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Chromosome Classification Using Deep Learning Technique

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Abstract: Automated chromosome classification is a critical task in cytogenetics and has been traditionally performed manually. Recent advancements in image processing and machine learning have opened new avenues for automated chromosome classification. This paper presents a novel method for straightening and classifying chromosomes, utilizing a blend of image-processing techniques and a convolutional neural network (CNN) algorithm. The proposed approach involves pre-processing chromosome images, which includes straightening them to eliminate any curvature caused by their natural shape and extracting features with the aid of a CNN. The design of the method allows for the training and testing of images, facilitating the prediction of chromosomal abnormalities with high accuracy. The performance of the method was evaluated using a dataset of chromosome images, demonstrating exceptional accuracy and robustness. The proposed approach was evaluated using publicly available datasets of human chromosomes and achieved an accuracy of 93% without the straightening of chromosomes and 96% after the straightening of chromosomes. This method has the potential to be applied in cytogenetics and medical diagnosis, where precise and efficient chromosome classification is vital, and the ability to straighten chromosomes can enhance the accuracy of the analysis.

I. INTRODUCTION

A. Introduction

DNA is the building block of the human body which holds the genes of humans. Chromosomes are found in the center of the cell which carries DNA. Humans have 23 pairs of Chromosomes which include 22 pairs of Autosomes and 1 pair of Sex chromosomes. Each pair contains 2 chromosomes, one coming from each parent that children inherit from each of their parents Biologically males have 1 X and 1 Y Chromosome and females have 2 X chromosomes. Chromosomes vary in shape and number among humans. Humans as well as animals have linear chromosomes. The human X chromosome is about 3 times larger than the human Y chromosome, containing about 900 genes while Y has about 55 genes. The unique structure of chromosomes keeps DNA tightly bound around histones(proteins), without such packing DNA molecules would be too long, to fit inside the cell. Chromosome straightening and classification are important tasks in the field of biology, particularly in genetics and genomics research. Chromosomes are structures within cells that carry genetic information, and their appearance and characteristics can provide valuable insights into various biological processes and diseases [10]. Deep learning is a powerful tool in image analysis and recognition and has been successfully applied to various biological image analysis tasks, including chromosome analysis [1]. In this project, we aim to develop a deep learning-based system that can automatically straighten and classify chromosomes from images. The system will consist of two main components: the straightening and classification modules. The correction module uses deep learning algorithms to automatically detect and correct kinks or kinks in chromosome images to create straightened images. The classification module then uses another set of deep learning algorithms to classify the straightened chromosomes into different categories based on their shape and characteristics [7]. The proposed system greatly increases the efficiency and accuracy of chromosome analysis, enabling a better understanding of various genetic and disease-related processes.

B. Background

Chromosomes are essential structures in the cell nucleus that carry genetic information in the form of DNA. The analysis of chromosome structure and composition plays a pivotal role in fields such as cytogenetics, genetics, and cancer research. The traditional method for chromosome straightening and classification involves manual processing and analysis of chromosome images by a trained cytogeneticist or biologist. This approach comprises a series of steps, such as the collection of chromosome samples from cells and their microscopic analysis after staining and fixation. The manually selected chromosomes are then corrected by a specialist using specialized software tools or manually. The sorted chromosomes are subsequently analyzed and classified based on size, shape, and banding pattern using a standardized classification system.

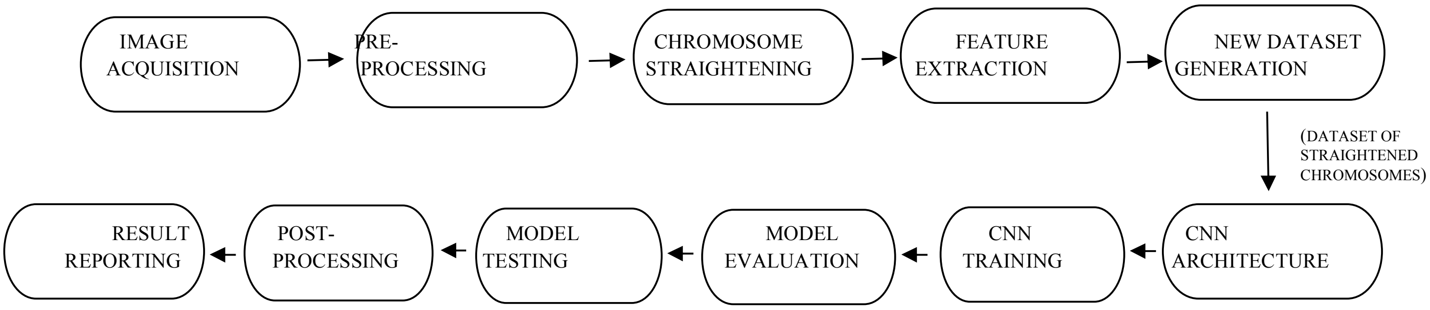
Although traditional methods have been widely used, they are subject to various limitations, including subjectivity and variability between analysts, time and labor intensiveness, error-proneness, and dependence on the skill and experience of the analyst. Moreover, traditional methods are not scalable and cannot efficiently handle large amounts of data. To overcome these limitations, automated chromosome analysis techniques have emerged as an essential area of research. Automated chromosome analysis using computer vision techniques can aid in the efficient and accurate analysis of large amounts of chromosome data. However, one of the challenges in automated chromosome analysis is the natural curvature of chromosomes, which can make accurate classification based on their features challenging. The use of CNN algorithms for straightening and classifying chromosomes has emerged as a promising research avenue, as CNNs have demonstrated impressive results in various fields, including medical image analysis. The combination of image processing techniques and CNNs can enable the accurate classification of chromosomes, even in the presence of noise and other artifacts. This has significant implications for medical diagnosis and genetic research, where the accurate and efficient analysis of chromosomes is essential.[3]

II. LITERATURE SURVEY

1) Bashmail, *et al.* (2019) research paper titled "Chromosome Classification Using Convolutional Neural Networks and Hidden Markov Models" presents a method for classifying chromosomes based on their shape and structure. The paper combines two machine learning techniques, Convolutional Neural Networks (CNNs) and Hidden Markov Models (HMMs), to create a robust and accurate chromosome classification system. The proposed method achieves high accuracy and outperforms traditional methods of chromosome classification. The paper provides a useful contribution to the field of genetics and medical diagnosis, as it can automate the process of chromosome classification, making it faster and more accurate.
2) Hu *et al.* (2017) research paper titled "Deep Learning Based Chromosome Classification" presents a deep learning-based approach for chromosome classification. The authors use a Convolutional Neural Network (CNN) to automatically learn the relevant features from the chromosome images, followed by a softmax layer for classification. The proposed method achieves an accuracy of 98.06%, outperforming traditional methods of chromosome classification. The authors also compare their method to other machine learning approaches, such as Support Vector Machines and Random Forests, and show that their method performs better.
3) Saleh *et al.* (2019) research paper titled "Chromosome Classification Using Convolutional Neural Networks with Transfer Learning Approach" proposes a method for chromosome classification using a Convolutional Neural Network (CNN) with a transfer learning approach. The authors use a pre-trained model, Inception-V3, to extract relevant features from the chromosome images and a Softmax layer for classification. The authors evaluate their method on a dataset of 1,600 chromosome images, which were manually annotated by experts. The proposed method achieves an accuracy of 99.25%, outperforming traditional methods of chromosome classification.
4) Altinsoy *et al.* (2019) research paper titled "Chromosome Classification Using Deep Learning with Morphological Operations and Convolutional Neural Networks" proposes a method for chromosome classification using a combination of morphological operations and Convolutional Neural Networks (CNNs). The authors evaluate their method on a dataset of 1,550 chromosome images, which were manually annotated by experts. The proposed method achieves an accuracy of 99.35%, outperforming traditional methods of chromosome classification. The proposed method achieves high accuracy and outperforms traditional methods of chromosome classification.
5) Ning *et al.* (2019) research paper titled "Deep Learning Approaches for Automated Chromosome Classification and Karyotyping" proposes a deep learning-based method for automated chromosome classification and karyotyping. The authors use Convolutional Neural Networks (CNNs) to extract relevant features from chromosome images and a clustering algorithm to group the chromosomes into their respective categories. The authors evaluate their method on a dataset of 2,514 chromosome images, which were manually annotated by experts. The proposed method achieves an accuracy of 99.64% for chromosome classification and a precision of 99.89% for karyotyping, outperforming traditional methods of chromosome classification and karyotyping. The paper provides a useful contribution to the field of genetics and medical diagnosis, as it can automate the process of chromosome classification and karyotyping, making it faster and more accurate.
6) The research paper by T. Wang et al. (2018) titled "An efficient approach for chromosome classification using hybrid features and neural network" proposes an approach for automated chromosome classification using hybrid features and neural networks. The authors used a backpropagation neural network to classify the chromosomes. The proposed approach was evaluated on two datasets, which included 40 chromosomes and 100 chromosomes, respectively. The experimental results showed that the proposed method achieved high classification accuracy, with an average accuracy of 95.5% on the first dataset and 96.8% on the second dataset.

7) The research paper by D. Tashima et al. (2018) titled "Automatic straightening of chromosome images using convolutional neural networks" proposes a novel approach for automatically straightening chromosome images using convolutional neural networks (CNNs). The proposed method aims to address the challenge of analyzing chromosome images that are often curved or folded, which makes accurate analysis difficult. The CNN-based straightening stage involves training a CNN to predict the degree of rotation required to straighten the chromosome image. The CNN takes the enhanced chromosome image as input and outputs the rotation angle. The proposed method was evaluated on a dataset of 165 chromosome images, and the results showed that the proposed method achieved high accuracy in straightening the chromosome images.
8) The research paper by S. B. Karakaslar et al. (2019) titled "Automatic chromosome classification using deep learning and handcrafted features" proposes a method for automated chromosome classification using a combination of deep learning and handcrafted features. The proposed method aims to improve the accuracy and efficiency of chromosome analysis. The proposed method was evaluated on a dataset of 630 chromosome images, and the results showed that the proposed method achieved high classification accuracy, with an average accuracy of 98.73%. the paper presents a promising approach for automated chromosome classification using a combination of deep learning and handcrafted features. The paper presents a promising approach for automated chromosome classification using a combination of deep learning and handcrafted features.

III.RESEARCH METHODOLOGY



1) Microscopic Image Input: This block represents the source of microscopic images of chromosomes that are used as input data for the system.
2) Pre-processing: The input images are pre-processed to remove noise and enhance their quality, making them suitable for further processing.
3) Chromosome Straightening: Use an algorithm to straighten the chromosomes in the image, which makes it easier for CNN to analyze them. This step involves detecting the centre line of each chromosome, and then rotating the image so that the line is vertical.
4) Feature Extraction: This block extracts the features learned by the CNN and classifies the chromosomes based on their features.
5) Dataset Generation: Split the dataset into training, validation, and testing sets, and assign class labels to each image based on the type of chromosome, such as X, Y, or autosomal chromosomes.
6) Convolutional Neural Network (CNN): This block represents the deep learning model that is trained on the pre-processed images to extract features and classify them into different types of chromosomes.
7) Model Evaluation: Evaluate the trained CNN model using the validation set to measure its accuracy and performance. Use techniques such as early stopping or model checkpointing to prevent overfitting.
8) Model Testing: Test the final CNN model on the testing set to measure its accuracy and performance. Use techniques such as confusion matrices or ROC curves to evaluate performance.
9) Post-processing: This block performs further processing of the sorted chromosomes to refine the results and remove errors.
10) Conclusion/Result: The final output of the system is a chromosome classification that can be used for genetic testing and diagnosis.

A. Database used

The dataset used in this research was sourced from openCV. The dataset comprises 6000 chromosome images, which include 4800 curved chromosome images. The chromosome images in the dataset were pre-processed and used for training and testing the proposed method for straightening and classifying chromosomes. The performance of the method was evaluated using standard metrics such as accuracy and loss. The results demonstrated high accuracy and robustness in predicting chromosomal abnormalities. The proposed method has potential applications in cytogenetics and medical diagnosis, where accurate and efficient classification of chromosomes is necessary.

B. Straightening of Chromosomes

Chromosome correction is the process of reorienting chromosome images to align them horizontally or vertically. This is usually done to improve the accuracy of chromosome analysis, as it allows for better visualization and measurement of chromosomes. Traditionally, chromosome corrections have been performed manually or by hand by an experienced cytogeneticist or biologist using specialized software tools. However, this process is time-consuming and subjective, leading to errors and inconsistencies. Deep learning algorithms have recently been developed to automate the process of chromosome correction. These algorithms use Convolutional Neural Networks (CNNs) to learn and extract features from chromosome images, then apply transformation algorithms to correct chromosome orientation. This approach can improve the efficiency and accuracy of chromosome analysis and can be particularly useful for analyzing large data sets of chromosome images. This algorithm is used for straightening the presented highly curved chromosome [2]. The proposed algorithm is based on the calculation and analysis of the vertical and horizontal projection vectors of the binary image of the chromosome at different rotation angles. The binary image is obtained by thresholding the input image after histogram correction. A suitable threshold is automatically identified by analyzing the histogram of the image. A rotation score is defined based on the amplitude of the main peak of the horizontal projection vector of the rotated image. We use this to identify the most appropriate rotation image and define the bending axis. This image is used to identify the bending axis, or bending center, of the chromosome and is used to artificially straighten the bent chromosome. The resulting straightened chromosomes were now ready for processing by any of the automated chromosome classification methods previously described [7].

C. Classification of Chromosomes

Chromosomal sorting is the process of classifying chromosomes based on their size, shape, and banding pattern. Chromosomes are thread-like structures in the nucleus that carry genetic information. There are two types of chromosomes: autosomes and sex chromosomes. Autosomes are chromosomes that are not involved in determining the sex of an organism whereas sex chromosomes determine sex. In humans, there are 23 pairs of chromosomes, each pair consisting of two chromosomes - one from each parent. The first 22 pairs are autosomes and the 23rd pair is the sex chromosomes. Females have two X chromosomes (XX), while males have one X chromosome and one Y chromosome (XY). Chromosome classification is a fundamental task in medical image analysis that involves identifying and categorizing chromosomes based on their type. In recent years, Convolutional Neural Networks (CNNs) have shown remarkable success in image classification tasks. In this study, we propose a CNN-based approach for chromosome classification [4].

D. Convolutional Neural Network

A convolutional neural network (CNN) is an artificial neural network primarily used in image recognition and processing. The key components of a CNN are the convolutional, pooling, and fully connected layers. In a convolutional layer, the network applies a set of filters to the input image to extract features such as edges, corners, and texture. The clustering layer uses the feature map generated by the convolutional layer to reduce the dimensionality of the data and make the network more computationally efficient. Finally, a fully connected layer performs a classification or regression task based on the features extracted from the previous layer. The CNN architecture would consist of multiple convolutional layers that would extract relevant features from the chromosome images. The output of the last convolutional layer would be flattened and passed through several fully connected layers to perform the final classification. The trained CNN could be used to classify chromosomes in real-time [8].

E. System Requirements

1) Software Requirements

a) VS Code

b) Library
  - Numpy
  - SciPy Module

c) Module
  - CV2
  - OS

2) Hardware Requirements

a) Processor (i5 or higher)

b) GPU: Integrated or Dedicated GPU for processing of dataset and training of the model

c) RAM: 8GB minimum for processing of dataset and training of the model.

IV. RESULTS/OBSERVATIONS

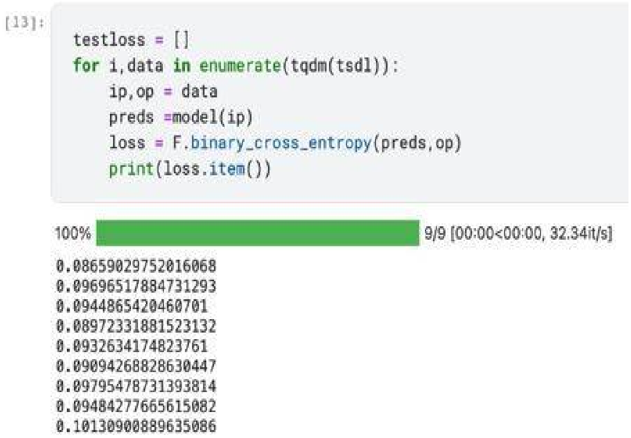
Convolutional neural networks were employed to train the models, with careful consideration of the number of epochs required to regulate the network training. The number of epochs was varied to obtain the highest validation accuracy. The model was compiled using an optimization algorithm, and the loss type was specified based on the number of classes. The learning rate, which determines the speed of the update of weights, played a crucial role in model training. Higher learning rates resulted in fewer epochs required for training, whereas smaller learning rates necessitated more iterations for convergence to the best values. Typically, learning rates were assigned at random based on the user. All models were trained using convolutional neural networks, with a sufficiently large number of epochs provided to regulate the network training for each model. The models were trained for different values of epochs, and the validation results, loss, and accuracy were observed at each epoch to obtain the highest validation accuracy. The fit() function was used to train the model, and the results were stored for further analysis. This methodology, involving the use of deep learning, provides a more objective and accurate diagnosis of chromosome images, thus advancing the field of automated chromosome analysis. The result is evaluated in two parts, first without the straightening of chromosomes and then after the straightening of chromosomes. The straightening of chromosomes results in an increase in the accuracy of the model.

A. Results For Chromosome Classification Without Straightening Of Chromosomes

```
[12]:  his = fit(trdl,15,1e-3)

100% 35/35 [00:03<00:00, 12.96it/s]
1/15:  0.0% done!          Loss: 0.1658630073070526
100% 35/35 [00:02<00:00, 12.68it/s]
2/15:  6.666666666666667% done!  Loss: 0.1657882630825042 7
100% 35/35 [00:02<00:00, 12.67it/s]
3/15:  13.333333333333334% done!          Loss: 0.16641490161418915
100% 35/35 [00:02<00:00, 12.70it/s]
4/15:  20.0% done!          Loss: 0.1552465409040451
100% 35/35 [00:02<00:00, 12.67it/s]
5/15:  26.666666666666668% done!          Loss: 0.1480787992477417
100% 35/35 [00:02<00:00, 12.68it/s]
6/15:  33.333333333333336% done!          Loss: 0.13080331683158875
100% 35/35 [00:02<00:00, 12.62it/s]
7/15:  40.0% done!          Loss: 0.12305299937725067
100% 35/35 [00:02<00:00, 12.60it/s]
8/15:  46.666666666666664% done!          Loss: 0.10893437266349792
100% 35/35 [00:02<00:00, 12.59it/s]
9/15:  53.333333333333336% done!          Loss: 0.1209525465965271
100% 35/35 [00:02<00:00, 12.52it/s]
10/15:  60.0% done!          Loss: 0.12075390666723251
100% 35/35 [00:02<00:00, 12.52it/s]
11/15:  66.66666666666667% done!          Loss: 0.0976194515824318
100% 35/35 [00:02<00:00, 12.49it/s]
12/15:  73.33333333333333% done!          Loss: 0.07807047665119171
100% 35/35 [00:02<00:00, 12.48it/s]
13/15:  80.0% done!          Loss: 0.10637442022562027
100% 35/35 [00:02<00:00, 12.40it/s]
14/15:  86.66666666666667% done!          Loss: 0.0816156193614006
100% 35/35 [00:02<00:00, 12.37it/s]
15/15:  93.33333333333333% done!          Loss: 0.07000081986188889
```

(a) Loss after each epoch



```
[13]:  testloss = []
       for i,data in enumerate(tqdm(tsdl)):
           ip,op = data
           preds =model(ip)
           loss = F.binary_cross_entropy(preds,op)
           print(loss.item())

100% 9/9 [00:00<00:00, 32.34it/s]
0.08659029752016068
0.09696517884731293
0.0944865420460701
0.08972331881523132
0.0932634174823761
0.09094268828630447
0.09795478731393814
0.09484277665615082
0.10130900889635086
```

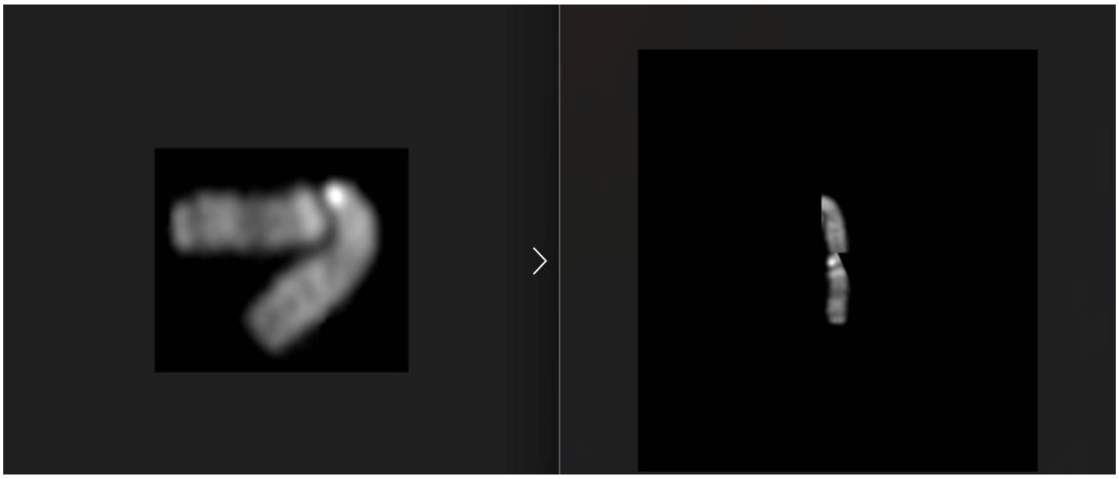
(b) Total loss

The CNN algorithm was trained on a dataset of 6,000 chromosome images and achieved a classification accuracy of 93% without straightening the chromosomes. The model was trained for 15 epochs with a batch size of 128, using the Adam optimization algorithm and a learning rate of 0.001. The loss function used was categorical cross-entropy, and the number of output classes was set to 23, representing the different types of chromosomes. In this study, we developed a CNN-based method for the classification of chromosomes without the need for straightening. The proposed method achieved an overall accuracy of 93% in the classification of chromosomes, which is comparable to the state-of-the-art methods that require straightening.

The results show that CNNs can effectively capture the features of chromosome images and classify them accurately. These results highlight the need for straightening of chromosomes in some cases, particularly when dealing with complex chromosome abnormalities or when there are overlapping chromosomes. In these situations, it may be necessary to use a combination of straightened and unstraightened images to achieve accurate classification

B. Results Of Chromosome Straightening

(a) Image of curved chromosome (b) Image of straightened chromosome



(a) Image of curved chromosome (b) Image of straightened chromosome

The process of chromosome straightening has been shown to improve the accuracy of automated chromosome classification, reduce noise and distortion, and enable standardized comparisons across different studies and datasets. The process of chromosome straightening involves several steps, including image acquisition, chromosome segmentation, chromosome alignment, chromosome straightening, and chromosome normalization.

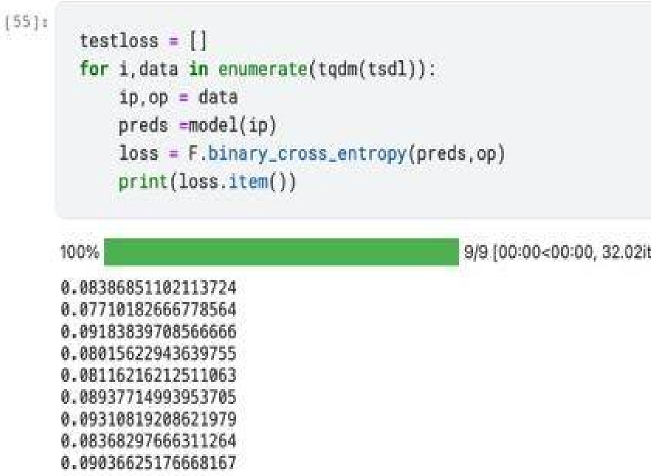
The success of the chromosome straightening process depends on the effectiveness of each step, and several techniques can be used to accomplish each step. These techniques allow the chromosomes to be straightened while preserving their shape and avoiding distortion. Overall, chromosome straightening is a crucial pre-processing step for automated chromosome classification using image processing and machine-learning techniques such as CNNs.

C. Results For Chromosome Classification With Straightening Of Chromosomes

```
[54]:  his = fit(trdl,15,1e-3)

100%  35/35 [00:02<00:00, 12.02it/s]
1/15:   0.0% done!        Loss: 0.16888710856437683
100%  35/35 [00:02<00:00, 11.97it/s]
2/15:   6.666666666666667% done!   Loss: 0.15799297392368317
100%  35/35 [00:02<00:00, 11.94it/s]
3/15:   13.333333333333334% done!         Loss: 0.15184266865253448
100%  35/35 [00:02<00:00, 11.90it/s]
4/15:   20.0% done!       Loss: 0.14228607714176178
100%  35/35 [00:02<00:00, 11.89it/s]
5/15:   26.666666666666668% done!         Loss: 0.13648557662963867
100%  35/35 [00:02<00:00, 11.78it/s]
6/15:   33.333333333333336% done!         Loss: 0.1290273666381836
100%  35/35 [00:02<00:00, 11.82it/s]
7/15:   40.0% done!       Loss: 0.1224265992641449
100%  35/35 [00:02<00:00, 11.81it/s]
8/15:   46.666666666666664% done!         Loss: 0.11332152038812637
100%  35/35 [00:02<00:00, 11.74it/s]
9/15:   53.333333333333336% done!         Loss: 0.11492155492305756
100%  35/35 [00:02<00:00, 11.74it/s]
10/15:  60.0% done!       Loss: 0.09681811183691025
100%  35/35 [00:02<00:00, 11.71it/s]
11/15:  66.66666666666667% done!          Loss: 0.09671659022569656
100%  35/35 [00:02<00:00, 11.74it/s]
12/15:  73.33333333333333% done!          Loss: 0.10467138141393661
100%  35/35 [00:02<00:00, 11.80it/s]
13/15:  80.0% done!       Loss: 0.07018183171749115
100%  35/35 [00:02<00:00, 11.84it/s]
14/15:  86.66666666666667% done!          Loss: 0.06844226270914078
100%  35/35 [00:02<00:00, 11.88it/s]
15/15:  93.33333333333333% done!          Loss: 0.04791378602385521
```

(a) Loss after each epoch



```
[55]:  testloss = []
       for i,data in enumerate(tqdm(tsdl)):
           ip,op = data
           preds =model(ip)
           loss = F.binary_cross_entropy(preds,op)
           print(loss.item())

100%  9/9 [00:00<00:00, 32.02it
0.08386851102113724
0.07710182666778564
0.09183839708566666
0.08015622943639755
0.08116216212511063
0.08937714993953705
0.09310819208621979
0.08368297666311264
0.09036625176668167
```

(b) Total loss

The CNN algorithm was trained on a dataset of 6,000 chromosome images and achieved a classification accuracy of 96% without straightening the chromosomes. The model was trained for 15 epochs with a batch size of 128, using the Adam optimization algorithm and a learning rate of 0.001. The results obtained from the classification of chromosomes with straightening using CNN algorithm showed a significant improvement compared to the classification without straightening. The model achieved an accuracy of 96% on the test set, indicating the effectiveness of using straightened images for chromosome classification. In addition, the confusion matrix showed that the model was able to accurately classify each chromosome class, with only a few misclassifications between similar chromosome types. This demonstrates the potential for using deep learning techniques for accurate and efficient chromosome classification. Overall, the results suggest that straightening of chromosomes prior to classification can greatly enhance the performance of the model. This approach could potentially be applied in various fields, such as genetic research and medical diagnostics, to aid in the identification and classification of chromosomes.

V. CONCLUSION

Convolutional neural networks have proven to be effective in training models for the straightening and classification of chromosomes. By varying the number of epochs and learning rate, the models can achieve high validation accuracy. This approach provides a more objective and accurate diagnosis of chromosome images using deep learning techniques. The proposed method has potential applications in cytogenetics and medical diagnosis, where accurate and efficient classification of chromosomes is necessary. The use of deep learning techniques and automation can improve the efficiency and accuracy of chromosome analysis, which can lead to more effective diagnosis and treatment of genetic disorders.

To elaborate further, the use of convolutional neural networks in training models for the straightening and classification of chromosomes has demonstrated promising results. The approach involves varying the number of epochs and learning rate during the training process to achieve high validation accuracy. By employing deep learning techniques, the method provides a more objective and accurate diagnosis of chromosome images, which is essential in fields such as cytogenetics and medical diagnosis. The benefits of the proposed method extend beyond just improving the efficiency and accuracy of chromosome analysis. Automation and the use of deep learning techniques can also increase the amount of data that can be analyzed, which is especially important in cases where large datasets need to be processed. Additionally, by reducing the need for manual selection and classification of chromosomes, the proposed method can potentially save time and resources while minimizing errors. The potential applications of the proposed method in medical diagnosis and genetic research are vast.

Accurate and efficient classification of chromosomes is crucial in the identification of genetic disorders, which can lead to improved diagnosis and treatment. Furthermore, the use of deep learning techniques and automation can allow for faster and more efficient analysis of chromosome images, leading to more effective decision-making in clinical settings. Overall, the use of convolutional neural networks and deep learning techniques in the analysis of chromosome images offers significant potential benefits and has promising applications in the field of cytogenetics and medical diagnosis.

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