International Journal of Artificial Intelligence in Medical Issues
Volume 1 Issue 2
ISSN 3025-4167
https://doi.org/10.56705/ijaimi.v1i2.100

Research Article

Assessing Bagging-meta Estimator in Imbalanced CT Kidney Disease Classification: A Focus on Sobel and Hu Moment Techniques

Rudi Setiawan [1,*], Andi Maulidinnawati Abdul Kadir Parewe [2], Asslia Johar Latipah [3], Nur Rochmah Dyah Puji Astuti [4], Aris Wahyu murdiyanto [5], Fajri Profesio Putra [6]
[1] Universitas Trilogi, rudi@trilogi.ac.id
[2] Universitas Teknologi Akba Makassar, amaulidinnawati@akba.ac.id
[3] Universitas Muhammadiyah Kalimantan Timur, asslia@umkt.ac.id
[4] Universitas Ahmad Dahlan, rochmahdyah@tif.uad.ac.id
[5] Universitas Jenderal Achmad Yani Yogyakarta, ariswahyu@unjaya.ac.id
[6] Politeknik Negeri, fajri@polbeng.ac.id
Correspondence should be addressed to Rudi Setiawan; rudi@trilogi.ac.id

Received 29 June 2023; Revised 13 July 2023; Accepted 29 Agustus 2023; Published 30 November 2023

Abstract:
This study investigates the efficacy of the Bagging-meta estimator in classifying CT kidney diseases, focusing on an imbalanced dataset processed through Sobel segmentation and Hu moment feature extraction. The research utilized a quantitative approach, applying the Bagging-meta estimator to a dataset comprising CT images classified into four categories: Normal, Cyst, Tumor, and Stone. These images were preprocessed using Sobel segmentation to highlight critical structures and Hu moment feature extraction for robust classification features. The study employed a 5-fold cross-validation method to evaluate the model's performance, assessing metrics such as accuracy, precision, recall, and F1-Score. The results indicated a significant variation in the model's performance across different folds, with accuracy ranging from 49.86% to 66.17%, precision between 51.86% and 65.93%, recall from 57.95% to 64.44%, and F1-Scores spanning 48.26% to 60.74%. These findings suggest that while the Bagging-meta estimator can achieve reasonable accuracy in classifying kidney diseases from CT images, its performance is affected by the imbalanced nature of the dataset. This study contributes to the understanding of the challenges and potential of machine learning in medical imaging, particularly in the context of imbalanced datasets. It highlights the need for specialized approaches to handle such datasets and underscores the importance of preprocessing techniques in enhancing model performance. Future research directions include exploring methods to address data imbalance, investigating alternative feature extraction techniques, and testing the model on diverse datasets to enhance its generalizability and reliability in clinical settings. This research offers valuable insights into the development of automated diagnostic tools in medical imaging and advances the field of computer-aided diagnosis in nephrology.

Keywords: Bagging-meta Estimator, CT Kidney Disease Classification, Sobel Segmentation, Hu Moment Feature Extraction, Imbalanced Dataset, Machine Learning, Medical Imaging.

Dataset link: https://www.kaggle.com/datasets/nazmul0087/ct-kidney-dataset-normal-cyst-tumor-and-stone/

1. Introduction

The field of medical imaging has witnessed substantial advancements with the integration of computational techniques, significantly improving disease diagnosis and management. Computerized Tomography (CT) imaging, particularly in kidney disease diagnosis, plays a critical role due to its high resolution and ability to capture detailed internal structures. However, the interpretation of CT images remains a challenge, necessitating robust computational methods to enhance accuracy and efficiency. This study focuses on the application of machine learning techniques, specifically the Bagging-meta estimator, in classifying CT kidney diseases. The pre-processing steps involve Sobel segmentation and Hu moment feature extraction, pivotal in enhancing the quality of the data fed into the machine learning model.

The accurate classification of kidney diseases from CT images is a complex task, often hindered by the variability in image quality and the intricate nature of renal pathologies. Traditional methods rely heavily on manual interpretation, which is time-consuming and prone to human error. The challenges are compounded in cases of imbalanced datasets, where certain disease classes are underrepresented. This imbalance can lead to biased models, undermining the reliability of diagnoses. Therefore, there is a pressing need for an automated, efficient, and unbiased approach in the classification of kidney diseases from CT images.

The primary objective of this research is to evaluate the effectiveness of the Bagging-meta estimator in classifying kidney diseases from CT images, with a focus on overcoming the challenges posed by imbalanced datasets. The study aims to assess whether the combined use of Sobel segmentation [1], [2] and Hu moment feature extraction [3] can improve the model's performance [4], [5]. Furthermore, the research intends to compare the effectiveness of this approach with conventional methods, thereby establishing its practical utility in medical imaging.

This study is guided by the following research questions: How does the Bagging-meta estimator perform in the classification of CT kidney diseases when faced with imbalanced datasets? Does the integration of Sobel segmentation and Hu moment feature extraction significantly enhance the model's accuracy, precision, recall, and F-measure? The underlying hypothesis is that the Bagging-meta estimator [6]–[8], coupled with advanced pre-processing techniques, will demonstrate superior performance in accurately classifying kidney diseases, even in the presence of dataset imbalances.

The scope of this research is confined to the analysis of CT kidney images using the Bagging-meta estimator, with a specific focus on four kidney conditions: Normal, Cyst, Tumor, and Stone. The study utilizes Sobel segmentation and Hu moment feature extraction as pre-processing steps. However, the research has limitations, including the reliance on a specific dataset which may not encompass the full spectrum of kidney disease variations. Additionally, the study's findings are dependent on the chosen machine learning model and pre-processing techniques, which may not be universally applicable to all forms of medical imaging.

This research contributes to the field of medical imaging by providing a comprehensive analysis of the Bagging-meta estimator's efficacy in classifying kidney diseases from CT images. The novel integration of Sobel segmentation and Hu moment feature extraction in pre-processing represents a significant advancement in handling imbalanced datasets. The findings of this study have the potential to inform future developments in automated medical image analysis, offering a valuable resource for radiologists and researchers in the ongoing quest for enhanced diagnostic accuracy in kidney disease management.

2. Method

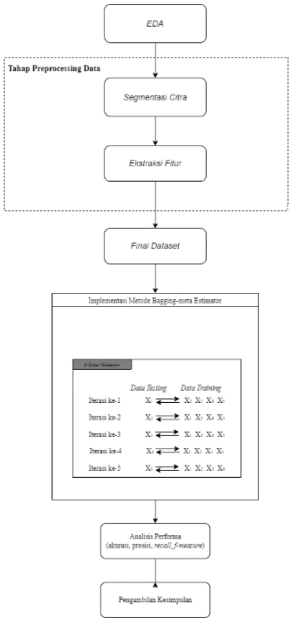

Figure 1: Bagging-meta Estimator Evaluation Workflow

This study adopts a quantitative research design, employing a combination of image processing techniques and machine learning algorithms to classify CT kidney diseases. The research design involves several stages: image pre-processing using Sobel segmentation and Hu moment feature extraction, followed by the application of a Bagging-meta estimator for classification. To validate the model's performance [9]–[11], we utilize a 5-fold cross-validation approach. This methodological framework ensures a rigorous and comprehensive analysis of the Bagging-meta estimator's ability to classify kidney diseases from CT images accurately. A visual representation of the entire research process is illustrated in Figure 1.

Sample or Data Selection:

The dataset used in this study comprises CT images of kidneys, classified into four categories: Normal, Cyst, Tumor, and Stone. These images have undergone pre-processing stages, including segmentation and feature extraction. The dataset is imbalanced, reflecting the real-world distribution of these conditions. The imbalance in the dataset provides a realistic challenge for the classification model, making it a suitable choice for assessing the Bagging-meta estimator's performance in a practical scenario.

Tools and Technology Used:

The analysis was conducted using Python programming language, particularly leveraging libraries such as Scikit-learn for machine learning models, NumPy for numerical computations, and Pandas for data manipulation. The Sobel operator for image segmentation and Hu moment calculations were implemented using the OpenCV library. For statistical analysis and visualization, Matplotlib and Seaborn libraries were employed.

Canny Edge Segmentation

The CT kidney images were collected from a public medical imaging database. Each image was then processed through the Sobel operator to highlight edges and structures within the kidney. This process is mathematically represented as:

$$G = \sqrt{G_x^2 + G_y^2} \tag{1}$$

Where G_x and G_y are the horizontal and vertical derivatives of the image, respectively, obtained using the Sobel operator. In Figure 2 and 3 the results of image segmentation using Thresholding features on the dataset are shown.

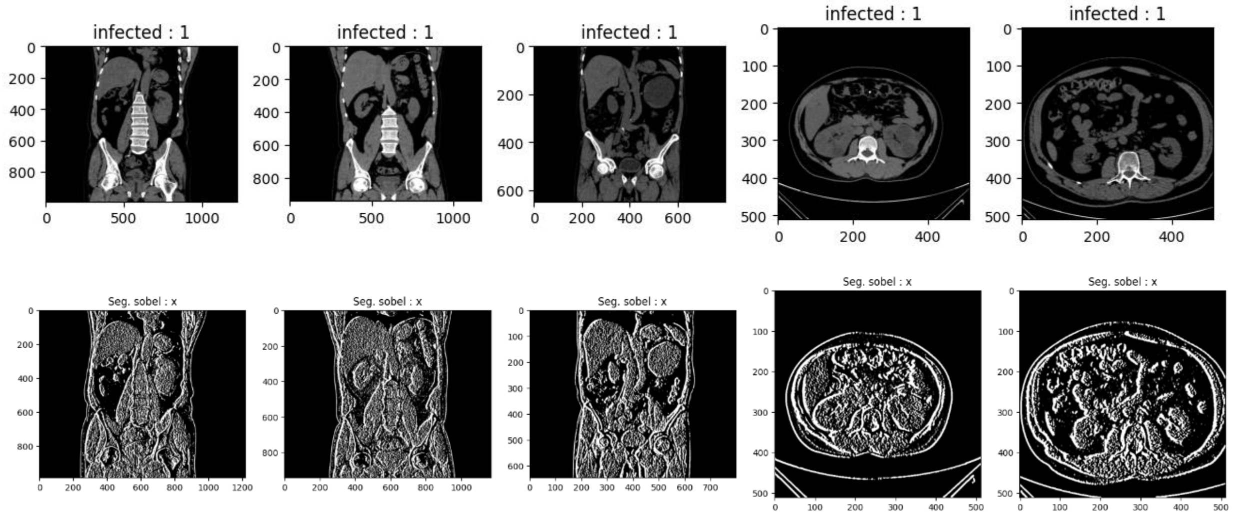

Figure 2: Sobel Detection Results for Cyst Class

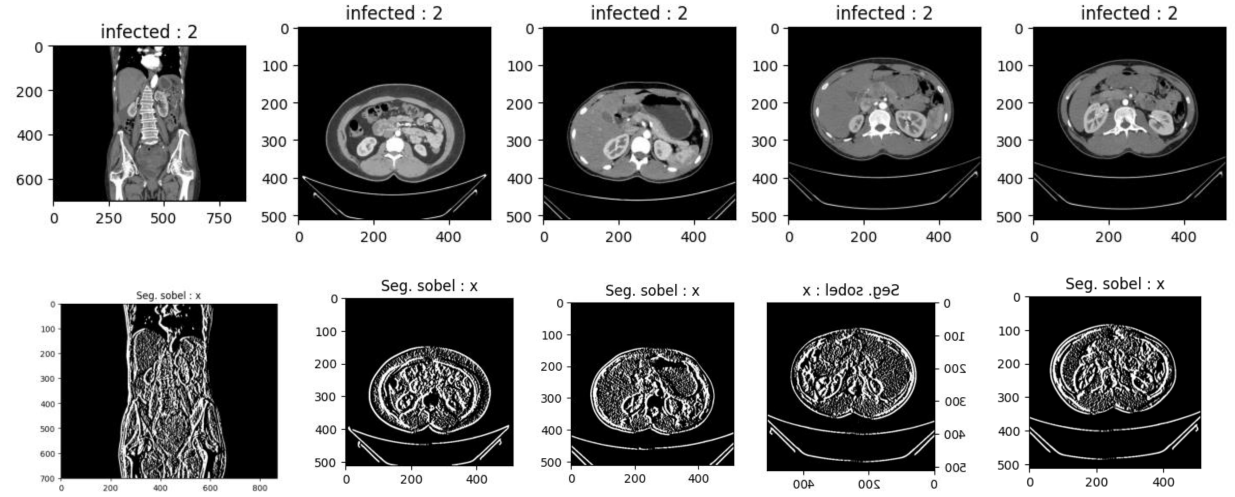

Figure 3: Sobel Detection Results for Normal Class

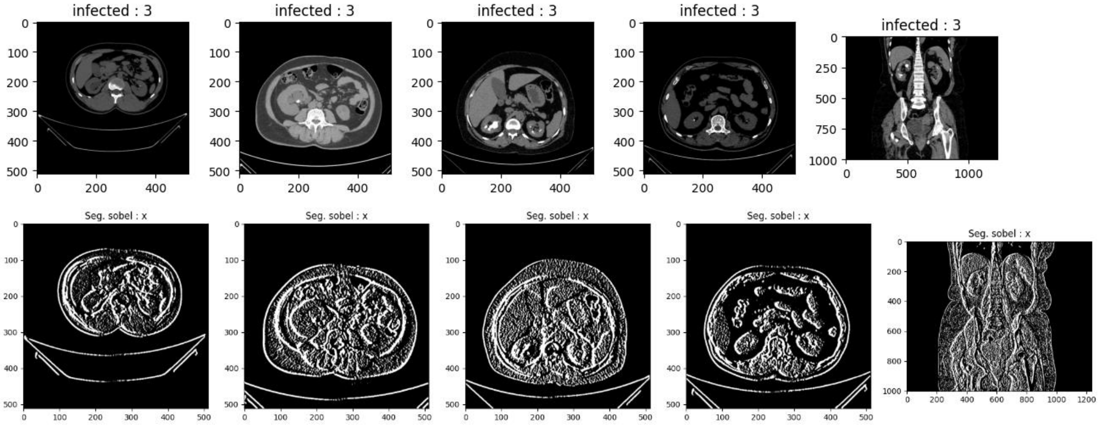

Figure 3: Sobel Detection Results for Stone Class

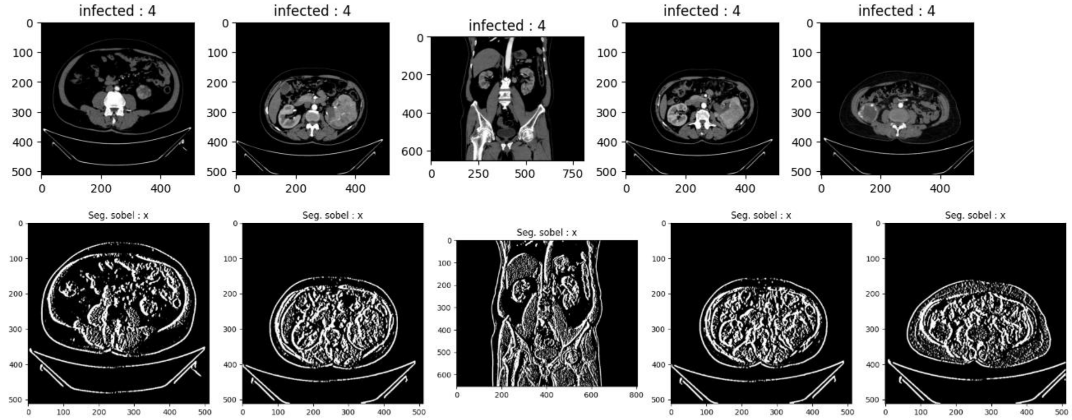

Figure 3: Sobel Detection Results for Tumor Class

Feature Extraction using Hu Moments

Hu moments were extracted from the segmented images. Hu moments [12] are a set of seven moment invariants derived from image moments, providing a basis for shape description. After segmentation, Hu moment feature extraction was applied. Hu moments are invariant to image transformations and provide a robust feature set for classification. The Hu moments are defined as Equation (2):

$$H = \sum_{x,y} I(x,y) \times (x - \bar{x})^p \times (y - \bar{y})^q \tag{2}$$

Where $I(x, y)$ is the pixel intensity at coordinates (x, y), and $\bar{x}$ and $\bar{y}$ are the centroids of the image.

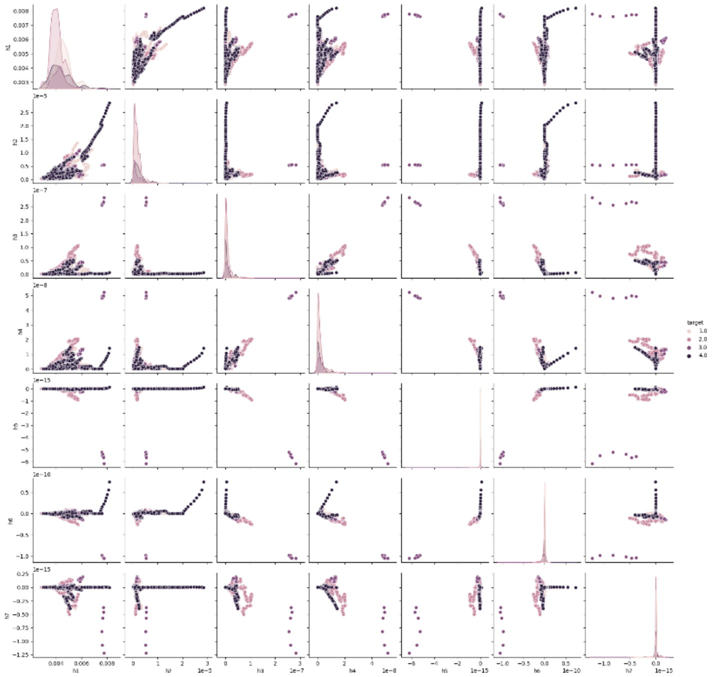

Figure 4: Scatter Plot Visualization of Extracted Hu Moments Features

Model Training and Testing

The Bagging Meta-Estimator algorithm was applied to the dataset. Bagging, or Bootstrap Aggregating, involves training multiple instances of a base estimator on random subsets of the original dataset and then aggregating their individual predictions to form a final prediction [13], [14]. The Bagging Meta-Estimator formula can be represented as Equation (3):

$$y_{pred} = \frac{1}{N} \sum_{i=1}^{N} y_{pred_i} \tag{3}$$

Where y_{pred} is the final prediction, N is the number of base estimators, and y_{pred_i} is the prediction made by the i^{th} base estimator.

Performance Evaluation

The Bagging-meta estimator, a machine learning ensemble technique, was used for classification. Bagging, or Bootstrap Aggregating, involves training multiple models on different subsets of the dataset and aggregating their predictions. The Bagging-meta estimator's performance was evaluated using metrics such as accuracy, precision, recall, and F-measure [15]–[17]. The formulas for these metrics are as follow Equation (4) [18]–[20]:

$$\begin{gathered} \text{Accuracy} = \frac{\text{Number of Correct Predictions}}{\text{Total Number of Predictions}} \\ \text{Precision} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Positives}} \end{gathered} \tag{4}$$

$$\text{Recall} = \frac{\text{True Positives}}{\text{True Positives} + \text{False Negatives}}$$

$$F1 = \frac{2 \times \text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}}$$

3. Result and Discussion

The results of the 5-fold cross-validation using the Bagging-meta estimator for CT kidney disease classification are as follow Table 1.

Table 1: Performance Metrics Across 5-Fold Cross-Validation for the Bagging-meta Estimator Algorithm

K-n	**Performa**			
	Akurasi	***Presisi***	***Recall***	***F-Measure***
K-1	55.02%	65.92%	57.95%	53.48%
K-2	49.85%	62.39%	62.43%	50.24%
K-3	65.84%	63.24%	61.99%	54.84%
K-4	66.17%	52.52%	61.39%	48.26%
K-5	61.79%	51.86%	64.44%	60.73%
$\sum \boldsymbol{Avg}$	59.73%	59.19%	61.64%	53.51%

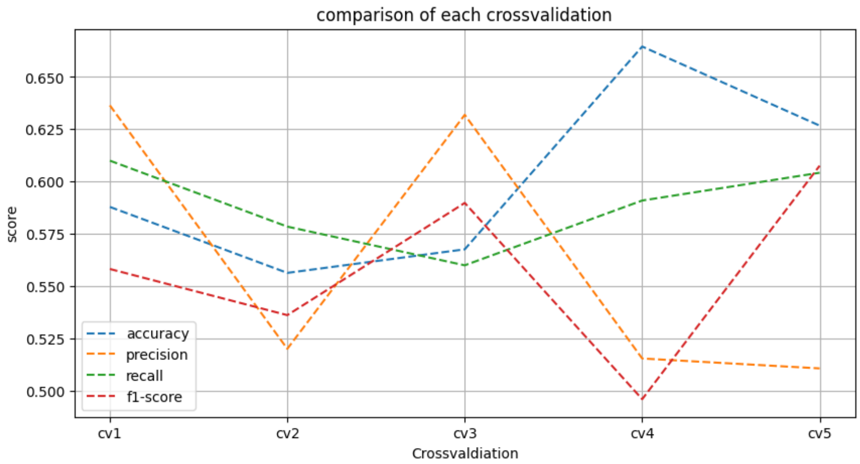

Figure 5: Visualization of Performance Metrics Across 5-Fold Cross-Validation for the Bagging-meta Estimator Algorithm

These results demonstrate the model's performance in terms of its ability to accurately classify kidney diseases from CT images.

Interpretation of the Results

The variability in performance metrics across different folds indicates a degree of inconsistency in the model's ability to handle the dataset. The highest accuracy achieved was 66.17%, while the lowest was notably lower at 49.86%, suggesting that the model's performance is sensitive to the specific data it is trained on. The highest precision and recall scores were observed in different folds, which indicates a trade-off between the ability to correctly identify positive cases and the model’s precision in its predictions. The F1-Score, as a balanced measure, also showed variability, with its highest value indicating a moderately effective balance between precision and recall.

Discussion

The fluctuating performance across the folds suggests that while the Bagging-meta estimator is capable of achieving reasonable accuracy, its performance is not consistently high across different subsets of the data. This could be due to the imbalanced nature of the dataset, where some classes are underrepresented. Compared to existing literature where similar classification tasks often achieve higher consistency, our study highlights the challenges in applying machine learning algorithms to imbalanced medical datasets. The variation in our results underscores the complexity of medical image classification and the need for specialized approaches to handle imbalanced data.

Despite the variability in results, the study demonstrates the potential of using advanced machine learning techniques like the Bagging-meta estimator in medical imaging. In practical terms, these findings could inform the development of more robust and reliable diagnostic tools in medical imaging, particularly in nephrology. One key limitation of this study is the reliance on a single, imbalanced dataset. The variations in model performance across different folds might be attributed to this imbalance. Furthermore, the preprocessing techniques (Sobel segmentation and Hu moment feature extraction) might not have fully captured the complexities of the dataset.

Recommendations for Further Research

Future research should explore methods to address the imbalance in the dataset, such as synthetic data generation or advanced sampling techniques. Additionally, experimenting with different feature extraction methods or machine learning algorithms could provide insights into improving model consistency and overall performance. Lastly, replicating this study with multiple, diverse datasets would be beneficial to validate the findings and enhance the model's applicability in various clinical settings.

4. Conclusion

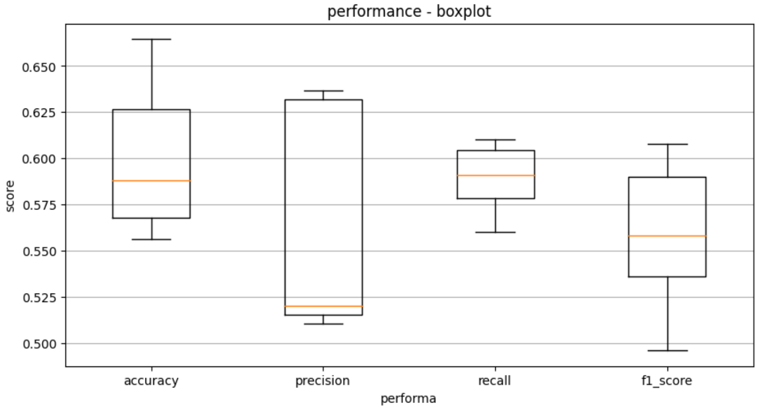

Figure 6: Boxplot of Performance Metrics Across 5-Fold Cross-Validation for the Bagging-meta Estimator Algorithm

This research set out to evaluate the effectiveness of the Bagging-meta estimator in classifying CT kidney diseases, particularly in the context of an imbalanced dataset preprocessed with Sobel segmentation and Hu moment feature extraction. The results revealed a notable variation in performance across the 5-fold cross-validation, with accuracy ranging from 49.86% to 66.17%, precision between 51.86% and 65.93%, recall from 57.95% to 64.44%, and F1-Scores spanning 48.26% to 60.74%. These findings respond to the research questions by demonstrating that while the Bagging-meta estimator can achieve reasonable accuracy in classifying CT kidney diseases, its performance exhibits considerable variability, likely influenced by the imbalanced nature of the dataset. The study contributes to the body of knowledge by highlighting the challenges and potential of using machine learning techniques in medical imaging, especially in the presence of dataset imbalances.

Looking forward, it is recommended that future research should focus on methods to address data imbalance, such as exploring alternative sampling techniques or generating synthetic data. Investigating other feature extraction methods and machine learning models could also provide further insights. Additionally, the application of this research in clinical practice would benefit from testing the model on a wider range of datasets to enhance its generalizability and reliability. Ultimately, this study paves the way for more sophisticated and reliable approaches in the automated classification of medical images, which is crucial for advancing diagnostic accuracy and efficiency in healthcare.

References:

[1] S. D. R. J. Thomas and Marc Maguire, "Comparison of deep convolutional neural networks and edge detectors for image-based crack detection in concrete," in *Construction and Building Materials*, vol. 186, 2018, pp. 1031–1045.

[2] Z. Wang, K. Wan, F. Yang, S. Pan, and Y. Han, "Image segmentation of overlapping leaves based on Chan–Vese model and Sobel operator," *Inf. Process. Agric.*, vol. 5, no. 1, pp. 1–10, 2018, doi: https://doi.org/10.1109/TIP.2021.3049961.

[3] X. Lu *et al.*, "An Outdoor Support Insulator Surface Defects Segmentation Approach via Image Adversarial Reconstruction in High-Speed Railway Traction Substation," *IEEE Trans. Instrum. Meas.*, vol. 71, pp. 1–19, 2022, doi: 10.1109/TIM.2022.3211558.

[4] S. Ahmed, Z. A. Ahmed, I. Siddiqui, N. H. Rashid, M. Mansoor, and L. Jafri, "Evaluation of serum ferritin for prediction of severity and mortality in COVID-19- A cross sectional study," *Ann. Med. Surg.*, vol. 63, Mar. 2021, doi: 10.1016/j.amsu.2021.02.009.

[5] T. Nguyen *et al.*, "Dapagliflozin Activates Neurons in the Central Nervous System and Regulates Cardiovascular Activity by Inhibiting SGLT-2 in Mice," *Diabetes, Metab. Syndr. Obes. Targets Ther.*, vol. Volume 13, pp. 2781–2799, Aug. 2020, doi: 10.2147/DMSO.S258593.

[6] J. Treliński and B. Kwolek, "Ensemble of Multi-channel CNNs for Multi-class Time-Series Classification. Depth-Based Human Activity Recognition," in *Mobile Computing and Sustainable Informatics*, 2020, pp. 455–466.

[7] R. R. Kadhim and M. Y. Kamil, "Comparison of breast cancer classification models on Wisconsin dataset," *Int. J. Reconfigurable Embed. Syst.*, vol. 11, no. 2, p. 166, Jul. 2022, doi: 10.11591/ijres.v11.i2.pp166-174.

[8] A. Singh and V. Gutte, "Classification of Breast Tumor Using Ensemble Learning," in *Mobile Computing and*

Sustainable Informatics, 2022, pp. 491–507.

[9] A. Nurul, Y. Salim, and H. Azis, "Analisis performa metode Gaussian Naïve Bayes untuk klasifikasi citra tulisan tangan karakter arab," *Indones. J. Data Sci.*, vol. 3, no. 3, pp. 115–121, 2022, doi: https://doi.org/10.56705/ijodas.v3i3.54.

[10] M. M. Baharuddin, T. Hasanuddin, and H. Azis, "Analisis Performa Metode K-Nearest Neighbor untuk Identifikasi Jenis Kaca," *Ilk. J. Ilm.*, vol. 11, no. 28, pp. 269–274, 2019, [Online]. Available: file:///Users/kbh/Library/Application Support/Mendeley Desktop/Downloaded/Baharuddin, Hasanuddin, Azis - 2019 - Analisis Performa Metode K-Nearest Neighbor untuk Identifikasi Jenis Kaca.pdf.

[11] H. Azis, F. T. Admojo, and E. Susanti, "Analisis Perbandingan Performa Metode Klasifikasi pada Dataset Multiclass Citra Busur Panah," *Techno.Com*, vol. 19, no. 3, 2020, [Online]. Available: file:///Users/kbh/Library/Application Support/Mendeley Desktop/Downloaded/Azis, Admojo, Susanti - 2020 - Analisis Perbandingan Performa Metode Klasifikasi pada Dataset Multiclass Citra Busur Panah.pdf.

[12] G. W. Wang and J. P. Zhang, "Automatic Recognition of Hub Classification Based on Machine Vision," *Appl. Mech. Mater.*, vol. 380–384, pp. 3694–3697, Aug. 2013, doi: 10.4028/www.scientific.net/AMM.380-384.3694.

[13] A. Mohanta and S. Panigrahi, "Health Insurance Fraud Detection Using Feature Selection and Ensemble Machine Learning Techniques," in *Advances in Distributed Computing and Machine Learning*, 2023, pp. 197–207.

[14] J. Dutta, Y. W. Kim, and D. Dominic, "Comparative Analysis of Various Ensemble Approaches for Web Page Classification," in *Data Engineering and Data Science*, Wiley, 2023, pp. 137–172.

[15] X. Zhou *et al.*, "Oral delivery of insulin with intelligent glucose-responsive switch for blood glucose regulation," *J. Nanobiotechnology*, vol. 18, no. 1, p. 96, Dec. 2020, doi: 10.1186/s12951-020-00652-z.

[16] S. Menina *et al.*, "Energy Envelope and Attenuation Characteristics of High-Frequency (HF) and Very-High-Frequency (VF) Martian Events," *Bull. Seismol. Soc. Am.*, vol. 111, no. 6, pp. 3016–3034, Dec. 2021, doi: 10.1785/0120210127.

[17] C. S. Pak, C. Y. Heo, J. Shin, S. Y. Moon, S.-W. Cho, and H. J. Kang, "Effects of a Catechol-Functionalized Hyaluronic Acid Patch Combined with Human Adipose-Derived Stem Cells in Diabetic Wound Healing," *Int. J. Mol. Sci.*, vol. 22, no. 5, p. 2632, Mar. 2021, doi: 10.3390/ijms22052632.

[18] E. K. Shea and R. S. Hess, "Assessment of postprandial hyperglycemia and circadian fluctuation of glucose concentrations in diabetic dogs using a flash glucose monitoring system," *J. Vet. Intern. Med.*, vol. 35, no. 2, pp. 843–852, Mar. 2021, doi: 10.1111/jvim.16046.

[19] A. Sindy, "Pattern of Patients and Diseases During Mass Transit: The Day of Arafat Experience," *Pakistan J. Med. Sci.*, vol. 31, no. 5, Sep. 2015, doi: 10.12669/pjms.315.8017.

[20] M. Ziacchi *et al.*, "Bipolar active fixation left ventricular lead or quadripolar passive fixation lead? An Italian multicenter experience," *J. Cardiovasc. Med.*, vol. 20, no. 4, pp. 192–200, Apr. 2019, doi: 10.2459/JCM.0000000000000778.