Journal of Holistic Medical Technologies
Vol.1 No.1 (2024) 1 – 9
Available online at https://journal.innoscientia.org/index.php/jhmt

Classification of mammographic image based on texture features with Random Forest method for identification of breast tumors

Rizal Krisdiyanto[1*] and Heni Sumarti[1]
[1] Department of Physics, Faculty of Science and Technology, Universitas Islam Negeri Walisongo Semarang, Indonesia
*Corresponding author's e-mail: rizal_krisdiyanto_2008026011@walisongo.ac.id

ABSTRACT

Breast cancer is one of the most common sorts of cancer in ladies around the world. One method that can be used to detect breast cancer is to use medical imaging. Purpose: This study was conducted to identify the types of breast tumors by combining feature extraction and classification using the Random Forest method. The research data comes from the DDSM repository, which consists of 20 benign and 20 malignant images aged 40 to 50 years. The research stages consist of preprocessing, feature extraction, and classification. The preprocessing and feature extraction stages use MATLAB R2021a, while the classification process uses the WEKA application. Texture feature extraction methods include Histograms and GLCM (Gray-Level Co-Occurrence Matrix). The histogram feature extraction results show that the benign image has a higher level of brightness and contrast and is symmetrical compared to the malignant image. Meanwhile, the malignant image has a more random or irregular histogram than the benign image. Then, the average value of GLCM texture features resulting from benign images is higher than malignant images. The texture feature-based breast tumor classification process using the Random Forest method from the Training Set stage obtained an accuracy of 100%. Meanwhile, at the cross-validation stage with variations of 5-Folds, 10-Folds, and 15-Folds, the same value was obtained for an accuracy of 95%. This shows that the Random Forest classification method can be used to identify breast tumor types with more accurate results and does not depend on an individual's ability to read medical imaging results.

Keywords:
Breast Tumors; Mammographic Classification; Random Forest; Texture Features; GLCM

Introduction

Breast cancer is one of the most common sorts of cancer in ladies around the world. According to (Trayes & Cokenakes, 2021), breast cancer is the second leading cause of death in women worldwide, after lung cancer. Breast cancer is one of the four cancers women are diagnosed with worldwide (GLOBOCAN, 2020). According to Ferlay et al. (2018) there were 3.91 million new cancer cases (excluding non-melanoma skin cancer) and 1.93 million cancer deaths in Europe in 2018. The most common causes of death from cancer are lung, colorectal, breast, and pancreatic cancer. According to Kemenkes (2022) breast cancer ranks as the most common type of cancer in Indonesia and is the main cause of death from cancer. Several risk factors that can increase a person's chances of developing breast cancer are age, family history, genetics, lifestyle, and environmental factors (Yedjou et al., 2019). Therefore, early detection of breast cancer is critical to increase the chances of healing and extend the life expectancy of sufferers.

One method that can be used to detect breast cancer is to use medical imaging (Houssein et al., 2021). Medical imaging is a technique used to obtain an overview of the tissues in the body, allowing doctors to see changes or abnormalities in breast tissue. Texture feature extraction was chosen as the first step in classification because images have special patterns that can cause differences in diagnosis. The pattern is a visual difference between benign and malignant tumors, and texture feature extraction is carried out based on the image's roughness, smoothness, and regularity —texture feature extraction in the form of Histograms and GLCM. The histogram in an image represents the gray level of the image (Thanki & Kothari, 2019). Meanwhile, GLCM is a technique that can be used to analyze the texture of

digital images (Narayan et al., 2023). This technique is often used in medical imaging to extract valuable features in diagnosing diseases, including breast tumors. This method makes it possible to measure the texture of medical images and show signs of breast tumors more clearly.

Several classification methods that can be used for tumor classification include Naive Bayes, Support Vector Machine (SVM), Fuzzy, Neural Networks, and Random Forest (Wibawa et al., 2018). Random Forest was chosen in the classification because it has several advantages, including producing relatively low errors, good classification performance, efficiently handling large amounts of training data, and an effective method for estimating missing data (Religia et al., 2021). Then, the Random Forest algorithm utilizes several decision trees to make a final decision based on the voting results of each decision tree, and this technique is considered successful for classification (Shah et al., 2020).

Julia et al. (2022), in their research classifying breast tumors based on textural features using the Naïve Bayes method, obtained an accuracy value of 80%. Another study performed GLCM feature extraction using the SVM method on mammographic images and obtained a probability value of 60% by testing ten composite images (five benign and five malignant) (Junita, 2017). Then, Dai et al. (2019) used the Random Forest algorithm to classify breast tumors to obtain an accuracy of 94.90%. From several references, it was found that feature extraction and Random Forest classification have a high accuracy value in classifying breast tumors. Therefore, this research was carried out by combining feature extraction and random forest classification to identify the type of breast tumor.

Methods

The research data came from the Digital Database for Screening Mammography (DDSM) repository, consisting of 20 benign and 20 malignant images aged 40 to 50. The stages of the research are preprocessing, feature extraction, and classification. The preprocessing and feature extraction stages use MATLAB R2021a, while the classification process uses the WEKA application.

Preprocessing

The preprocessing process is in the form of filtering, cropping, and resizing. Preprocessing starts from the raw image taken from the DDSM dataset, which is processed with a filtering step to filter the image while removing tumor markers and converting the image to grayscale (Djunaidi et al., 2022). Then, the image is cropped to remove or cut out parts of the image that are not needed. Next, resize the image to equalize the size of all data and adjust the image pixels.

Texture Feature Extraction

Texture feature extraction retrieves information or features related to an image's texture. Texture feature extraction method in the form of Histogram and GLCM.

Histogram

An image's histogram represents the relative frequency of different shades of gray in that image. It gives an overall picture of the appearance of the image. The level of enhancement and type of histogram distribution can reflect the characteristics of the image being observed. By using a histogram, images can be identified based on the gray distribution pattern on the histogram. Dark images tend to have their histogram components concentrated in the lower gray levels, and bright images tend to have their histogram components concentrated in the upper gray levels. (Salamah & Ekawati, 2021). Some statistical techniques used to extract features from histograms (Malik & Baharudin, 2013):

a. Mean (m) is the average value of the brightness level of an object.

$$m = \sum_{i=0}^{L-1} i.p(i) \tag{2.1}$$

Where i is the gray level in image f and p(i) represents the probability of occurrence of i and L denotes the highest gray level value.

b. The standard deviation (σ) is a measure that indicates how far the data is spread out from the average value.

$$\sigma = \sqrt{\sum_{i=0}^{L-1}(i-m)^2 p(i)} \tag{2.2}$$

c. A variant is a measure that describes the variation or difference in color intensity in an image.

$$\sigma^2 = \sum_{i=0}^{L-1}(i-m)^2 p(i) \tag{2.3}$$

where σ^2 is called the second-order normalized moment because p(i) is a probability function.

d. Skewness is an indicator that describes the extent to which the average intensity distribution tends to be asymmetrical.

$$Skewness = \sum_{i=0}^{L-1}(i-m)^3 p(i) \tag{2.4}$$

e. Kurtosis is a metric that describes the spiciness or flatness of a histogram curve in a data.

$$Kurtosis = \sum_{i=0}^{L-1}(i-m)^4 p(i) \tag{2.5}$$

f. Entropy is a measure that describes the level of complexity of the image.

$$Entropy = -\sum_{i=0}^{L-1} log_2(p(i)) \tag{2.6}$$

Gray Level Co-Occurrence Matrix (GLCM)

GLCM is one of the methods used in texture analysis or feature extraction. A GLCM is a matrix representing the frequency of occurrence of two pixels with a given intensity in a given direction and distance. The feature extraction stage uses the GLCM method with image feature outputs in contrast, energy, homogeneity, and correlation (Lin & Irsyad, 2021). With the following calculations (Preethi & Sornagopal, 2014):

a. Contrast
Contrast measures the moment difference between the GLCM image and spatial frequency. Contrast is a measure of the presence of variations in the gray level.

$$Contrast = \sum_i \sum_j (i-j)^2 p(i,j) \tag{2.7}$$

where $p(i,j)$ is the probability of co-occurrence between pairs of pixels with gray levels i and j in the image.

b. Energy
Energy is a parameter that describes how homogeneous the image is.

$$Energy = \sum_{i,j=0}^{N-1} p(i,j)^2 \tag{2.8}$$

Where N is the number of gray levels in the image.

c. Homogeneity
Homogeneity is an indicator that measures the uniformity of the gray level in a certain area in an image.

$$Homogeneity = \sum_i \sum_j \frac{p(i,j)}{1+(i-j)} \tag{2.9}$$

d. Correlation
Correlation reflects the grayscale association of image textures. Higher matrix element values and smoother image textures are associated with higher correlation values.

$$Correlation = \frac{1}{\sigma_x \sigma_y} \sum_i = 1 \sum_j = 1(1-\mu_x)(1 - \mu_y)p(i,j) \tag{2.10}$$

Where μ_x and μ_y are the average gray levels of i and j in the image, $\sigma_x \; and \; \sigma_y$ are the standard deviation values of the image's gray levels of i and j.

Classification

The random forest method is used for image classification (Sheykhmousa et al., 2020). Random Forest is a popular machine learning algorithm belonging to the family of group learning algorithms. Then, the Random Forest algorithm utilizes several decision trees to make a final decision based on the voting results of each decision tree, and this technique is considered successful for classification (Gupta et al., 2021; Shah et al., 2020). Meanwhile, Random Forest can be used to rank characteristics depending on their influence on classification, and the importance of these features is assessed by the index of Gini impurity criteria. The Gini index measures the predictive potential of a variable in a regression or classification. The Gini index can be determined by (Smys et al., 2019):

$$Gini\ Impurity = 1 - \sum_{j=1}^{n} (p_j)^2 \tag{2.11}$$

where n is the number of target classes, j is the target class, and p is the target class ratio.

The Random Forest classification process involves two important stages, namely using the Training Set and the Cross-Validation method. In Cross-Validation, the dataset will be divided into several subsets called k-fold validation, which are then used as test data for model evaluation. K-Fold Cross-Validation is a cross validation testing method used to evaluate the performance of an algorithmic method by dividing the data sample into several groups (folds) as many as K values, then testing the algorithm method randomly at each fold to produce a performance value (Cahyanti et al., 2020).

Data Analysis

After the classification results were obtained using the Random Forest method, then the data analysis stage was carried out to test accuracy, precision, and recall using the Confusion Matrix method. In classification, accuracy refers to the percentage of success in correctly classifying data after being tested based on the classification results. Precision is the ratio between the number of cases predicted as positive and true positive to the overall genuinely positive data. Meanwhile, recall is the ratio between the number of truly positive cases predicted to be correctly favorable to all truly positive data (Shah et al., 2020). With the following calculations (Frank et al., 2017):

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \times 100\% \tag{2.12}$$

$$Precision = \frac{TP}{TP+FP} \times 100\% \tag{2.13}$$

$$Recall = \frac{TP}{TP + FN} \times 100\% \quad (2.14)$$

where TP (true positive) refers to data the system finds positive and classifies as positive. TN (true negative) refers to data the system finds negative and classifies it as negative. FN (false negative) refers to data that is negative but is classified as positive by the system. FP (false positive) refers to data that is positive but is classified as negative by the system.

Results and Discussions

Result

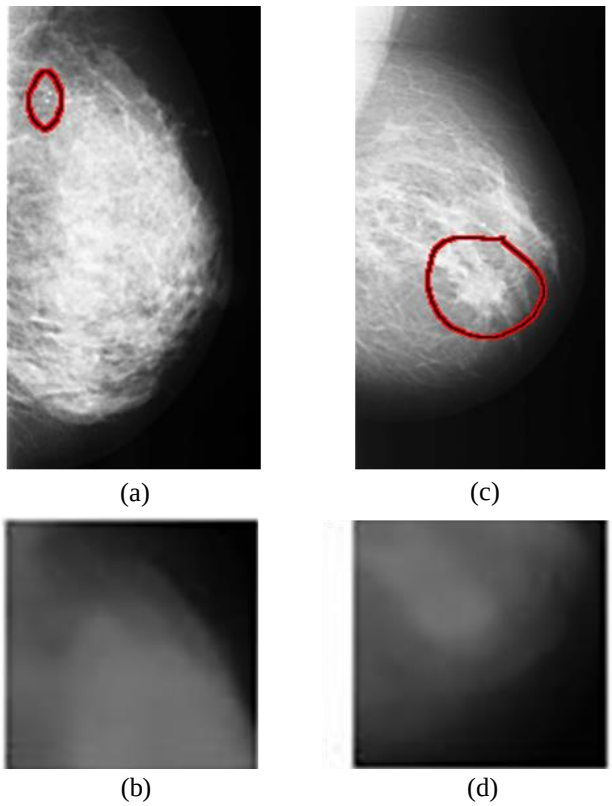
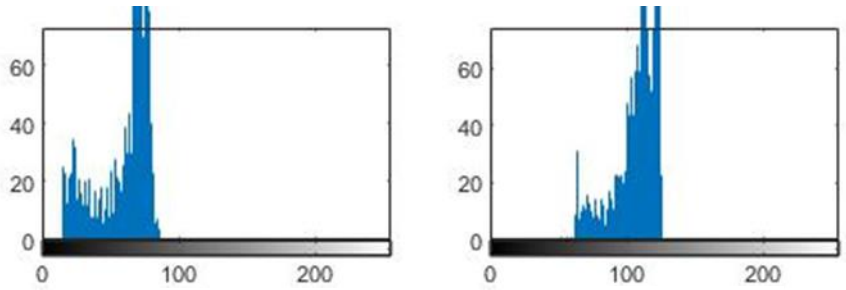


Figure 1. Mammographic Image (a) Benign Tumor before Preprocessing, (b) Benign Tumor After Preprocessing, (c) Malignant Tumor Before Preprocessing, and (d) Malignant Tumor After Preprocessing

Figure 1 shows the results of mammography images before and after preprocessing. The image results obtained from preprocessing are images filtered by markers in the form of grayscale images when filtering occurs. Then, the image results were cropped, and the pixel sizes of all images were the same. The results of this preprocessing are used for the Histogram and GLCM feature extraction stages (Julia et al., 2022).

Figure 2 shows the histogram results of mammography images. The graphical forms of the two images have different gray levels; in benign images, the gray levels are spread in the range 0-100; in malignant images, the gray levels are spread in the range 100-150. It shows that the gray level of benign tumors shows a dark image and that of a malignant tumor shows a light image.



(a) (b)

Figure 2. Mammographic Image Histogram (a) Benign Tumor and (b) Malignant tumor

The results of texture feature extraction are shown in Table 1. The standard deviation value of the average texture feature value is added to see the data distribution. Values with a random data distribution are mean, standard deviation, and variance texture features, while other texture feature values have a uniform data distribution. Histogram texture features are mean, standard deviation, variance, skewness, and entropy. Meanwhile, the texture features of GLCM are contrast, energy, homogeneity, and correlation.

Table 1. Average Histogram and GLCM Feature Values

Texture Features	**Benign**	**Malignant**
Mean	73.6407 ± 13.5873	71.075 ± 14.8677
Standard Deviation	23.2247 ± 8.5660	23.0435 ± 11.5477
Variant	611.7192 ± 421.0545	664.3871 ± 570.7704
Skewness	-1.1305 ± 0.6119	-0.7452 ± 0.6431
Kurtosis	4.5772 ± 2.7030	3.391 ± 1.5879
Entropy	5.7151± 0.4530	5.7896 ± 0.6707
Contrast	0.0955 ± 0.1892	0.0675 ± 0.0377
Energy	0.489 ± 0.1660	0.4358 ± 0.2052
Homogeneity	0.9738 ± 0.0117	0.9675 ± 0.0157
Correlation	0.9384 ± 0.0392	0.9064 ± 0.0990

Table 2. Confusion Matrix Prediction Results

Parameters	**Random Forest Classification**			
	Training Set	**5-Folds**	**10-Folds**	**15-Folds**
TP	20 Data	19 Data	19 Data	19 Data
FP	0 Data	0 Data	0 Data	0 Data
TN	20 Data	20 Data	20 Data	20 Data
FN	0 Data	1 Data	1 Data	1 Data
Accuracy	100%	95%	95%	95%
Precision	100%	100%	100%	100%
Recall	100%	95%	95%	95%

After feature extraction, the classification stage is carried out using the Random Forest method. Table 2 shows the results of the Random Forest classification, which obtained the Confusion Matrix values in the form of TP, namely benign images that read as benign. FP, namely malignant images that read as benign. TN, namely malignant images that read as malignant. Furthermore, FN, namely benign images that read as malignant. The table shows that at the cross-validation stage, the number of benign tumors detected as benign was 19, while the number of benign tumors detected as malignant was 1. The prediction results of the mammography image are shown in Figure 3.

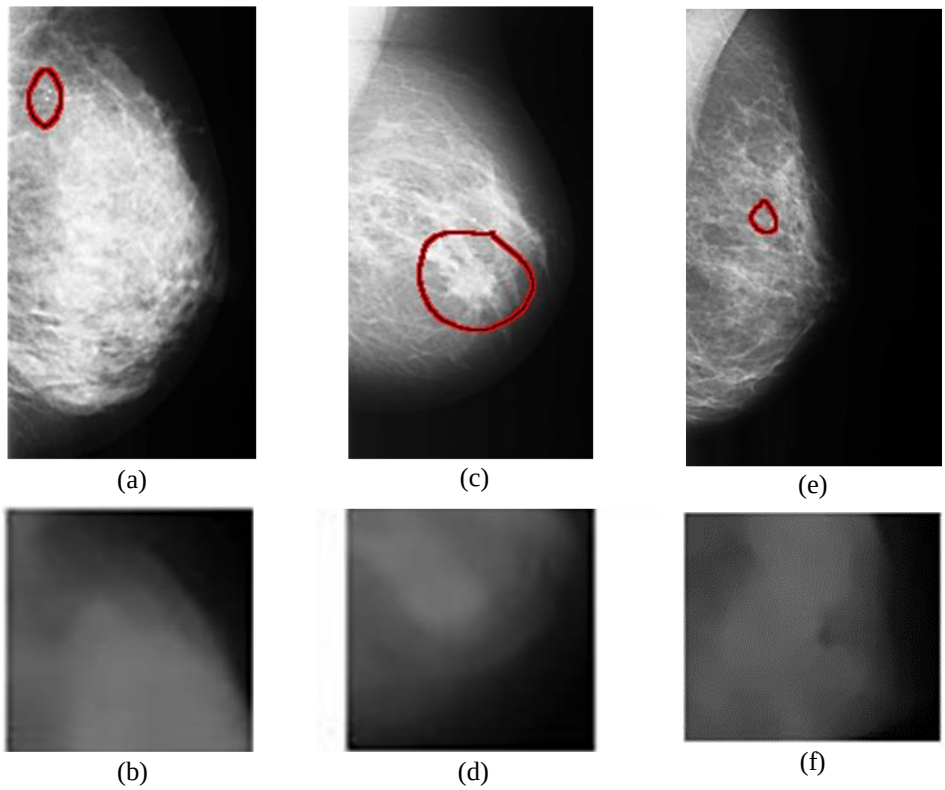


Figure 3. The Results of Mammographic Image Predictions (a) True Prediction of Benign Image Before Preprocessing, (b) True Prediction of Benign Image After Preprocessing, (c) True Prediction of Malignant Image Before Preprocessing, (d) True Prediction of Malignant Image After Preprocessing, (e) False Prediction of Benign Image Before Preprocessing, and (f) False Prediction of Benign Image After Preprocessing

The value of accuracy, precision, and recall of the training set is 100%. Then, the results of variations in the k-Fold validation values (5-Folds, 10-Folds, and 15-Folds) obtained 95% accuracy, 100% precision, and 95% recall value.

Based on Table 1, the average value of histogram texture features in the form of mean, standard deviation, and kurtosis has a higher value in benign tumor images. It shows that the benign image has a higher brightness and contrast and is symmetrical compared to the malignant image. Meanwhile, the average value of variance, skewness, and entropy is higher in the image of a malignant tumor. These findings indicate that malignant images have a more random or irregular histogram than benign images because the features of variance, skewness, and entropy are used to measure histogram diversity. It is consistent with the nature of malignant tumors, which tend to have a higher level of complexity and diversity. The results of the Histogram texture characteristics obtained are in line with research conducted by Julia et al. (2022), used the Naïve Bayes method based on textural features to classify breast tumors and obtained textural features in the form of mean, standard deviation, kurtosis, and entropy for benign images, which were higher, while the variance and skewness for malignant images were higher than for benign images. The texture feature values are similar because they are the same stages as those in the research conducted, where the stages are preprocessed with the resulting images in the form of grayscale. Then, the average value of GLCM texture features resulting from benign images is higher than that of malignant images.

The confusion matrix in the form of TP, FP, TN, and FN is shown in Table 2. In these results, a false prediction occurs where a benign tumor is detected as malignant (false positive). False predictions occur because the textural features of the tame image are similar to the average value of the texture features of the malignant image, so that the predicted results of the confusion matrix show the results as a malignant image. The prediction results of the mammography image are shown in Figure 3.

The accuracy value is shown in Table 2 with variations of 5-Folds, 10-Folds, and 15-Folds obtained a value of 95%. Mashudi et al. (2021) used several methods to classify breast tumors in their research. One of the methods used is the Random Forest method with variations in k-fold values of 2,

3, and 5. The accuracy results obtained were 97.36%, 97.72%, and 97.72%, respectively. The accuracy value in this study is greater and results in different accuracy with different k-fold variations. This is because the number of datasets used is 569 data and includes large data compared to the research conducted. Then, the image used in the previous study used fine needle aspiration (FNA) examination, which is a type of biopsy, so the classification process is more accurate.

The Random Forest classification method based on textural features can be an additional method for medical diagnosis with more accurate results and does not depend on an individual's ability to read medical imaging results, especially imaging for tumor identification. This is because in this study, an accuracy value of 95% was obtained and included high accuracy. Even so, there are research constraints in data input, such the data is still input manually and not automatically.

Conclusion

The texture feature-based breast tumor classification process results using the Random Forest method from the Training Set stage obtained an accuracy value of 100%. Meanwhile, at the cross-validation stage with variations of 5-Folds, 10-Folds, and 15-Folds obtained Accuracy values of 95%, Precision 100%, and Recall 95%. This shows that the Random Forest classification method can be used as an additional means of identifying breast tumor types with more accurate results and does not depend on an individual's ability to read medical imaging results.

Acknowledgments

We thank Dr. Hamdan Hadi Kusuma for his invaluable guidance and support throughout this research. Thanks to Universitas Islam Negeri Walisongo Semarang for providing the necessary facilities and resources for this work.

Conflicts of interest

The authors affirm that they have no conflicts of interest.

References

Cahyanti, D., Rahmayani, A., & Husniar, S. A. (2020). Analisis Performa Metode KNN pada Dataset Pasien Pengidap Kanker Payudara. *Indonesian Journal of Data and Science*, *1*(2), 39–43. https://doi.org/10.33096/ijodas.v1i2.13

Dai, B., Chen, R. C., Zhu, S. Z., & Zhang, W. W. (2019). Using Random Forest Algorithm for Breast Cancer Diagnosis. *Proceedings - 2018 International Symposium on Computer, Consumer and Control, IS3C 2018*, 449–452. https://doi.org/10.1109/IS3C.2018.00119

Djunaidi, K., Lanang, N., Syahdu, A., & Kuswardani, D. (2022). *Penerapan Metode Thresholding : Entropy dan Mathematical Morphology Pada Segmentasi Citra USG Kanker Payudara*. *11*(2), 1–7. https://doi.org/10.33322/kilat.v11i2.1503

Ferlay, J., Colombet, M., Soerjomataram, I., Dyba, T., Randi, G., Bettio, M., Gavin, A., Visser, O., & Bray, F. (2018). Cancer Incidence and Mortality Patterns in Europe: Estimates for 40 Countries and 25 Major Cancers in 2018. *European Journal of Cancer*, *103*, 356–387. https://doi.org/10.1016/j.ejca.2018.07.005

Frank, E., Hall, M. A., & Witten, I. H. (2017). The WEKA Workbench. *Data Mining*, 553–571. https://doi.org/10.1016/b978-0-12-804291-5.00024-6

GLOBOCAN. (2020). *New Global Cancer Data*.

Gupta, V. K., Gupta, A., Kumar, D., & Sardana, A. (2021). Prediction of COVID-19 confirmed, death, and cured cases in India using random forest model. *Big Data Mining and Analytics*, *4*(2), 116–123. https://doi.org/10.26599/BDMA.2020.9020016

Houssein, E. H., Emam, M. M., Ali, A. A., & Suganthan, P. N. (2021). Deep and Machine Learning Techniques for Medical Imaging-Based Breast Cancer: A Comprehensive Review. *Expert Systems with Applications*, *167*, 114161. https://doi.org/10.1016/j.eswa.2020.114161

Julia, B., Sumarti, H., & Kusuma, H. H. (2022). *Klasifikasi Tumor Payudara Berbasis Ciri Tekstur pada Citra Mammografi Menggunakan Metode Naive Bayes*. *7*(2), 165–176.

Junita, B. D. (2017). Ekstraksi Fitur dan Klasifikasi Menggunakan Metode GLCM dan SVM pada Citra Mammogram untuk Identifikasi Kanker Payudara. *Jurnal Ilmiah Teknologi Dan Rekayasa*, *22*(1), 2089–8088.

Kemenkes. (2022). *Kanker Payudara Paling Banyak di Indonesia, Kemenkes Targetkan Pemerataan Layanan Kesehatan*. https://sehatnegeriku.kemkes.go.id/baca/umum/20220202/1639254/kanker-payudaya-paling-banyak-di-indonesia-kemenkes-targetkan-pemerataan-layanan-kesehatan/

Lin, J., & Irsyad, H. (2021). Klasifikasi Pneumonia Pada Citra X-Rays Paru-Paru Menggunakan GLCM Dan LVQ. *Jurnal Algoritme*, *1*(2), 184–194. https://doi.org/10.35957/algoritme.v1i2.897

Malik, F., & Baharudin, B. (2013). Analysis of Distance Metrics in Content-Based Image Retrieval Using Statistical Quantized Histogram Texture Features in The DCT Domain. *Journal of King Saud University - Computer and Information Sciences*, *25*(2), 207–218. https://doi.org/10.1016/j.jksuci.2012.11.004

Mashudi, N. A., Rossli, S. A., Ahmad, N., & Noor, N. M. (2021). Comparison on Some Machine Learning Techniques in Breast Cancer Classification. *Proceedings - 2020 IEEE EMBS Conference on Biomedical Engineering and Sciences, IECBES 2020*, 499–504. https://doi.org/10.1109/IECBES48179.2021.9398837

Narayan, V., Mall, P. K., Awasthi, S., Srivastava, S., & Gupta, A. (2023). FuzzyNet: Medical Image Classification Based on GLCM Texture Feature. *2023 International Conference on Artificial Intelligence and Smart Communication (AISC)*, 769–773.

Preethi, G., & Sornagopal, V. (2014). MRI Image Classification Using GLCM Texture Features. *Proceeding of the IEEE International Conference on Green Computing, Communication and Electrical Engineering, ICGCCEE 2014*. https://doi.org/10.1109/ICGCCEE.2014.6922461

Religia, Y., Nugroho, A., & Hadikristanto, W. (2021). Analisis Perbandingan Algoritma Optimasi pada Random Forest untuk Klasifikasi Data Bank Marketing. *Jurnal RESTI (Rekayasa Sistem Dan Teknologi Informasi)*, *5*(1), 187–192. https://doi.org/10.29207/resti.v5i1.2813

Salamah, U. G., & Ekawati, R. (2021). *Pengolahan Citra Digital*. Media Sains Indonesia.

Shah, K., Patel, H., Sanghvi, D., & Shah, M. (2020). A Comparative Analysis of Logistic Regression, Random Forest and KNN Models for the Text Classification. *Augmented Human Research*, *5*(1). https://doi.org/10.1007/s41133-020-00032-0

Sheykhmousa, M., Mahdianpari, M., Ghanbari, H., Mohammadimanesh, F., Ghamisi, P., & Homayouni, S. (2020). Support Vector Machine Versus Random Forest for Remote Sensing Image Classification: A Meta-Analysis and Systematic Review. *IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing*, *13*, 6308–6325. https://doi.org/10.1109/JSTARS.2020.3026724

Smys, S., Tavares, J., Balas, V. E., & Iliyasu, A. M. (2019). Computational Vision and Bio-Inspired Computing. In *Advances in Intelligent Systems and Computing: Vol. 1108 AISC*. Springe. https://doi.org/https://doi.org/10.1007/978-3-030-37218-7

Thanki, R. M., & Kothari, A. M. (2019). *Digital Image Processing Using Scilab.* Springer International Publishing.

Trayes, K. P., & Cokenakes, S. E. (2021). Breast Cancer Treatment. *American Family Physician*.

Wibawa, A. P., Purnama, M. G. A., Akbar, M. F., & Dwiyanto, F. A. (2018). Metode-Metode Klasifikasi. *Prosiding Seminar Ilmu Komputer Dan Teknologi Informasi*, *3*(1), 134.

Yedjou, C. G., Sims, J. N., Miele, L., Noubissi, F., Lowe, L., Fonseca, D. D., Alo, R. A., Payton, M., & Tchounwou, P. B. (2019). Health and Racial Disparity in Breast Cancer. *Advances in Experimental Medicine and Biology*, *1152*, 31–49. https://doi.org/10.1007/978-3-030-20301-6_3