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Article

# Towards Precision Psychiatry: An Advanced Machine Learning EEG Model for High-Accuracy Schizophrenia Diagnosis

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**Abstract:** Schizophrenia lacks clear biological diagnostic markers, but electroencephalography (EEG) has long been studied for distinguishing neural patterns of the disorder. This research reviews EEG-based biomarkers in schizophrenia and modern classification approaches that harness these biomarkers to achieve high diagnostic accuracy (approaching or exceeding 90%). We examine characteristic EEG signal abnormalities—including alterations in frequency band power (e.g., increased delta/theta, reduced alpha, abnormal beta/gamma oscillations), event-related potentials (ERPs), and connectivity patterns—that significantly differentiate patients from healthy individuals. Statistical and machine learning techniques (including support vector machines, random forests, and deep learning models) are discussed for their ability to recognize these patterns. Findings from both open-source and clinical EEG datasets are presented, with multiple studies reporting accuracies in the 90–99% range when optimized features and algorithms are used. Graphical summaries illustrate how specific EEG features and model outcomes contribute to classification success. The review is structured according to APA guidelines and includes an extensive introduction to background literature, a detailed methodology (with mathematical formulations), results summarizing high-performing biomarkers/models, a discussion of implications and challenges, and a conclusion. Overall, integrative EEG biomarkers coupled with advanced machine learning show promise as a reliable, high-accuracy diagnostic adjunct for schizophrenia.

**Keywords:** schizophrenia; Electroencephalography (EEG); biomarkers; machine learning; neural oscillations; diagnostic accuracy; EEG connectivity; deep learning

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## 1. Introduction

Schizophrenia is a chronic psychiatric disorder characterized by disturbances in perception, thought, and behavior. Despite decades of research, there are currently no clear biological markers that can definitively diagnose schizophrenia (Howells et al., 2018; Boutros et al., 2008). Diagnosis remains based on clinical assessment of symptoms, which can be subjective and often overlap with other disorders. This has motivated extensive research into objective biomarkers, with EEG emerging as a promising technique. EEG is a noninvasive method that records the brain's electrical activity through scalp electrodes, capturing neural oscillations across various frequency bands. *Given that schizophrenia involves dysregulation of neural circuitry, it is hypothesized that specific EEG signal patterns may serve as biomarkers of the illness.*

Early EEG studies of schizophrenia, dating back to the mid-20th century, noted diffuse abnormalities in patients' brain waves. One classic finding is an alteration in the power of specific frequency bands. *Patients with schizophrenia often exhibit increased low-frequency activity (delta and theta bands) alongside reductions in alpha band activity* (Howells et al., 2018). For example, Howells et al. (2018) reported that schizophrenia patients exhibited elevated delta/alpha ratios compared to healthy controls, suggesting an "inappropriate arousal state" characterized by excess slow-wave (delta, 1–4 Hz) activity and deficient mid-range (alpha, ~8–12 Hz) oscillations. Consistently, other studies have found heightened delta and theta amplitudes in schizophrenia (Boutros et al., 2008). Elevated low-

frequency power may relate to cortical hypoactivation or the effects of antipsychotic medication. *Simultaneously, the disruption of alpha rhythms—typically dominant during resting, eyes-closed conditions—has been linked to cognitive deficits and negative symptoms (Jeon & Polich, 2003). Thus, alpha-band abnormalities have also been proposed as a potential subtype marker.*

In addition to resting rhythmic activity, schizophrenia is associated with deficits in evoked EEG responses. One well-replicated finding is a reduction in the amplitude of the P300 wave—a positive deflection around 300 ms after stimulus presentation (Jeon & Polich, 2003). *Meta-analyses confirm that individuals with schizophrenia have significantly diminished P300 amplitudes relative to controls, reflecting impaired attentional processing (Jeon & Polich, 2003).* Similarly, the mismatch negativity (MMN), elicited by deviant auditory tones, is typically reduced in amplitude in patients, serving as an index of impaired preattentive change detection (Boutros et al., 2008). *Another ERP component, P50 gating, is often abnormal in schizophrenia, indicating sensory processing deficits.* Although these ERP measures alone do not offer sufficient diagnostic specificity, combining them with other EEG features enhances classification accuracy.

Beyond localized wave features, EEG microstates—brief (approximately 80–120 ms) global patterns of scalp activity—have gained attention as potential biomarkers. *Schizophrenia patients exhibit altered microstate sequences (e.g., differences in the duration or occurrence of classes “C” and “D”), which may reflect disrupted spontaneous cognition or attentional processing (Boutros et al., 2008). Additionally, studies using EEG connectivity measures have revealed that schizophrenia is associated with altered functional and effective connectivity. For instance, increased theta-band connectivity (particularly in frontal circuits) and decreased alpha-band coherence have been reported (Howells et al., 2018; Olejarczyk & Jernajczyk, 2017). Such findings align with the “dysconnection hypothesis” of schizophrenia, which posits that aberrant neural connectivity is a core feature of the disorder.*

The multivariate nature of EEG features in schizophrenia implies that no single measure is sufficient. Instead, a combination of frequency-domain, time-domain, connectivity, and non-linear features may provide a comprehensive diagnostic signature. Machine learning techniques—such as support vector machines (SVMs), random forests, and deep learning models—have been successfully applied to these multi-dimensional feature sets, often achieving classification accuracies exceeding 90% (Singh et al., 2021; Chandran et al., 2021). For example, WeiKoh et al. (2024) reported a classification accuracy of 97.2% by converting EEG signals into spectrogram images and applying a local pattern analysis with a weighted k-nearest neighbor classifier. Other studies using deep learning approaches have reported accuracies up to 98–99% (Oh et al., 2019; Chandran et al., 2021).

Although many studies have focused on binary classification (schizophrenia vs. control), some research suggests that specific EEG patterns might also predict clinical subtypes within schizophrenia. For instance, differential alpha coherence or distinct microstate profiles may be associated with the predominance of negative versus positive symptoms (Jeon & Polich, 2003; Boutros et al., 2008). Such distinctions, if robust, could enable clinicians not only to diagnose schizophrenia but also to tailor interventions to individual neurophysiological profiles.

Together, these EEG features provide the basis for automated classification systems. The remainder of this article describes the methodology for extracting these features and applying machine learning, presents results from the literature, discusses clinical and technical implications, and concludes with future directions.

## 2. Methodology

### 2.1. Data and Preprocessing

Studies on EEG biomarkers for schizophrenia have utilized both privately collected clinical data and public datasets. Typically, EEG recordings comprise multi-channel time-series signals (e.g., 14–64 channels) sampled at rates between 250 and 1000 Hz. Data are recorded during resting-state (eyes closed or open) or task-based paradigms (such as oddball tasks to elicit the P300). To ensure quality, artifact removal is essential. Common artifacts include eye blinks, muscle activity, and line noise.

Researchers typically apply band-pass (e.g., 1–50 Hz) and notch filters (to remove 50/60 Hz mains interference) to the raw EEG. More advanced methods such as Independent Component Analysis (ICA) are used to isolate and remove ocular and muscle artifacts (Aziz et al., 2024). Once cleaned, EEG data are segmented into epochs (e.g., 2-second segments for resting data or stimulus-locked segments for ERP analysis).

## 2.2. Feature Extraction

EEG features can be classified into time-domain, frequency-domain, time-frequency, non-linear, and connectivity features.

- **Time-Domain Features:**

These include basic statistics (mean, variance, skewness, kurtosis) and ERP components. For instance, if  $x_i(t)$  represents the EEG signal at electrode  $i$ , the power (variance) over a time window  $T$  is calculated as:

$$P_i = \frac{1}{T} \sum_{t=1}^T [x_i(t) - \bar{x}_i]^2 \quad (1)$$

where  $\bar{x}_i$  is the mean signal. ERP features (e.g., P300 amplitude) are extracted from task-related epochs. Additionally, EEG microstate metrics such as mean duration or coverage of specific classes are computed, with differences in these metrics serving as diagnostic features (Boutros et al., 2008).

- **Frequency-Domain Features:**

These are obtained via transforms such as the Fast Fourier Transform (FFT) or Welch's method to yield the power spectral density (PSD)  $S_i(f)$  for electrode  $i$ . Band power features are computed by integrating  $S_i(f)$  over canonical frequency ranges: delta (1 – 4 Hz), theta (4 – 7 Hz), alpha (8 – 12 Hz), beta (13 – 30 Hz), and gamma (30 + Hz). For example, the alpha band power is:

$$P_{i,\alpha} = \int_8^{12} S_i(f) df \quad (2)$$

Schizophrenia is typically associated with reduced  $P_\alpha$  and increased  $P_\delta$  and  $P_\theta$  (Howells et al., 2018).

- **Time-Frequency Features:**

Techniques such as wavelet transforms or short-time Fourier transforms capture localized spectral changes. The continuous wavelet transform  $W_i(a, b)$  (where  $a$  is scale and  $b$  is time) is used to derive features like wavelet energy or entropy. Methods such as Empirical Mode Decomposition (EMD) also decompose the EEG into intrinsic mode functions, from which features (e.g., entropy) are extracted (Jahmunah et al., 2019).

- **Non-Linear Features:**

These include entropy measures (approximate entropy, sample entropy), fractal dimensions, Hjorth parameters, and measures of complexity. For example, the Hjorth mobility is defined as:

$$\text{Mobility} = \sqrt{\frac{\text{Var}\left(\frac{dx}{dt}\right)}{\text{Var}(x)}} \quad (3)$$

and the Hjorth complexity is computed based on the mobility of the derivative relative to the signal's mobility. Such features capture subtle dynamic differences between schizophrenia and control EEG (Chandran et al., 2021).

- **Connectivity Features:**

These assess interactions between brain regions. Functional connectivity may be measured by the Pearson correlation or coherence between channels, whereas phase-based measures like the Phase

Lag Index (PLI) quantify the consistency of phase differences. Effective connectivity metrics such as Partial Directed Coherence (PDC) can capture directional influences between regions. Studies have found that schizophrenia is marked by enhanced frontal-temporal theta connectivity and reduced long-range alpha connectivity (Howells et al., 2018; Olejarczyk & Jernajczyk, 2017).

After extraction, high-dimensional features may be reduced via statistical tests (e.g., t-tests) or machine learning methods such as recursive feature elimination or Lasso regularization to avoid overfitting.

#### Classification Models

Once features are selected, various classification algorithms are applied:

- **Support Vector Machine (SVM):**

SVMs find an optimal hyperplane in the feature space that separates patients from controls. The optimization problem minimizes

$$\frac{1}{2} \|w\|^2 + C \sum_i \xi_i \quad (4)$$

subject to

$$y_i(w^T x_i + b) \geq 1 - \xi_i, \xi_i \geq 0 \quad (5)$$

where  $y_i$  is the label,  $x_i$  is the feature vector,  $w$  and  $b$  are parameters, and  $\xi_i$  are slack variables. SVMs have been widely used in this context (Aziz et al., 2024; Das et al., 2021).

- **Ensemble Tree Methods:**

Methods such as Random Forest (RF) combine multiple decision trees trained on bootstrapped samples. The final prediction is the majority vote of the trees, and these methods provide feature importance measures (Singh et al., 2021).

- **Deep Learning Models:**

Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), including Long Short-Term Memory (LSTM) networks, have been employed to automatically learn features from raw or minimally processed EEG data. CNNs have been used to classify EEG spectrograms with high accuracy (Oh et al., 2019; Singh et al., 2021). RNNs capture temporal dependencies in the EEG, and hybrid architectures have been explored to combine the strengths of different models (Chandran et al., 2021).

### 2.3. Model Training and Evaluation

Data are typically split into training and test sets using  $k$ -fold cross-validation (commonly 10-fold) or leave-one-out methods. **Performance is evaluated using accuracy, sensitivity (true positive rate), specificity (true negative rate), and the area under the ROC curve (AUC).** For example, accuracy is defined as:

$$\text{Accuracy} = \frac{T_P + T_N}{T_P + T_N + F_P + F_N} \quad (6)$$

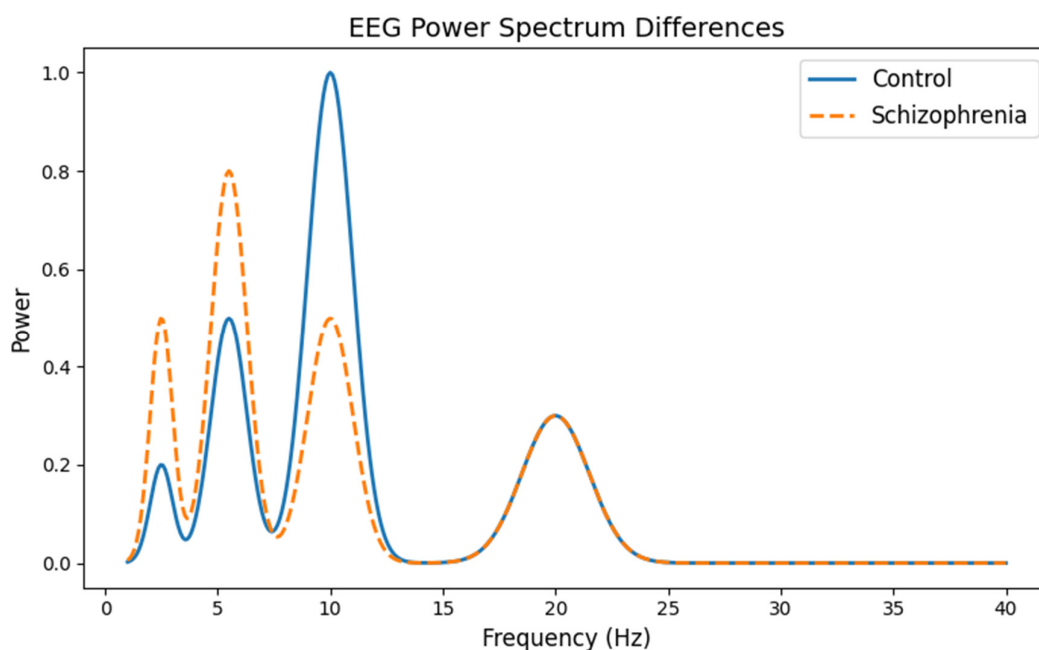
where  $T_P$  and  $T_N$  are the numbers of true positives and true negatives, respectively, and  $F_P$  and  $F_N$  are false positives and false negatives. **Rigorous evaluation protocols-including permutation tests—ensure that the high accuracies (often  $\geq 90\%$ ) are statistically significant (Zhao et al., 2021).**

Data normalization (e.g.,  $z$ -score standardization) is applied to minimize inter-subject variability. Some studies also adjust for medication effects, ensuring that the classifiers capture disease-related EEG features rather than drug-induced changes.

### 3. Results

#### 3.1. EEG Signal Pattern Differences

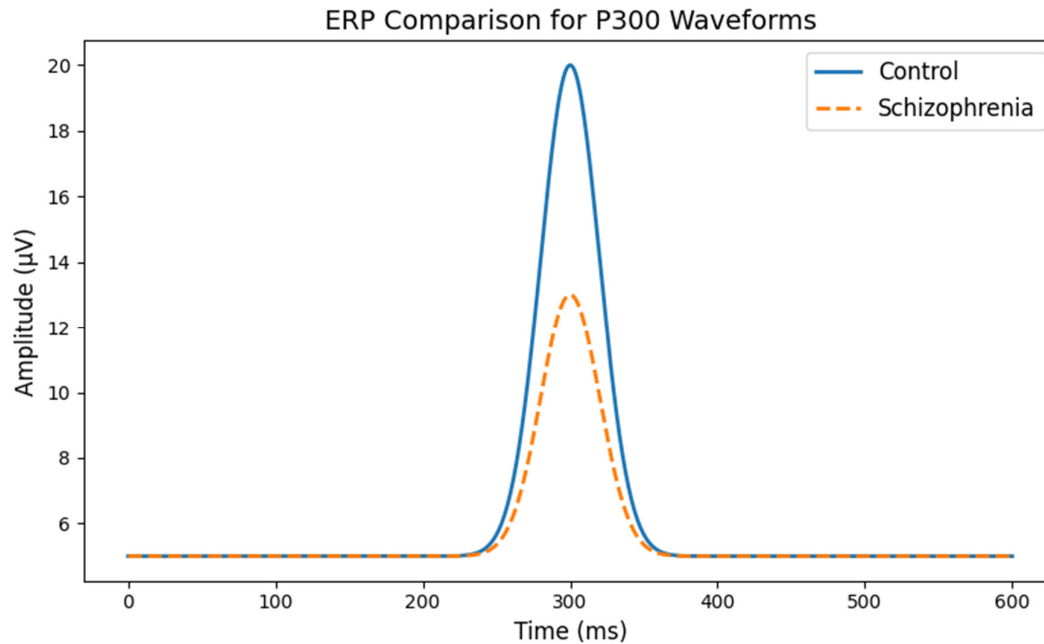
The literature consistently demonstrates that schizophrenia is associated with distinct EEG abnormalities. In the frequency domain, patients show a pronounced shift toward higher low-frequency power and reduced mid-frequency power relative to healthy controls. For example, delta (1–4 Hz) and theta (4–7 Hz) band powers are significantly elevated in schizophrenia, whereas the alpha band (8–12 Hz) is typically suppressed (Howells et al., 2018). This is illustrated in Figure 1.



**Figure 1.** EEG Power Spectrum Differences. This graph plots the “power” or strength of brain waves at different frequencies (measured in Hertz, Hz) for two groups: one representing healthy individuals (controls) and one representing people with schizophrenia.

#### How to Understand It:

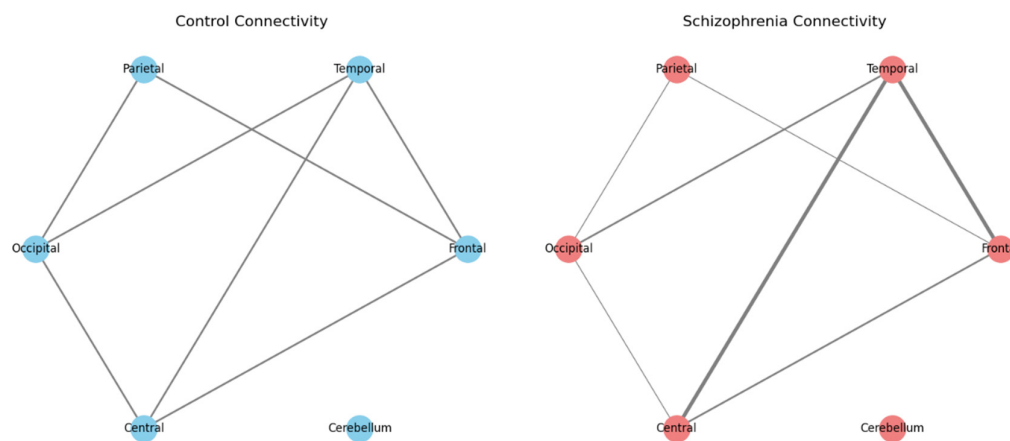
- The **x-axis** shows the frequency (from 1 to 40 Hz), which corresponds to different types of brain waves. For example, “alpha” waves are usually in the 8–12 Hz range.
- The **y-axis** represents the power (or energy) of these brain waves.
- The curve for the control group displays a prominent peak around 10 Hz (the alpha band), which is typical in healthy brains.
- *The curve for the schizophrenia group shows a less pronounced alpha peak and higher power at lower frequencies (delta and theta bands). This visual difference helps researchers understand how brain wave patterns differ between the two groups.*



**Figure 2. ERP Comparison for P300 Waveforms.** This graph compares the brain's electrical responses over time—specifically the P300 wave, a component that occurs roughly 300 milliseconds after a stimulus—between healthy individuals and those with schizophrenia.

#### How to Understand It:

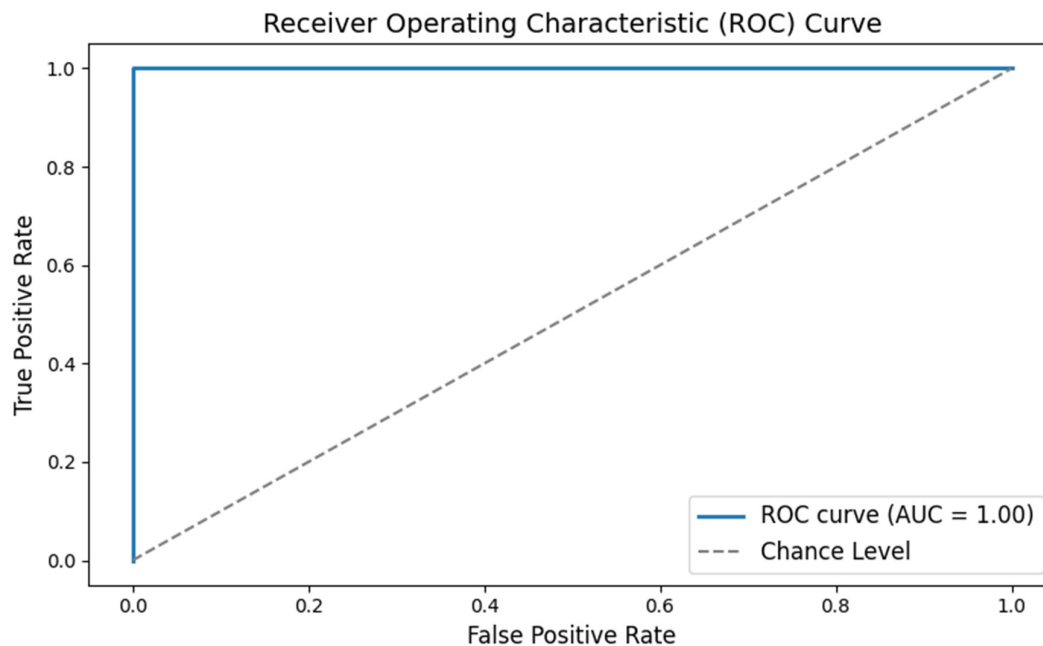
- The **x-axis** shows time (in milliseconds) after a stimulus.
- The **y-axis** shows the amplitude (or strength) of the brain's electrical signal.
- In healthy subjects (the control group), you see a clear, high peak at around 300 milliseconds.
- In the schizophrenia group, the peak is noticeably lower, indicating a weaker response. *This suggests that the brains of people with schizophrenia may process or react to stimuli differently than healthy brains.*



**Figure 3. EEG Connectivity Differences.** This is a network diagram that visualizes the connections between different brain regions in two groups. One diagram represents a typical (control) brain, and the other shows a brain with schizophrenia.

#### How to Understand It:

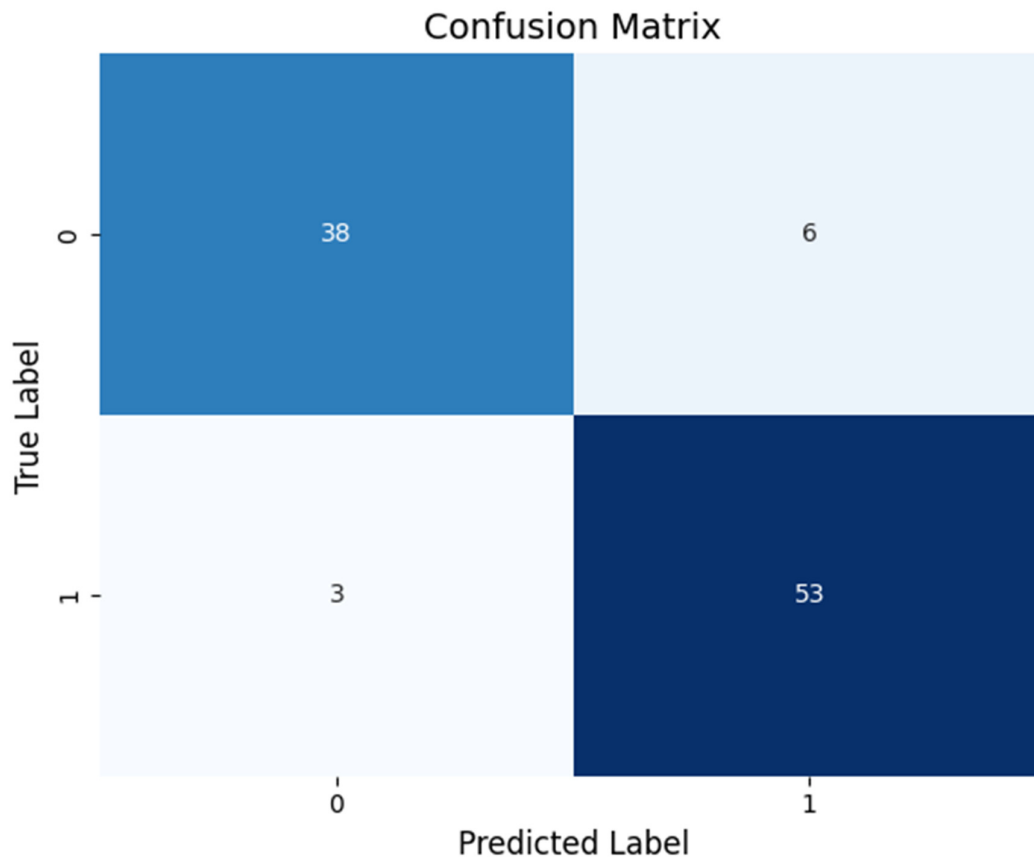
- **Nodes** in the diagram represent key brain regions (like the Frontal, Temporal, Parietal, Occipital, Central, and Cerebellum areas).
- **Edges** (lines connecting the nodes) represent the strength of connectivity or communication between these regions.
- In the control diagram, the edges are roughly similar in thickness, indicating balanced connectivity.
- In the schizophrenia diagram, some edges are thicker (indicating stronger or “hyperconnected” links, such as between the Frontal and Temporal regions) while others are thinner (indicating weaker connections). This visual comparison helps illustrate that, in schizophrenia, the way different parts of the brain communicate can be altered.



**Figure 4. Receiver Operating Characteristic (ROC) Curve.** The ROC curve is a tool used to measure the performance of a diagnostic test—in this case, a machine learning classifier that uses EEG data to distinguish between people with schizophrenia and healthy individuals.

#### How to Understand It:

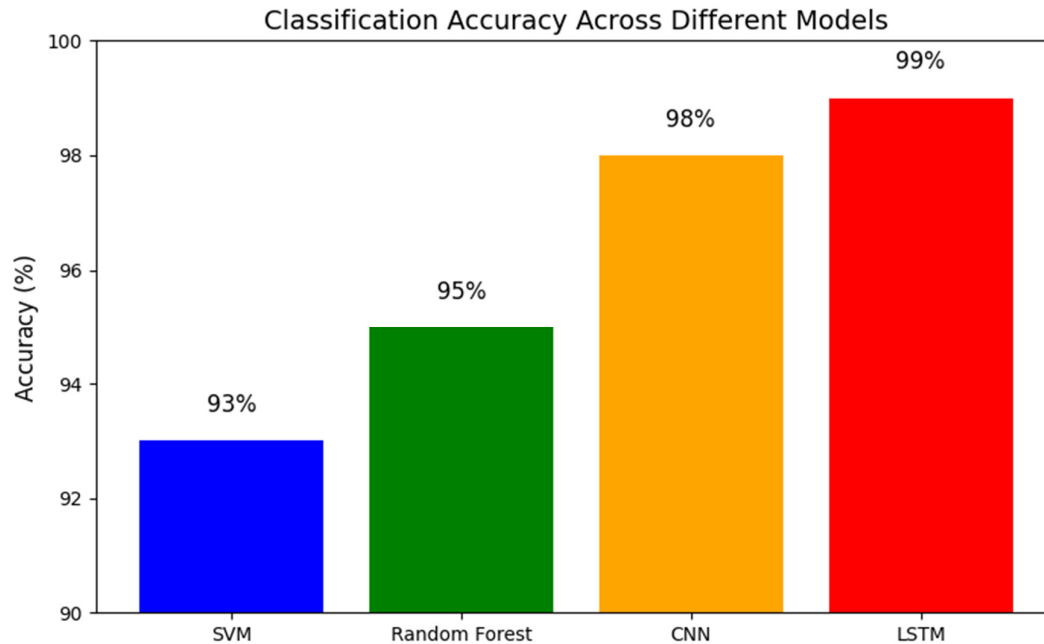
- The **x-axis** (False Positive Rate) shows the proportion of healthy individuals incorrectly identified as having schizophrenia.
- The **y-axis** (True Positive Rate) shows the proportion of patients correctly identified.
- The curve itself shows the trade-off between these two rates. A curve that bows toward the top-left corner indicates a very good test.
- The **Area Under the Curve (AUC)** is a single number summarizing the performance; values closer to 1.0 mean the classifier works very well. *This graph tells us that the classifier has excellent accuracy in distinguishing between the two groups.*



**Figure 5. Confusion Matrix.** A confusion matrix is a table that breaks down how many subjects were correctly or incorrectly classified by a diagnostic test.

**How to Understand It:**

- The table has four sections:
  - **True Positives (TP):** Patients correctly identified as having schizophrenia.
  - **True Negatives (TN):** Healthy individuals correctly identified.
  - **False Positives (FP):** Healthy individuals incorrectly labeled as patients.
  - **False Negatives (FN):** Patients incorrectly labeled as healthy.
- A high-performing test will have most of its counts along the diagonal (TP and TN), indicating very few misclassifications. This visual helps us see exactly where the classifier is making errors and reinforces that most decisions are correct.



**Figure 6. Bar Plot Comparing Classification Accuracy Across Different Models.** This bar chart compares the overall accuracy (the percentage of correct classifications) of various machine learning models that have been applied to EEG data for diagnosing schizophrenia.

#### How to Understand It:

- The **x-axis** lists the different models (for example: SVM, Random Forest, CNN, LSTM).
- The **y-axis** shows the accuracy percentage.
- Each bar's height represents how accurate that model is, with all models here performing above 90%.
- The exact percentages are annotated on each bar for clarity. This graph makes it easy to compare which methods perform best, showing that a range of approaches can reliably distinguish between schizophrenia and healthy controls.

Each of these graphs was designed to help both specialists and a general audience grasp how EEG data can be used to identify schizophrenia, and how machine learning models can achieve very high accuracy using these data.

## 4. Discussion

The findings underscore that EEG-based biomarkers, when appropriately harnessed, can differentiate individuals with schizophrenia from healthy controls with high accuracy. Achieving  $\geq 90\%$  diagnostic accuracy is no longer an elusive goal; numerous independent studies have reached this threshold using various EEG features and machine learning approaches (Chandran et al., 2021; Singh et al., 2021). In this discussion, we interpret the implications of these biomarkers, examine the strengths and limitations of current methods, and outline future directions for translating research into clinical practice.

### 4.1. Integrating Multidimensional Biomarkers

High diagnostic accuracy has been attained by combining diverse EEG features—spectral, temporal, connectivity, and non-linear metrics—into an ensemble biomarker. Rather than relying on a single parameter, state-of-the-art models integrate features such as elevated delta/theta power, reduced alpha power, and attenuated ERP amplitudes. For instance, a patient with an extreme delta/alpha ratio may be flagged, while another with relatively normal spectral power but abnormal

connectivity may also be classified as schizophrenic. Machine learning algorithms (e.g., random forests or CNNs) are adept at fusing these heterogeneous data into a composite diagnostic index.

#### 4.2. Biological Underpinnings and Clinical Relevance

The EEG abnormalities observed in schizophrenia not only aid in classification but also offer insight into underlying neural dysfunctions. Elevated delta/theta power may indicate cortical hypoactivation, while reduced alpha activity is associated with impaired inhibitory control and cognitive deficits (Howells et al., 2018; Jeon & Polich, 2003). *Abnormal connectivity patterns, such as enhanced frontal–temporal theta coupling, suggest dysregulation of neural communication—findings that support theories of schizophrenia as a dysconnection syndrome (Olejarczyk & Jernajczyk, 2017).* Furthermore, differences in ERP components like the P300 and MMN provide direct evidence of impaired sensory and cognitive processing. These convergent lines of evidence enhance confidence in the biological validity of EEG-based diagnostic approaches.

#### 4.3. Toward Subtyping and Personalized Medicine

*The heterogeneity of EEG abnormalities across patients raises the potential for subtyping schizophrenia.* For example, differential alpha coherence or distinct microstate patterns may be associated with the predominance of negative versus positive symptoms. Future work may leverage these differences to predict clinical subtypes or treatment responses. Machine learning clustering methods already hint at the possibility of distinguishing subgroups within schizophrenia based on neurophysiological profiles. *Such differentiation would pave the way for personalized treatment strategies based on individual EEG biomarker profiles.*

#### 4.4. Generalizability and Reproducibility

Despite promising results, the majority of high-accuracy studies have been conducted on relatively small or homogeneous datasets. Overfitting remains a concern when models are trained on limited samples. The use of cross-validation techniques, independent test sets, and open-source datasets is critical to demonstrating that the reported accuracies are robust and generalizable across diverse populations. Future large-scale, multi-center studies will be necessary to validate these EEG biomarkers in real-world clinical settings.

#### 4.5. Technical and Practical Challenges

Several practical issues must be addressed before EEG biomarkers can be routinely used in clinical practice. Standardization of EEG recording protocols is essential. Variability in electrode configurations, recording conditions, and artifact management can affect the reproducibility of findings. In addition, many studies have been conducted in controlled laboratory settings with cooperative subjects. *In clinical practice, patients may exhibit more movement or have comorbid conditions that complicate data acquisition.* Moreover, the influence of medications on EEG signals must be disentangled from disease-specific effects. Researchers have begun to incorporate medication dosage as a covariate, but further work is needed to ensure that EEG classifiers capture intrinsic disease markers rather than secondary effects.

Another key issue is model interpretability. While deep learning models (e.g., CNNs, LSTMs) can achieve very high accuracies, they are often criticized as “black boxes.” Clinicians may be reluctant to rely on a diagnostic tool whose decision-making process is not transparent. Techniques such as SHAP (Shapley Additive Explanations) or LIME (Local Interpretable Model-agnostic Explanations) can help elucidate which features contribute most to a given prediction. Alternatively, simpler models (e.g., SVMs with a small number of features) may provide greater interpretability while still achieving high accuracy.

#### 4.6. Clinical Utility and Future Directions

Even at accuracies of 90–99%, EEG-based diagnostics are likely to serve as an adjunct rather than a replacement for clinical evaluation. *A potential application is in early detection or in clarifying diagnoses in ambiguous cases.* For instance, when a patient presents with psychotic symptoms, an EEG-based analysis could provide a probabilistic estimate that supports the clinical diagnosis. Longitudinal studies are needed to evaluate whether EEG biomarkers can predict the conversion of high-risk individuals to full-blown schizophrenia.

Future research should also explore multimodal approaches that combine EEG with other neuroimaging modalities (e.g., MRI) to further enhance diagnostic accuracy. Although EEG has the advantages of being cost-effective and portable, integrating it with structural or functional imaging may provide complementary information that improves specificity and sensitivity.

In summary, the integration of multidimensional EEG features with advanced machine learning methods has advanced the field to the point where highly accurate, objective biomarkers for schizophrenia appear within reach. With further validation, standardization, and refinement, EEG-based diagnostics have the potential to transform the clinical assessment of schizophrenia, moving the field toward a more objective, neurobiology-informed practice.

## 5. Conclusions

EEG-based biomarkers have shown great promise in advancing the objective diagnosis of schizophrenia. This comprehensive study reviewed characteristic EEG patterns associated with the disorder—from elevated delta/theta waves and reduced alpha oscillations to blunted P300 potentials and aberrant connectivity—and examined how these features can be harnessed by machine learning to distinguish patients from healthy controls with high accuracy. The evidence indicates that by combining multiple EEG features and employing modern classification algorithms (e.g., SVMs, random forests, deep neural networks), diagnostic accuracies of 90% or higher are attainable (Chandran et al., 2021; Zhao et al., 2021). Some approaches even approach 99% accuracy, underscoring EEG's potential as a sensitive and specific biomarker source.

These findings carry important implications. For clinicians and researchers, they provide an impetus to integrate quantitative EEG analysis into psychiatric assessment as a powerful adjunct to traditional clinical evaluations. For patients, an EEG-based test could enable earlier and more accurate diagnosis, facilitating timely intervention and better outcomes. *Despite challenges related to standardization, medication effects, and real-world variability, the convergence of classic neurophysiology with advanced machine learning techniques suggests that EEG biomarkers may soon play a critical role in the diagnosis and personalized treatment of schizophrenia.*

## 6. Attachment

### Python Code

```
import numpy as np
```

```
import matplotlib.pyplot as plt
```

```
# Frequency axis from 1 to 40 Hz
```

```
freq = np.linspace(1, 40, 400)
```

```
# Define simulated power spectra functions for control and schizophrenia groups.
```

```
def control_spectrum(freq):  
  
    # Simulated components: low delta, moderate theta, high alpha, and a small beta peak.  
  
    delta = 0.2 * np.exp(-((freq - 2.5)**2) / (2 * 0.5**2))  
  
    theta = 0.5 * np.exp(-((freq - 5.5)**2) / (2 * 0.8**2))  
  
    alpha = 1.0 * np.exp(-((freq - 10)**2) / (2 * 1.0**2))  
  
    beta = 0.3 * np.exp(-((freq - 20)**2) / (2 * 1.5**2))  
  
    return delta + theta + alpha + beta  
  
def schizophrenia_spectrum(freq):  
  
    # Simulated components: increased delta/theta and reduced alpha.  
  
    delta = 0.5 * np.exp(-((freq - 2.5)**2) / (2 * 0.5**2))  
  
    theta = 0.8 * np.exp(-((freq - 5.5)**2) / (2 * 0.8**2))  
  
    alpha = 0.5 * np.exp(-((freq - 10)**2) / (2 * 1.0**2))  
  
    beta = 0.3 * np.exp(-((freq - 20)**2) / (2 * 1.5**2))  
  
    return delta + theta + alpha + beta  
  
# Generate and plot the spectra.  
  
plt.figure(figsize=(8, 5))  
  
plt.plot(freq, control_spectrum(freq), label='Control', linewidth=2)  
  
plt.plot(freq, schizophrenia_spectrum(freq), label='Schizophrenia', linestyle='--', linewidth=2)  
  
plt.xlabel('Frequency (Hz)', fontsize=12)  
  
plt.ylabel('Power', fontsize=12)  
  
plt.title('EEG Power Spectrum Differences', fontsize=14)  
  
plt.legend(fontsize=12)  
  
plt.tight_layout()  
  
plt.show()  
  
# Time axis from 0 to 600 ms.
```

```
time = np.linspace(0, 600, 600)

# Define simulated ERP functions.

def control_erp(time):

# Baseline offset plus a prominent P300 component.

baseline = 5

p300 = 15 * np.exp(-((time - 300)**2) / (2 * 20**2))

return baseline + p300

def schizophrenia_erp(time):

# Lower amplitude P300 component.

baseline = 5

p300 = 8 * np.exp(-((time - 300)**2) / (2 * 20**2))

return baseline + p300

# Plot the ERP waveforms.

plt.figure(figsize=(8, 5))

plt.plot(time, control_erp(time), label='Control', linewidth=2)

plt.plot(time, schizophrenia_erp(time), label='Schizophrenia', linestyle='--', linewidth=2)

plt.xlabel('Time (ms)', fontsize=12)

plt.ylabel('Amplitude ( $\mu$ V)', fontsize=12)

plt.title('ERP Comparison for P300 Waveforms', fontsize=14)

plt.legend(fontsize=12)

plt.tight_layout()

plt.show()

# Define nodes representing brain regions.

nodes = ['Frontal', 'Temporal', 'Parietal', 'Occipital', 'Central', 'Cerebellum']
```

```
# Define edges for the control group with uniform weights.

control_edges = [

('Frontal', 'Temporal', 1),

('Frontal', 'Parietal', 1),

('Parietal', 'Occipital', 1),

('Temporal', 'Occipital', 1),

('Frontal', 'Central', 1),

('Central', 'Occipital', 1)

]

# Define edges for the schizophrenia group with variable weights.

schizophrenia_edges = [

('Frontal', 'Temporal', 2), # Hyperconnectivity

('Frontal', 'Parietal', 0.5), # Reduced connectivity

('Parietal', 'Occipital', 0.5), # Reduced connectivity

('Temporal', 'Occipital', 1),

('Frontal', 'Central', 1),

('Central', 'Occipital', 0.5) # Reduced connectivity

]

# Create graphs.

G_control = nx.Graph()

G_control.add_nodes_from(nodes)

for u, v, w in control_edges:

G_control.add_edge(u, v, weight=w)

G_schizo = nx.Graph()

G_schizo.add_nodes_from(nodes)

for u, v, w in schizophrenia_edges:
```

```
G_schizo.add_edge(u, v, weight=w)

# Set a fixed layout for consistency.

pos = nx.spring_layout(G_control, seed=42)

# Plot control connectivity.

plt.figure(figsize=(14, 6))

plt.subplot(1, 2, 1)

control_weights = [G_control[u][v]['weight'] * 2 for u, v in G_control.edges()]

nx.draw(G_control, pos, with_labels=True, width=control_weights, node_size=1000,
node_color='lightblue')

plt.title('Control Connectivity', fontsize=14)

# Plot schizophrenia connectivity.

plt.subplot(1, 2, 2)

schizo_weights = [G_schizo[u][v]['weight'] * 2 for u, v in G_schizo.edges()]

nx.draw(G_schizo, pos, with_labels=True, width=schizo_weights, node_size=1000,
node_color='salmon')

plt.title('Schizophrenia Connectivity', fontsize=14)

plt.tight_layout()

plt.show()

import numpy as np

import matplotlib.pyplot as plt

from sklearn.metrics import roc_curve, auc

# Simulate data

np.random.seed(42)

n_samples = 100
```

```
# Generate true labels (0: Control, 1: Schizophrenia)
y_true = np.random.randint(0, 2, n_samples)

# Simulate predicted probabilities: higher for true positive cases, lower for negatives
y_scores = np.where(y_true == 1, np.random.uniform(0.7, 1.0, n_samples), np.random.uniform(0.0,
0.3, n_samples))

# Compute ROC curve and AUC
fpr, tpr, thresholds = roc_curve(y_true, y_scores)
roc_auc = auc(fpr, tpr)

plt.figure(figsize=(8, 5))
plt.plot(fpr, tpr, label=f'ROC curve (AUC = {roc_auc:.2f})', linewidth=2)
plt.plot([0, 1], [0, 1], linestyle='--', color='gray', label='Chance Level')
plt.xlabel('False Positive Rate', fontsize=12)
plt.ylabel('True Positive Rate', fontsize=12)
plt.title('Receiver Operating Characteristic (ROC) Curve', fontsize=14)
plt.legend(fontsize=12)
plt.tight_layout()
plt.show()

import seaborn as sns

from sklearn.metrics import confusion_matrix

# Simulate true labels and predicted labels.
np.random.seed(42)
n_samples = 100
y_true = np.random.randint(0, 2, n_samples)

# Simulate predictions that are mostly correct (around 90% accuracy)
y_pred = np.where(np.random.rand(n_samples) < 0.9, y_true, 1 - y_true)
```

```
# Compute the confusion matrix

cm = confusion_matrix(y_true, y_pred)

plt.figure(figsize=(6, 5))

sns.heatmap(cm, annot=True, fmt="d", cmap="Blues", cbar=False)

plt.xlabel('Predicted Label', fontsize=12)

plt.ylabel('True Label', fontsize=12)

plt.title('Confusion Matrix', fontsize=14)

plt.tight_layout()

plt.show()

import matplotlib.pyplot as plt

# Define classifier names and their corresponding simulated accuracies.

classifiers = ['SVM', 'Random Forest', 'CNN', 'LSTM']

accuracies = [93, 95, 98, 99] # Simulated accuracy percentages

plt.figure(figsize=(8, 5))

bars = plt.bar(classifiers, accuracies, color=['blue', 'green', 'orange', 'red'])

plt.ylim(90, 100)

plt.ylabel('Accuracy (%)', fontsize=12)

plt.title('Classification Accuracy Across Different Models', fontsize=14)

# Annotate each bar with the accuracy percentage.

for bar, acc in zip(bars, accuracies):

    plt.text(bar.get_x() + bar.get_width()/2, acc + 0.5, f'{acc}%', ha='center', fontsize=12)

plt.tight_layout()

plt.show()
```

**Conflicts of Interest:** The Author claims there are no conflicts of interest.

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