

УДК 004.032.26

Ternytskyi V.¹, Shyrokorad D.²

¹асп. гр. А-124.14 НУ «Запорізька політехніка»

²доц. НУ «Запорізька політехніка»

MACHINE LEARNING APPROACHES TO BIOTYPE CLASSIFICATION USING HURST EXPONENT FEATURES: A METHODOLOGICAL EVALUATION

Abstract: The Bipolar-Schizophrenia Network for Intermediate Phenotypes (B-SNIP) established psychosis biotypes based on neurobiological measurements [1,2]. These biotypes, derived from cognitive, electrophysiological, and neuroimaging data, cut across conventional diagnostic boundaries [3]. Recent studies have explored resting-state fMRI biomarkers, including excitation/inhibition ratio analysis, as potential tools for distinguishing psychiatric conditions, including autism and schizophrenia [4].

Objective: This study evaluates the applicability of machine learning classification methods to distinguish B-SNIP-derived psychosis biotypes using Hurst exponent features derived from resting-state fMRI, and assesses the methodological challenges inherent in biomarker-based psychiatric classification.

Methods: We analyzed a dataset of 846 participants (308 Biotype 1, 241 Biotype 2, 297 Biotype 3) characterized by 53 Hurst exponent measurements derived from functional connectivity analysis. A comprehensive machine learning pipeline was implemented, including: (1) proper train-test stratification (80/20 split), (2) feature standardization, (3) SMOTE-based class imbalance correction, (4) evaluation of eight classification approaches ranging from traditional methods (Logistic Regression, Support Vector Machines) to advanced techniques (Neural Networks, Stacking Ensembles), (5) rigorous cross-validation, and (6) hyperparameter optimization via GridSearchCV. Feature engineering included 11 statistical summary features (mean, median, standard deviation, quartiles, range, skewness, kurtosis, median absolute deviation). Performance was assessed using balanced accuracy to account for class imbalance, with detailed per-class metrics and confusion matrix analysis.

Results: All classification models achieved modest performance, with balanced accuracies ranging from 31,2% to 36,5% (random baseline: 33,3%). The

best-performing model was a stacking ensemble combining Random Forest, Gradient Boosting, and SVM with logistic regression meta-learner (36,5% test balanced accuracy). PCA analysis revealed that the first principal component explained 51% of variance but captured patterns common across all biotypes rather than discriminative features. Statistical testing (ANOVA with FDR correction) revealed no features with statistically significant differences between biotypes after multiple testing correction (minimum corrected p-value = 0,092). Biotype 2 showed consistently poorest classification performance across all models (recall: 20,8-31,2%), likely reflecting both minority class size and genuine feature overlap with other biotypes.

Discussion: The modest classification performance, despite implementation of the latest machine learning techniques, reveals fundamental challenges in using Hurst exponent features alone for biotype differentiation. Several critical insights emerged: (1) The consistency of poor performance across diverse algorithmic approaches (linear models, tree-based methods, neural networks, ensembles) suggests the limitation lies in feature informativeness rather than methodological sophistication. (2) The weak statistical signals (no significant features post-FDR correction) presaged the machine learning outcomes, demonstrating the value of preliminary statistical testing. (3) The narrow performance range (32-37%) across eight different methods indicates a likely ceiling effect for this feature set. (4) Advanced techniques (neural networks, stacking) provided only marginal improvements (3-4 percentage points) over simpler methods, questioning the cost-benefit ratio of complex models for this application.

Our findings align with the B-SNIP consortium's own observations that biomarker-based classification of psychosis presents substantial challenges. While the original B-SNIP studies successfully identified three distinct biotypes using multimodal biomarker integration (cognition, eye-tracking, EEG/ERP), our results suggest that Hurst exponents derived from resting-state fMRI, when used in isolation, may not capture sufficient discriminative information for reliable biotype classification. This contrasts with successful applications of Hurst analysis in distinguishing autism from schizophrenia (84% AUC), suggesting that Hurst features may be more effective for categorical diagnostic distinctions than for within-psychosis biotype differentiation.

The consistent underperformance of Biotype 2 across all models warrants investigation into whether this reflects: (a) true biological heterogeneity within this biotype, (b) overlapping feature distributions with other biotypes, or (c) insufficient sample size ($n = 241$ vs. $308/297$). The absence of natural clustering in unsupervised analyses (K-means silhouette scores < 0.17) further supports the hypothesis of limited separability in this feature space.

Conclusion: This study provides valuable negative evidence regarding the sufficiency of Hurst exponent features for B-SNIP biotype classification. The

consistent modest performance across diverse machine learning approaches, corroborated by weak statistical signals, suggests that either: (1) Hurst exponents capture variance orthogonal to biotype-defining characteristics, or (2) Successful biotype classification requires multimodal feature integration as employed in the original B-SNIP studies. Future research should explore: (a) integration of Hurst features with cognitive and electrophysiological biomarkers [5,6], (b) investigation of alternative temporal complexity metrics beyond Hurst exponents, (c) feature selection based on biotype-specific rather than diagnosis-specific criteria, and (d) examination of whether Hurst features predict treatment response or functional outcomes even if they fail to discriminate biotypes.

СПИСОК ВИКОРИСТАНОЇ ЛІТЕРАТУРИ

1. Tamminga C.A., Pearlson G., Keshavan M., Sweeney J., Clementz B., Thaker G. Bipolar and Schizophrenia Network for Intermediate Phenotypes: Outcomes Across the Psychosis Continuum. *Schizophrenia Bulletin*. 2014. Vol. 40. Suppl. 2. P. S131–S137.
2. Clementz B.A., Sweeney J.A., Hamm J.P. etc. Identification of Distinct Psychosis Biotypes Using Brain-Based Biomarkers. *American Journal of Psychiatry*. 2016. Vol. 173. № 4. P. 373–384.
3. Clementz B.A., Parker D.A., Trotti R.L. etc. Psychosis Biotypes: Replication and Validation from the B-SNIP Consortium. *Schizophrenia Bulletin*. 2022. Vol. 48. № 1. P. 56–68.
4. Uscătescu L.C., Hyatt C.J., Dunn J., Kronbichler M., Calhoun V., Corbera S., Pelphrey K., Pittman B., Pearlson G., Assaf M. Using the Excitation/Inhibition Ratio to Optimize the Classification of Autism and Schizophrenia. 2022. URL: <https://doi.org/10.1101/2022.05.24.22275531>. (дата звернення : 16.04.2026).
5. Hill S.K., Reilly J.L., Keefe R.S.E. etc. Neuropsychological Impairments in Schizophrenia and Psychotic Bipolar Disorder: Findings from the Bipolar-Schizophrenia Network on Intermediate Phenotypes (B-SNIP) Study. *American Journal of Psychiatry*. 2013. Vol. 170. № 11. P. 1275-1284.
6. Ethridge L.E., Hamm J.P., Shapiro J.R. etc. Neural Activations During Auditory Oddball Processing Discriminating Schizophrenia and Psychotic Bipolar Disorder. *Biological Psychiatry*. 2012. Vol. 72. № 9. P. 766-774.