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functional MRI (fMRI), to learn patterns and perform classification tasks. The most prevalent models used in diagnosing SZ are supervised learning models. More recently, neural network models have also been employed for SZ detection. This paper evaluates the diagnostic and classification potential of ML for SZ across different modalities, including EEG, MRI, fMRI, behavioral, and genetic data, in hopes of identifying implications for future research and clinical practice.

2. Overview of Schizophrenia

Schizophrenia (SZ) is a psychiatric disorder with positive symptoms, such as hallucinations, delusions, and thought disorders, and negative symptoms, including loss of motivation, loss of interest, and withdrawal, as well as cognitive impairment, characterized by problems with attention and memory [1].

A combination of genetic and environmental factors contributes to a person's risk of developing SZ. SZ has a high heritability rate of ~80%, but the etiology and progression of this disease are extremely complicated [3]. Research in molecular genetics has established thousands of alleles with varying frequencies contributing to liability, including variants such as STAG1 that encodes a subunit of cohesion, which is an essential protein in chromosomal division [4]. Other studies have found genes associated with glucuronidation, ascorbate, and aldarate metabolic pathways in the body [5]. Previous research established genetic variations in genes regulating glutamatergic and dopaminergic signaling (e.g., GRIN2A, NRG1, and COMT) may contribute to the onset of SZ. Apart from genetic factors, environmental influences relating to risk exposure during early neurodevelopment during pregnancy are also potential risk factors for SZ. These influences include maternal stress, nutritional deficiencies, autoimmune diseases, and more. However, these influences are not specific to SZ and could be risk factors for common neurodevelopmental disorders, including autism, ADHD, and epilepsy.

Understanding the neurophysiological mechanisms of SZ progression is crucial for biomarker identification and treatment development. Studies have shown that the imbalance of excitatory and inhibitory neurons in the cerebral cortex may be an important component of SZ pathology [6]. Abnormalities in interneurons (inhibitory), particularly parvalbumin-positive neurons and pyramidal neurons (excitatory) lacking dendritic spines, are identified in SZ patients. Recent research suggests that microglia, or glial cells that mediate brain inflammation, are involved in synaptic pruning in adolescence, which is the process by which the brain eliminates or weakens synapses. Abnormalities in microglia cells can lead to chemical imbalances in the brain and potentially lead to schizophrenia.

Current diagnostic models, including those proposed in the Diagnostic and Statistical Manual of the American Psychiatric Association (DSM) or the International Classification of Diseases (ICD) of the World Health Organization, evaluate patients based on the presence of specific symptoms such as psychotic episodes. However, due to the heterogeneity of symptoms, the diagnostic accuracy is 33% among 30 influential international psychiatrists, and there are no biomarkers or tests for the accurate diagnosis of SZ [7].

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3. Machine learning principles in the diagnosis of Schizophrenia

3.1. Data sources

The diagnosis of SZ using machine learning requires data input, such as neuroimaging features, behavior, history, and genetic data, and specific biomarkers. Neuroimaging techniques have emerged as useful tools for mapping the structure and physiology of the brain. Magnetic resonance imaging (MRI) uses the magnetic field and radiofrequency currents to discern brain structure and small changes in brain anatomy. Functional MRI (fMRI) is also commonly used in schizophrenia diagnosis because of its ability to highlight functional connectivity, a potential biomarker for schizophrenia. fMRI tracks brain activity by measuring changes in blood oxygenation level. CT scans use X-rays to detect structural abnormalities of the brain and tumors, and lesions. MRI, fMRI, and CT scans all have high spatial resolutions, allowing for more accurate depictions of distinct brain tissues and areas. Meanwhile, the electroencephalogram (EEG) achieves high temporal resolution through implementing scalp electrodes to measure brain electrical activity. EEG has been effective in detecting neural patterns associated with schizophrenia.

Beyond medical imaging, handwriting, gene expression patterns, and immune-based metabolites and cytokines are also used as biomarkers for SZ diagnosis. Handwriting analysis differentiates patients with SZ from healthy controls by their motor dysfunctions. These motor abnormalities are prominent in patients suffering from chronic conditions and children who are diagnosed with SZ years later. Genetic alterations that disrupt neuroimmune system modulation are also associated with the onset of schizophrenia. The abnormal expression of cytokines and receptors could trigger brain inflammatory responses that disrupt neural function.

3.2. Feature extraction and selection

Studies have found that SZ is not caused by abnormality in one specific brain region or several distinct brain areas; rather, it involves the interplay of interconnected neural systems. Connections between different brain regions are reflected in functional networks, where multiple brain areas show coordinated activity. One region can influence another and may suggest causal relationships across areas. Thus, functional connectivity serves as a notable biomarker for SZ diagnosis. Functional connectivity is quantified by first extracting fMRI data, then preprocessing it with the Data Processing Assistant for Resting-State fMRI (DPARSF) and the Data Processing and Analysis of Brain Imaging (DPABI) toolbox. Specifically, the process includes removal of the first few time points to eliminate noise, slice-timing correction, and realignment. Then, the functional images are spatially normalized to the Montreal Neurological Institute (MNI) standard space and undergo spatial smoothing if needed. Linear trends caused by slow drifts in the signal are removed, and temporal bandpass filtering is executed. Nuisance regression is carried out to remove unwanted signals. Finally, the functional connectivity matrix is calculated using Pearson's correlation analysis.

Structural MRI plays a major role in the diagnosis of schizophrenic subtypes. Specifically, studies have shown that patients with the paranoid subtype of schizophrenia have reduced cortical folding [8]. To retrieve and analyze structural data, raw data undergoes motion correction and bias field correction to remove artifacts and scanner-related distortions. Then, the MRI image is aligned to a template space. After skull stripping and segmentation are executed, the data is processed using structural measuring tools to calculate cortical and subcortical volumes. Data preprocessing of CT scans uses similar methods.

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EEG recordings of SZ patients show abnormal brain rhythms and disrupted connectivity. Although EEG signals can successfully capture neural abnormalities in schizophrenia, their high dimensionality and complexity make them difficult to interpret. Therefore, analyzing raw EEG data requires extensive preprocessing steps. Raw signals are first filtered to remove noise, followed by artifact removal and segmentation into epochs. The preprocessed EEG data undergoes further data transformation, such as image encoding, to enable a machine learning application.

A combination of kinematic and geometrical features is extracted from handwriting data. Classical measures of handwriting data include pressure, the number of peaks, length, velocity, and acceleration. Other variables, such as lacunarity or density of points, are also extracted from raw data [9].

Immune biomarkers for SZ are assessed by analyzing cytokines and KP metabolites in blood. These raw measurements first undergo quality control to ensure reliability. After quality control, the cleaned data are used to identify specific biomarkers for distinguishing SZ patients from controls. For genetic data, raw gene expression data is harvested from databases and then transformed. Probe identifiers are matched to their corresponding genes, and differential expression analysis is performed.

3.3. Overview of common machine learning models

3.3.1. Feature selection

In machine learning, feature selection is a crucial step to select relevant features from the large sets of raw data, thereby improving model performance. The three common types of feature selection methods are filter methods, wrapper methods, and embedded methods. The filter method is used as a data preprocessing step to evaluate each feature independently and does not consider feature interactions. This method is suitable for efficiently evaluating features without training the model and removing redundant features for high-dimensionality and multi-modal datasets. The wrapper method iteratively trains a model on different feature subsets, assesses its performance, and refines the subset to maximize accuracy. This method excels at accounting for feature interactions (e.g., functional connectivity) and selecting the most relevant features, though it can be computationally expensive for larger datasets. The embedded method is typically contained in ML algorithms such as decision trees and lasso regression, allowing for the model to select the most relevant features automatically and making it more efficient and scalable than the wrapper method.

3.3.2. Supervised learning

One of the most widely used ML approaches in SZ diagnosis is supervised learning. Supervised learning involves training a model to learn the relationship between input variables and an output variable, which can then be used to predict outcomes for new data [10]. In SZ detection, supervised learning provides more interpretable results, which is crucial in clinical decision-making. Machine learning models are typically divided into two main types: regression and classification. Regression models predict a continuous numeric target value, whereas classification models predict discrete categorical variables.

Linear regression is an example of a regression model, where labeled data is implemented to learn the best-fitting linear function for the given inputs. Logistic regression, a classification model, uses a sigmoid function to predict the probability that an input belongs to one of two classes.

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Tree-based methods split data into groups by decision trees, enabling a hierarchical representation of complex relationships between features. Random forest is an ensemble method that involves combining multiple decision trees and randomly excluding features to reduce overfitting. Boosting decision tree models in sequence.

Support Vector Machines (SVMs) are a supervised learning technique that locates the optimal decision boundary—the hyperplane that maximally separates classes by the largest possible margin to the nearest support vectors—thereby enhancing generalization to unseen data. K Nearest Neighbors (KNN), a non-parametric model, considers the k closest existing data points in the dataset. For classification, it assigns the class that most of those neighbors belong to. For regression, it takes the average of their values. The Naïve Bayes Classifier is a probabilistic algorithm based on Bayes' theorem. It assumes conditional independence, making it suitable for straightforward classification.

3.3.3. Deep learning

Deep learning is a type of ML that mimics neural networks in the brain to allow computers to find patterns in unstructured data. Graph Convolutional Networks (GCN) are a type of neural network that is designed for effectively learning from graph-structured data. Each graph has nodes and edges (connections between nodes), and each layer updates the features of a node by aggregating the features of its neighbors. Thus, each node ends up with a vector that summarizes both its own features and its neighborhood's structure. When processing EEG data, each electrode is a node, and the connections between electrodes are the edges. The nodes have feature matrices that include signal features. The adjacency matrix encodes the connections between nodes—or brain regions—transforming EEG data into a graph. By exploiting this structure, graph convolutional networks simultaneously capture localized electrode dynamics and global brain connectivity, rendering them exceptionally powerful for dissecting complex neural signals.

Convolutional Neural Networks (CNNs) are designed to extract grid-like matrices, making them suitable for analyzing spatial information in image data like MRIs. To train CNN models on EEG signals, the raw EEG data needs to be converted into visual data using image encoding. The converted EEG data showcases both temporal (how the signals change over time) and spectral (frequency of the signals) information.

4. Applications of machine learning in Schizophrenia diagnosis

4.1. EEG-based machine learning approaches in Schizophrenia diagnosis

Yin et al. developed a three-dimensional adaptive CNN model: 3D-AGCN for SZ diagnosis. The 3D attention module applies attention on three axes of the EGG data: frequency band, spatial domain, and feature dimension, and outputs data that reflects functional connectivity. The resulting data is fed into the Graph Attention Network (GAT) + GCN model for classification. Overall, the model achieved a classification accuracy of 87.64% with patients with first-episode schizophrenia [11].

Aich et al. introduced a three-stage framework for SZ detection from EEG signals in 2 separate datasets. First, raw EEG data is encoded into scalogram images using Continuous Wavelet Transform (CWT). Feature extraction is performed using transfer learning with 2 pretrained densely connected convolutional networks. The features are classified using KNN in the wrapper-based feature selection. The framework yielded classification accuracies of 99.67% and 99.97% across 2 independent EEG datasets while using a smaller number of features [12].

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Abrar et al. proposed a four-stage framework combining multichannel EEG, Crossover-Boosted Archimedes Optimization Algorithm (CAOA), and Rough Set Theory (RST) to handle high-dimensional EEG data. The features extracted through the multivariate empirical mode function (MEMF) and entropy measures are classified using SVM. The model yielded an average accuracy of 94.9% [13].

Sarisik et al. classified patients with SZ using EEG recordings trained on SVMs and repeated nested cross-validation, correctly identifying 179 out of 250 patients. The study also found that the global alpha oscillation power decrease is a predictive marker of SZ [14].

Mazroa et al. proposed a deep learning model: Cascaded Atrous Convolutional Network with Adaptive Weight Fusion (CA-AWFM) trained on EEG data. The model integrates cascaded networks with atrous convolutions to allow the model to capture a larger temporal context and refine representations of the data. The model yielded a 99.5% accuracy [15].

4.2. Immune-based biomarkers and machine learning applications in Schizophrenia

Skorobogatov et al. employed supervised learning models to diagnose SZ using peripheral kynurenine metabolites and cytokines. After extracting and quantifying metabolites and cytokines from schizophrenia (SZ) patients and controls, the authors applied regression and tree-based models with nested cross-validation for sensitivity analysis, achieving an AUC of 0.804. Key immune-related biomarkers—xanthurenic acid, tryptophan, and tumor necrosis factor-α—were identified for SZ detection [16].

4.3. CT imaging and machine learning applications in Schizophrenia

Li et al. proposed a deep learning model, DenseMD, to diagnose SZ with CT scans. The model includes the feature extraction model based on the 3D DenseNet model, the fusion module, which concatenates separate vectors into a combined feature vector, and the classification module. The model yielded accuracies of 0.745 and 0.742 in the internal and external validation sets [17].

4.4. Handwriting data and its analysis using machine learning in Schizophrenia

Javeed et al. developed a three-stage ML framework called SRF-SMOTE-NET and validated it using handwriting features. In the first stage, the Kruskal-Wallis statistical test is implemented to select the statistically significant features. The SMOTE algorithm is performed in the second stage, and the neural network is trained to classify these features. Overall, the architecture achieved a classification accuracy of 96% [9].

4.5. MRI and fMRI-based machine learning approaches in Schizophrenia research

Tavakoli et al. used conventional ML methods to classify SZ patients from healthy controls with structural MRI and resting-state fMRI data. They extracted graph-based measures, such as degree, betweenness centrality, participation coefficient, and local efficiency, from 116 intracranial regions. The study achieved an accuracy of 79%. They also used SVMs to classify different subtypes of SZ, which yielded a classification accuracy of 64% [8].

Liu et al. analyzed the fractional amplitude of low-frequency fluctuations, regional homogeneity, and degree centrality of resting-state fMRI and used the selected features to train ML models. The highest-performing model, SVM, yielded an accuracy of 0.9464 [18].

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C. Li et al. utilized resting-state fMRI features to evaluate an SVM classifier for chronic medicated and first-episode unmedicated patients, achieving 69% classification accuracy [19].

Shevchenko et al. evaluated functional connectivity, gradients, and gradient dispersion features extracted from fMRI using ML models and found that functional connectivity achieved significantly higher accuracy than those using gradient-based features (Mann–Whitney test, $p < 0.005$). The study also proposed a scalable pipeline to test over 1 million features [20].

4.6. Diagnosis of Schizophrenia based on genetic information using machine learning

Lin et al. used a 3D Deep Aggregation Network (3D DANet) to analyze gene expression and MRI brain imaging together. The study found the strongest correlation between default mode networks with KLRD1 and CD244 genes, deepening our understanding of the physiopathology of SZ and identifying potential genetic biomarkers [21].

5. Challenges and limitations of machine learning in the diagnosis of Schizophrenia

One problem to be tackled in future research is overfitting. Many SZ datasets have relatively few participants, while the features, specifically those of EEG and neuroimaging methods, have high dimensions. Moreover, EEG, MRI, fMRI, handwriting, immune-based, and genetic features are all unique features in SZ diagnosis. By implementing multimodal ML approaches, researchers could attain more robust and comprehensive diagnostic models.

It is also important to address challenges related to data biases. Though data processing techniques and feature selection methods are designed to minimize redundancies and errors in ML models, the quality of the original data is the ultimate deciding factor for classification accuracy. Class imbalance might impact the performance of ML models in real-world scenarios, because healthy people constitute the majority in the general population. Moreover, the diversity of the datasets may also impact the generalizability of ML models to the real world. Future studies can reduce selection bias by sourcing patient cases from a variety of backgrounds and regions.

Another problem to be addressed is the interpretability and explainability of ML models. Often, ML models include “black box” algorithms or models that correctly classify patients without explicitly explaining which features were used to achieve the result. This lack of transparency can hinder further research and broader clinical applications. Thus, implementing and developing explainable models will alleviate ethical concerns from a patient perspective while also allowing clinicians to incorporate the framework into routine diagnostic practice.

6. Conclusion

Recent years have seen a rising trend in the use of ML for psychiatric research and the incorporation of ML algorithms into medical practices. Schizophrenia (SZ), a chronic mental illness, traditionally lacks accurate diagnostic strategies due to its complicated pathophysiology. The novel implementation of ML models for SZ diagnosis has shown promising results. This review examined the application of machine learning techniques for diagnosing schizophrenia across various modalities, including EEG, MRI, fMRI, genetic, and behavioral data, while also highlighting the effectiveness of different ML algorithms. Across the reviewed studies, supervised learning and deep learning models trained on EEG signals excelled at diagnosing SZ patients from healthy controls. Surprisingly, handwritten data also yielded high classification accuracy. ML models were also used to identify potential biomarkers of SZ, including functional connectivity, genetic, immune-based,

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and behavioral markers. These findings not only enable more accurate and efficient diagnosis of SZ but also open up new possibilities for predictive analytics and treatment targets.

Despite these advances, challenges in model generalization, data biases, and the explainability of ML models remain. Biases in data collection and the limited interpretability of ML algorithms could hinder widespread adoption of ML in real-world settings. Future research should prioritize improving the explainability of ML models, adopting larger and more diverse datasets, and incorporating multimodal algorithms to increase the generalizability of these models. Beyond diagnosis, ML has the potential to transform biomarker identification, treatment outcome prediction, and more. If these challenges are mitigated, ML models could become powerful tools in assisting psychiatrists in the diagnosis, classification, and treatment of SZ.

References

[1] National Institute of Mental Health (NIMH). (2025) Schizophrenia https://www.nimh.nih.gov/health/statistics/schizophrenia
[2] Ahsan M.M., Luna S.A., Siddique Z. (2022) Machine-Learning-Based Disease Diagnosis: A Comprehensive Review. Healthcare (Basel), 10(3): 541.
[3] Merikangas A.K., Shelly M., Knighton A., Kotler N., Tanenbaum N., Almasy L. (2022) What genes are differentially expressed in individuals with schizophrenia? A systematic review. Mol Psychiatry, 27(3): 1373–83.
[4] Chick S.L., Holmans P., Cameron D., Grozeva D., Sims R., Williams J., et al. (2025) Whole-exome sequencing analysis identifies risk genes for schizophrenia. Nat Commun., 16(1): 7102.
[5] Shokrgozar A., Rahimi M., Shoraka S. (2025) Identification of key genes and pathways in schizophrenia: a bioinformatics analysis based on GWAS and GEO. Front Psychiatry, 16: 1464676.
[6] Owen M.J., Sawa A., Mortensen P.B. (2016) Schizophrenia. Lancet, 388(10039): 86–97.
[7] Urkin B., Parnas J., Raballo A., Koren D. (2024) Schizophrenia Spectrum Disorders: An Empirical Benchmark Study of Real-world Diagnostic Accuracy and Reliability Among Leading International Psychiatrists. Schizophr Bull Open, 5(1): sgae012.
[8] Tavakoli H., Rostami R., Shalbaf R., Nazem-Zadeh M. (2024) Diagnosis of Schizophrenia and Its Subtypes Using MRI and Machine Learning. Brain Behav., 15(1): e70219.
[9] Javeed A., Ali L., Nour R., Noor A., Amiri Golilarz N.A. (2025) Handwriting-based detection of schizophrenia and bipolar disorder using machine learning. IEEE Sensors J. 25(5): 9113–9120.
[10] Iyortsuun N.K., Kim S.H., Jhon M., Yang H.J., Pant S. (2023) A Review of Machine Learning and Deep Learning Approaches on Mental Health Diagnosis. Healthcare (Basel)., 11(3): 285.
[11] Yin G., Yuan J., Chen Y., Guo G., Shi D., Wang L., et al. (2025) Schizophrenia recognition based on three-dimensional adaptive graph convolutional neural network. Sci Rep., 15(1): 4067.
[12] Aich U., Saha A., Woźniak M., Ijaz M.F., Singh P.K. (2025) Schizophrenia detection from electroencephalogram signals using image encoding and wrapper-based deep feature selection approach. Sci Rep., 15(1): 21390.
[13] Abrar M., Salam A., Albugmi A., Al-otaibi F., Amin F., de la Torre I., et al. (2025) Enhanced schizophrenia detection using multichannel EEG and CAOA-RST-based feature selection. Sci Rep., 15(1): 21814.
[14] Sarisik E., Popovic D., Keeser D., Khuntia A., Schiltz K., Falkai P., et al. (2024) EEG-based Signatures of Schizophrenia, Depression, and Aberrant Aging: A Supervised Machine Learning Investigation. Schizophr Bull., 51(3): 804–17.
[15] Al Mazroa A., Eltahir M.M., Ebad S.A., Alotaibi F.A., K V., Cho J. (2025) EEG-based schizophrenia diagnosis using deep learning with multi-scale and adaptive feature selection. PeerJ Comput Sci., 11: e2811.
[16] Skorobogatov K., De Picker L., Wu C.L., Foiselle M., Richard J.R., Boukouaci W., et al. (2024) Immune-based Machine learning Prediction of Diagnosis and Illness State in Schizophrenia and Bipolar Disorder. Brain Behav Immun., 122: 422–32.
[17] Li M., Hou X., Yan W., Wang D., Yu R., Li X., et al. (2024) Identification of Bipolar Disorder and Schizophrenia Based on Brain CT and Deep Learning Methods. J Imaging Inform Med., 38(3): 1653–60.
[18] Liu Y., Wan B., Liu Z., Zhang S., Liu P., Ding N., et al. (2025) Classifying schizophrenia using functional MRI and investigating underlying functional phenomena. Brain Res Bull., 223: 111279.
[19] Li C., Chen J., Dong M., Yan H., Chen F., Mao N., et al. (2025) Classification of schizophrenia spectrum disorder using machine learning and functional connectivity: reconsidering the clinical application. BMC Psychiatry, 25(1): 372.

DOI: 10.54254/2753-8818/2025.AU27288

[20] Shevchenko V., Benn R.A., Scholz R., Wei W., Pallavicini C., Klatzmann U., et al. (2025) A comparative machine learning study of schizophrenia biomarkers derived from functional connectivity. Sci Rep., 15(1): 2849.
[21] Lin J., Wang B., Chen S., Cao F., Zhang J., Lu Z. (2025) Association of the characteristics of brain magnetic resonance imaging with genes related to disease onset in schizophrenia patients. SLAS Technol., 32: 100281.