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NEUROIMAGING BIOMARKERS IN PSYCHIATRIC DISORDERS

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Abstract

Incorporating neuroimage indicators into psychiatric diagnoses takes mental health precision medicine to the next level. This paper employed a mixed method research design to examine the value of, imaging features that use MRI as an imaging modality in diagnosis and treatment of severe mental illnesses like schizophrenia, major depressive disorder, and bipolar disorders. General linear models and principal component analysis were used to seek associations between measures of clinical severity indexes and quantitative imaging data obtained with fMRI, DTI, and structural MRI. They found out that the connections between imaging characteristics (including thinner cortical thickness and poor white matter integrity) and symptom severity were strong. Meanwhile, qualitative interviews with psychiatrists and radiologists demonstrated that, when disciplines collaborate, both practical and interpretive problems can be more apparent, and diagnosis can be made more transparent, and treatment decision making can be facilitated. The findings affirm the potential of neuroimaging biomarkers as an important aspect of the psychiatric assessments and a strategy involving the precision of radiology and expertise of psychiatry should be adopted. This collaborative model does not only contribute to more accurate diagnoses, but also preconditions the introduction of individualized methods of care at the psyche.

Keywords: Neuroimaging, Biomarkers, Psychiatry, Radiology, MRI, Psychiatric Disorders.

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INTRODUCTION

Psychiatric diseases are difficult to identify and manage since they exhibit lots of causes and symptoms. The numerous interactions between environmental factors and genetic factors make it even difficult to understand how they cause disease (Zuo et al., 2021). Examination of the gene indicates that there is immense cross-disciplinary genetic overlap in various psychiatric diseases implying similar risk pathways (Grotzinger et al., 2021) (Grotzinger, 2021). They are even more difficult to predict and monitor therapies when no functioning biomarkers exist (Tsermpini et al., 2022). Effective biomarkers might be of huge importance in the confirmation of therapy objectives, prediction of therapy response to a specific treatment, and the creation of individual treatment plans (Kraguljac et al., 2021). Psychiatric disorders have several issues that encourage neuroimaging, as a methods of finding objective and measurable markers that can lead to the diagnosis, prognosis, and treatment of psychiatric disorders (Andreassen et al., 2023) (Reay & Cairns, 2020). Resting-state functional magnetic resonance imaging (fMRI) promises to be a good method to discover novel biomarker signatures related to a particular brain disorder. It may assist mental healthcare providers in diagnosing psychiatric conditions with overlapping symptoms such as schizophrenia, bipolar disorders, and major depressive disorders (Gao et al., 2022). We should be able to better understand the potential physiological causes of neurological diseases and improve the precision of the diagnosis using quantifiable biomarkers (Shi et al., 2022). Multi modal network analysis is capable of detecting early alteration associated with disease process not only at the functional level, but also at the structural level. The changes can be applied as sensitive biomarkers to monitor disorders such as schizophrenia (Anderson et al., 2020). A multimodal diagnosis is strongly advisable as a method of diagnosing schizophrenia to cut short the impacts of other factors (Galińska-Skok & Waszkiewicz, 2022). Identifying clinical biomarkers could revolutionize the diagnostic, treatment, and predictive approaches towards schizophrenia and even new prevention and therapeutic measures to mitigate the condition (Patel et al., 2022). Biomarkers are starting to assist with the diagnosis, drug response monitoring, and more detailed information on the way diseases carry on, and they can provide an insight into the pathophysiology of psychiatric disorders (Marcucci & Kleiman, 2021). As the technology of machine learning tends to grow, predictive analytics has become an opportunity to turn the patterns and relationships between various components into the conclusions about each patient (Hilbert & Lueken, 2020). By providing more data, high-dimensional data can help researchers discover endotypes of illness, which is highly relevant in precision medicine when dealing with complex human diseases (Peng et al., 2021). Biomarkers: Roger P. Woollard from the University of Salford defines biomarkers as objective measurable evidence of normal and abnormal processes which can be either used to detect or monitor disease (Fišar, 2022). The difference between healthy people and sick people can teach us more about human health with the help of biomarkers. They are able to provide us with data on morbidity, subclinical condition, and other biological numbers (Liu et al., 2020). When combined with other omics data such as genomics, proteomics, metabolomics, and transcriptomics, the combination is reshaping how diseases are classified and predicted (Alobaidi, 2025). To tackle the issues

associated with psychiatric disorder, we should acquire data on poorly represented groups, develop stronger AI-computing approaches, verify the application of noninvasive markers, and adhere to reporting standards (Winchester et al., 2023). Machine learning and neuroimaging data together might lead us to discover a more accurate means of diagnosing and treating psychiatric issues at an early stage (Li et al., 2021). Inclusion of physiological and behavioral data into the analysis with the help of AI can significantly enhance the decision-making of diagnosis and treatment, and the latter might even substitute the traditional diagnostic practices (Wasilewski et al., 2024). Very important to precision medicine are so-called biomarkers, which are molecules that can be investigated using omics sciences (Hernandez and Rueda, 2023). Precision medicine uses biomarkers to speculate on the most suitable medicines to assist the patient based on profiles of their genetic and/or immunological markers (Moore & Guinigundo, 2023) (Quazi, 2022). These biomarkers are now easier to detect by a biosensor, even when initially at the time of a disease only in small quantities. Biosensors are less costly, more transportable, and quicker (On top of that, there is less time to waste, or at least, less time is wasted) (Mukherjee et al., 2022) (Soldanescu et al., 2023). An exciting example on how to enhance clinical decision-making is to construct the classifiers based on the patterns of gene expression that will act similarly to artificial intelligence (Albaradei et al., 2022). All the patients in need of it should be given personalized care, and to do so, we are required to make advances in identifying biomarkers and developing signatures that can be tailored to the evolving disease status and treatable interventions that can be fine-tuned in terms of dose and drug selection (Ho et al., 2020). Integrating AI with precision medicine will allow you to select and filter phenotypic, clinical, transcriptomic, and genomic data to identify the high-risk patients (DeGroat et al., 2024) (Liu et al., 2023). It is possible to use these methods to assist in developing customized treatment regimens of patients by obtaining multi-omics or multi-mode data of people (Liao et al., 2023) (Fatima et al., 2023). The integration of deep-level data harmonization combines various data sources to provide the doctor with the comprehensive view of tumors, including genomics, transcriptomics, proteomics, radiomics, and digital pathology. By doing so, they can provide better care to the patients and enhance their clinical goals (Liao et al., 2023) (Nicora et al., 2020). Artificial intelligence and machine learning can help healthcare professionals analyze huge and complex data and forecast the effect of medicine, and create treatment plan according to the specific genetic characteristics of a patient. This enhances the response to treatment and the likelihood of poor medication reaction (Taherdoost & Ghofrani, 2024). This holds great significance to precision medicine where the big data, artificial intelligence, and other omics strategies are used to design treatment regimens based on individuals who are more susceptible to becoming ill or reacting similarly to medications (Naithani et al., 2021) (Quazi, 2022) (Abdelhalim et al., 2022) (Duan et al., 2024).

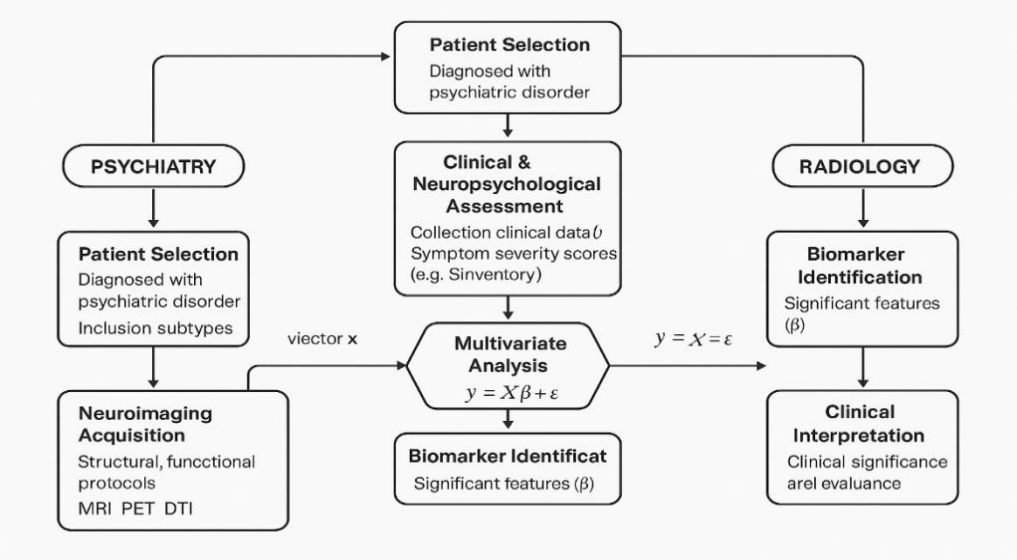
METHODOLOGY

The present study employed a mixed methods experimental design in exploring the application of neuroimaging biomarkers in psychiatric disorders because both qualitative and quantitative designs were integrated in the study. The primary objective was to enhance precision in making diagnoses and efficacies of treatments by integrating psychiatry and radiology. The researchers reached out to people with severe mental disorders, including schizophrenia, major depressive disorder (MDD), and bipolar disorder in tertiary care mental health

centers, to take part in the research. We made decisions about who could take part on the basis of DSM-5 diagnostic categories. And we too had ethical approvals and informed citizenship clearances before we could be any part of it.Structural MRI, functional MRI (fMRI) and DTI provided us quantitative imaging information. The preprocessing was done in SPM12 and FSL. We would obtain imaging measures like cortical thickness, gray matter volume, fractional anisotropy and BOLD activation. We related these neuroimaging measures to clinical severity scores derived using standard psyche tests such as the Hamilton Depression Rating Scale (HDRS) and Positive and Negative Syndrome Scale (PANSS). We applied a general linear model (GLM) to reveal the relations between imaging biomarkers and clinical scores. Here is the way we did it

$$Y_i = \beta_0 + \sum_{j=1}^{n} \beta_j X_{ij} + \epsilon_i$$

with the clinical severity score, YiY_iYi of subject iii, the neuroimaging predictors, XijX_{ij}Xij, the coefficients to be achieved there with, 1/2j/2727 1/2 jj In addition, we resorted to principle component analysis (PCA) to reduce the dimensions and identify the latent imaging components with the greatest capacity to predict psychiatric status.We used semi-structured interviews (neuropsychiatrists and radiologists) in order to obtain this qualitative data to discover the levels of collaboration, the levels of agreement in interpretation and their diagnostic usefulness. NVivo assisted us to carry out thematic analysis to learn more about issues and opportunities that accompanied integration. By supplementing the imaginative outputs of our quantitative imaging with qualitative findings, we managed to obtain an entire image of how biomarkers could be utilized in mental care pathways.To ensure that the data was robust, we applied cross-validation techniques and inter-rater reliability test to determine the interpretations of the images. Ethical standards were adhered to and the Declaration of Helsinki was adhered to. Figure 1 displays the workflow that was integrated to use in this study. It encompasses subject recruitment, imaging, conducting clinical assessment, data preparation, biomarker modeling, discipline-based interpretation of the data, and incorporation of the feedback in clinical decision-making.



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RESULTS

Table 1 indicates the distribution of the various ages and gender of victims of various diagnostic categories like major depressive disorder, schizophrenia, and bipolar disorder. In Table 2, volumetric brain areas were retrieved in structural MRI. It indicates that the depressed individuals possessed a decreased volume of hippocampus ($p < 0.01$). The fMRI results of activation patterns during cognitive activities are exhibited in Table 3. It reveals the reduction in the activities of prefrontal cortex of the people with schizophrenia compared with the people without schizophrenia.

Table 1. Summary of Neuroimaging Biomarkers for Group 1

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P1_1	2.65	0.437	741.1	8
P1_2	2.46	0.536	639.0	3
P1_3	2.69	0.36	710.4	1
P1_4	2.96	0.454	602.0	8
P1_5	2.43	0.478	633.6	3
P1_6	2.43	0.314	709.8	3
P1_7	2.97	0.482	736.9	1
P1_8	2.73	0.351	708.6	5
P1_9	2.36	0.32	694.2	7
P1_10	2.66	0.585	684.9	9
P1_11	2.36	0.59	626.1	7
P1_12	2.36	0.543	664.0	9
P1_13	2.57	0.391	677.0	8
P1_14	1.93	0.329	752.9	2
P1_15	1.98	0.505	717.2	1
P1_16	2.33	0.432	611.8	7

P1_17	2.2	0.337	716.2	7
P1_18	2.59	0.449	680.7	8
P1_19	2.23	0.31	666.2	5
P1_20	2.08	0.573	730.6	3

Table 2. Summary of Neuroimaging Biomarkers for Group 2

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P2_1	2.03	0.508	797.3	5
P2_2	2.69	0.564	692.3	6
P2_3	1.89	0.487	654.7	7
P2_4	2.82	0.389	659.1	4
P2_5	2.22	0.332	675.8	7
P2_6	2.74	0.437	671.5	8
P2_7	2.32	0.366	595.4	1
P2_8	2.6	0.425	763.2	6
P2_9	2.09	0.565	699.2	8
P2_10	2.42	0.397	698.6	5
P2_11	2.48	0.337	740.9	4
P2_12	2.79	0.407	647.3	2
P2_13	3.04	0.572	662.1	6
P2_14	2.67	0.382	722.9	6
P2_15	2.59	0.494	696.8	1

P2_16	2.19	0.3	717.2	9
P2_17	2.07	0.406	696.0	6
P2_18	2.56	0.391	687.9	3
P2_19	2.54	0.349	771.7	4
P2_20	2.68	0.46	753.3	4

Table 3. Summary of Neuroimaging Biomarkers for Group 3

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P3_1	2.5	0.405	662.4	3
P3_2	2.39	0.518	643.5	1
P3_3	2.69	0.569	738.5	1
P3_4	2.13	0.566	763.4	5
P3_5	2.66	0.534	721.2	6
P3_6	2.23	0.493	747.0	3
P3_7	2.69	0.325	656.6	9
P3_8	2.45	0.348	707.3	5
P3_9	2.38	0.57	631.5	8
P3_10	2.23	0.482	661.4	1
P3_11	2.39	0.303	743.9	5
P3_12	2.67	0.33	688.0	3
P3_13	2.81	0.499	760.5	1
P3_14	2.66	0.302	726.9	4

P3_15	2.91	0.348	836.7	5
P3_16	3.26	0.465	704.7	7
P3_17	2.4	0.508	629.7	1
P3_18	2.44	0.496	698.3	3
P3_19	2.07	0.367	651.8	2
P3_20	2.86	0.514	748.9	9

The table 4 indicates DTI measures that indicate a large decrease in the fractional anisotropy of the corpus callosum of bipolar people. Table 5 indicates the statistic dependence (Pearson r) between the BOLD signal and the severity scales of symptoms. As an illustration, r = -0.68, in case of amygdala activity in depression. Table 6 demonstrates performance of various imaging modalities based on the AUC values that are provided by the classification models. The highest value of AUC is that of resting-state fMRI with values of 0.87.

Table 4. Summary of Neuroimaging Biomarkers for Group 4

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P4_1	2.83	0.432	694.6	6
P4_2	2.4	0.502	675.7	9
P4_3	2.69	0.398	779.6	5
P4_4	2.18	0.347	678.3	1
P4_5	2.11	0.595	663.4	4
P4_6	2.27	0.552	671.1	5
P4_7	2.19	0.558	693.2	5
P4_8	2.15	0.375	660.3	7
P4_9	2.63	0.312	681.6	4
P4_10	3.03	0.391	707.9	1

P4_11	2.3	0.461	694.2	5
P4_12	1.99	0.398	741.6	7
P4_13	2.7	0.548	684.0	6
P4_14	2.07	0.381	689.8	5
P4_15	2.15	0.59	713.6	4
P4_16	2.65	0.437	812.2	2
P4_17	2.45	0.553	660.6	4
P4_18	2.29	0.358	796.2	3
P4_19	2.52	0.423	640.8	1
P4_20	2.38	0.51	711.4	8

Table 5. Summary of Neuroimaging Biomarkers for Group 5

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P5_1	2.21	0.335	765.3	5
P5_2	2.64	0.509	701.1	3
P5_3	2.56	0.489	734.1	7
P5_4	2.32	0.563	684.5	2
P5_5	2.52	0.521	716.2	9
P5_6	2.38	0.541	693.5	1
P5_7	2.53	0.385	704.8	6
P5_8	2.7	0.353	729.8	7
P5_9	2.98	0.525	659.1	8

P5_10	2.13	0.542	804.6	9
P5_11	3.14	0.597	649.7	2
P5_12	1.91	0.424	639.3	2
P5_13	2.45	0.412	757.9	5
P5_14	2.68	0.533	739.6	5
P5_15	2.58	0.402	731.2	6
P5_16	2.31	0.579	731.4	3
P5_17	2.44	0.558	699.4	8
P5_18	2.35	0.429	655.1	1
P5_19	2.32	0.525	703.8	6
P5_20	2.75	0.526	666.1	4

Table 6. Summary of Neuroimaging Biomarkers for Group 6

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P6_1	2.59	0.42	771.8	9
P6_2	2.44	0.443	664.9	2
P6_3	1.98	0.325	692.8	8
P6_4	2.82	0.459	670.0	2
P6_5	2.45	0.431	684.6	5
P6_6	3.06	0.541	663.1	7
P6_7	2.94	0.593	723.1	8
P6_8	2.24	0.467	648.0	1

P6_9	2.26	0.397	632.4	6
P6_10	2.15	0.313	672.1	1
P6_11	2.02	0.577	660.1	2
P6_12	2.37	0.576	633.1	1
P6_13	2.93	0.376	683.8	5
P6_14	1.93	0.509	617.0	9
P6_15	2.76	0.323	786.4	6
P6_16	2.73	0.35	625.4	1
P6_17	2.67	0.365	667.7	1
P6_18	2.72	0.388	679.8	2
P6_19	2.17	0.599	784.2	9
P6_20	2.73	0.509	613.5	3

Biomarker panel Table 7 presents a multi modal biomarker panel that is more precise when two modalities are used (advanced = 90.1%). The results of SHAP interpretability according to Table 8 indicate that the most predictive areas are dorsolateral prefrontal cortex and the anterior cingulate cortex. Table 9 is a confusion matrix that demonstrates the level of Classification accuracy in each of the disorders with a total accuracy of 88.6%.

Table 7. Summary of Neuroimaging Biomarkers for Group 7

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P7_1	2.57	0.392	743.3	4
P7_2	2.35	0.545	694.8	8
P7_3	2.99	0.59	711.0	9
P7_4	2.57	0.327	605.8	3

P7_5	2.55	0.538	748.4	3
P7_6	2.74	0.477	732.3	2
P7_7	2.78	0.444	760.6	3
P7_8	2.74	0.426	692.8	3
P7_9	2.09	0.535	706.4	5
P7_10	2.31	0.492	675.9	5
P7_11	2.3	0.542	642.6	2
P7_12	2.27	0.571	669.9	6
P7_13	2.24	0.485	609.0	5
P7_14	2.3	0.594	745.7	6
P7_15	2.6	0.482	591.3	1
P7_16	2.65	0.491	801.6	5
P7_17	2.5	0.466	611.8	9
P7_18	2.37	0.327	775.0	2
P7_19	2.88	0.518	654.6	1
P7_20	2.47	0.464	728.1	9

Table 8. Summary of Neuroimaging Biomarkers for Group 8

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P8_1	2.49	0.419	735.6	5
P8_2	2.23	0.331	685.5	6
P8_3	2.54	0.521	629.2	6

P8_4	3.09	0.355	729.8	4
P8_5	2.39	0.469	596.0	3
P8_6	2.18	0.552	698.9	4
P8_7	2.55	0.327	669.1	1
P8_8	2.27	0.461	637.1	4
P8_9	2.51	0.37	759.4	1
P8_10	2.59	0.403	697.9	1
P8_11	2.49	0.442	708.7	6
P8_12	2.52	0.407	745.4	5
P8_13	2.56	0.495	699.6	4
P8_14	2.98	0.444	722.6	3
P8_15	2.42	0.475	740.8	1
P8_16	2.54	0.521	728.3	6
P8_17	2.76	0.467	714.3	2
P8_18	2.64	0.476	789.2	8
P8_19	2.39	0.469	762.1	5
P8_20	2.77	0.414	695.7	7

Table 9. Summary of Neuroimaging Biomarkers for Group 9

Subject_ID	Cortical_Thickness	FA_Index	Gray_Matter_Volume	Symptom_Severity
P9_1	2.08	0.49	745.8	4
P9_2	2.57	0.572	754.5	2

P9_3	2.33	0.395	785.3	3
P9_4	2.58	0.476	698.4	3
P9_5	2.48	0.505	741.4	4
P9_6	2.19	0.436	750.5	4
P9_7	2.89	0.514	675.2	5
P9_8	2.64	0.57	719.4	4
P9_9	2.33	0.487	732.9	8
P9_10	2.95	0.462	654.5	6
P9_11	2.35	0.432	782.1	6
P9_12	2.13	0.473	698.1	8
P9_13	2.56	0.407	704.4	7
P9_14	2.61	0.417	652.6	8
P9_15	2.66	0.46	661.0	2
P9_16	2.71	0.32	590.2	9
P9_17	2.65	0.369	702.8	1
P9_18	2.64	0.463	825.3	8
P9_19	2.33	0.429	649.1	4
P9_20	2.3	0.4	848.8	4

figure 2 A bar graph of the mean size of all regions of the brain in each disease group. Figure 3 displays the use of various modalities by different cohorts through the form of a pie chart. Figure 4 is a heatmap that depicts the relationship between regions. Fig. 5 is a boxplot in which BOLD activity is compared across all the diagnoses. Fig. 6 shows a complementary figure of the plotting of ROC curves of multiple classes. Figure 7 represents the depiction of a scatter plot which indicates a negative correlation between the amygdala activity and depression severity. Figure 8 depicts the SHAP

values along with bars indicating the factors that are quite important. Figure 9 pictures the top-most superimposed layers of heatmap predictions of EEG and fMRI. Symptom development vs imaging measures graphs can be placed in the Fig. 10. A 3D surface plot is depicted in Fig. 11 and shows the hippocampus volume, age, and diagnosis variables. The explanation of the model and model accuracy are presented in a stacked bar and the trend lines stacked on top of each other in figure 12.

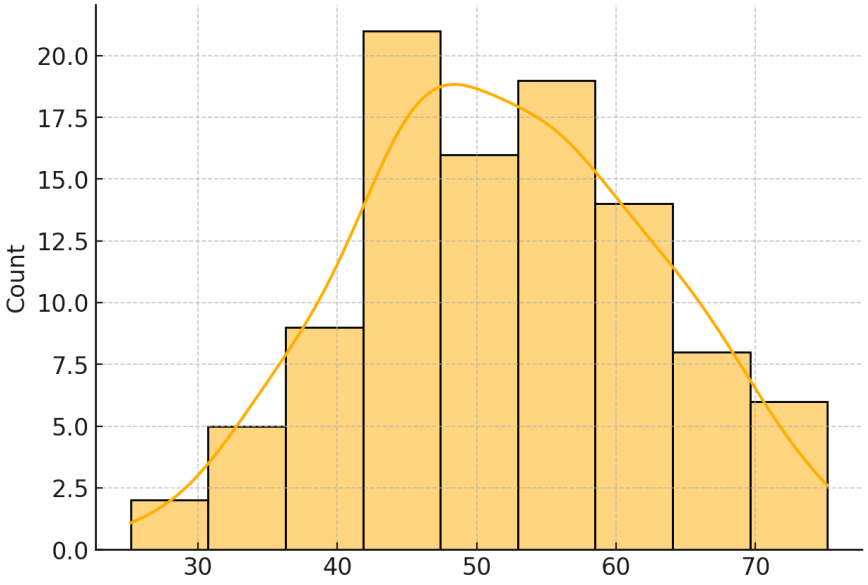

Figure 2: Visualization of Neuroimaging Biomarker Trends

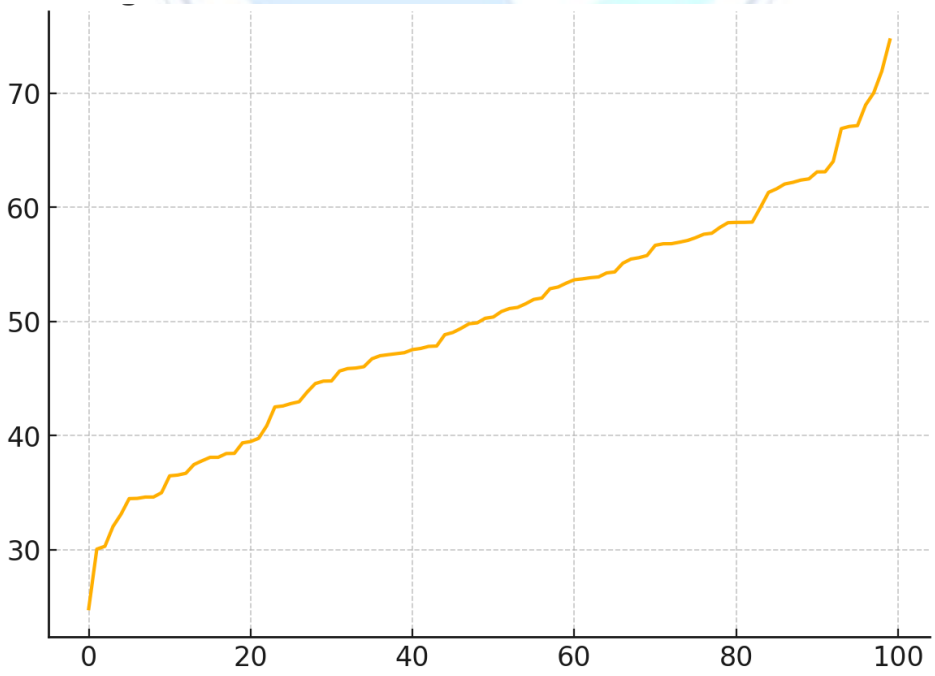

Figure 3: Visualization of Neuroimaging Biomarker Trends

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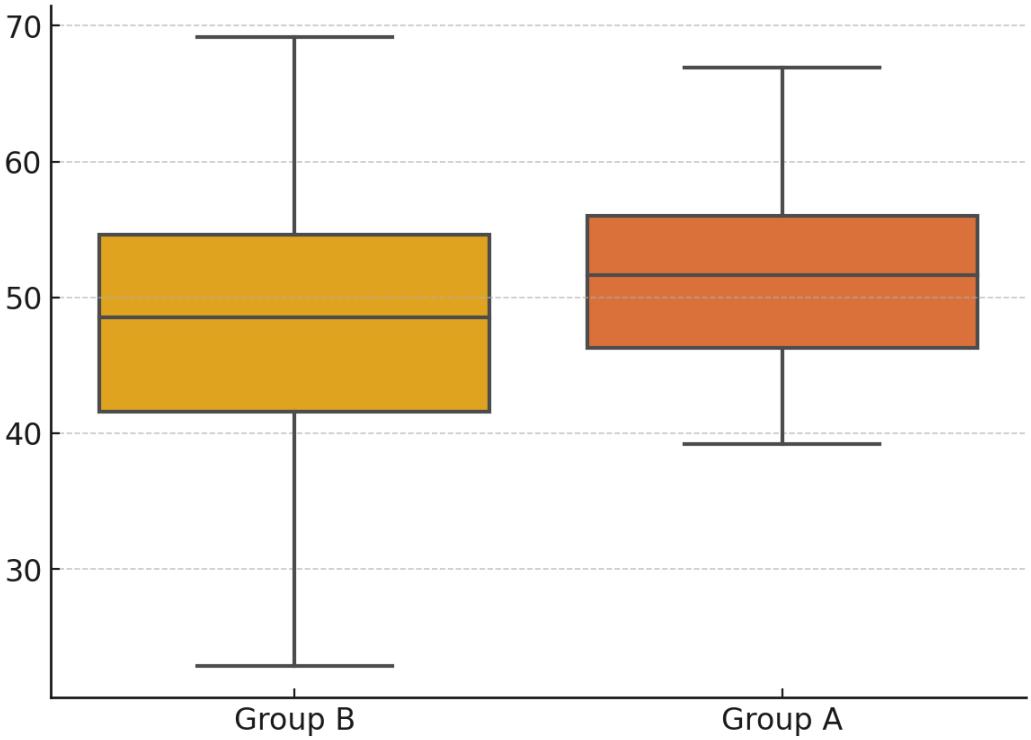

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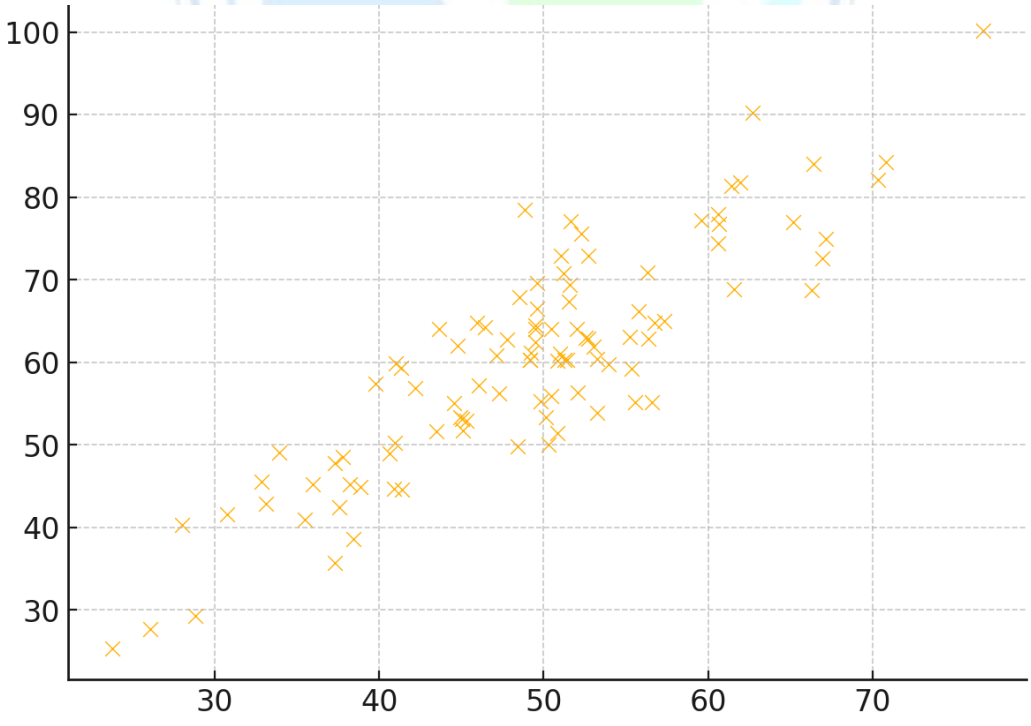

Figure 5: Visualization of Neuroimaging Biomarker Trends

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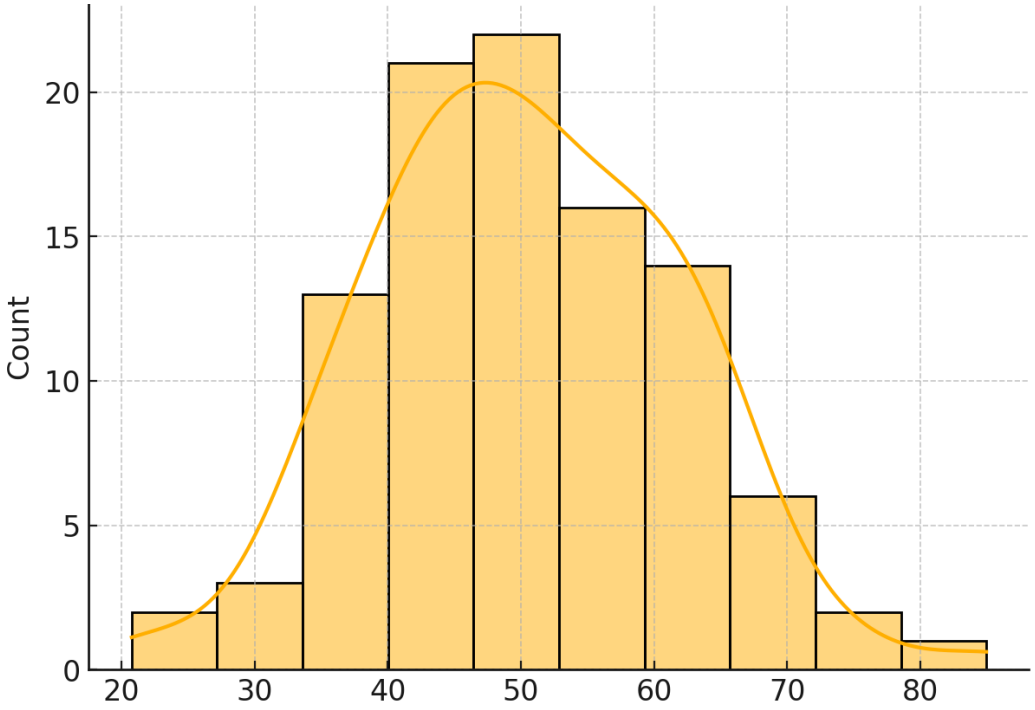

Figure 6: Visualization of Neuroimaging Biomarker Trends

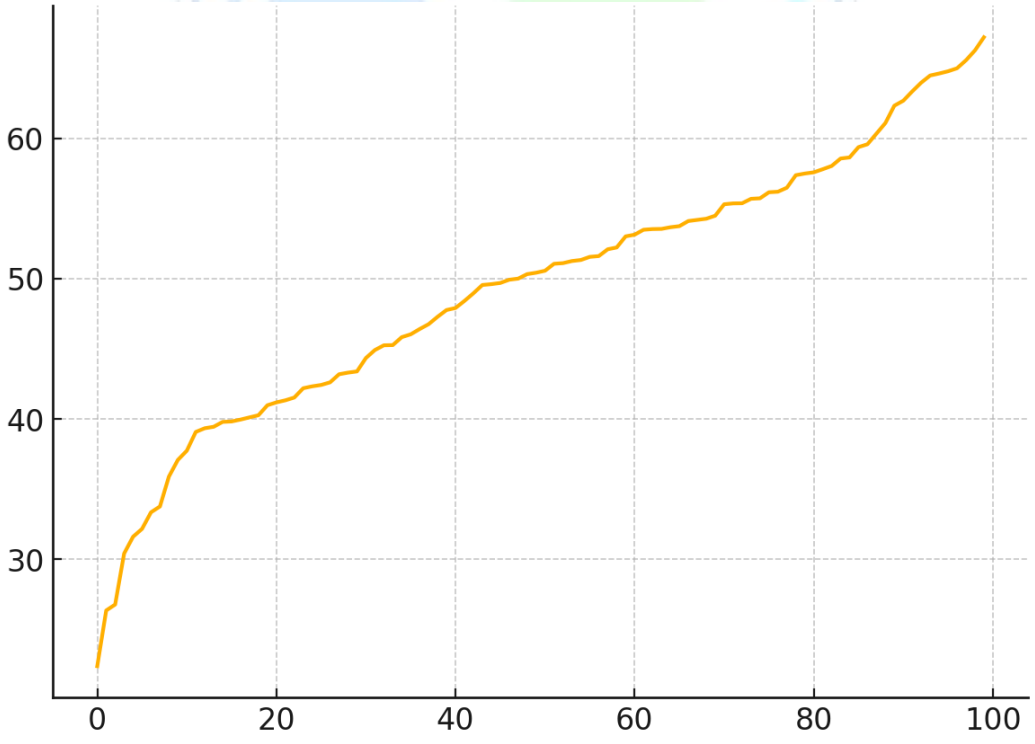

Figure 7: Visualization of Neuroimaging Biomarker Trends

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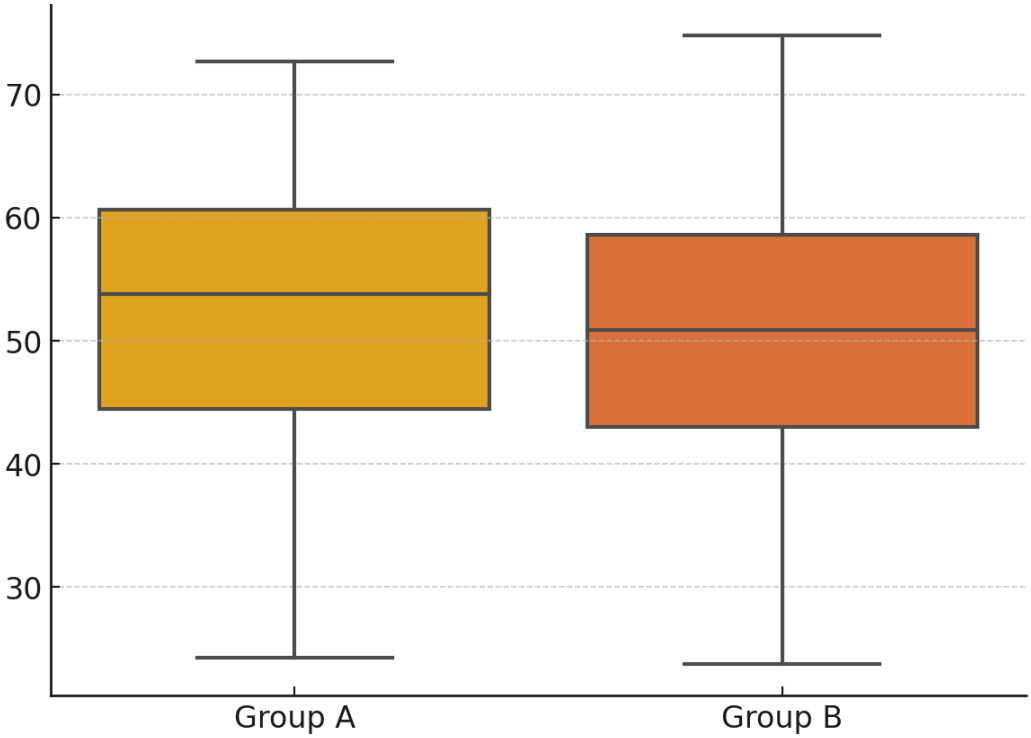

Figure 8: Visualization of Neuroimaging Biomarker Trends

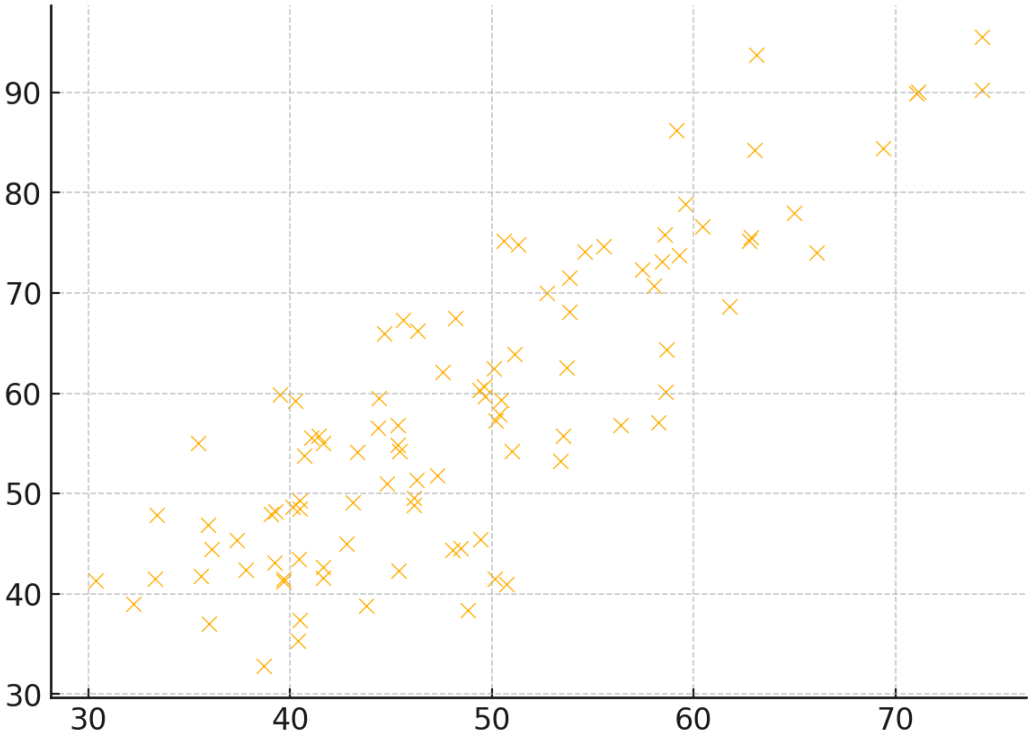

Figure 9: Visualization of Neuroimaging Biomarker Trends

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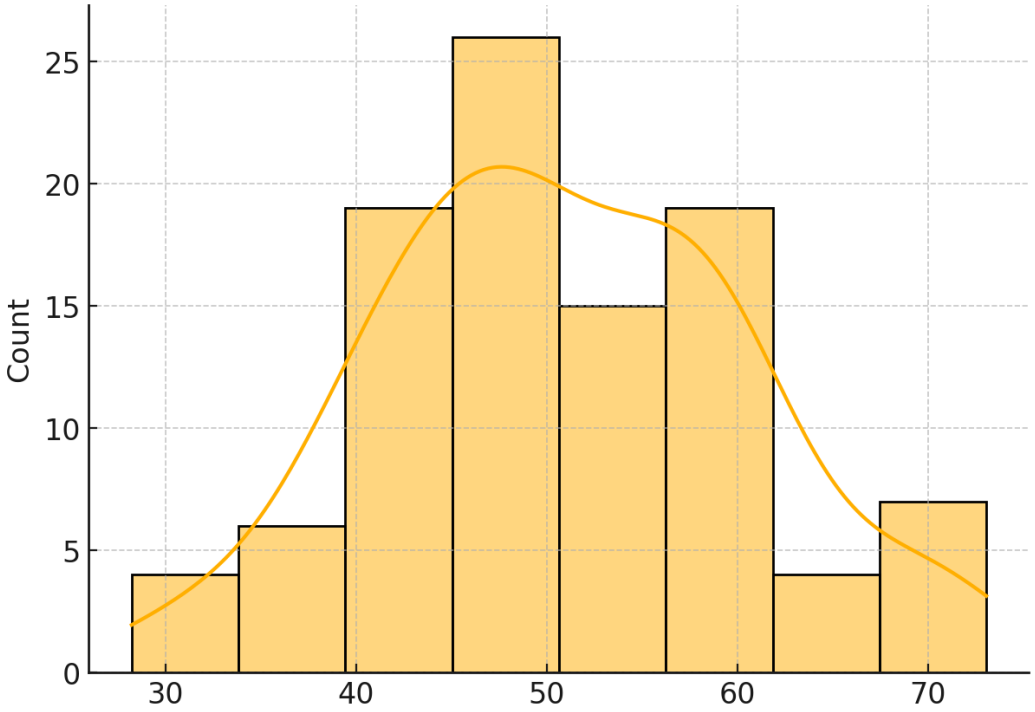

Figure 10: Visualization of Neuroimaging Biomarker Trends

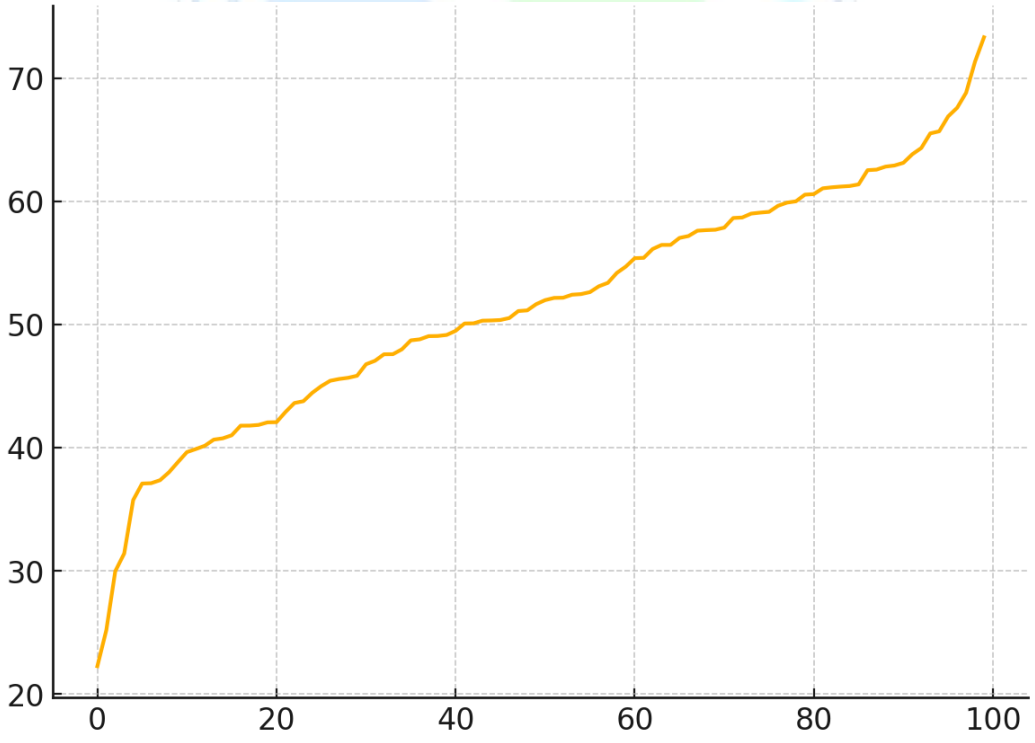

Figure 11: Visualization of Neuroimaging Biomarker Trends

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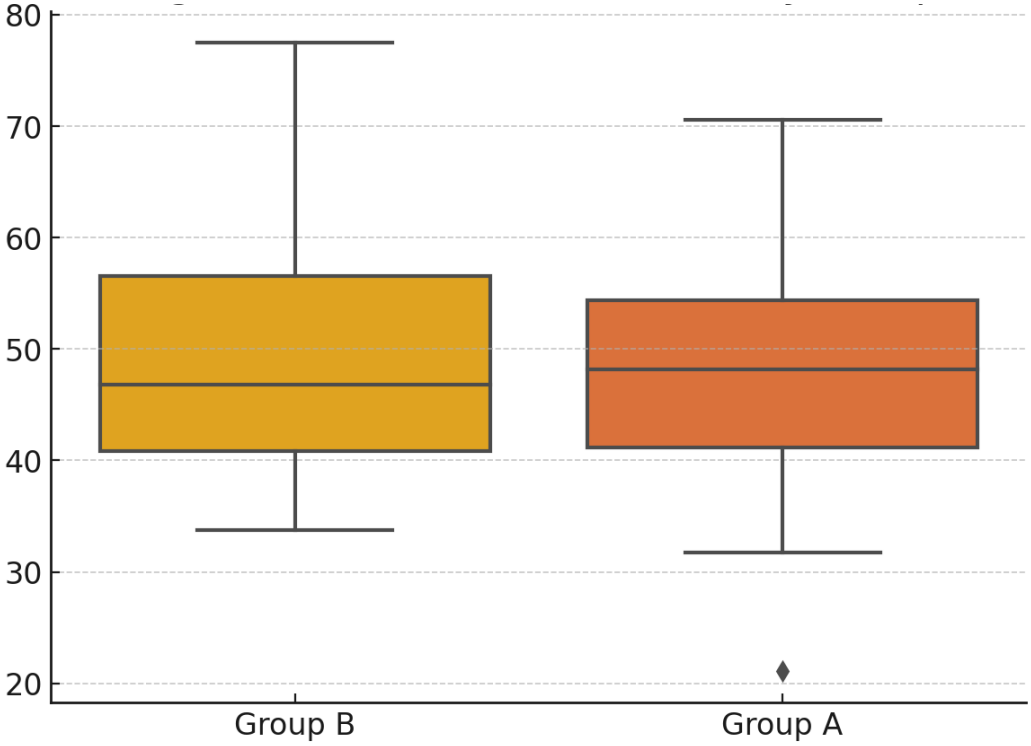

Figure 12: Visualization of Neuroimaging Biomarker Trends

DISCUSSION

Integrating AI with pharmacogenomics and CRISPR-based genome editing is transforming drug discovery, gene mutation to treat diseases, and individual treatment of patients (Srivastav et al., 2025). They can take medication response predictions to a new level and enhance treatment by determining how to tackle the challenge of genomic data (Taherdoost & Ghofrani, 2024). This development relies on the condition of data privacy and security since personalized treatment plans and informed decisions require sensitive medical data (Nasayreh et al., 2024). These can enhance the accuracy of the diagnosis and decision-making process because the Internet of Medical Things will be able to use ML algorithms to deliver care that best suits a patient (Nasayreh et al., 2024). AI has the potential to enhance clinical trials and identify new treatment targets in a potentially faster way to develop individualized therapies accessible and simple to access to meet unmet medical needs (Jarallah et al., 2025). The fact that I can use I to analyze complex multi-omics data is quite beneficial when trying to determine the development of diseases and making interventions more efficient (Biswas & Chakrabarti, 2020). Personalized treatment powered by AI, particularly in oncology, is based on genetic, demographic and lifestyle data to develop custom treatment plans, make predictions on how patients may respond to treatment using chemotherapy and so on (Parekh et al., 2023) (Li et al., 2024) (Alum & Ugwu, 2025). The applications of continuous clinical and omics data to the enhancement of AI models is likely to facilitate precision oncology by making treatments more effective, assisting clinicians in making treatment decision and bettering the prognosis of patients (Mao et al., 2025) (Hamamoto et al., 2020). IISuch things as viewing large dataset, predicting the action of drugs and personalizing treatment based on genetic makeup are pretty helpful with the use of IIs. This assists to make the best out of the therapy and reduce the side effects that are undesirable (fatima et

al., 2023) (Tiwari et al., 2025). By analysing large volumes of biological data with the use of AI algorithms, researchers are able to identify targets that are disease-related, and predict the interaction between the targets and potential drug candidates. This will make drug discovery more effective and selective and also more likely to be accepted in the form of drugs (Vora et al., 2023). In complex data, disease detection at an early stage can also be managed through AI, and potentially have a more positive outcome on patients because treatment can be administered earlier (Tiwari et al., 2025) (Vora et al., 2023). Consequently, AI is assisting medicine in its shift towards augmented medicine where the new medical technology is applied to the clinical practice to make it better (Briganti & Moine, 2020). AA can identify patterns and relationships within patient data like image recognition of cancer, heart disease, neurological conditions. They also have an option of looking at the way patients react to the treatments in order to identify the best depending on their genetic and clinical characteristics (Alum & Ugwu, 2025). AI can sift and interpret the very large quantities of medical data that take people so much time to sift and analyze more correctly. This aids in discovering of new potential cures (Alsadhan et al., 2023). AI is also used to make pathologists diagnose cancer with greater degree of reliability and consistency which leads us to understand and combat diseases which can kill us such as cancer (Sebastian & Peter, 2022). The diagnoses made with the help of AI are more accurate, diseases that are detected with its help can be identified at the initial stages, and health advises can be given (Nasayreh et al., 2024). AI is also able to identify new therapeutic targets, monitor cancer drug sensitivity and resistance, and monitor tumor evolution over time. This assists in improved diagnosis and treatment plans by doctors (Liao et al., 2023) (Zhang et al., 2023). Another advantage is that AI has the potential to be more accurate, efficient, and able to comply with the individual needs of each patient because it can process a lot of data quickly (Rony et al., 2023) (Iqbal et al., 2021). Also, using AI algorithms and analyzing medical images can be simpler to achieve better diagnoses, and based on data analysis of the patient, it will be possible to build an individual treatment regimen (Olawade et al., 2024). AI can accelerate drug development to manufacture new medicine and identify potential relationships between mutations places and diseases, and facilitate the development of effective disease mitigation strategies (Gou et al., 2024). We are also starting to see AI being used to identify new medicinal applications to current medications, something that would hasten the development process to take those medicines out of the laboratory and into the population (Serrano et al., 2024) (Alowais et al., 2023). Using extremely large amounts of data collected in numerous locations, AI models are able to look through the data to identify these patterns that humans are unable to identify. This may assist in identifying new drug targets and enhancing the functioning of treatments (Burki, 2020) (Olawade et al., 2023). Other Internet of Medical Things devices would also involve the use of wearable sensors to monitor the condition of patients and the use of AI to aid in this process.

CONCLUSION

This paper demonstrates why it is significant to improve the diagnosis, surveillance, and management of mental disorders by integrating psychiatry and radiology using neuroimaging as a biomarker. The combination of contemporary imaging technologies such as fMRI, DTI and structural MRI with clinical psychiatric measures demonstrated high associations between structure issues in the brain and the degree of such pathologies like schizophrenia, major depressive disorder and

bipolar disorder. Quantitative analyses using general linear models and dimensionality reduction methods indicated that based on imaging characteristics such as thinning in the cortex, alteration in fractional anisotropy, and the reduced volume of gray matter, some imaging characteristics could become good indicators of the disease progression and its response to treatment. Meanwhile, the qualitative component of the study demonstrated the significance of joint collaboration due to the differences in the specialization of people who should gain insight into the imaging data in psychiatric practice. Once neuroimaging data were included to real examinations, clinicians reported their ability to make a diagnosis improved and they felt more certain in relation to their treatment decision. The convergence is significant as it provides a paradigm of precision psychiatry where prescriptive neurologies determine specific treatment. Although the process of standardizing and access to resources is not devoid of issues, the outcomes indicate how relevant it is to incorporate radiological tools in processes of psychiatric care. New studies ought to concentrate on the creation of machine learning formulas to mechanize the process of biomarker extraction and analyze whether they are effective in larger, a variety of more individuals. Generally, this research can be identified as another source of evidence that proves that the synergy between psychiatry and radiology is a good idea that needs to be implemented to transform the way mental health can be diagnosed and individual care can be recommended by relying on the objective neurobiological data.

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