Convolutional Neural Network for Classifying the Stages of the Cell Cycle

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**Abstract**

The cell cycle is a highly coordinated process, and its improper regulation can lead to diseases such as cancer. The detailed observation of the cell cycle constitutes a fundamental starting point for diagnosing and preventing diseases. One way to observe the cell cycle is through computational techniques such as deep learning, which have consolidated as tools contributing to a more precise and practical observation. Nevertheless, existing tools still tend to make errors. In this context, the present study aims at methodological improvement by introducing a convolutional neural network model designed to achieve a more accurate classification of cell cycle states through images. A convolutional neural network model was trained using images of Jurkat cells corresponding to different cell cycle phases. Subsequently, it underwent a comprehensive comparison with models designed by other researchers who also addressed the classification of cell cycle stages using the same dataset. The results

revealed that the proposed model demonstrated a notable ability to classify the various phases of the cell cycle. With a weighted average of 93.72% using the F1 metric, it significantly outperformed models previously documented by other authors in similar research studies. The developed model demonstrated greater consistency with the inherent characteristics of the data used, resulting in a more accurate classification of cell cycle stages. This outcome underscores the distinct ability of a convolutional neural network to identify patterns in the cell cycle more precisely than human perception, which, at times, may be susceptible to errors.

**Keywords:** Jurkat cells, machine learning, data imbalanced, cycle analysis

# Introduction

The cell cycle is a highly coordinated process encompassing two general states: interphase and mitosis. Each of these states is divided into specific phases. In that order, the interphase is subdivided into G1, S, and G2. Mitosis, on the other hand, is split into Prophase, Metaphase, anaphase, and telophase [[1](#_bookmark13)].

In studying a cancer cell, cell cycle analysis is fundamental. When the cell cycle is not properly regulated, a cell can transform into a cancerous state, triggering anomalies in its functioning [[2](#_bookmark14)]. The observation and detailed analysis of each cell cycle phase is essential for preventing and diagnosing these anomalies.

The study of cancer cells is commonly conducted through cell lines, which are immortalized cells with continuous growth [[3](#_bookmark15)]. The Jurkat cell line, originating from acute lymphoblastic leukemia and obtained in 1977 from a child’s blood, has been particularly prominent in cell cycle research.

The alterations in cellular morphology during the various phases of the cell cycle tend to be ambiguous from a visual perspective. In this context, we briefly explain the events in each phase and the visible transformations in cellular morphology. During the initial phase of the cell cycle, known as G1, the cell undergoes protein and ribonucleic acid (RNA) synthesis. In this period, the cell maintains a constant morphology. The S phase constitutes the second stage of the cell cycle. At this point, the cell duplicates the DNA and shows morphological changes, exhibiting irregular shapes and undergoing an increase in size. During the third phase, known as G2, the cell initiates the duplication process of its organelles, leading to significant morphological changes compared to the two preceding phases of the cell cycle. In the prophase and metaphase stages, which belong to mitosis, no visible morphological differences are observed at a glance compared to the G2 phase. In the anaphase, notable differences become evident as the cell initiates the separation into two daughter cells. In the telophase, preceding cytokinesis, the cell is practically divided into two new cells, resulting in a visually evident morphological change [[4](#_bookmark16)].

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The observation of cell alterations is carried out mainly through microscopy techniques. Also, other methods used in cell cycle analysis include flow cytometry [[5](#_bookmark17)] for calculating DNA content in the cell [[6](#_bookmark18)]. Biomarkers, such as FUCCI technology [[7](#_bookmark19)], are also utilized. However, it is important to note that the above techniques do not provide extensive details about cell morphology in each cell cycle phase [[8](#_bookmark20)].

Data analysis plays a pivotal role in virtually all research areas. There is no exception in the study of the cell cycle, as the application of computer vision techniques or machine learning enables the classification of cell cycle phases through images. Deep learning networks are the most commonly employed cell cycle phase classification tool.

Abin et al. [[9](#_bookmark21)] utilized a recurrent neural network combined with convolutional gated recurrent unit layers in two works for cell cycle classification [[9](#_bookmark21)]. In both studies, a comparison was made with a ResNet model [[10](#_bookmark22)].

Narotamo et al. [[7](#_bookmark19)] utilized FUCCI technology as an indicator to determine the cell cycle phases. This study emphasized using the compound DAPI to identify the cellular nucleus. Subsequently, they employed a Support Vector Machine (SVM) to classify cell cycle phases. In another study [[11](#_bookmark23)], they proposed three approaches based on the Fast YOLO algorithm and the use of the DAPI for cell staining, primarily aimed at classifying phases corresponding to the interphase of the cell cycle. On the other hand, Rappez et al. [[12](#_bookmark24)] developed a deep neural network called DeepCycle to reconstruct the trajectory of the cell cycle. In this approach, similar to previous works, they utilized FUCCI technology.

The methodology proposed in this work is situated within a broader context and is closely related to various previous studies, especially concerning the employed dataset. To emphasize the current contributions in the field, the following works are presented chronologically.

Blasi et al. [[13](#_bookmark25)] were the creators and the first to use the dataset in a classification. They obtained images of individual cells using flow cytometry to predict DNA content and quantify cell cycle phases. The method developed proved to be effective for cell cycle analysis.

Eulenberg et al. [[14](#_bookmark26)] conducted the reconstruction of the cell cycle to elucidate its behavior in the progression of diabetic retinopathy. For this, they implemented a neural network called DeepFlow based on MXNet; they classified the different states of the cell cycle, achieving an accuracy of 79.40% considering the seven states of the cycle. However, in some phases, the algorithm’s classification proved deficient due to the limited number of available images [[14](#_bookmark26)]. Jin et al. [[8](#_bookmark20)] introduced the use of the WGAN-GP data augmentation technique to mitigate the issue of data imbalance, particularly in the phases of cell division. Subsequently, they implemented a ResNet-41 model. Considering the classification of the seven phases, they reported an accuracy of 82.10%.

Rana et al. presented two studies that classified the cell cycle [[15](#_bookmark27)][[16](#_bookmark28)]. Like Jin et al., they addressed the issue of data imbalance by combining two data augmentation techniques: WGAN and mixup. In their results, they

achieved an accuracy of 85%. Their second study combined three data augmentation techniques: WGAN, mixup, and nonlinear mixup, resulting in an accuracy of 85.6%.

The various methodologies employed in this dataset have yielded promising results for cell cycle classification. However, a significant gap persists, presenting an opportunity for further investigation to find a methodology that classifies the cell cycle more effectively. This study introduces a methodology that utilizes a convolutional neural network model capable of classifying cell cycle phases with higher accuracy than the algorithms mentioned earlier. The improvement is particularly focused on phases involving mitosis.

# Methodology

This section describes the methodology employed for creating the proposed Convolutional Neural Network model (CNN) in this study. Initially, details of the dataset used are provided. Subsequently, the architecture of the developed CNN model is comprehensively outlined. Finally, a concise explanation of the methods used for comparisons is provided, accompanied by a description of the metrics used to evaluate the performance of the developed model.

The development of the proposed model is detailed in Figure [1](#_bookmark0), a block diagram divided into two distinct sections. Procedures are highlighted using colors to illustrate each step, and each process is described in detail in the following paragraphs. The upper section, depicted in Figure [1](#_bookmark0)a, focuses on the overall development of the CNN model. The model is fed with images of Jurkat cells in various cell cycle phases obtained through imaging flow cytometry. The training phase involves the model learning to assign output labels to the received images, contributing to its recognition and classification capabilities. The lower section (Figure [1](#_bookmark0)b) showcases two different procedures used to analyze the behavior of the developed CNN. In Procedure [1](#_bookmark0)b.1, similar to the process in Figure [1](#_bookmark0)a, the model is fed with images of the Jurkat cell line. The key difference lies in using images corresponding to mitosis phases, which are employed to feed a data augmentation network, generating synthetic images. Regarding Procedure [1](#_bookmark0)b.2, the model is fed with images from another channel linked to imaging flow cytometry. Once again, images related to the mitosis phase are augmented using data augmentation techniques.

## Dataset

The dataset used to train and validate the performance of the CNN developed in this study was extracted from the research by Blasi et al. [[13](#_bookmark25)]. This dataset consists of four channels (brightfield, darkfield, and fluorescence channels), each with 32,266 images (G1=14333, S=8616, G2=8601, prophase=606, metaphase=68, anaphase=15,

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General procedure with the original data

(a)



**Data** **samples**

G1 S G2

pro meta ana

telo

training set: 80% samples

Train

CNN

model

test set: 20% samples

Predicted values

G1:0 **S:1** G2:0 pro:0 meta:0 ana:0 telo:0

Shuffle split

Test

General procedure with data augmentation

**Data** **samples**



(b)

(b.1)

(b.2)

**Data** **Samples**

G1 under sampling

S G2

pro meta ana telo

G1 S G2

pro meta ana telo

WGAN-GP

Data augmentation

pro WGAN-GP meta WGAN-GP ana WGAN-GP telo WGAN-GP

**Synthetic** **samples**

**created**

proWGAN-div + mixup + pro metaWGAN-div + mixup + meta anaWGAN-div + mixup + ana teloWGAN-div + mixup + telo

WGAN-div + mixup

Data augmentation

**Synthetic** **samples** **created**

training set: 80% samples

Shuffle split

test set:

20% samples

training set: 80% samples

Shuffle split

test set: 20% samples

Train

Test

CNN

model

Train

Test

Predicted values

G1:0 **S:1** G2:0 pro:0 meta:0 ana:0 telo:0

CNN

model

Predicted values

G1:0 **S:1** G2:0 pro:0 meta:0 ana:0 telo:0

**Fig. 1**: General methodology used in developing the model and its evaluation with other methods. (a) Methodology carried out for the developed model (b) General procedures with data augmentation (b.1) Procedure carried out with the WGAN-GP technique (b.2) Procedure carried out with the WGAN-div and mixup technique.

telophase=27, respectively). These images correspond to the Jurkat cell line cancer cells and were captured through imaging flow cytometry.

In our study, we employed the brightfield and darkfield channels analogous to the approaches used in the studies against which we compared our proposed model. The dataset has been categorized into seven classes (states) corresponding to the different phases of the cell cycle: G1, S, and G2, constituting the interphase, and Prophase, Metaphase, Anaphase, and Telophase, which are part of mitosis. Figure [2](#_bookmark1) presents an example of representative images for each class. The original dimensions of the images are 66*×*66 pixels, and they are displayed in a color format.

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Prophase

Metaphase

Anaphase

Telophase

Brightfield

G1

S

G2

Darkfield 

**Fig. 2**: Examples of the cell cycle images used in this study. The images are organized by phases and categorized according to the type of imaging flow cytometry used.

## Developed CNN model

A CNN model was constructed following the standard conventions of the field. A CNN is an artificial neural network that employs the convolution operation to extract significant features from an image. The developed CNN model was designed to consist of two convolutional layers, each followed by a max-pooling layer. The convolutional layers are configured with kernels of 64 and 32, which learn the features of the image. The kernel sizes are 10 and 5, respectively. The activation function used in each of these layers is the Rectified Linear Unit (ReLU). Subsequently, the flattening technique was implemented and connected to a dense layer composed of 32 neurons, followed by a dropout layer to mitigate the risk of overfitting. Then, another dense layer with 16 neurons was used; the ReLU activation function was applied in both layers. Finally, a dense layer with 7 neurons was incorporated, each representing one of the cell cycle states to be classified. Consequently, a softmax activation function was applied to the last layer, facilitating the classification of the different categories (see Figure [3](#_bookmark3)).



 **Conv2D** **MaxPooling** **2D** **Flatten** **Dense** **Dropout**

**Fig. 3**: Architecture of developed convolutional neural network.

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* + 1. **Training model**

The network was trained with the dataset mentioned above, which was split into two sets: training data (80% of the images) and test data (20% of the images). The categorical cross-entropy loss function was commonly employed in multiclass classification problems. Additionally, the Adam optimization function was utilized with a learning rate of 0.0001, *beta*1=0.9, and *beta*2=0.999, along with a batch size of

32. Finally, accuracy was used to evaluate the model’s performance during training and evaluation.

## Procedure for observing the behavior of the developed CNN model

Since other methodologies already classified the dataset, we adopted their approaches to compare our results. This process allowed us to observe the behavior of the developed model. Based on the methodology proposed by Jin et al. [[8](#_bookmark20)], we employed the data augmentation technique WGAN-GP [[17](#_bookmark29)] (see Figure [1](#_bookmark0)b). This network is an improvement of a Generative Adversarial Network (GAN) that focuses on gradient penalty to address the issue of gradient fading. It stands out for its fast convergence rate and greater stability than its predecessor, WGAN. The WGAN-GP was trained using a batch size of 4 for Anaphase and Telophase and 16 for Metaphase and Prophase. The training was carried out for 7000 epochs with a learning rate of 0.00001, *beta*1 = 0.01, and *beta*2 = 0.999. The image size was adjusted from 66 *×* 66 *×* 3 to 64 *×* 64 *×* 3. Network hyperparameters were maintained at their default values. Additionally, the G1 class had excess samples, so subsampling was applied by randomly removing images (see Figure [1](#_bookmark0)). All these steps were taken to balance mitosis and interphase class samples.

Once the new dataset was prepared, we trained the model described in Section [2.2](#_bookmark2) using the hyperparameters initially assigned. T his process led to acquiring new performance values for classifying cell cycle states.

On the other hand, following the methodology proposed by Rana et al. [[15](#_bookmark27)], we implemented the data augmentation technique WGAN-div in combination with the mixup technique (see Figure [1](#_bookmark0)c). Like WGAN-GP, WGAN-div [[18](#_bookmark30)] is an improvement over WGAN that approximates Wasserstein divergence to provide greater stability during training. On the other hand, mixup [[19](#_bookmark31)] blends two images to create a hybrid of them. For more details about these techniques, it is recommended to refer to the mentioned references. The hyperparameters used to train the WGAN-div are described below. The batch size for all classes was 64, with a learning rate 0.0001 for Prophase, Metaphase, and Anaphase and 0.00001 for Telophase. *beta*1 was 0.01, and *beta*2 was 0.999. Similar to WGAN-GP, the image size was adjusted from 66 *×* 66 *×* 3 to 64 *×* 64 *×* 3. The number of training steps per iteration for the discriminator was 10 for Prophase and 4 for Metaphase, Anaphase, and Telophase. Network hyperparameters were kept at their default values. Half of the images obtained by WGAN-GP underwent the mixup technique and were combined with images obtained by WGAN and the original images. With this new dataset, the

model developed in Section [2.2](#_bookmark2) was trained using the initially assigned hyperparameters.

## F1-Score

The F1 metric, widely recognized in the assessment of classification models, was employed to evaluate the results of the proposed CNN model. The F1-score metric combines two key metrics: precision and recall. Standard practice involves using these metrics together to assess model performance comprehensively. The F1 score reaches its optimal value at 1 and its minimum at 0 [[20](#_bookmark32)]. The F1 score is calculated using Formula [1](#_bookmark4).

2 *·* (*Precision · Recall*)

*F* 1 =

where F1 is given by [2](#_bookmark5) and [3](#_bookmark6)

*Precision* =

(*Precision* + *Recall*)

*TruePositives*

(1)

(2)

*Recall* =

*TruePositives* + *FalsePositives*

*TruePositives TruePositives* + *FalseNegatives*

(3)

This metric measures the values predicted by our model compared to the labels or ground truth of each cell cycle image. Additionally, it provides a measure to compare the results of our model with those obtained through methodologies mentioned by other authors previously.

# Results

This work introduces a convolutional neural network (CNN) model designed to classify the different phases of a cancerous cell cycle. This model was trained using images from the Jurkat cell line. To validate the efficiency of the developed model, a comprehensive comparison was conducted between the obtained results and those of other deep learning models utilizing the same database, as detailed in the introduction and methodology. The selected metrics for model evaluation include precision, recall, the F1 score, and the weighted average of the F1 score. It is crucial to note that a 5-fold stratified cross-validation was employed in assessing the proposed model. In this section, the evaluation and discussion are divided into two parts: the first regarding the dataset without modifications, the second concerning the data set with data augmentation using the WGAN-GP and WGAN-div

+ mixup techniques.

## Evaluation of CNN on original data

This study's adoption of a Convolutional Neural Network (CNN) was based on several considerations. The utilization of a CNN is characterized by reduced complexity and heightened suitability, primarily owing to the available volume of data, which aligns seamlessly with the requisites of a moderately deep network. Furthermore, the

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deployment of a CNN is associated with reduced computational overhead and faster data processing.

The magnitude and heterogeneity of the training dataset constitute pivotal determinants for the efficacy of the developed model. In particular, for phases G1, S, and G2, a substantial volume of data facilitated the assimilation of common patterns by the model. However, the remarkable resemblance observed among images from distinct phases presents a challenge to the model’s classification accuracy, particularly concerning phase S. This intricacy is discernible in the confusion matrix illustrated in Figure [4](#_bookmark7), in which the model exhibits a propensity to misclassify the data for S as G1 and G2, thereby contributing to a reduction in overall model accuracy. Conversely, the data associated with mitosis exhibit a significant scarcity of images in both the training and validation sets. This data limitation adds complexity to the model’s task, as it fails to grasp the specific patterns inherent in these categories adequately.

2500



2585 273 8

0

0

0

0

383 1158 183

0

0

0

0

27

244 1444

5

0

0

0

1

2

48

69

1

0

0

0

0

8

6

0

0

0

0

0

2

1

0

0

0

0 0 0 0 0 0 5



G1

S 2000

G1 0.9 0.095 0.0028 0 0 0 0

S 0.22 0.67 0.11 0 0 0 0

1.0

0.8



G2

1500

True label

G2 0.016 0.14 0.84 0.0029 0 0 0

True label

0.6

Pro

Pro 0.0083 0.017 0.4 0.57 0.0083 0 0

Meta Ana Telo

1000

500

Meta Ana Telo

0 0 0.57 0.43 0 0 0

0 0 0.67 0.33 0 0 0

0 0 0 0 0 0 1

0.4

0.2

0

G1 S G2 Pro Meta Ana Telo

Predicted label

(a)

G S G2 Pro Meta Ana Telo Predicted label

(b)

0.0

**Fig. 4**: (a) Confusion matrix of the classification of the original dataset. (b) Normalized confusion matrix of the classification of the original dataset.

Due to inherent characteristics in the employed data, such as the disparity in the number of samples per class and the overall dataset size, the neural network tends to experience overfitting in those classes with higher representation, leading to poor performance and directly impacting the overall model performance. Model training was halted at epoch 22, considering the observed variations in the loss function on the validation data. An increase in the loss function of the validation data is evident, contrary to expectations, and a decrease in accuracy is observed instead of an improvement.

To assess the performance of the proposed model, a detailed comparison was conducted, as illustrated in Table [1](#_bookmark8), between the outcomes achieved by our model and those obtained by Jin et al. [[8](#_bookmark20)]. This table shows that the imbalance in the data distribution per class emerges as a determining factor in the model’s performance. Positive outcomes stand out in the G1, G2, and Telophase stages, mainly attributable to the abundance of data and the clarity of the object to be classified

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in the images, in contrast to other phases of the cell cycle. The metrics reveal a significant difference favoring our model compared to that developed by Jin et al. [[8](#_bookmark20)]. This analysis highlights the importance of managing the imbalance in the quantity of data per class to enhance the model’s generalization. The quality and quantity of available data are fundamental elements that directly impact the model’s ability to classify the various phases of the cell cycle effectively.

**Table 1**: Comparison of the classification results between our model and those of Jin et al., using the original dataset.

Phase Precision Recall F1

Jin et al.’s model Proposed model Jin et al.’s model Proposed model Jin et al.’s model Proposed model

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| G1 | 0.8316 | **0.8628** | 0.8403 | **0.9020** | 0.8359 | **0.8820** |
| S | 0.6765 | **0.6905** | **0.7052** | 0.6717 | **0.6905** | 0.6810 |
| G2 | 0.8453 | **0.8529** | 0.8012 | **0.8395** | 0.8241 | **0.8462** |
| Prophase | **0.8521** | 0.8519 | **1.0000** | 0.5702 | **0.9202** | 0.6832 |
| Metaphase | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Anaphase | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |
| Telophase | 0.0000 | **1.0000** | 0.0000 | **1.0000** | 0.0000 | **1.0000** |
| Weighted Average | 0.7835 | **0.8117** | 0.7844 | **0.8152** | 0.7853 | **0.8127** |

## Results of the CNN architecture trained with data augmentation

Jin et al. proposed implementing the WGAN- GP data augmentation technique to address the data imbalance, coupled with under-sampling in the G1 phase. The methodology of Jin et al. was adopted to assess the performance of the proposed CNN model, now incorporating data augmentation techniques.

Figure [5](#_bookmark9) displays the results in a confusion matrix of the model trained with data augmentation and G1 under-sampling. Recalling the challenges encountered with imbalanced data, an increase in the number of true positives in class S was observed, while the count of true negatives and false negatives slightly decreased. Furthermore, in states associated with mitosis, a notable increase in true positives was evident from incorporating new data provided by the data augmentation technique.

Table [2](#_bookmark10) showcases improvements in most phases in terms of metrics, unlike the imbalanced dataset, for both the methodology proposed by Jin et al. and the proposed CNN model. The results of our model, in particular, are superior, suggesting that the utilization of a conventional CNN model can yield classification results similar to or even better than other deep learning architectures.

Rana et al. conducted a study in which they trained a ResNet using images generated by combining data augmentation techniques WGAN-div + mixup. To assess the performance of our CNN model in this work, we relied upon the methodology proposed in [[15](#_bookmark27)]. The proposed CNN was trained using data generated through the mentioned augmentation techniques, achieving superior performance. This contrasts with the approach taken in [[8](#_bookmark20)], highlighting the model’s strong performance

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G1 1493 225 4 0 0 0 0



1400

G1 0.87 0.13 0.0023 0 0 0 0

1.0

S G2

True label

Pro Meta Ana

Telo

294 1242 186 1 0 0 0

35 255 1429 0 0 1 0

0 0 0 1212 0 0 0

0 0 0 0 135 1 0

0 0 0 0 0 30 0

0 0 0 0 0 0 54

1200

1000

800

600

400

200

S G2

Pro Meta Ana

True label

Telo

0.17 0.72 0.11 0.00058 0 0 0

0.02 0.15 0.83 0 0 0.00058 0

0 0 0 1 0 0 0

0 0 0 0 0.99 0.0074 0

0 0 0 0 0 1 0

0 0 0 0 0 0 1

0.8

0.6

0.4

0.2

0

G S G2 Pro Meta Ana Telo

Predicted label

(a)

G S G2 Pro Meta Ana Telo Predicted label



(b)

0.0

**Fig. 5**: (a) Confusion matrix of the dataset classification using the WGAN- GP data augmentation. (b) Normalized confusion matrix of the dataset classification using the WGAN-GP data augmentation.



**Table 2**: Class-wise comparison between the proposed model and Jin et al. using the dataset with WGAN-GP data augmentation and oversampling in the G1 stage.

Phase Precision Recall F1

Jin et al.’s model Proposed model Jin et al.’s model Proposed model Jin et al.’s model Proposed model

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| G1 | 0.8181 | **0.8194** | 0.8490 | **0.8670** | 0.8333 | **0.8426** |
| S | 0.6700 | **0.7213** | 0.6918 | **0.7208** | 0.6808 | **0.7210** |
| G2 | 0.8456 | **0.8826** | 0.7895 | **0.8308** | 0.8166 | **0.8559** |
| Prophase | 0.9934 | **0.9992** | 0.9909 | **1.0000** | 0.9922 | **0.9996** |
| Metaphase | 0.8125 | **1.0000** | 0.9559 | **0.9926** | 0.8784 | **0.9963** |
| Anaphase | **1.0000** | 0.9375 | 0.0667 | **1.0000** | 0.1250 | **0.9677** |
| Telophase | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 | 1.0000 |
| Weighted Average | 0.8210 | **0.8490** | 0.8184 | **0.8481** | 0.8174 | **0.8481** |

both on data without applying augmentation techniques and on data with augmentation.

In the confusion matrix of Figure [6](#_bookmark11), a notable scarcity of false positives and false negatives is evident. Specifically focusing on classes associated with mitosis, a virtually flawless classification is achieved, thanks to data augmentation techniques. It is crucial to consider that, superficially, mitotic states may exhibit variations, underscoring the importance of differentiation through the inclusion of more examples.

In general, we can affirm that the developed model, fueled by examples provided by a WGAN-div, demonstrated superior performance. Table [3](#_bookmark12) shows a comparison with the methodology proposed in [[15](#_bookmark27)], focusing specifically on the F1 metric, where the algorithm shows promising results in most cell cycle states. We can confirm that incorporating additional data enhances the proposed model's efficiency.

The results show significant improvements in each of the classes. As anticipated, the G1, S, and G2 phases exhibit notable similarities. However, the most significant differences are observed in the classification of phases associated with mitosis, with

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G1 2725 141 0 0 0 0 0



2500



1.0

S G2

True label

Pro Meta Ana

Telo

314 1288 122 0 0 0 0

1 215 1502 2 0 0 0

0 0 0 2221 0 0 0

0 0 0 25 2078 0 0

0 0 0 29 0 2074 0

0 0 0 9 0 0 1044

2000

1500

True label

1000 M

A

500

T

0.8

0.6

0.4

0.2

0

G1 S G2 Pro Me Ana Telo

Predicted label

(a)

G1 S G2 Pro Meta Ana Telo Predicted label



G1 0.95 0.049 0 0 0

0

0

S 0.18 0.75 0.071 0 0

0

0

G2 0.00058 0.12 0.87 0.0012 0

0

0

Pro

0

0

0

1 0

0

0

eta

0

0

0

0.012 0.99

0

0

na

0

0

0

0.014 0

0.99

0

elo

0

0

0 0.0085 0

0

0.99



(b)

0.0

**Fig. 6**: (a) Confusion matrix of the dataset classification using the WGAN- GP data augmentation. (b) Normalized confusion matrix of the dataset classification using the WGAN-GP data augmentation.

**Table 3**: Class-wise comparison between the proposed model and Rana et al.’s [[15](#_bookmark27)] using the dataset with WGAN-div data augmentation and mixup.

|  |  |  |
| --- | --- | --- |
| Phase | Rana et al.’s model | Proposed model |
| G1 | **0.9300** | 0.9280 |
| S | 0.7500 | **0.7648** |
| G2 | 0.8400 | **0.8983** |
| Prophase | 0.9200 | **0.9856** |
| Metaphase | 0.5700 | **0.9940** |
| Anaphase | **1.0000** | 0.9931 |
| Telophase | **1.0000** | 0.9951 |
| Weighted Average | 0.8600 | **0.9372** |

Metaphase is the most affected. This is attributed to the achieved differentiation between Prophase and Telophase classes, which visually resemble Metaphase the most. The weighted average also reflects a higher number of successful predictions per phase in favor of the proposed model, indicating superior overall performance.

# Conclusions

This project successfully classified the 7 states in the cell cycle of a cancerous cell. It was demonstrated that a standard CNN model can effectively classify cell cycle phases even in an imbalanced dataset. The results indicate that conventional CNN can yield similar or even better classification outcomes without a profound network structure. It is also noteworthy that the efficiency of the CNN model improves when data augmentation is applied. Cell cycle phases, which can be challenging for the human eye, can

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be accurately classified using a deep learning model. Data augmentation techniques prove invaluable when a dataset lacks sufficient images per class. This approach allows for more robust model training, enhancing performance when evaluating the model’s accuracy with diverse data.

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