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Classification of Alzheimer's Disease Based on Texture Characteristics in Magnetic Resonance Imaging Images Using the Random Forest Method

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ABSTRACT

Alzheimer's disease (AD) is a progressive neurodegenerative disorder and one of the leading causes of dementia worldwide. Early detection is critical to slowing disease progression and improving patient outcomes. While Magnetic Resonance Imaging (MRI) is commonly used for AD diagnosis, analyzing the high-dimensional data remains challenging. This study explores the use of texture features from MRI images to improve the accuracy of AD classification using machine learning. This research utilized MRI brain images from publicly available datasets to classify early-stage Alzheimer's disease. The Random Forest algorithm handled large, complex datasets while minimizing overfitting. Texture features, including Histogram, Gray Level Co-Occurrence Matrix (GLCM), and Gray Level Run-Length Matrix (GLRLM), were extracted to highlight microstructural changes in the brain, particularly in the hippocampus and cortex—critical areas affected by AD. The model achieved an accuracy of 88%, precision of 85%, and Recall of 92% in the 10th fold using the WEKA platform, demonstrating its effectiveness in detecting early neurodegenerative changes. The Random Forest model, combined with texture feature extraction, provides a computationally efficient approach for the early detection of Alzheimer's disease. By identifying subtle changes in brain tissue, this method can potentially support clinicians in early diagnosis and intervention planning. Future research should focus on integrating additional imaging modalities and clinical data to enhance diagnostic accuracy and reliability.

Keywords:

Alzheimer's disease; Magnetic Resonance Imaging (MRI); Random Forest; Texture Feature Extraction; Gray Level Co-Occurrence Matrix (GLCM); Gray Level Run-Length Matrix (GLRLM); Machine Learning; Early Detection; Neurodegenerative Disease.

Introduction

Alzheimer's disease is one of the leading causes of dementia, affecting more than 55 million people worldwide, and is expected to continue to increase to reach 139 million cases by 2050 due to the growing elderly population (Fernandez et al., 2024). Alzheimer's is characterized by progressive damage to brain tissue, which affects the patient's cognitive function and behavior. Early symptoms usually include difficulty remembering new information, which develops into critical thinking disorders, confusion, and an inability to carry out daily activities (Mortara et al., 2023; Bhagya Shree, 2016). In the clinical context, early diagnosis of Alzheimer's is a crucial step to slow down the course of the disease, improve the quality of life of patients, and optimize treatment (Pourranjbar et al., 2024).

Magnetic Resonance Imaging (MRI) is one of the most reliable and widely used technologies for detecting Alzheimer's early. MRI uses strong magnetic fields and radio waves to produce high-resolution structural images of the brain, allowing the identification of morphological changes typical of the early stages of the disease (Bhade & Bamnote, 2023; Bhagya Shree & Sheshadri, 2014; Saikia & Kalita, 2024; Patil et al., 2023). This technology is safe to use by various age groups, including individuals with other comorbidities, making it the diagnostic tool of choice in neuroimaging (Jatmiko, 2021; Jack et al., 2015). Several recent studies have highlighted the potential of texture analysis on MRI

images to identify microstructural changes that conventional visual analysis cannot detect (Almumtazah et al., 2023).

However, the main challenge in MRI image analysis is the high dimensionality of the data, which requires data processing methods that can efficiently summarize important information without compromising accuracy. For example, a study showed that using Principal Component Analysis (PCA), the dimensions of an MRI image (256×256 pixels) can be summarized into 50 principal components. These components were then analyzed using artificial neural networks, resulting in an accuracy of up to 91.0% and an AUC of 0.941 on the test data (Olle Olle et al., 2024). Although promising, this method has limitations in terms of complexity and high computational resource requirements, so it requires exploring other more practical and efficient approaches.

One of the prominent approaches in medical data processing is Random Forest, a supervised machine learning algorithm that combines results from many decision trees to generate more accurate predictions (Tran et al., 2025; Chen et al., 2024; Mirzadeh & Omranpour, 2024). The algorithm has been successfully applied to a wide range of medical image classification studies, including detecting heart disease, cancer, and other neurological disorders, with a competitive accuracy rate compared to other methods (Qi et al., 2024; Luo & Qiao, 2024). As an ensemble method, Random Forest combines multiple decision trees to improve prediction accuracy, with an accuracy rate of 91.56% for Alzheimer's detection (Iqbal et al., 2023).

However, to harness the full potential of Random Forest, a tool that can efficiently support the implementation and evaluation of these algorithms is needed. WEKA (Waikato Environment for Knowledge Analysis) is an essential tool in implementing Random Forest, especially for researchers looking for an intuitive and efficient solution for data analysis. WEKA offers a graphical interface that simplifies the classification process, model parameter settings, and visualization of results, such as setting the Number of decision trees or the maximum depth of trees that can significantly affect model performance (Hussain & Gogoi, 2022; Sai Madhuri et al., 2024; Awojoyogbe & Dada, 2024). With its ability to support the exploration of model parameters, WEKA ensures that the applied algorithm can achieve optimal results, even on complex datasets such as MRI images.

WEKA simplifies the visualization of results and provides the option to set algorithm parameters, such as the Number of trees (*Number of trees*) or the maximum depth of the tree (*maximum depth*), which can affect the model's performance. WEKA allows this study to ensure the efficiency and validity of the methods used to classify MRI images (Qamar & Raza, 2023).

Previous research has demonstrated that the *Inception V3* architecture, a variant of the *Convolutional Neural Network* (CNN), has been successfully utilized to classify MRI data related to Alzheimer's disease, achieving a validation accuracy of 87.79% and a precision rate of 92% for the *Non-Demented* category. These results highlight the computational efficiency of *Inception V3*, particularly in handling large-scale, high-resolution data such as MRI images (Fitriyani et al., 2023). However, this study adopts a different approach by analyzing MRI images for Alzheimer's detection using the *Random Forest* algorithm via the *WEKA* platform, leveraging texture feature extraction methods such as histograms, GLCM, and GLRLM. This approach aims to provide a simpler and more computationally efficient alternative for detecting microscopic changes in brain tissue associated with Alzheimer's, thereby enhancing the accuracy of early diagnosis through ensemble-based machine-learning techniques.

This study aims to explore the use of the Random Forest algorithm in analyzing MRI images based on texture features to improve the accuracy of early detection of Alzheimer's. With a machine learning technology-based approach, this research is expected to advance medical diagnosis significantly, support more timely clinical decision-making, and open up new opportunities in neurodegenerative research.

Methods

Data Processing Procedures

The study used brain MRI scan images from the kaggle.com database, which included 100 images of mild impairment and 100 images of no impairment. Brain MRI and scan image extraction were performed using Python in Google Colab, and classification was carried out using the WEKA machine

learning algorithm. Figure 1 shows the stages of the research. There are three main stages: preprocessing, extraction of texture features, and using the Random Forest method for classification.

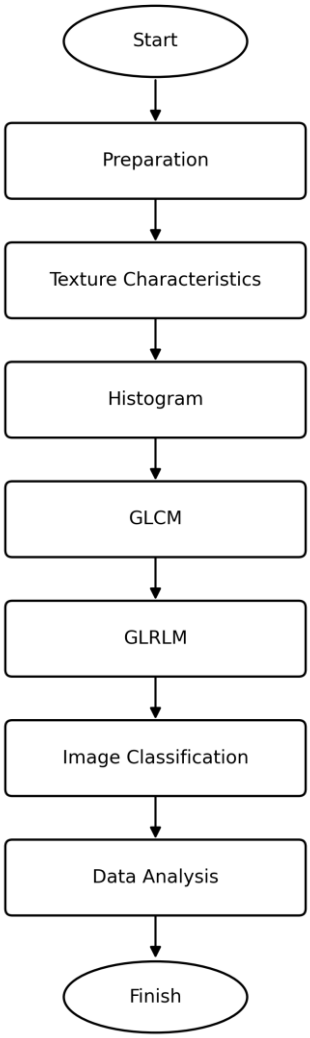

Figure 1. Research Flowchart

Preprocessing
There are several processes, namely, taking an image from kaggle.com, collecting it, and converting the RGB input image to grayscale.

Texture Feature Extraction
This extraction process produces essential data that can then be used to obtain important information. The information, in turn, can provide a thorough overview and interpretation of an object (Almumtazah et al., 2023). Texture feature extraction in this study includes a Histogram, a Gray-Level Co-Occurrence Matrix (GLCM), and a Gray-Level Run-Length Matrix (GLRLM) (Rizal et al., 2019).

Histogram
Histogram equalization will increase the brightness and contrast of dark, low-contrast images so that features not visible in the initial image become visible. This method works by distributing the greyness levels across the image so that each greyness level has an even distribution (Choukali et al., 2023; Li et al., 2024; Zhao et al., 2024).

Mean

$$\mu = \sum_{n=0}^{N} z_n p\,(z_n) \tag{1}$$

Variant

$$\sigma^2 = \sum_{i=0}^{l} (z_n - \mu)^2\ p(z_n) \tag{2}$$

Slope

$$\propto_3 = \frac{1}{\propto_3} \sum_{n=0}^{N} (z_n - \mu)^3\ p(z_n) \tag{3}$$

Entropy

$$S = -\sum_{n=0}^{N} p(z_n)^2\, log_2\, p(z_n) \tag{4}$$

Standard deviation

$$\sigma = \sqrt{\sigma^4} \tag{5}$$

Kurtosis

$$\propto^4 = \frac{1}{\propto^4} \sum_{n=0}^{N} (F_n - \mu)^4\ p(F_n) - 3 \tag{6}$$

where i is the grayness level in image f and p(i) represents the probability of an L occurring, the highest greyness level value is shown. Where σ² is called the second-order normalized moment because P(I) is a probability function.

Gray-Level Co-occurrence Matrix (GLCM)

The Gray-Level Co-occurrence Matrix (GLCM) is a texture analysis method used to measure how pixels of a certain intensity in an image relate to each other at certain distances and angles (Dheepak et al., 2023).

Homogeneity

$$\sum_{i,j=0}^{g=1} \frac{Pij}{1 + |i-j|} \tag{7}$$

Contrast measures the extent to which pixel intensity differences in a shared event matrix

$$\sum_{i,j=0}^{l-1} |i-j|^2\ Pij \tag{8}$$

Correlation

$$\sum_{i,j=0}^{g=1} \frac{(i-\mu_i)(j-\mu_j)Pij}{\sigma_i \times \sigma_j} \tag{9}$$

Energy represents the homogeneity of texture

$$\sum_{i,j=0}^{l=1} Pij \tag{10}$$

where p(i,j) is the probability of co-occurrence between pairs of pixels with greyness levels i and j in the image, N is the Number of greyness levels in the image. Where μx and μy are the average greyness levels i and j in the image, σx and σy are the standard greyness deviation values of the image.

Gray Level Run-Length Matrix (GLRLM)

The Gray Level Run-Length Matrix (GLRLM) is a matrix used to extract various texture features to support texture analysis. Texture in this context refers to the grey pixel intensity pattern formed in 18 specific directions of the reference pixel. The long *run* refers to the number of consecutive pixels with the same level of grey intensity in a given direction (Durgamahanthi et al., 2021).

Short-Term Emphasis (SRE)

$$SRE = \frac{1}{S}\sum_{i=1}^{M}\sum_{j=1}^{N}\frac{p(i,j)}{j^2} = \sum_{j=1}^{N}\frac{r(i,j)}{j^2} \quad (11)$$

Long-Term Emphasis (LRE)

$$LRE = \frac{1}{S}\sum_{i=1}^{M}\sum_{j=1}^{N}\frac{p(i,j)}{j^2} = \sum_{j=1}^{N} j^2 r\,(j)/S \quad (12)$$

Non-Uniform Gray Level (GLN)

$$GLN = \frac{1}{S}\sum_{i=1}^{M}\left(\sum_{j=1}^{N} p(i,j)\right)^2 = \sum_{i=1}^{N} g(i)^2\,/S \quad (13)$$

Non-Uniform Running Length (RLN)

$$RLN = \frac{1}{S}\sum_{i=1}^{M}\left(\sum_{j=1}^{N} p(i,j)\right)^2 = \sum_{i=1}^{N} r(j)^2\,/S \quad (14)$$

Low Gray Level Running Emphasis (LGRE)

$$LGRE = \frac{1}{S}\sum_{i=1}^{M}\sum_{j=1}^{N}\frac{p(i,j)}{i^2} \quad (15)$$

High Gray Level Running Emphasis (HGRE)

$$HGRE = \frac{1}{S}\sum_{i=1}^{M}\sum_{j=1}^{N} p\,(i,j)i^2 \quad (16)$$

Execution Percentage (RP)

$$RP = \frac{S}{\sum_{i=1}^{M}\sum_{j=1}^{N} p\,(i,j)} = \frac{1}{n}\sum_{i=1}^{M}\sum_{j=1}^{N} p\,(i,j) \quad (17)$$

where S is the Total sum of all values run on an image, M is the Number of greyness ordinances (Gray level) (0, 1, 2, …, 255), N is the Number of sequences Running length (1, 2, 3, …), I is Grayness value (Gray level) (0; 1; 2; …; M-1), J is Value Running length (1; 2; 3; …; N), r(j) is Number of run-lengths by sequence, j g(I) is Number of run-lengths by sequence, I (grey level) n is Number of rows × Number of columns, p(I, j) is Matrix set I and j.

Random Forest

Random Forest is an ensemble-based machine learning algorithm that improves classification accuracy by combining several decision trees (Mirzadeh & Omranpour, 2024). Each decision tree in Random Forest is trained using a randomly drawn sample from the initial data and using only a random subset of the available features. This method allows Random Forest to handle complex and large data effectively, as each tree is trained with only a portion of the information, thus reducing the potential for overfitting (Jin et al., 2020).

Random Forest's main advantage lies in its resilience to lost and outlier data and its ability to handle large amounts of data with complex parameters. This method also has a built-in feature selection process, assigning each feature an importance rating that shows its contribution to the model's accuracy. With these features, Random Forest can improve model performance in complex classification or regression tasks, such as medical image processing and bioinformatics, where accurate prediction is critical.

$$Gini\ Impurity = 1 - \sum_{j=1}^{n}(pj)^2 \quad (18)$$

where n is the Class target number, J is the Target class, p is the Class target ratio.

Data Analysis Techniques

The accuracy of the diagnostic values in the classification can be shown through the evaluation index values obtained from the data classification results using the WEKA machine learning algorithm. In this analysis, accuracy, precision, and *Recall* will be described and measured as follows.

Accuracy

This is the ratio of the overall correct prediction to the total data.

$$Akurasi = \frac{TP + TN}{TP + TN + FP + FN} \quad (19)$$

Precision
The Number of correct positive predictions divided by the total positive predictions shows how many classes predicted to be positive turned out to be positive. This measure measures how accurate the model is in detecting disease.

$$Presisi = \frac{TP}{TP + FP} \quad (20)$$

Recall
The Number of correct optimistic predictions divided by the total actual positive events. This shows how many actual positive events were successfully predicted as positive.

$$Recall = \frac{TN}{TP + FN} \quad (21)$$

TP *(True Positive)* is the Number of patients classified as Alzheimer's by the classification system, FP *(False Positive)* is the Number of Non-Alzheimer's patients who are classified as Alzheimer's by the classification system, FN *(False Negative)* is the Number of Alzheimer's patients classified as Non-Alzheimer's by the classification system, TN *(True Negative)* is the Number of Non-Alzheimer's patients classified as Non-Alzheimer's by the classification system.

Results and Discussion

Figure 2(b) shows an overview of diagnosing normal brain tissue biopsied using Magnetic Resonance Imaging. Normal brains tend to have a well-defined structure and no dark areas or conspicuous shrinkage, as in the picture of Alzheimer's disease. A normal brain shows stable and regular development and growth of nerve cells. The brain consists of several critical regions, such as the cortex, hippocampus, and brainstem. In Figure 2(a), some cells in the hippocampus or cortex area undergo abnormal degeneration, which can lead to symptoms of Alzheimer's disease. The feature extraction used is texture features using histograms, GLCM, and GLRLM.

(a) (b)

Figure 2. MRI of Alzheimer's brain tissue (a) Mild Impairment (b) No Impairment

The analysis results in Table 1 use the Random Forest method, a cross-sectional approach, and diagnostic tests. The table helps calculate the accuracy value in classifying brain tissue in Alzheimer's patients. Based on the results of the experiment, the highest accuracy was obtained in fold 10 with a value of 88%, followed by fold 20 (87.5%), fold 15 (85%), fold 25 (83%), and fold 5 (80%). This accuracy value is beneficial in identifying brain tissue affected by Alzheimer's, where a more accurate classification can provide a clear picture of the condition of nerve cells. The highest precision is achieved at fold 10 with a value of 85%, while folds 5, 15, 20, and 25 show precision varying between 79% and 84%. The highest Recall of 92% is achieved in folds 10 and 20, while the other folds show a consistent recall of 91% and the lowest Recall in fold 5 with a value of 76%. The Random Forest method provides a classification of brain tissue with a reasonable degree of accuracy in detecting the presence of Alzheimer's, especially with the characteristics of neurodegeneration in the hippocampus and cortex

that is central to cognitive decline in Alzheimer's patients. This classification is essential to aid in early diagnosis and further management of the disease. Compared to previous research by Almumtazah et al. (2023), the results of the study in the form of sensitivity of 90.27%, accuracy of 88.60%, and specificity of 87.15%, where these results are good values to be used as a decision support system for medical personnel in diagnosing Alzheimer's patients. The amount of data, brain image processing methods, and data processing techniques can cause this difference in results.

Table 1. Performance Evaluation of the Random Forest Model by Fold, in Terms of Accuracy, Precision, and Recall

Fold	TP (data)	FP (data)	FN (data)	TN (data)	Accuracy (%)	Precision (%)	Recall (%)
Training	100	0	0	100	100.00	100.00	100.00
5	76	17	24	83	80	81.70	76.00
10	92	16	8	84	88	85	92.00
15	91	20	9	80	85	81	91.00
20	92	17	8	83	87.5	84	92.00
25	91	24	9	76	83	79	91.00

The model's ability to detect texture features associated with pathological changes in Alzheimer's disease can benefit doctors and diagnosticians in conducting early detection and planning more appropriate interventions (Fernandez et al., 2024). Alzheimer's disease, as a progressive neurodegenerative disease, causes damage to brain tissue, especially in areas such as the hippocampus and cortex that play a role in memory, learning, and cognition (Mortara et al., 2023). This texturing feature-based model can distinguish healthy brain tissue from tissue degenerated due to the accumulation of beta-amyloid plaques and neurofibrillary tangles, characteristic of Alzheimer's.

Texture feature extraction techniques such as histograms, GLCM, and GLRLM provide a deeper understanding of the microscopic changes in brain tissue, even before the clinical symptoms of Alzheimer's appear (Li et al., 2024; Dheepak et al., 2023). Through this analysis, the model can identify patterns of changes in the structure and distribution of nerve cells and other supporting tissues, such as astrocytes and microglia, which are often difficult to recognize through mere visual observation. This early detection is critical, given that Alzheimer's is often diagnosed late when damage to the brain is already widespread.

Although this study offers great potential in helping the diagnostic process and evaluation of the progression of Alzheimer's disease, some limitations need to be considered. The study did not include detailed information on the stages of disease progression, the size and distribution of plaque and tangle, and its association with more specific clinical manifestations. In addition, there are no clear guidelines regarding the treatment steps that should be taken based on the analysis of these texture features. So, although this model can be a precious tool, a holistic approach involving clinical examination and other imaging is still needed to provide an accurate and thorough diagnosis of Alzheimer's patients.

This study employs the Random Forest algorithm, an ensemble-based machine learning method that enhances classification accuracy by combining multiple decision trees. One of its primary strengths is its ability to handle high-dimensional data while minimizing overfitting. Using WEKA as an analysis platform facilitates the implementation of Random Forest, from parameter configuration to result visualization; parameters such as the Number of trees and maximum tree depth were optimized to achieve the best performance in distinguishing healthy brain tissue from tissue affected by Alzheimer's.

Texture feature extraction from MRI images plays a critical role in identifying microstructural changes invisible through conventional visual analysis. Three primary techniques were employed in this study: the Histogram, which enhances image contrast and evenly distributes grayscale levels, revealing hidden features, with parameters such as mean, variance, entropy, and kurtosis describing the grayscale distribution; the Gray Level Co-Occurrence Matrix (GLCM), which measures the spatial relationship between pixels with specific grayscale values at defined distances and angles, with

parameters like homogeneity, contrast, correlation, and energy providing information on texture patterns; and the Gray Level Run-Length Matrix (GLRLM), which measures the run-length patterns of pixels with similar grayscale intensity in a specific direction, with parameters such as Short Run Emphasis (SRE), Long Run Emphasis (LRE), and Gray Level Non-Uniformity (GLN) describing the distribution of pixel intensities.

The texture-based model developed in this study effectively detects neurodegenerative changes at an early stage, even before significant clinical symptoms appear. The hippocampus and cortex, critical for cognitive function, were the primary focus areas for detection. The classification results demonstrate the model's effectiveness in differentiating between healthy and degenerated brain tissue, a key indicator of Alzheimer's disease. The model demonstrates competitive results compared to prior research; for instance, a study by Almumtazah et al. (2023) reported a sensitivity of 90.27%, accuracy of 88.60%, and specificity of 87.15%. Variations in image processing techniques, dataset size, and analysis methods likely account for the differences in outcomes.

Despite its potential, the model has certain limitations that warrant consideration. The study does not provide detailed information on the stages of disease progression, which could influence classification accuracy. Broader clinical implementation requires integrating other imaging modalities, such as PET scans or fMRI, and comprehensive clinical evaluations, and the texture feature analysis still needs to offer clear guidance on therapeutic interventions based on diagnostic results. Nonetheless, this study makes a significant contribution to the application of machine learning in diagnosing neurodegenerative diseases. Future research should focus on developing more complex models that integrate multimodal data such as genetic information, biomarkers, and functional imaging to enhance diagnostic accuracy and provide more precise guidance for medical interventions.

Conclusion

This study demonstrates that the Random Forest algorithm provides good classification performance in detecting brain tissue affected by Alzheimer's disease, with the highest accuracy of 88%, precision of 85%, and Recall of 92% in the 10th fold. Texture feature extraction techniques such as histograms, GLCM, and GLRLM successfully detected neurodegeneration patterns in the hippocampus and cortex areas before clinical symptoms appeared. This texture-based model has the potential to serve as an effective diagnostic tool for early detection of Alzheimer's, although a more holistic approach is necessary for comprehensive clinical application.

Conflicts of interest

The authors hereby declare that there are no known conflicts of interest, financial or otherwise, that could have appeared to influence the results or interpretation of this study.

References

Almumtazah, N., Kiromi, M. S., & Ulinnuha, N. (2023). Klasifikasi Alzheimer Berdasarkan Data Citra MRI Otak Menggunakan Fcm Dan Anfis. Jurnal Teknologi Informasi dan Ilmu Komputer, 10(3), 613-622. https://doi.org/10.25126/jtiik.20231036826

Awojoyogbe, B. O., & Dada, M. O. (2024). Performance Evaluation of Machine Learning Classification of Brain Tumors with WEKA and Python Programming. In B. O. Awojoyogbe, & M. O. Dada (Eds.), Digital Molecular Magnetic Resonance Imaging (pp. 229-246). Springer Nature Singapore. https://doi.org/10.1007/978-981-97-6370-2_9

Bhade, A. W., & Bamnote, G. R. (2023). Performance Evaluation of Machine and Deep Transfer Learning Techniques for the Classification of Alzheimer Disease Using MRI Images. In H. Sharma, A. K. Saha, & M. Prasad (Eds.), Proceedings of International Conference on Intelligent Vision and Computing (ICIVC 2022) (pp. 314-327). Springer Nature Switzerland.

Bhagya Shree, S. R., & Sheshadri, H. S. (2014). A review on the method of diagnosing Alzheimer's disease using data mining. International Journal of Engineering Research, 3(3), 2417-2420.

Bhagya Shree, S. R. (2016). Diagnosis of Alzheimer's Disease using Rule based Approach. Indian Journal of Science and Technology, 9(13). https://doi.org/10.17485/ijst/2016/v9i13/84496

Chen, J. H., Wang, X. L., & Lei, F. (2024). Data-driven multinomial random forest: a new random forest variant with strong consistency. Journal of Big Data, 11(1). https://doi.org/10.1186/s40537-023-00874-6

Choukali, M. A., Valizadeh, M., Amirani, M. C., & Mirbolouk, S. (2023). A desired histogram estimation accompanied with an exact histogram matching method for image contrast enhancement. Multimedia Tools and Applications, 82(18), 28345-28365. https://doi.org/10.1007/s11042-023-14830-2

Dheepak, G., J, A. C., & Vaishali, D. (2023). Brain tumor classification: a novel approach integrating GLCM, LBP and composite features. Frontiers in Oncology, 13(January), 1-12. https://doi.org/10.3389/fonc.2023.1248452

Durgamahanthi, V., Anita Christaline, J., & Shirly Edward, A. (2021). GLCM and GLRLM Based Texture Analysis: Application to Brain Cancer Diagnosis Using Histopathology Images. In S. S. Dash, S. Das, & B. K. Panigrahi (Eds.), Intelligent Computing and Applications (pp. 691-706). Springer Singapore.

Fernandez, M. V., Liu, M., Beric, A., Johnson, M., Cetin, A., Patel, M., Budde, J., Kohlfeld, P., Bergmann, K., Lowery, J., Flynn, A., Brock, W., Sanchez Montejo, B., Gentsch, J., Sykora, N., Norton, J., Gentsch, J., Valdez, O., Gorijala, P., ... Cruchaga, C. (2024). Genetic and multi-omic resources for Alzheimer disease and related dementia from the Knight Alzheimer Disease Research Center. Scientific Data, 11(1), 1-19. https://doi.org/10.1038/s41597-024-03485-9

Fitriyani, F., Fahira, S. N., Rotua, S. S., Mitra, A. P., Pravitasari, A. A., & Hendrawati, T. (2023). Klasifikasi Penyakit Alzheimer pada Citra Magnetic Resonance Imaging menggunakan Inception V3 Architecture. BIAStatistics: Jurnal Statistika Teori dan Aplikasi: Biomedics, Industry & Business And Social Statistics, 2023(1), 265-276.

Hussain, M. A., & Gogoi, L. (2022). Performance analyses of five neural network classifiers on nodule classification in lung CT images using WEKA: a comparative study. Physical and Engineering Sciences in Medicine, 45(4), 1193-1204. https://doi.org/10.1007/s13246-022-01187-3

Iqbal, M., Nawawi, H. M., Rezki, M., Hamid, A., & Rahayu, S. (2023). Pendekatan Algoritma Klasifikasi Machine Learning untuk Deteksi Penyakit Demensia. Computer Science (CO-SCIENCE), 3(2), 94-99. https://doi.org/10.31294/coscience.v3i2.1987

Jack, C. R., Barnes, J., Bernstein, M. A., Borowski, B. J., Brewer, J., Clegg, S., Dale, A. M., Carmichael, O., Ching, C., DeCarli, C., Desikan, R. S., Fennema-Notestine, C., Fjell, A. M., Fletcher, E., Fox, N. C., Gunter, J., Gutman, B. A., Holland, D., Hua, X., ... Weiner, M. (2015). Magnetic resonance imaging in Alzheimer's Disease Neuroimaging Initiative 2. Alzheimer's and Dementia, 11(7), 740-756. https://doi.org/10.1016/j.jalz.2015.05.002

Jatmiko, A. W. (2021). Efek Pemakaian Kontras Untuk Optimalisasi Citra Pada Pemeriksaan Diagnostik Magnetic Resonance Imaging (MRI). Jurnal Biosains Pascasarjana, 23(1), 28. https://doi.org/10.20473/jbp.v23i1.2021.28-39

Jin, Z., Shang, J., Zhu, Q., Ling, C., Xie, W., & Qiang, B. (2020). RFRSF: Employee Turnover Prediction Based on Random Forests and Survival Analysis. Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics), 12343 LNCS, 503-515. https://doi.org/10.1007/978-3-030-62008-0_35

Li, Z., Wu, Y., Liu, M., Miao, D., Zhang, D., & Ding, W. (2024). A novel quantitative method to evaluate lumbar disc degeneration: MRI histogram analysis. European Spine Journal, 33(6), 2420-2429. https://doi.org/10.1007/s00586-024-08279-6

Luo, D., & Qiao, X. (2024). Regional agricultural drought vulnerability prediction based on interpretable Random Forest. Environmental Monitoring and Assessment, 196(11), 1123. https://doi.org/10.1007/s10661-024-13203-y

Mirzadeh, H., & Omranpour, H. (2024). Extended random forest for multivariate air quality forecasting. International Journal of Machine Learning and Cybernetics. https://doi.org/10.1007/s13042-024-02329-7

Mortara, A. A., Permatasari, M., Desiani, A., Andriani, Y., & Arhami, M. (2023). Perbandingan Algoritma C4.5 dan Adaptive Boosting dalam Klasifikasi Penyakit Alzheimer. Jurnal Teknologi dan Informasi, 13(2), 196-207. https://doi.org/10.34010/jati.v13i2.10525

Olle Olle, D. G., Zoobo Bisse, J., & Abessolo Alo'o, G. (2024). Application and comparison of K-means and PCA based segmentation models for Alzheimer disease detection using MRI. Discover Artificial Intelligence, 4(1). https://doi.org/10.1007/s44163-024-00106-7

Patil, A., Tiple, B., & Phatak, M. (2023). Deep Learning Framework for Brain Tumor and Alzheimer Disease Prognosis Using MRI Images. In A. J. Kulkarni (Ed.), Optimization Methods for Product and System Design (pp. 217-232). Springer Nature Singapore. https://doi.org/10.1007/978-981-99-1521-7_12

Pourranjbar, S., Mameghani, A. S., Gholami, M., & Abbasi-Maleki, S. (2024). Probiotic Agents for Alzheimer and Dementia. In N. Moradikor, I. Chatterjee, & W. Mohamed (Eds.), Nutrition in Brain Aging and Dementia (pp. 223-233). Springer Nature Singapore. https://doi.org/10.1007/978-981-97-4117-5_11

Qamar, U., & Raza, M. S. (2023). Practical Data Science with WEKA. In U. Qamar, & M. S. Raza (Eds.), Data Science Concepts and Techniques with Applications (pp. 393-448). Springer International Publishing. https://doi.org/10.1007/978-3-031-17442-1_12

Qi, X., Xu, B., Wang, Z., & Hsu, L. T. (2024). Random forest-based multipath parameter estimation. GPS Solutions, 28(3), 1-16. https://doi.org/10.1007/s10291-024-01667-x

Rizal, R. A., Gulo, S., Della, O., Sihombing, C., Bernandustahi, A., Napitupulu, M., Gultom, A. Y., & Siagian, T. J. (2019). Analisis Gray Level Co-Occurrence Matrix (Glcm) Dalam Mengenali Citra Ekspresi Wajah. Jurnal Mantik Augustus: Manajemen, Teknologi Informatiak Dan Komunikasi, 3(2), 31-38.

Sai Madhuri, K., Prathusha, B., Manish Reddy, G., Deshmukh, G., Bhuvan Sai Kumar, K., & Markos, A. (2024). Performance Analysis of Machine Learning Algorithms by Using WEKA and Scikit-Learn. In D. Mishra, X. S. Yang, A. Unal, & D. S. Jat (Eds.), Data Science and Big Data Analytics (pp. 633-644). Springer Nature Singapore.

Saikia, P., & Kalita, S. K. (2024). Alzheimer Disease Detection Using MRI: Deep Learning Review. SN Computer Science, 5(5), 507. https://doi.org/10.1007/s42979-024-02868-4

Tran, T. T., Phan, N. Q., & Huynh, H. X. (2025). Random Forest Model Parameters Optimization. In N. Thai-Nghe, T. Do, & S. Benferhat (Eds.), Intelligent Systems and Data Science (pp. 237-247). Springer Nature Singapore.

Zhao, Z., Zhang, J., Yuan, S., Zhang, H., Yin, H., Wang, G., Pan, Y., & Li, Q. (2024). The value of whole tumor apparent diffusion coefficient histogram parameters in predicting meningiomas progesterone receptor expression. Neurosurgical Review, 47(1), 235. https://doi.org/10.1007/s10143-024-02482-1