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MICRO ORGANISM IMAGE DETECTION USING DEEP LEARNING

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ABSTRACT

Despite tremendous recent interest, the application of deep learning in microbiology has still not reached its full potential. To tackle the challenges faced by human-operated microscopy, deep-learning-based methods have been proposed for microscopic image analysis of a wide range of microorganisms, including viruses, bacteria, fungi, and parasites. We believe that deep-learning technology-based systems will be on the front line of monitoring and investigation of microorganisms. Hence, here we are proposing a model that which can classify and detects the type of organism using the CNN based transfer learning algorithm of deep learning. Once after the detection of the organism, the spread of diseases are also predicted from the detected output.

Keywords: *Microorganism, deep learning, CNN, Transfer learning.*

INTRODUCTION

A microorganism, or microbe, is an organism of microscopic size, which may exist in its single-celled form or as a colony of cells. The possible existence of unseen microbial life was suspected from ancient times, such as in Jain scriptures from sixth century BC India. The scientific study of microorganisms began with their observation under the microscope in the 1670s by Anton van Leeuwenhoek. In the 1850s, Louis Pasteur found that microorganisms caused food spoilage, debunking the theory of spontaneous generation. In the 1880s, Robert Koch discovered that microorganisms caused the diseases tuberculosis, cholera, diphtheria, and anthrax.

Microbes are important in human culture and health in many ways. Microbes are essential tools in biology as model organisms and have been put to use in biological warfare and bioterrorism. In the human body, microorganisms make up the human microbiota, including the essential gut flora. The pathogens responsible for many infectious diseases are microbes and, as such, are the target of hygiene measures. The recognition of various genera and species of bacteria is useful in diagnostic Process. The classic techniques of bacteria recognition mainly use biological techniques such as gram staining and identify from contained specified metabolism of bacteria.

In this paper the most important features of bacteria that can be recognized on the images is the color of gram stained and the shape of its cell. The purpose of this research is to study possibility to use image classification and deep learning method for classify bacteria species by distinguish two basic shapes of long-rod and spherical.

LITERATURE REVIEW

S. NO	Journal Type with year	Authors	Title	Outcomes
1	Lancet Digit Health 1, 271–297, 2019	Liu, X	A comparison of deep learning performances against health-care professionals in detecting diseasesfrom medical imaging: a systemic review and meta-analysis	A comparison of deep learning performances against health-care professionals in detectingdiseases
2	Trends Cancer 5, 157–169,2019	Levine, A.B	Rise of the machines: advances indeep learning for cancer diagnosis	Study of deep learning for cancer diagnosis
3	Sci. Adv. 6, eabd5354,2020	Daz, M.S	Virus detection using nanoparticles and deep neuralnetwork-enabled smartphone system	Virus detection using nanoparticles and deepneural network-enabled
4	Trends Biotechnol. 37, 310–324, 2019	Riordon, J	Deep learning with microfluidicsfor biotechnology	Study of Deep learningwith microfluidics

EXISTING METHOD

In the existing there is no methods are implemented to check or detect the types of microorganisms. The only way is to do the process manually in the labs and predict the microorganisms using the microscopes that which consumes a lot of time and more human effort.

DISADVANTAGES

1. Time consuming
2. More human

PROPOSED METHOD

In our proposed method we are proposing a model that which can classify and detects the type of organism using the CNN based transfer learning algorithm (MobileNet) of deep learning. Here we are considering the four classes of four microorganisms. After the preprocessing of the considered dataset, we perform the training with the transfer learning method that which is used for the testing purpose and we will be detecting the type of microorganisms. Once after the detection of the organism, the spread of diseases are also predicted from the detected output. The flow of the proposed method is shown in the below block diagram.

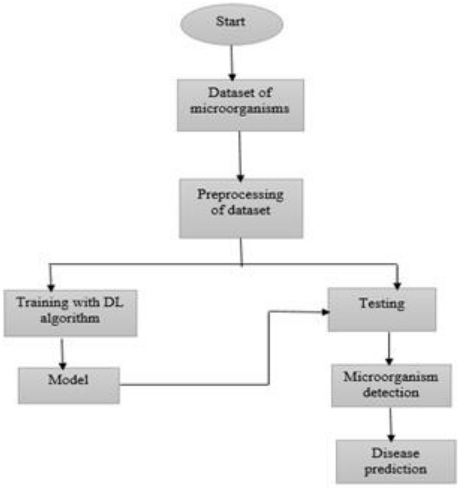


Fig 1: Block diagram of proposed method

METHODS OR TECHNIQUES USED

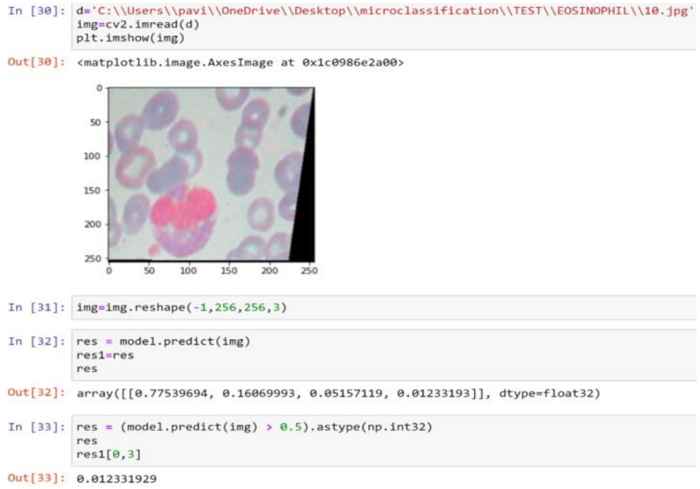
CNN:

In deep learning, a convolutional neural network (CNN, or ConvNet) is a class of deep neural networks, most commonly applied to analyzing visual imagery. A convolutional neural network consists of an input layer, hidden layers and an output layer. In any feed-forward neural network, any middle layers are called hidden because their inputs and outputs are masked by the activation function and final convolution. In a convolutional neural network, the hidden layers include layers that perform convolutions. Typically this includes a layer that does multiplication or other dot product, and its activation function is commonly RELU. This is followed by other convolution layers such as pooling layers, fully connected layers and normalization layers.

SIMULATION RESULT

Testing of four Categories

INPUT1:

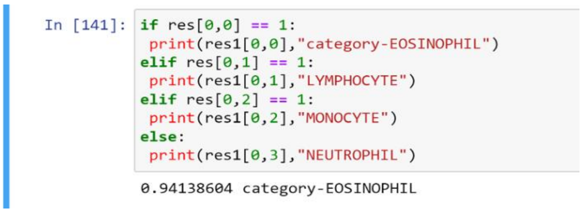


```
In [30]: d='C:\\Users\\pavi\\OneDrive\\Desktop\\microclassification\\TEST\\EOSINOPHIL\\10.jpg'
         img=cv2.imread(d)
         plt.imshow(img)

Out[30]: <matplotlib.image.AxesImage at 0x1c0986e2a00>
```

```
In [31]: img=img.reshape(-1,256,256,3)

In [32]: res = model.predict(img)
         res1=res
         res

Out[32]: array([[0.77539694, 0.16069993, 0.05157119, 0.01233193]], dtype=float32)

In [33]: res = (model.predict(img) > 0.5).astype(np.int32)
         res
         res1[0,3]

Out[33]: 0.012331929
```

Fig 2: Category 1

OUTPUT1:



```
In [141]: if res[0,0] == 1:
           print(res1[0,0],"category-EOSINOPHIL")
          elif res[0,1] == 1:
           print(res1[0,1],"LYMPHOCYTE")
          elif res[0,2] == 1:
           print(res1[0,2],"MONOCYTE")
          else:
           print(res1[0,3],"NEUTROPHIL")

          0.94138604 category-EOSINOPHIL
```

Fig 3: Detection of range and image

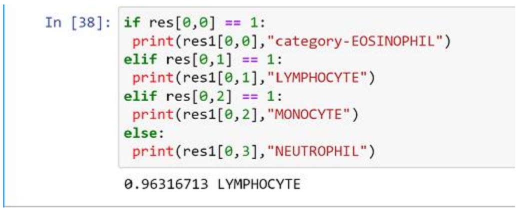
INPUT2:

```
In [34]: d='C:\\Users\\pavi\\OneDrive\\Desktop\\microclassification\\TEST\\LYMPHOCYTE\\10.jpg'
         img=cv2.imread(d)
         plt.imshow(img)

Out[34]: <matplotlib.image.AxesImage at 0x1c098777cd0>
```

```
In [35]: img=img.reshape(-1,256,256,3)

In [36]: res = model.predict(img)
         res1=res
         res

Out[36]: array([[0.00804759, 0.96316713, 0.02609701, 0.00268824]], dtype=float32)

In [37]: res = (model.predict(img) > 0.5).astype(np.int32)
         res
         res1[0,3]

Out[37]: 0.0026882405
```

Fig 4: Category 2

OUTPUT2:



```
In [38]: if res[0,0] == 1:
          print(res1[0,0],"category-EOSINOPHIL")
         elif res[0,1] == 1:
          print(res1[0,1],"LYMPHOCYTE")
         elif res[0,2] == 1:
          print(res1[0,2],"MONOCYTE")
         else:
          print(res1[0,3],"NEUTROPHIL")

         0.96316713 LYMPHOCYTE
```

Fig 5: Detection of range and image

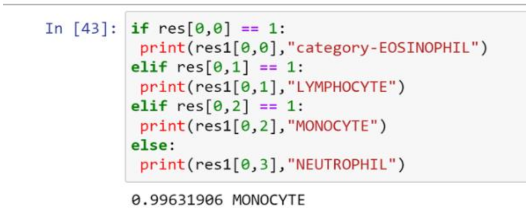
INPUT3:

```
In [39]: d='C:\\Users\\pavi\\OneDrive\\Desktop\\microclassification\\TEST\\MONOCYTE\\10.jpg'
         img=cv2.imread(d)
         plt.imshow(img)

Out[39]: <matplotlib.image.AxesImage at 0x1c0987dde80>
```

```
In [40]: img=img.reshape(-1,256,256,3)

In [41]: res = model.predict(img)
         res1=res
         res

Out[41]: array([[2.1410050e-04, 5.1742676e-04, 9.9631906e-01, 2.9493421e-03]],
               dtype=float32)

In [42]: res = (model.predict(img) > 0.5).astype(np.int32)
         res
         res1[0,3]

Out[42]: 0.0029493421
```

Fig 6: Category 3

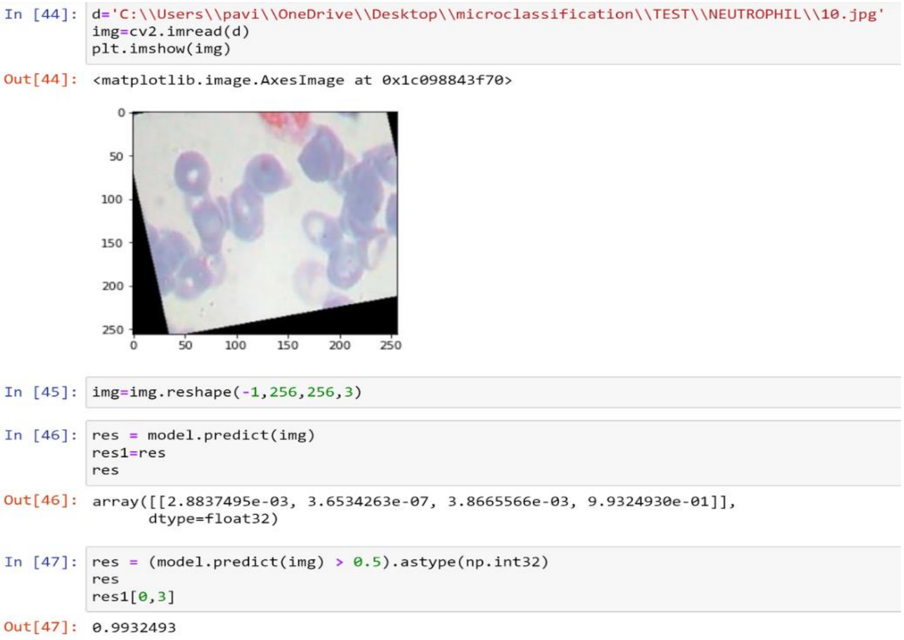
OUTPUT3:



```
In [43]: if res[0,0] == 1:
          print(res1[0,0],"category-EOSINOPHIL")
         elif res[0,1] == 1:
          print(res1[0,1],"LYMPHOCYTE")
         elif res[0,2] == 1:
          print(res1[0,2],"MONOCYTE")
         else:
          print(res1[0,3],"NEUTROPHIL")

         0.99631906 MONOCYTE
```

Fig 7: Detection of range and image

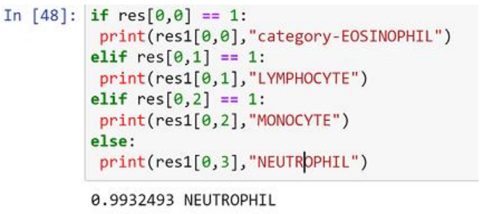
INPUT4:



```
In [44]: d='C:\\Users\\pavi\\OneDrive\\Desktop\\microclassification\\TEST\\NEUTROPHIL\\10.jpg'
         img=cv2.imread(d)
         plt.imshow(img)

Out[44]: <matplotlib.image.AxesImage at 0x1c098843f70>

In [45]: img=img.reshape(-1,256,256,3)

In [46]: res = model.predict(img)
         res1=res
         res

Out[46]: array([[2.8837495e-03, 3.6534263e-07, 3.8665566e-03, 9.9324930e-01]],
               dtype=float32)

In [47]: res = (model.predict(img) > 0.5).astype(np.int32)
         res
         res1[0,3]

Out[47]: 0.9932493
```

Fig 8: Category 3

OUTPUT4:



```
In [48]: if res[0,0] == 1:
          print(res1[0,0],"category-EOSINOPHIL")
         elif res[0,1] == 1:
          print(res1[0,1],"LYMPHOCYTE")
         elif res[0,2] == 1:
          print(res1[0,2],"MONOCYTE")
         else:
          print(res1[0,3],"NEUTROPHIL")

         0.9932493 NEUTROPHIL
```

Fig 9: Detection of range and image

ADVANTAGES

1. Accurate classification
2. Less complexity
3. High performance enables Scheduled Monitoring.

APPLICATIONS

1. Diagnostic process especially for infected patients.
2. Used in Laboratories.
3. Mainly used in analyzing visual imagery.

HARDWARE&SOFTWARE REQUIREMENTS

H/W Configuration:

1. Processor - I3/Intel Processor
2. Hard Disk -160GB
3. RAM -8Gb

S/W Configuration:

Operating System:

1. Windows :7/8/10
2. Server side Script : HTML, CSS & JS
3. IDE : Pycharm
4. Libraries Used : Numpy, IO, OS, Flask, keras
5. Technology : Python 3.6+

CONCLUSION

In this project we have successfully classified the different microorganism's images using the deep learning. Here, we have considered the dataset of four different microorganism classes and trained using CNN based transfer learning model. After the training user can test by uploading the image and can check for the classified results and after the classification of type of microorganism, the disease of the microorganism is predicted**.**

FUTURE SCOPE

This process can be extended in future to classify the more number of microorganism types with a large dataset that which can lead to the easy way for classifying and predicting the different microorganisms and also predicting their diseases easily without more human efforts**.**

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