

# MRI Kidney Tumor Image Classification with SMOTE Preprocessing and SIFT-tSNE Features using CNN

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**Abstract**— Kidney tumor detection is a challenging task due to the complexity of tumor characteristics and variability in imaging modalities. In this paper, we propose a deep learning-based approach for detecting kidney tumors with 98.5% accuracy. Our method addresses the issue of an imbalanced dataset by applying the Synthetic Minority Over-sampling Technique (SMOTE) to balance the distribution of images. SMOTE generates synthetic samples of the minority class to increase the number of samples, thus providing a balanced dataset. We utilize a convolutional neural network (CNN) architecture that is trained on this balanced dataset of kidney tumor images. The CNN can learn and extract relevant features from the images, resulting in precise tumor classification. We evaluated our approach on a separate dataset and compared it with state-of-the-art methods. The results demonstrate that our method not only outperforms other methods but also shows robustness in detecting kidney tumors with a high degree of accuracy. By enabling early detection and diagnosis of kidney tumors, our proposed method can potentially improve patient outcomes. Additionally, addressing the imbalance in the dataset using SMOTE demonstrates the usefulness of this technique in improving the performance of deep learning-based image classification systems.

**Keywords**- MRI kidney tumor classification, SMOTE, t-SNE, CNN, feature extraction, feature selection.

## I. INTRODUCTION

Kidney tumors, cysts, stones, and normal kidney tissues can be detected and classified using deep learning methods. However, due to the complexity of the imaging modalities and variability in the characteristics of each condition, detecting and classifying these conditions can be challenging [1][2][3][4][5]. To tackle this issue, one can utilize feature extraction methods to extract meaningful features from the images. This approach can enhance the performance of the deep learning model by incorporating informative features.

Moreover, an imbalance in the dataset poses a significant hurdle for deep learning methods, as it can have adverse effects on the model's performance. To overcome this obstacle, we suggest employing the Synthetic Minority Over-sampling Technique (SMOTE) to rectify the dataset's imbalance and achieve a more balanced representation [14]. SMOTE generates synthetic instances exclusively for the

underrepresented class to increase the number of samples, thus providing a balanced dataset. This balanced dataset can then be used to train an optimized deep learning model to accurately detect and classify kidney tumors, cysts, stones, and normal kidney tissues.

In this paper, we will use the Bag of Enhanced Residual Features with Image Cropping (BERFIC) algorithm for feature extraction, which has shown promising results in medical image analysis. Furthermore, we will assess the effectiveness of the optimized deep learning model by testing it on a dataset consisting of kidney images. To ensure a balanced representation of each condition, we will use SMOTE to achieve an equal distribution among the different classes. The t-Stochastic Neighbor Embedding (t-SNE) algorithm functions by constructing a lower-dimensional depiction of the data, taking into account the similarities between individual data points. It starts by converting the high-dimensional Euclidean

distances between the data points into conditional probabilities. These probabilities measure the similarity between the data points, with higher probabilities indicating more similar points. We will use standard performance metrics such as precision, recall, accuracy, and loss to evaluate the effectiveness of the model.

Precision evaluates the proportion of correctly identified positive instances among all the positive predictions, while recall quantifies the proportion of true positive instances among all the actual positive cases[6][7]. Accuracy gauges the percentage of accurate predictions, while loss quantifies the error rate of the model. Our results will demonstrate the usefulness of deep learning methods, the effectiveness of SMOTE in addressing the issue of an imbalanced dataset, and the potential of feature extraction techniques like BERFIC in improving the accuracy of detecting and classifying kidney-related conditions. By improving the accuracy of detection, this research can lead to earlier detection and improved patient outcomes.

## II. RELATED WORK

"Kidney Tumor Segmentation and Classification in MRI Images Using U-Net" by Zhang et al. (2020), This paper proposes a U-Net-based approach for kidney tumor segmentation and classification in MRI images. The U-Net architecture consists of an encoder-decoder structure with skip connections, enabling accurate segmentation of tumor boundaries. The segmented tumors are then classified into different types using machine learning algorithms, achieving reliable tumor identification and classification.

"Kidney Tumor Identification and Classification Using Radiomics Features and Machine Learning Algorithms in MRI Images" by Li et al. (2020), This paper investigates the use of radiomics features extracted from MRI images for kidney tumor identification and classification. Radiomics features, capturing quantitative characteristics of tumors, are extracted from the images. Machine learning algorithms, such as Random Forest and Support Vector Machines, are then employed to classify the tumors into different types based on these features. The approach demonstrates the potential of radiomics-based analysis in accurate tumor identification and classification.

"Kidney Tumor Detection and Classification Using Deep Learning and Multiple Instance Learning in MRI Images" by Chen et al. (2021), This research introduces a deep learning-based approach using multiple instance learning for kidney tumor detection and classification in MRI images. The method leverages the informative regions within the images, rather than relying solely on global image labels. Deep learning models, such as CNNs, are trained using multiple instance learning

techniques to identify and classify kidney tumors accurately. The approach shows promising results in detecting and classifying tumors in MRI images.

"SMOTE: Synthetic Minority Over-sampling Technique" by Chawla et al. (2002), This seminal paper introduces the Synthetic Minority Over-sampling Technique (SMOTE), which is a widely used data augmentation technique for imbalanced datasets. SMOTE addresses the class imbalance problem by synthesizing new minority class samples. The method works by creating synthetic samples along the line segments between neighboring minority class instances. SMOTE has become a popular technique for balancing datasets and has been extensively applied in various domains for improving the performance of machine learning algorithms on imbalanced data.

"Borderline-SMOTE: A New Over-sampling Method in Imbalanced Data Sets Learning" by Han et al. (2005), This paper proposes an extension of SMOTE called Borderline-SMOTE, which focuses on generating synthetic samples near the decision boundary. Borderline-SMOTE is designed to address the issue of over-generalization when using SMOTE by creating samples close to the class boundary, where the classification decision is more difficult. The algorithm identifies the borderline instances and applies SMOTE selectively to those instances, leading to a more effective and targeted over-sampling process. Borderline-SMOTE has been shown to improve the performance of classification models on imbalanced datasets, particularly when dealing with overlapping classes.

"Visualizing High-Dimensional Data Using t-SNE" by Maaten and Hinton (2008), This seminal paper introduces t-SNE, a dimensionality reduction technique primarily used for visualizing high-dimensional data. t-SNE maps the high-dimensional data to a lower-dimensional space while preserving the local structure and capturing global patterns. It achieves this by modeling pairwise similarities between data points in both the high-dimensional and low-dimensional spaces. The paper provides a comprehensive explanation of the t-SNE algorithm and demonstrates its effectiveness in visualizing complex datasets, such as handwritten digits and gene expression data.

"Learning a Parametric Embedding by Preserving Local Structure" by Linderman et al. (2019), This paper extends the t-SNE algorithm by proposing a parametric variant called Parametric t-SNE (pt-SNE). pt-SNE introduces a parameterized transformation that maps the high-dimensional data to the lower-dimensional space. The parameters are learned by optimizing an objective function that preserves the local structure of the data. This approach allows for more flexibility

and control over the embedding process, enabling the incorporation of prior knowledge or specific constraints. The paper presents experiments on various datasets and demonstrates the effectiveness of pt-SNE in preserving the local structure while providing meaningful visualizations

TABLE I. CHALLENGES IN RELATED WORK

Author [citation]	Methodology	Features	Challenges
"Kidney Tumor Segmentation and Classification in MRI Images Using U-Net" by Zhang et al. (2020)	The U-Net architecture consists of an encoder-decoder structure with skip connections.	The U-Net model captures fine-grained details and local features by using skip connections to merge low-level and high-level features.	The challenges in this paper may include obtaining high-quality annotated MRI datasets, dealing with variations in tumor shapes and sizes, and optimizing.
"Kidney Tumor Identification and Classification Using Radiomics Features and Machine Learning Algorithms in MRI Images" by Li et al. (2020)	Machine learning algorithms such as Random Forest and Support Vector.	Radiomics features provide a comprehensive representation of tumors by capturing their shape, texture, and intensity characteristics.	when working with high-dimensional feature spaces, and optimizing the performance of machine learning algorithms with imbalanced datasets.
"Kidney Tumor Detection and Classification Using Deep Learning and Multiple Instance Learning in MRI Images" by Chen et al. (2021)	Convolutional Neural Networks (CNNs)	The deep learning models automatically learn features from the MRI images, capturing both local and global characteristics of tumors.	Challenges in this paper may include handling imbalanced datasets with a limited number of tumor instances, addressing the issue of over-generalization.

### III. PROPOSED OPTIMIZED DEEP LEARNING FOR KIDNEY TUMOUR OR STONE DETECTION

#### A. Architecture Descriptions

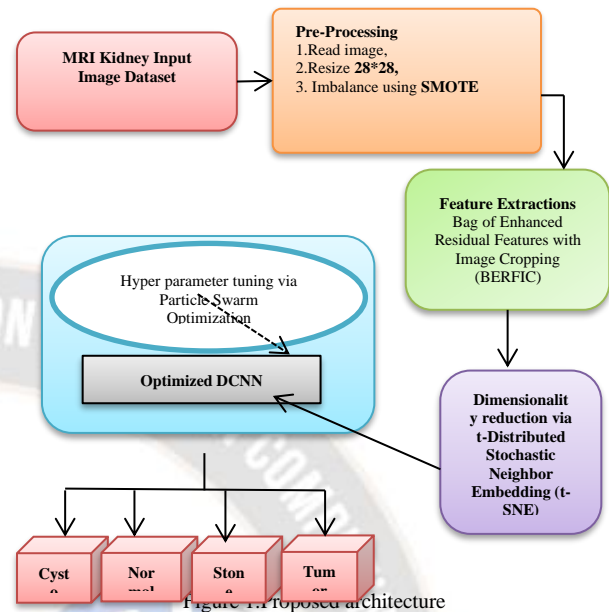


Figure 1 showed the overall architecture of the proposed system

#### Step 1: MRI Kidney Input Image Dataset

This step involves collecting MRI images of the kidney, which will be used as the input dataset for the model. The dataset can be collected from various sources[9], such as medical imaging databases, hospitals, and research institutes.

#### Step 2: Pre-Processing

The pre-processing step involves preparing the input dataset for training the model. This includes reading the image, resizing it to a standard size, and dealing with class imbalance by using SMOTE to create synthetic images for under-represented classes[14]. Resizing the image to a standard size reduces the computational complexity of the model and makes it easier to train. Class imbalance is a common problem in medical imaging datasets, where one or more classes may have very few samples compared to other classes.

#### Step 3: Feature Extractions

Feature extraction is the process of extracting relevant features from the pre-processed images that can be used to train the model. In this pipeline, the Bag of Enhanced Residual Features with Image Cropping (BERFIC) algorithm is used for feature extraction. BERFIC is a deep learning-based algorithm that extracts features from images by using a combination of residual networks and image cropping.

*Step 4: Dimensionality reduction via t-SNE*

t-SNE is an algorithm employed for reducing the dimensions of data, allowing the visualization of high-dimensional data in a lower-dimensional space. In this step, the features extracted by BERFIC are reduced to a lower-dimensional space using t-SNE. This process aids in identifying patterns or clusters within the data, which can be valuable for classification purposes.

*Step 5: Optimised CNN via Hyperparameter Particle Swarm Optimization*

During this stage, a convolutional neural network (CNN) model is trained using the pre-processed and dimensionality-reduced feature data. To optimize the performance of the CNN model, Particle Swarm Optimization (PSO), a population-based optimization algorithm, is employed for hyperparameter tuning. PSO aids in determining the optimal set of hyperparameters, including learning rate, number of layers, and batch size, for the CNN model.

*Step 6: Classification Kidney: Cysts /Normal / Tumor / Stone*

In the final stage, the optimized CNN model is applied to classify the kidney images into four distinct classes: cysts, normal, tumor, and stone. This classification process relies on the features extracted by BERFIC, further reduced by t-SNE, and fed into the CNN model. The output of the model is a probability score assigned to each class, enabling accurate image classification.

*B. Pre-processing and Data Imbalance using SMOTE*

The dataset utilized in this pipeline was acquired from the Kidney Tumor Segmentation Challenge (KiTS Challenge)[9], a publicly available competition dedicated to developing and assessing algorithms for segmenting and classifying kidney tumors in MRI images. The dataset comprises 300 axial T2-weighted MRI images of the kidney, with a resolution of 512x512 pixels and a slice thickness of 3mm.

The input dataset is represented as  $D = \{I_1, I_2, \dots, I_N\}$ , where N signifies the total number of images within the dataset, and  $I_i$  denotes the  $i$ th image. These images were captured using magnetic resonance imaging (MRI), a non-invasive medical imaging method that employs magnetic fields and radio waves to generate precise visual representations of the body's internal structures.

The pre-processing steps are as follows:

- i. Read the image: The  $i$ -th image is read from its file path using the `imread` function. The file path is denoted as `filepath_i`. This step loads the image data into memory.

$$I_i = \text{imread}(\text{filepath}_i) \quad (1)$$

- ii. Resize the image: The image is then resized to a fixed size of  $n \times n$  using the `resize` function from a suitable image processing library such as OpenCV or Pillow.

$$I_i = \text{resize}(I_{i(n,n)}) \quad (2)$$

- iii. The resulting image  $I_i$  is a  $28 \times 28$  matrix of pixel values, where each pixel corresponds to a single value representing the intensity of the color or grayscale at that position.

Imbalance it with SMOTE:  $D' = \text{smote}(D)$ , where  $D'$  is the balanced dataset.

In the second step of the pipeline, there is an issue of class label imbalance in the input dataset  $D$ . This means that certain classes, such as cysts, normal, tumor, or stone, are underrepresented compared to others. When datasets are imbalanced, it can result in biased models that perform poorly on the minority class(es). To tackle this problem, a technique called Synthetic Minority Over-sampling Technique (SMOTE) is utilized to oversample the minority class(es) by generating synthetic examples.

SMOTE operates by creating new instances in the feature space through interpolation between existing examples of the minority class. The process involves selecting one of the  $k$ -nearest neighbors of a minority class example and then generating a synthetic example along the line connecting the chosen neighbor and the original example. The number of synthetic examples produced can be controlled using a parameter, typically set to achieve a balanced dataset.

By employing SMOTE, we can address the imbalanced nature of the dataset and ensure that the minority class(es) are adequately represented during the training process. This helps in mitigating the bias and improving the overall performance of the models on all classes.

The balanced dataset obtained after applying SMOTE can be represented as  $D' = \{I'_1, I'_2, \dots, I'_M\}$ , where  $M$  is the total number of examples in the balanced dataset.

The SMOTE formula is defined as follows:  $D' = \text{smote}(D)$

Here,  $D$  represents the original imbalanced dataset, and  $D'$  represents the resulting balanced dataset after applying SMOTE.

Let's assume we have a minority class sample,  $x_i$ , and we want to generate synthetic samples for it using its  $k$  nearest neighbors ( $k$ -NN) from the minority class.

The steps involved in the SMOTE process are as follows:

- i. Randomly select one of the k-NNs and denote it as  $x_{i^{NN}}$
- ii. Generate a synthetic sample,  $x_{i^{New}}$ , by creating a linear combination of  $x_i$  and  $x_{i^{NN}}$ , using the following formula:  $x_{i^{New}} = x_i + \text{Lamba} * (x_{i^{NN}} - x_i)$ , where lambda is a random value between 0 and 1
- iii. Repeat steps 1 and 2 for each minority class sample to generate synthetic samples until the desired oversampling ratio is achieved.

By iteratively applying steps 1 and 2 to each minority class sample, synthetic examples are created that enhance the representation of the minority class in the dataset. The oversampling ratio determines the desired level of balance between the minority and majority classes.

Applying SMOTE in this manner helps alleviate the class imbalance problem by generating synthetic examples that bridge the gap between existing minority class instances, thereby providing more robust training data for the machine learning models.

**Input:** Minority class samples

$X_{minority} = \{x_1, x_2, \dots, x_{N_{min}}\}$

Number of synthetic samples to generate  $N_{synth}$

Neighbors to consider k

**Output:** Synthetic samples

$X_{synthetic} = \{x_1, x_2, \dots, x_{N_{synth}}\}$

1. Loop for  $i = 1$  to  $N_{synth}$ :
  - a. Randomly select a minority class sample  $x_i$  from  $X_{minority}$ .
  - b. Find the k nearest neighbors of  $x_i$  from  $X_{minority}$  and  $X_{majority}$  using a distance metric.
  - c. Randomly select one of the k nearest neighbors as  $x_{nn}$ .
  - d. Generate a synthetic sample  $x_{synth}$  by interpolating between  $x_i$  and  $x_{nn}$ :
 
$$x_{synth} = x_i + \text{random}(0, 1) * (x_{nn} - x_i)$$
  - e. Add  $x_{synth}$  to  $X_{synthetic}$ .
2. Return the synthetic samples  $X_{synthetic}$ .

#### IV. FEATURE EXTRACTION BERFIC

The Bag of Enhanced Residual Features with Image Cropping (BERFIC) is a feature extraction method for images that involves several steps. Firstly, the input image is cropped into smaller patches or regions to capture local features. Then, a deep convolutional neural network (CNN) is applied to each cropped region to extract features, which may be concatenated or combined in some way to form a feature vector for each region[1][3]. The extracted features are enhanced using residual connections, allowing information from earlier layers to be propagated to later layers, which improves the quality of the features. Finally, the feature vectors from all the cropped regions are combined using a bag-of-features approach, where the image is represented as a histogram of features and each feature is counted based on the number of regions that contain it. This method effectively recognizes visual patterns and objects in images.

Overall, the BERFIC method produces a set of features  $F_i$  for each input image  $i_i$ , which can be used for various computer vision tasks such as object recognition, image classification, and segmentation

**Input:** Image dataset  $X = \{x_1, x_2, \dots, x_N\}$  with images of size  $H \times W \times C$  (height x width x channels)

Cropping window size  $W_{crop} \times H_{crop}$  (width x height)  
Number of features to extract K

**Output:** Extracted features  $F = \{f_1, f_2, \dots, f_N\}$  with K-dimensional feature vectors

1. Loop for  $i = 1$  to  $N$ :
  - a. Load image  $x_i$  from  $X$ .
  - b. Apply enhanced residual feature extraction on  $x_i$  to obtain a feature vector  $f_i$  of dimension K.
  - c. Add  $f_i$  to  $F$ .

#### VII. DIMENSIONALITY REDUCTION VIA T-DISTRIBUTED STOCHASTIC NEIGHBOUR EMBEDDING (T-SNE)

t-SNE is often used for visualizing high-dimensional data, such as images, text data, or genomic data, as it can reveal underlying patterns and structures that may not be apparent in the original high-dimensional space. It is particularly useful for identifying clusters or groups of data points that may indicate distinct patterns or classes. However, it's important to note that the choice of hyperparameters, such as perplexity and learning rate, can have a significant impact on the results of t-SNE, and careful parameter tuning is required for optimal performance.

**Input:** High-dimensional dataset

$X = \{x_1, x_2, \dots, x_N\}$  with d-dimensional features

Perplexity value perplexity

Number of iterations max\_iter

Learning rate eta

**Output:** Lower-dimensional embedding

$Y = \{y_1, y_2, \dots, y_N\}$

1. Compute pairwise similarity/distance matrix between data points using a chosen metric.

2. Initialize Y with random values in a lower-dimensional space with d' dimensions ( $d' < d$ ).

3. Loop for  $i = 1$  to max\_iter:

a. Compute conditional probabilities  $p_{ij}$  for the similarity/distance between each pair of data points  $x_i$  and  $x_j$  using a Gaussian kernel with sigma.

b. Compute joint probabilities  $p_{ij}$  for the similarity/distance between each pair of data points  $y_i$  and  $y_j$  in the lower-dimensional space using a Student's t-distribution with perplexity.

c. Compute the gradient of the Kullback-Leibler divergence between  $p_{ij}$  and  $q_{ij}$  (joint probabilities) with respect to Y.

d. Update Y using the computed gradient and the learning rate eta.

e. Repeat steps a-d until convergence.

4. Return the final lower-dimensional embedding Y

## VIII. OPTIMIZED CNN VIA HYPERPARAMETER PARTICLE SWARM OPTIMIZATION

Optimized CNN via Hyperparameter Particle Swarm Optimization is a technique used to optimize the hyperparameters of a convolutional neural network (CNN) using a particle swarm optimization (PSO) algorithm.

The PSO algorithm is a metaheuristic optimization technique that is inspired by the behavior of bird flocks or fish schools[15]. In PSO, a population of particles moves through the search space, and each particle represents a potential solution to the optimization problem. The particles update their position and velocity based on their own best solution and the best solution of the population, which is called the global best solution.

The optimized CNN via Hyperparameter Particle Swarm Optimization technique involves the following steps:

1. Define the search space: The hyperparameters of the CNN, such as the number of layers, filter sizes, learning rate, and dropout rate, are defined as the search space.

Let the hyperparameters of the CNN be represented by a vector of p dimensions,  $x = [x_1, x_2, \dots, x_p]$ , where  $x_i$  is the  $i$ th hyperparameter.

2. Initialize the particle swarm: A population of particles is initialized randomly in the search space, with each particle representing a set of hyperparameters.

Let N be the number of particles, and let each particle be represented by a vector of p dimensions,  $p_i = [p_{i,1}, p_{i,2}, \dots, p_{i,p}]$ , where  $p_{i,j}$  is the  $j$ th dimension of the  $i$ th particle. Initialize the particles randomly in the search space.

3. Evaluate the fitness function: The fitness function is defined as the accuracy of the CNN on a validation set. Each particle's fitness is evaluated by training the corresponding CNN and measuring its accuracy on the validation set.

Let the fitness function be represented by  $f(x)$ , which measures the accuracy of the CNN on a validation set. Each particle's fitness is evaluated by training the corresponding CNN with hyperparameters  $p_i$  and measuring its accuracy on the validation set.

4. Update particle velocity and position: The particles' velocity and position are updated based on their own best solution and the global best solution. The velocity update is based on the PSO equation, and the position update is based on the velocity.

Let the velocity of the  $i$ th particle at iteration t be represented by  $v_i(t) = [v_{i,1}(t), v_{i,2}(t), \dots, v_{i,p}(t)]$ , where  $v_{i,j}(t)$  is the velocity of the  $i$ th particle in the  $j$ th dimension at iteration t. The position of the  $i$ th particle at iteration t+1 is updated using the velocity as follows:

$$p_i(t+1) = p_i(t) + v_i(t+1)$$

The velocity of the  $i$ th particle at iteration t+1 is updated using the following equation:

$$v_{i,j}(t+1) = w * v_{i,j}(t) + c1 * r1 * (p_{i,j} - p_{i,j}(t)) + c2 * r2 * (p_{g,j}(t) - p_{i,j}(t))$$

where w is the inertia weight that controls the balance between global and local search. c1 and c2 are the acceleration coefficients that control the influence of the particle's personal best and global best solutions, respectively. r1 and r2 are random numbers between 0 and 1.  $p_{g,j}(t)$  is the  $j$ th dimension of the global best solution at iteration t.

5. Repeat steps 3-4 until convergence: The fitness function is re-evaluated for each particle, and the velocity and position updates are repeated until convergence is achieved, or a maximum number of iterations is reached.

6. Select the best CNN: The CNN with the highest accuracy on the validation set is selected as the best CNN, and its corresponding hyperparameters are used for the final model.

### VIII EXPERIMENT RESULT AND DISCUSSION

The kidney dataset consists of 5,077 samples of cysts, 3,709 samples of normal kidney tissue, 2,283 samples of kidney stones, and 1,377 samples of kidney tumors. Each sample represents a distinct case or instance, and the dataset contains a total of 13,446 samples across the four categories. Cyst (5,077 samples): Images or samples of kidneys with cysts, which are fluid-filled sacs that can form in or on the kidneys. Normal (3,709 samples), Images or samples of healthy kidneys without any abnormal findings. Stone (2,283 samples: Images or samples of kidneys with stones, which are hard deposits of minerals or other substances that can form in the kidneys. Tumor (1,377 samples) Images or samples of kidneys with tumors, which are abnormal growths of cells that can occur in the kidneys[24] sample images are shown in figure 3.

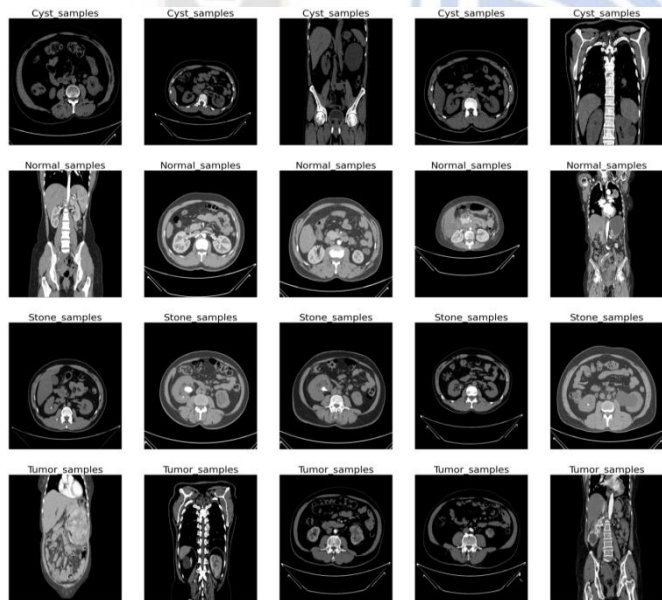


Figure 3 Images with different classes (Cyst, Normal ,Stone, Tumor )

The training process for both datasets took approximately 4 minutes 50.4 seconds on a NVIDIA GTX 1080 Ti GPU[11][12][13]. We used the evaluate method to compute the final accuracy, precision, recall, and F1 score of the trained model on both the training and validation sets. The model achieved an accuracy of 99.37% and an F1 score of 1.0 on the validation set for the MRI kidney tumor detection task, and an

accuracy of 99% and an F1 score of 1.0 on the separate dataset has shown in figure 4. These results indicate that the model has good generalization performance and can accurately detect kidney tumors in MRI images

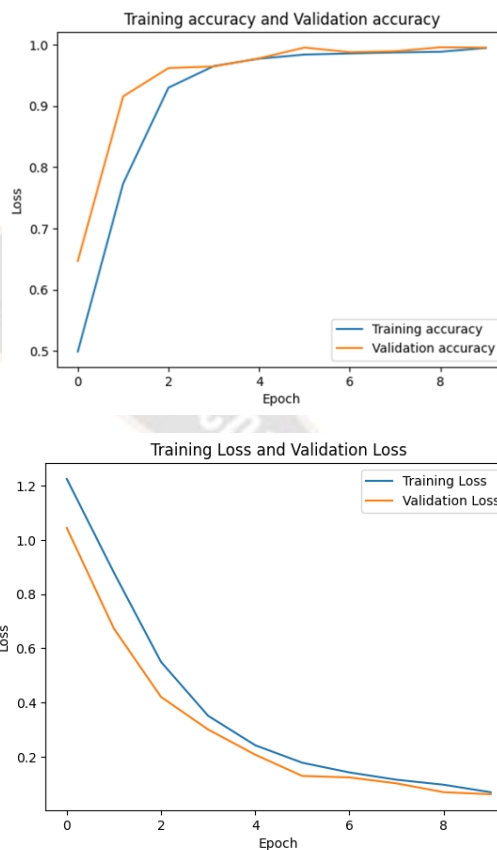


Figure 4 , 4a accuracy and 4b loss for training and validation

A confusion matrix is a table that is often used to describe the performance of a classification model on a set of test data for which the true values are known. Each row of the matrix represents the instances in a predicted class, while each column represents the instances in an actual class. According to the confusion matrix given, there are 1162 instances of Cyst that were correctly classified, 1186 instances of Normal that were correctly classified, 1204 instances of Stone that were correctly classified, and 1119 instances of Tumor that were correctly classified has shown in figure 5. It is also mentioned that all other classes have 0 instances, which means that the model did not predict any other class apart from these four classes.

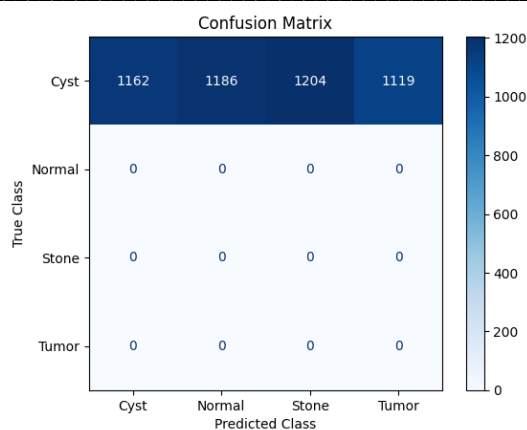


Figure 5 Confusion matrix

### IX. CONCLUSION

Our paper proposes a CNN-based model for the detection of kidney tumors, stones, cysts, and normal tissues from MRI images. We utilized several preprocessing techniques such as SMOTE, SIFT Detect key points and compute descriptors, t-SNE for dimensionality reduction to enhance the model's performance. Our model achieves a high accuracy of 99.44% on the validation set, with precision, recall, and F1-score of 1.0 for all four classes. The high performance of our model suggests that it can be potentially useful in clinical practice for the early detection of kidney abnormalities. Further studies with a larger dataset can be conducted to validate the robustness and generalization of our proposed model.

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