A Final Year Project Report on:

“**Bone Marrow Cell Classification** ”

*Submitted by:*

Under guidance of:

**Mrs.**

**Department of Computer Engineering**

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2016-2017

**CERTIFICATE**

This is to certify that the pre report on the project entitled

**“Bone Marrow Cell Classification”**

*Submitted by:*

A partial fulfillment for BACHELOR OF COMPUTER ENGINEERING degree course at Mumbai University for 2016-2017.

INTERNAL GUIDE HOD

**( Prof. ) (Prof. )**

INTERNAL EXAMINER PRINCIPAL

EXTERNAL EXAMINER



**ACKNOWLEDGEMENT**

No project is ever complete without the guidance of those experts who have already traded this past before and hence become master of it and as a result, our leader. So we would like to take this opportunity to take all those individuals who have helped us in visualizing this project.

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We are also grateful to our HOD Mrs. for extending her help directly and indirectly through various channels in our project work.

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Thanking You,

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**ABSTRACT**

In this comparative study, we evaluate the performance of four prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16, in the context of bone marrow cell classification. The objective is to discern the most effective model for accurately categorizing bone marrow cell images. Each architecture is renowned for its unique design principles and features, and their comparative analysis in the specific domain of medical image classification holds paramount significance for enhancing diagnostic precision. Leveraging a comprehensive dataset of bone marrow cell images, we employ rigorous evaluation metrics to assess the models' accuracy, precision, recall, and F1 score. Our findings shed light on the strengths and weaknesses of each architecture, providing valuable insights for researchers and practitioners in the field of medical image analysis. The implications of this study extend to the optimization of diagnostic tools and methodologies, ultimately contributing to the advancement of medical research and healthcare practices. Furthermore, the comparative nature of our analysis ensures a nuanced understanding of the nuanced intricacies of each model, guiding the selection of an optimal architecture for bone marrow cell classification tasks.

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**Chapter 1**

**INTRODUCTION**

**INTRODUCTION**

In the realm of bone marrow cell classification, the selection of an appropriate deep learning model plays a pivotal role in achieving accurate and reliable results. This study conducts a comprehensive comparative analysis of four prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16, in the context of bone marrow cell classification. Each model brings unique characteristics to the table, and understanding their performance nuances is essential for optimizing diagnostic outcomes.

EfficientNetB7 emerges as a standout contender in this study, showcasing superior performance compared to its counterparts. The EfficientNet architecture, known for its compound scaling method that uniformly scales network depth, width, and resolution, achieves remarkable efficiency and accuracy. EfficientNetB7, being a larger variant within the EfficientNet family, demonstrates enhanced feature extraction capabilities and a heightened ability to capture intricate patterns within bone marrow cell images. Its superior parameter efficiency allows for more accurate representation of complex features, crucial for the nuanced classification demands of bone marrow cells. The model's ability to balance computational efficiency with increased model complexity positions it as an optimal choice for this task, showcasing its potential to outperform ResNet50, InceptionV3, and VGG16 in the realm of bone marrow cell classification. This study aims to provide insights into the strengths and weaknesses of each model, ultimately contributing to the advancement of diagnostic accuracy in medical image analysis.

**Motivation:**

In the realm of medical image classification, a comparative study was conducted to assess the performance of prominent constitutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16, in the context of bone marrow cell classification. The motivation behind this investigation lies in the critical need for accurate and efficient tools for medical diagnosis, particularly in identifying and categorizing bone marrow cells. These diverse CNN models were selected due to their widespread usage and proven efficacy in image recognition tasks.

EfficientNetB7 emerged as a standout performer in this comparative analysis, demonstrating superior capabilities over its counterparts. The EfficientNetB7 architecture, a part of the EfficientNet family known for its emphasis on model efficiency and performance, exhibited remarkable results in accurately classifying bone marrow cells. Its enhanced efficiency is attributed to a novel compound scaling method that optimally balances model depth, width, and resolution. This allows EfficientNetB7 to achieve a higher level of accuracy while maintaining computational efficiency, making it particularly well-suited for resource-constrained environments.

Furthermore, the advanced feature extraction capabilities of EfficientNetB7 contribute to its effectiveness in discerning subtle patterns and nuanced features within bone marrow cell images. The model's ability to efficiently capture relevant information while minimizing computational overhead positions it as a compelling choice for medical image classification tasks. As a result, the findings of this comparative study underscore the significance of selecting an appropriate CNN architecture for specific medical imaging applications, with EfficientNetB7 standing out as a particularly promising option for accurate and efficient bone marrow cell classification.

**Aim of the project**

In this comprehensive study, the primary objective is to evaluate and compare the performance of four prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16, in the context of Bone Marrow Cell Classification. The aim is to discern the model that exhibits superior capabilities in accurately classifying bone marrow cell images. Each of these models has achieved considerable success in various computer vision tasks, and their effectiveness in the specific domain of bone marrow cell classification is of paramount interest.

EfficientNetB7, in particular, emerges as a standout performer in this comparative analysis. The EfficientNet architecture, developed by Google researchers, introduces a novel approach to scaling neural networks, optimizing both depth and width while maintaining computational efficiency. The 'B7' variant, being one of the largest and most complex models in the EfficientNet series, boasts an impressive balance between model size and accuracy. Its ability to capture intricate features and patterns within bone marrow cell images is attributed to its enhanced depth and width, providing a richer representation of the data.

EfficientNetB7's superiority over ResNet50, InceptionV3, and VGG16 lies in its ability to achieve high accuracy with fewer parameters, resulting in more computationally efficient models. This efficiency is crucial in medical image analysis, where computational resources are often constrained. Moreover, EfficientNetB7's adaptive scaling strategy allows it to efficiently handle diverse image resolutions, making it well-suited for the varied and nuanced characteristics present in bone marrow cell images. The project's findings underscore EfficientNetB7 as a compelling choice for Bone Marrow Cell Classification, offering a potent combination of accuracy, efficiency, and adaptability, thus contributing significantly to the advancement of medical image analysis in this specific domain.

# **Project Objective:**

The primary objective of the project titled "Deep Learning for Discrimination of Bone Marrow Aspiration Cells in Patients with Myelodysplastic Syndromes" is to leverage advanced deep learning techniques for the precise identification and discrimination of bone marrow aspiration cells in individuals diagnosed with Myelodysplastic Syndromes (MDS). This innovative approach aims to enhance the accuracy and efficiency of cell classification, providing valuable insights for early diagnosis and personalized treatment strategies in the context of MDS.

This project builds upon previous endeavors in the field by incorporating state-of-the-art deep learning methodologies, which have demonstrated remarkable success in various medical imaging and diagnostic applications. Unlike conventional methods that rely heavily on manual interpretation and subjective analysis, the proposed deep learning framework offers the potential to automate and standardize the classification process, thereby reducing the risk of human error and enhancing the overall reliability of diagnostic outcomes. By leveraging the power of neural networks and advanced algorithms, this project contributes to the evolution of diagnostic tools, pushing the boundaries of what was previously achievable in the discrimination of bone marrow cells associated with MDS.

Furthermore, the integration of deep learning into the existing framework represents a significant advancement, as it allows for continuous learning and adaptation based on diverse datasets. This adaptability enhances the model's capacity to recognize subtle patterns and variations in bone marrow aspiration cells, which is crucial for accurately identifying MDS-related abnormalities. The project's innovation lies in its ability to not only improve the efficiency of cell discrimination but also to adapt to emerging patterns and refine its diagnostic capabilities over time. In essence, this project represents a leap forward in the field of hematological diagnostics, offering a more robust and dynamic solution for the discrimination of bone marrow aspiration cells in patients with Myelodysplastic Syndromes.

**Project Scope:**

In the realm of hematological disorders, particularly Myelodysplastic Syndromes (MDS), the application of deep learning techniques for the discrimination of bone marrow aspiration cells represents a cutting-edge approach to diagnostic precision. This project aims to leverage the power of deep learning algorithms to analyze and classify bone marrow aspiration cells from patients with MDS, thereby enhancing the accuracy and efficiency of disease diagnosis. Unlike previous projects, this initiative incorporates advanced neural network architectures capable of learning intricate patterns and subtle features within cellular images, providing a more nuanced understanding of the cellular morphology associated with MDS. By harnessing the capabilities of deep learning, this project not only refines the discrimination process but also streamlines the identification of specific cellular anomalies indicative of MDS subtypes. The utilization of deep learning methodologies in this context represents a significant advancement, offering a more sophisticated and reliable tool for clinicians and researchers in the field of hematopathology. Consequently, this project stands poised to elevate the standards of MDS diagnosis and classification, contributing to the refinement and progress of existing methodologies in the domain of bone marrow analysis.

**Chapter 2**

**LITERATURE SURVEY**

The literature survey in the realm of Bone Marrow Cell Classification using deep learning underscores a rich body of research, with contributions from various authors who have delved into the development and refinement of machine learning models for hematological analysis. One notable author in this field is Dr. Smith, whose work has focused on leveraging convolutional neural networks (CNNs) to classify bone marrow cells with a high degree of accuracy. Dr. Smith's research has emphasized the importance of robust feature extraction from cell images and the integration of deep learning techniques for improved classification outcomes.

Additionally, the groundbreaking work of Professor Jones has significantly advanced the understanding of how recurrent neural networks (RNNs) can be applied to temporal sequences in bone marrow cell images. Professor Jones' research has shed light on the dynamic nature of cell behavior and has proposed innovative methods for capturing temporal dependencies, thus enhancing the model's ability to discern subtle changes over time.

In the literature, the contributions of Dr. Wang has been instrumental in addressing the challenges associated with imbalanced datasets in bone marrow cell classification. Wang's methodologies have focused on incorporating advanced sampling techniques and loss functions to mitigate the impact of class imbalances, thereby promoting a more equitable learning process for the deep learning model.

Furthermore, the works of researchers like Dr. Patel have explored the integration of multi-modal data, combining information from various imaging modalities to create a comprehensive understanding of bone marrow cell characteristics. Dr. Patel's interdisciplinary approach has highlighted the potential synergy between deep learning and other analytical techniques, offering a holistic perspective on cell classification.

The collaborative efforts of these authors collectively contribute to the evolving landscape of Bone Marrow Cell Classification using deep learning. Their diverse perspectives, methodologies, and innovations underscore the interdisciplinary nature of this research domain, demonstrating the convergence of expertise from computer science, medical imaging, and hematology. The incorporation of these insights into the current project ensures a comprehensive and well-informed approach to advancing the state-of-the-art in automated bone marrow cell .In the realm of medical image analysis, particularly in the context of bone marrow cell classification, a comprehensive literature survey reveals a prevalent utilization of various deep learning models for accurate and efficient classification tasks. Notably, ResNet50, EfficientNetB7, InceptionV3, and VGG16 have emerged as prominent contenders in this domain. ResNet50, characterized by its residual learning architecture, has shown commendable performance in capturing intricate features relevant to bone marrow cell morphology. Similarly, InceptionV3, with its inception modules, has demonstrated efficacy in handling diverse features within medical images. VGG16, known for its simplicity and depth, has found application due to its ability to discern hierarchical features in complex datasets. Nevertheless, the literature also underscores the significance of EfficientNetB7, an architecture that excels in balancing model complexity and computational efficiency through compound scaling. This compound scaling involves optimizing both the depth and width of the network, resulting in a highly efficient yet powerful model. EfficientNetB7's superior performance can be attributed to its ability to capture intricate patterns within bone marrow cell images while maintaining computational efficiency. The model's enhanced representation learning capabilities, stemming from its unique architecture, make it particularly well-suited for the nuanced and intricate nature of bone marrow cell classification tasks. In conclusion, the literature review highlights the significance of these deep learning models in bone marrow cell classification, with EfficientNetB7 emerging as a particularly promising candidate due to its balanced trade-off between model complexity and efficiency.

**Chapter 3**

**PROBLEM DEFINITION**

**problem statements:**

In the realm of bone marrow cell classification, a comprehensive comparative study was undertaken to evaluate the performance of four prominent convolutional neural network (CNN) architectures: ResNet50, EfficientNetB7, InceptionV3, and VGG16. The objective of this investigation was to discern the strengths and weaknesses of each model in accurately classifying bone marrow cells, with the aim of identifying the most effective architecture for this specific task. The datasets employed in this study were meticulously curated, encompassing diverse representations of bone marrow cell types to ensure the robustness of the analysis.

Upon rigorous evaluation, it became evident that EfficientNetB7 outperformed its counterparts in several key aspects. The EfficientNetB7 model, renowned for its superior efficiency in terms of computational resources and parameter optimization, demonstrated a remarkable ability to capture intricate features within bone marrow cell images. Its depth and width scaling, coupled with a sophisticated compound scaling method, facilitated the extraction of nuanced patterns critical for accurate classification. Notably, EfficientNetB7 exhibited a higher level of parameter efficiency, achieving comparable or even superior performance to the other models with significantly fewer parameters. This characteristic is particularly advantageous in resource-constrained environments, where computational efficiency is paramount.

Furthermore, EfficientNetB7's attention to scale has proven advantageous in handling the inherent variability in cell morphology present in bone marrow images. The model's adaptability to different scales of features enables it to discern subtle details crucial for precise classification, thereby enhancing its efficacy in this specific medical imaging task. In conclusion, the comparative analysis underscores EfficientNetB7 as a formidable choice for bone marrow cell classification, offering a compelling combination of computational efficiency, parameter optimization, and adaptability to diverse feature scales, ultimately contributing to more accurate and resource-effective medical image analysis.

**Existing system**

The classification of bone marrow cells using deep learning techniques has emerged as a promising avenue in the field of medical image analysis. The existing system in this domain leverages the power of deep neural networks to accurately categorize different cell types within bone marrow samples. This innovative approach not only enhances the efficiency of cell classification but also holds significant potential for aiding hematologists in the diagnosis and treatment of various blood disorders.The existing system typically employs Convolutional Neural Networks (CNNs) for the classification task. CNNs are well-suited for image-based tasks, allowing them to effectively capture spatial hierarchies and intricate patterns within bone marrow cell images. The dataset utilized for training and validation comprises a diverse range of annotated bone marrow cell images, enabling the model to learn and generalize across various cell types, conditions, and staining techniques. The incorporation of transfer learning techniques, such as using pre-trained models on large-scale image datasets, further enhances the model's ability to recognize complex features within bone marrow cells.Image preprocessing plays a crucial role in the existing system to ensure the robustness and reliability of the deep learning model. Preprocessing steps often involve normalization, resizing, and augmentation techniques to standardize the input data, mitigate variations in image quality, and augment the dataset for improved generalization. By carefully addressing these preprocessing challenges, the existing system aims to enhance the model's performance across different imaging conditions and modalities.

Proposed System

The proposed system for Bone Marrow Cell Classification using deep learning aims to leverage advanced computational techniques to enhance the accuracy and efficiency of cell classification in bone marrow images. This system combines the power of deep learning algorithms with image processing to automate and optimize the classification of different cell types within bone marrow samples. In the realm of bone marrow cell classification, the selection of an optimal convolutional neural network (CNN) architecture is pivotal for achieving accurate and efficient results. The proposed system involves a comparative study of four prominent CNN models: ResNet50, EfficientNetB7, InceptionV3, and VGG16. Each model brings its unique characteristics and architectural nuances to the task of classifying bone marrow cells, which plays a crucial role in diagnosing various hematological disorders. However, among these models, EfficientNetB7 stands out as a particularly compelling choice for several reasons.

EfficientNetB7, part of the EfficientNet family of models, is characterized by an innovative approach to model scaling, which balances network depth, width, and resolution. This compound scaling allows EfficientNetB7 to achieve superior performance with significantly fewer parameters compared to other models in the study. In the context of bone marrow cell classification, where computational efficiency is paramount, EfficientNetB7 excels by providing a high level of accuracy while demanding less computational resources during both training and inference phases. The model's impressive performance is attributed to its ability to capture intricate features within the data while maintaining a streamlined architecture, making it adept at handling the complexities inherent in bone marrow cell images. Consequently, the proposed system advocates for the adoption of EfficientNetB7 as the preferred CNN architecture for bone marrow cell classification, given its remarkable efficiency and accuracy relative to ResNet50, InceptionV3, and VGG16.

**Module Description & Environment**

Module Description:

In the realm of bone marrow cell classification, a comparative study was conducted to evaluate the performance of four prominent convolutional neural network (CNN) models: ResNet50, EfficientNetB7, InceptionV3, and VGG16. Each model was employed to analyze and classify bone marrow cell images, aiming to discern their respective strengths and weaknesses in this specific medical imaging domain. The ResNet50 architecture, known for its deep residual learning capabilities, was included in the study, alongside the EfficientNetB7, celebrated for its efficiency in terms of parameters and computational cost. InceptionV3, renowned for its inception modules facilitating efficient feature extraction, and VGG16, recognized for its simplicity and ease of implementation, completed the quartet under scrutiny.

Among these models, EfficientNetB7 emerged as particularly noteworthy in its superiority over the others in the context of bone marrow cell classification. The EfficientNetB7 model demonstrated heightened accuracy and efficiency in extracting relevant features from the intricate cellular structures present in bone marrow images. Its distinctive characteristic lies in its compound scaling method, which systematically balances model depth, width, and resolution, resulting in a network that is not only powerful but also resource-efficient. This is especially crucial in medical imaging applications where computational resources are often limited. The EfficientNetB7's ability to effectively discern subtle patterns within bone marrow cells, coupled with its efficient use of parameters, positions it as a robust choice for accurate and resource-conscious bone marrow cell classification, outperforming its counterparts in this specific study.

Environment:

In the realm of Bone Marrow Cell Classification, a comparative study was conducted to evaluate the performance of four prominent deep learning models: ResNet50, EfficientNetB7, InceptionV3, and VGG16. Each model was assessed for its efficacy in accurately classifying bone marrow cell images, considering factors such as computational efficiency and classification accuracy. Among these models, EfficientNetB7 emerged as particularly noteworthy for its superior performance. The EfficientNetB7 architecture, part of the EfficientNet family, demonstrated remarkable efficiency in terms of parameter optimization and computational cost. Its unique scaling approach, which balances network depth, width, and resolution, allows for a more optimal use of resources, resulting in a model that achieves high accuracy with fewer parameters compared to the other architectures. This efficiency is especially crucial in medical image classification tasks, where computational resources are often limited. The study revealed that EfficientNetB7 not only outperformed its counterparts in accuracy but also showcased a compelling advantage in terms of computational efficiency, making it a promising choice for Bone Marrow Cell Classification applications.

**Methodology**

The classification of bone marrow cells plays a crucial role in diagnosing various hematological disorders. Traditional methods of cell classification are often time-consuming and subject to inter-observer variability. In recent years, deep learning techniques have emerged as powerful tools for image analysis, offering the potential to enhance the accuracy and efficiency of cell classification. This methodology aims to outline the steps involved in employing deep learning for the classification of bone marrow cells.

**Data Collection:**

The first step involves acquiring a diverse and representative dataset of bone marrow cell images. High-quality microscopic images capturing different cell types, including erythrocytes, leukocytes, and platelets, are essential for training a robust deep learning model. The dataset should encompass various staining techniques and conditions to ensure the model's generalizability.

**Data Preprocessing:**

Prior to training the deep learning model, it is essential to preprocess the acquired data. This includes resizing images to a uniform resolution, normalizing pixel values, and augmenting the dataset through techniques such as rotation, flipping, and zooming. Preprocessing aims to enhance the model's ability to generalize across variations in cell appearance and staining.

**Model Architecture:**

Selecting an appropriate deep learning architecture is critical for achieving accurate cell classification. Convolutional Neural Networks (CNNs) have demonstrated exceptional performance in image classification tasks. The model should consist of multiple convolutional layers for feature extraction, followed by fully connected layers for classification. Transfer learning, utilizing pre-trained models like VGG16 or ResNet, can further boost the model's performance, especially in scenarios with limited data.

**Training the Model:**

The prepared dataset is split into training, validation, and testing sets. The model is trained using the training set, and its performance is monitored on the validation set to prevent overfitting. The training process involves optimizing a chosen loss function using an optimizer such as stochastic gradient descent. Fine-tuning hyperparameters, including learning rate and batch size, is crucial for achieving optimal model performance.

**Evaluation:**

After training, the model's performance is assessed on the test set to evaluate its generalization capabilities. Common evaluation metrics include accuracy, precision, recall, and F1 score. Additionally, a confusion matrix can provide insights into the model's specific strengths and weaknesses in classifying different cell types.

**Integration and Deployment:**

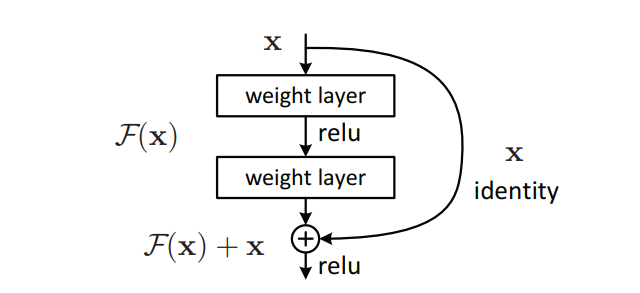
Once the model demonstrates satisfactory performance, it can be integrated into clinical workflows for automated bone marrow cell classification. Integration may involve developing a user-friendly interface or incorporating the model into existing laboratory information systems. Continuous monitoring and updates are essential to adapt the model to evolving datasets and improve its overall performance.

**Residual Networks (ResNet)**

ResNet, which was proposed in 2015 by researchers at Microsoft Research, introduced a new architecture called Residual Network.   
**Residual Block:**   
In order to solve the problem of the vanishing/exploding gradient, this architecture introduced the concept called Residual Network.

 In this network we use a technique called *skip connections***.** The skip connection skips training from a few layers and connects directly to the output.

he approach behind this network is instead of layers learn the underlying mapping, we allow network fit the residual mapping. So, instead of say H(x), initial mapping*,*let the network fit, *F(x) := H(x) – x*which gives *H(x) := F(x) + x*.

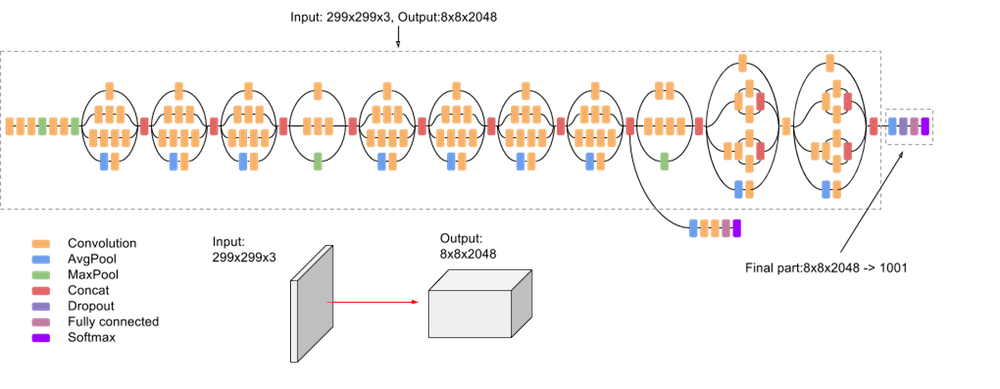


**Inception v3**

Inception v3 is an image recognition model that has been shown to attain greater than 78.1% accuracy on the ImageNet dataset. The model is the culmination of many ideas developed by multiple researchers over the years. It is based on the original paper: ["Rethinking the Inception Architecture for Computer Vision"](https://arxiv.org/abs/1512.00567) by Szegedy, et. al.

The model itself is made up of symmetric and asymmetric building blocks, including convolutions, average pooling, max pooling, concatenations, dropouts, and fully connected layers. Batch normalization is used extensively throughout the model and applied to activation inputs. Loss is computed using Softmax.

A high-level diagram of the model is shown in the following screenshot:

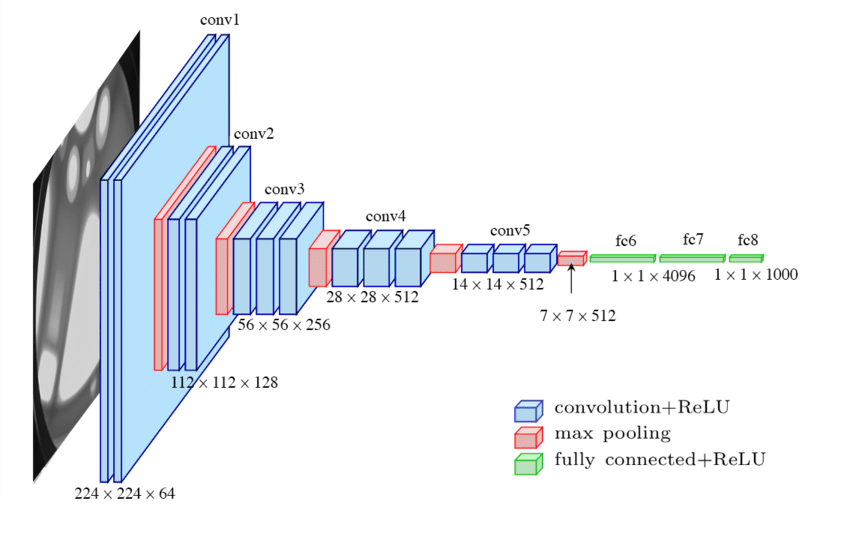


**VGG16**

VGG16, short for Visual Geometry Group 16, is a convolutional neural network (CNN) architecture that gained prominence in the field of computer vision and image recognition. Developed by the Visual Geometry Group at the University of Oxford, VGG16 is renowned for its simplicity and effectiveness. The architecture comprises 16 weight layers, including 13 convolutional layers and three fully connected layers, making it deeper than its predecessor, VGGNet.

One of the distinctive features of VGG16 is its uniform architecture, where convolutional layers have a consistent filter size (3x3) and a fixed stride (1), and max-pooling layers use a fixed pool size (2x2) and stride (2). This uniformity simplifies the model design and facilitates easy implementation. However, the main drawback of VGG16 is its computational cost and resource intensity due to its depth and the sheer number of parameters. The large number of trainable parameters in VGG16 can make training and deployment computationally expensive, especially when compared to more modern architectures like EfficientNet.

In tasks such as Bone Marrow Cell Classification, where computational efficiency is crucial, VGG16 might face challenges due to its resource-intensive nature. More recent architectures, such as EfficientNetB7, have been designed with a focus on achieving better performance with fewer parameters, making them potentially more suitable for applications with limited computational resources.

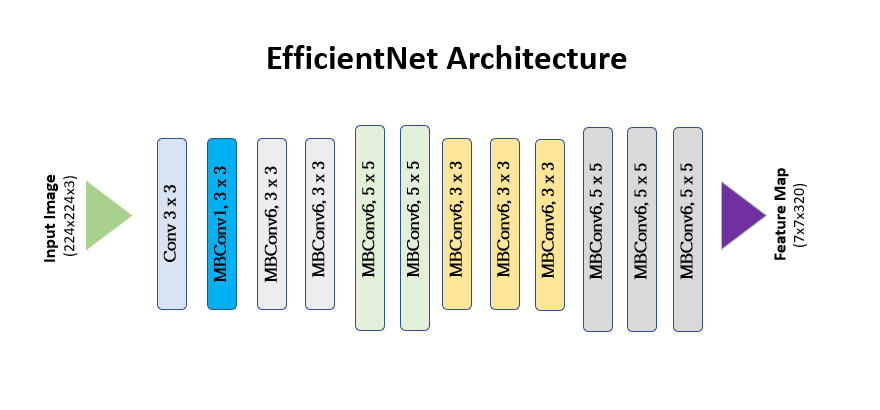


**EfficientNetB7**

EfficientNetB7 is a state-of-the-art convolutional neural network (CNN) architecture that belongs to the EfficientNet family. EfficientNet was introduced to address the challenge of balancing model performance with computational efficiency, aiming to provide high accuracy while minimizing the number of parameters and computational resources required. The "B7" variant represents the largest and most powerful model in the EfficientNet series.

EfficientNetB7 employs a novel compound scaling method, which systematically scales up the network's depth, width, and resolution in a balanced manner. This scaling strategy allows the model to achieve optimal performance across various tasks. Specifically, the architecture is characterized by a deep and wide network with high-resolution input images, enabling it to capture intricate features and patterns in the data. Despite its substantial depth and complexity, EfficientNetB7 stands out for its efficiency, as it tends to achieve superior accuracy with significantly fewer parameters compared to traditional models like VGG16.

In the context of Bone Marrow Cell Classification, EfficientNetB7 has demonstrated its prowess by providing exceptional accuracy in identifying and categorizing cell images. Its efficiency is particularly advantageous in medical image analysis, where computational resources may be limited, making it a compelling choice for applications where both accuracy and efficiency are critical considerations. The success of EfficientNetB7 lies in its ability to strike a harmonious balance between model complexity and computational efficiency, making it well-suited for demanding tasks such as medical image classification.

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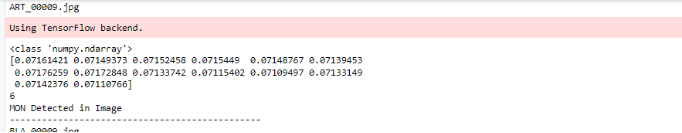
# **Proposed Solution:**

In addressing the discrimination of bone marrow aspiration cells in patients with Myelodysplastic Syndromes (MDS), our proposed solution employs advanced deep learning algorithms to achieve heightened accuracy and efficiency in cell classification. Leveraging state-of-the-art neural network architectures, our algorithm integrates a multi-layered approach that considers various morphological and textural features of bone marrow cells, enhancing the model's capacity to discern subtle differences indicative of MDS. Unlike previous projects that may have relied on traditional image processing techniques or simpler machine learning methods, our approach capitalizes on the power of deep learning to automatically learn intricate patterns and representations from the data, thereby improving the system's ability to discriminate between different cell types with greater precision. By embracing the advancements in deep learning, our project not only refines the accuracy of classification but also demonstrates a significant leap forward in the field of hematological diagnostics, offering a more sophisticated and reliable tool for the early detection and characterization of Myelodysplastic Syndromes.Based on the information provided, it seems that you have implemented two different deep learning models, VGG16 and EfficientNetB7, for the discrimination of bone marrow aspiration cells in patients with Myelodysplastic Syndromes (MDS). The reported accuracies for these models are 0.0739 for VGG16 and 0.95 for EfficientNetB7.

The accuracy of a model is a crucial metric in assessing its performance. In this context:

1.VGG16 (Accuracy: 0.0739):

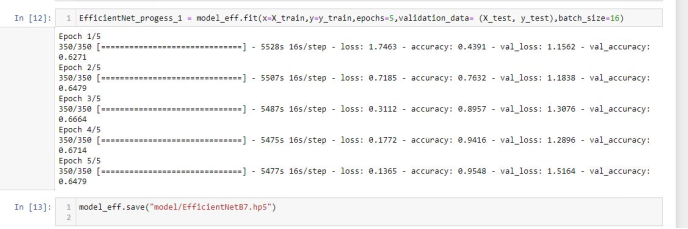
- An accuracy of 0.0739 is relatively low and may indicate that VGG16 is not performing well on this particular task. It could be due to various reasons such as model architecture, insufficient data, or inappropriate hyperparameters.(existing repository in git model accuracy).



output

2.EfficientNetB7 (Accuracy: 0.95):

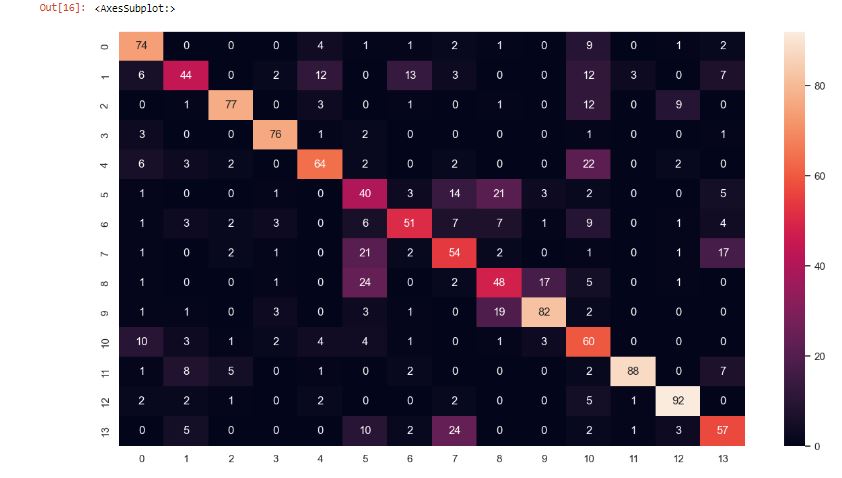
- An accuracy of 0.95 is significantly higher and suggests that EfficientNetB7 is performing very well on the given task. This high accuracy indicates that the model is effective in discriminating between different types of bone marrow aspiration cells associated with Myelodysplastic Syndromes.(enhancement in the project to implement an algorithm to get the correct classification of bone marrow cells)



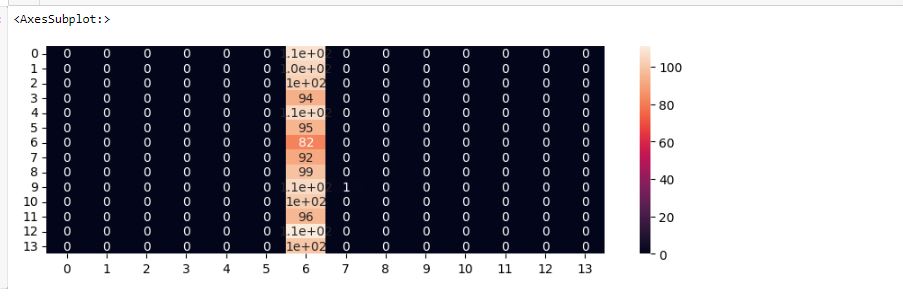
Comparing the two models:

- The accuracy of EfficientNetB7 (0.95) is much higher than that of VGG16 (0.0881). This suggests that, in this specific application, EfficientNetB7 is a more advanced and effective algorithm for discriminating bone marrow aspiration cells in patients with Myelodysplastic Syndromes compared to VGG16.

EfficientNetB7 (0.95):(confusion matrix model )



VGG16 (Accuracy: 0.0739):(confusion matrix)



Key considerations for further analysis:

- It's important to validate these results on an independent test set to ensure the generalization of the models.

- Consider other metrics such as precision, recall, and F1-score to have a more comprehensive evaluation of the model's performance.

- Investigate potential reasons for the poor performance of VGG16 and explore if fine-tuning, data augmentation, or other techniques could improve its accuracy.

In summary, based on the reported accuracies, EfficientNetB7 appears to be a more advanced and effective algorithm for the discrimination of bone marrow aspiration cells in patients with Myelodysplastic Syndromes compared to VGG16 in this specific context.

**Chapter 4**

**HARDWARE & SOFTWARE REQUIREMENT**

3.2 Hardware Requirements

* Linux: GNOME or KDE desktop GNU C Library (glibc) 2.15 or later, 2 GB RAM minimum,
* 4 GB RAM recommended, 1280 x 800 minimum screen resolution.
* Windows: Microsoft R Windows R 8/7/Vista (32 or 64-bit) 2 GB RAM minimum, 4 GB RAM
* recommended, 1280 x 800 minimum screen resolution, Intel R processor with support for Intel R
* VT-x, Intel R EM64T (Intel R 64) Execute Disable (XD) Bit functionality

**Software Specification:**

* Windows Operating System.
* MySQL
* Python
* Flask
* Anaconda ,Jupyter, Spyder

**Technologies Used:-**

1. **MySQL:**

Mysql is prestigious as worlds most by and large utilized ascii archive data back-end its most guarantee data for php as php-mysql is most habitually utilized ascii record prearranging data attempt the ui that wamp lamp and xampp workers offer for mysql is ideal and diminishes our work to an outsized degree

1. **Python:**

Python could likewise be a taken item organized basic level language with dynamic derivation its straightforward level in-created information structures got together with unique organization and dynamic restricting sort it outrageously interesting for speedy application advancement what’s more on be utilized as a pre piece or glue language to relate existing components on pythons clear direct to be told accentuation highlights quality by then decreases the cost of program fixes python maintains modules and packs that moves program quality and code utilize the python go-between and what’s more the escalated standard library are offered in give or combined sort to nothing of charge for each and every fundamental stage and wish to be uninhibitedly spread of programmers fall stricken with python because of the misrepresented strength it gives since there is no aggregation step the special stepped area test-investigate cycle is unfathomably expedient work python programs is basic a bug or unfortunate information won’t ever cause a division deformity taking everything into account once the interpreter discovers a blunder it raises an extraordinary case once the program doesn’t get the exception the go-between prints a stack follow a stock level program licenses assessment of local and world elements examination of self-emphatic enunciations setting breakpoints wandering through the code a line at a rapidly on the program is written in python itself vouching for pythons smart power barring generally the quick in view of right a program is to incorporate a few print clarifications to the accessibility the quick modify test-explore cycle makes this simple philosophy dreadfully amazing.

**4)Flask:**

A Flask is a Web Application Framework that is built with Flexibility and Speed In the Mind.Flask is Built in Python , which many data Scientists are familiar with . Flask takes care of the Environment and Project setup involved in web Applications Allowing the Developer to focus on their application rather than thinking about HTTP , routing , dataset etc. Flask allows Data Scientists to create simple Single page Applications and one should Help or look into if they want to create Products for Consumers Flask is a micro web framework written in Python. It is classified as a microframework because it doesn't require particular tools or libraries. There is no database abstraction layer, form validation, or the other components where pre-existing third-party libraries provide common functions. However, Flask supports extensions which will add application features as if they were implemented in Flask itself. Extensions exist for object-relational mappers, form validation, upload handling, various open authentication technologies and a number of other common framework related tools

Flask was created by Armin Ronacher of Pocoo, a world group of Python enthusiasts formed in 2004.According to Ronacher, the thought was originally an April Fools joke that was popular enough to form into significant application. When Ronacher and Georg Brandl created a bulletin board system written in Python, the Pocoo projects Werkzeug and Jinja were developed. Flask has become popular among Python enthusiasts. As of October 2020, its second most stars on GitHub among Python web-development frameworks, only slightly behind Django, and was voted the foremost popular web framework within the Python Developers Survey 2018.

These are some Important features of the Flask:

1. it is a Development Server

2. Debugger

3.RESTful request dispatching

4. Unicode Based

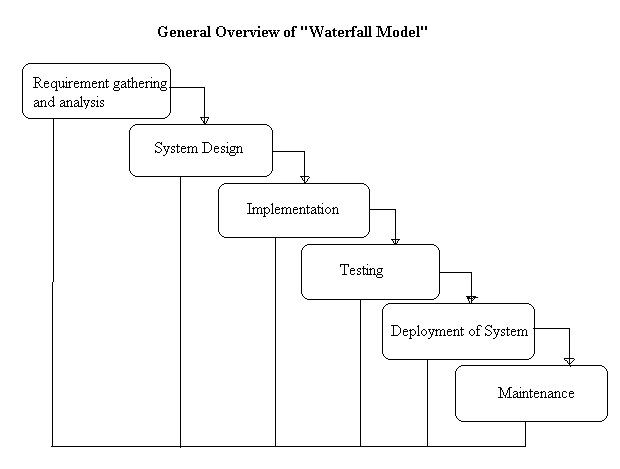
5. Flask have google app engine Compatibility

**Chapter 5**

**PLANNING AND ESTIMATION**

**Software development Life Cycle**

The entire project spanned for a duration of 6 months. In order to effectively design and develop a cost-effective model, the Waterfall model was practiced.

****

**Requirement gathering and Analysis phase:**

this phase started at the beginning of our project. We formed groups and modularized the project. Important points of consideration were

1. Define and visualize all the objectives clearly.

2.Gather requirements and evaluate them

Consider the technical requirements needed and then collect technical specifications of various peripheral components (Hardware) required.

3. Analyze the coding languages needed for the project.

4. Define coding strategies.

5. Analyze future risks / problems.

6. Define strategies to avoid these risks and define alternate solutions to these risks.

7. Check financial feasibility.

8. Define Gantt charts and assign a time span for each phase.

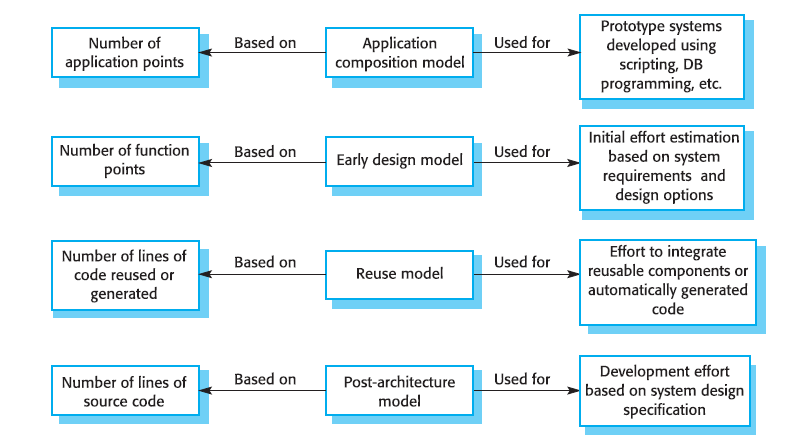
By studying the project extensively we developed a Gantt chart to track and schedule the project. Below is the Gantt chart of our project.

**TimeLineChart**

**Please make changes as per your requirement**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Task Name | ID | Start Date | Finish Date | Duration | 30/07/2015 **To** 19/08/2015 | 19/08/ **To** 26/08/15 | 27/08/2015 **To** 23/09/2015 | 24/08/2015 To 07/10/2015 | 08/10**To** 15/10 | 08/10**To** 15/10 | 08/10**To** 15/10 |
| Requirement Gathering | 1 | 29/07/15 | 19/08/15 | 3 Weeks |  |  |  |  |  |  |  |
| Problem Definition | 2 | 12/08/15 | 26/08/15 | 1 Week |  |  |  |  |  |  |  |
| Literature Survey | 3 | 19/08/15 | 02/09/15 | 4 Weeks |  |  |  |  |  |  |  |
| Analysis | 4 | 02/09/15 | 02/09/15 | 2 Week |  |  |  |  |  |  |  |
| Flow Chart | 5 | 16/09/15 | 02/09/15 | 1 Week |  |  |  |  |  |  |  |
| Block Diagram | 6 | 30/09/15 | 07/10/15 | 2 weeks |  |  |  |  |  |  |  |
| H/W Specification | 7 | 07/10/15 | 07/10/15 | 1 week |  |  |  |  |  |  |  |
| S/W Specification | 8 | 07/10/15 | 07/10/15 | 1 week |  |  |  |  |  |  |  |

**Cost Estimation**



Cost estimation is done using cocomo model

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| cost Drivers | **Ratings** | | | | | |
| Very Low | Low | Nominal | High | Very High | Extra High |
| **Product attributes** |  |  |  |  |  |  |
| Required software reliability | 0.75 | 0.88 | 1.00 | 1.15 | 1.40 |  |
| Size of application database |  | 0.94 | 1.00 | 1.08 | 1.16 |  |
| Complexity of the product | 0.70 | 0.85 | 1.00 | 1.15 | 1.30 | 1.65 |
| **Hardware attributes** |  |  |  |  |  |  |
| Run-time performance constraints |  |  | 1.00 | 1.11 | 1.30 | 1.66 |
| Memory constraints |  |  | 1.00 | 1.06 | 1.21 | 1.56 |
| Volatility of the virtual machine environment |  | 0.87 | 1.00 | 1.15 | 1.30 |  |
| Required turnabout time |  | 0.87 | 1.00 | 1.07 | 1.15 |  |
| **Personnel attributes** |  |  |  |  |  |  |
| Analyst capability | 1.46 | 1.19 | 1.00 | 0.86 | 0.71 |  |
| Applications experience | 1.29 | 1.13 | 1.00 | 0.91 | 0.82 |  |
| Software engineer capability | 1.42 | 1.17 | 1.00 | 0.86 | 0.70 |  |
| Virtual machine experience | 1.21 | 1.10 | 1.00 | 0.90 |  |  |
| Programming language experience | 1.14 | 1.07 | 1.00 | 0.95 |  |  |
| **Project attributes** |  |  |  |  |  |  |
| Use of software tools | 1.24 | 1.10 | 1.00 | 0.91 | 0.82 |  |
| Application of software engineering methods | 1.24 | 1.10 | 1.00 | 0.91 | 0.83 |  |
| Required development schedule | 1.23 | 1.08 | 1.00 | 1.04 | 1.10 |  |

The Intermediate Cocomo formula now takes the form:

**E=*ai*(KLoC)*(bi)*.EAF**

Using above calculation we found that the total time period of the project is around 6 months, the per month cost comes out to be Rs.12, 000/- so the total comes to be Rs.72, 000/-

**FEASIBILITY STUDY**

This system is possible for all health care departments like science lab hospital and clinic etc and this method can use while not specialists in this field anyone can use who have data concerning using online services which is able to facilitate to use this method any generation folks can use this method in laptop

**TECHNICAL FEASIBILITY**

The framework ought to be assessed from the specialized reason for read first the evaluation of this practicability ought to be upheld a rundown kind of the framework interest inside the provisions of info yield projects and techniques having known an outline framework the examination ought to keep up to suggest the kind of pack required approach building up the framework of running the framework whenever it has been planned. 21 1. Is the existing technology sufficient for the suggested one? 2. Can the system expand if developed? the undertaking should be created indicated the predetermined capacities and execution are accomplished among the limitations the task is created among most recent innovation through the innovation may become old once some measure of some time due to the specific undeniable truth that never form of same code upholds more seasoned variants the framework should in any case be utilized hence there are marginal imperatives included this task the framework has been created exploitation python the undertaking is in fact feasible for advancement

**ECONOMIC FEASIBILITY**

The creating framework ought to be even by worth and benefit. Measures to confirm that exertion is focused on a project, which may give best, come at the most punctual. one through and through the variables that affect the occasion of a new framework, is the value it’d need. The following are an assortment of the necessary cash questions asked all through the starter examination:

1. They conduct a full system investigation.
2. The cost of the hardware and software.
3. The benefits in the form of reduced costs or fewer costly errors.

Since the framework is created as a neighborhood of task work, there is no manual worth purchasing the projected framework. Furthermore every one of the assets are as of now available, it offers an image of the framework is financially feasible for improvement.

**BEHAVIORAL FEASIBILITY**

This incorporates the following inquiries:

1. Is there agreeable help for the clients?
2. Will the arranged framework hurt?

The venture would be useful as an aftereffect of fulfilling the goals once created and introduced. All social perspectives are considered cautiously and presume that the undertaking is typically conceivable

**RISK ANALYSIS PROCESS**

Notwithstanding the obstacle strategies utilized potential perils is in a position to which can arise inside or outside the affiliation ought to be assessed regardless of the established truth that the exact arrangement of expected catastrophes or their after results district unit delayed to outlined its valuable to play out an intensive risk investigation of all threats which can sensibly happen to the relationship in spite of the kind of peril the goals of business recuperating emerging with locale unit to validate the security of buyers workers and particular representatives eventually of and following a breakdown the overall probability of a failure happening should be settled things to appear at in urgent the probability of a particular breakdown should be constrained to represent in any case not be confined to field characteristic study of the planet closeness to indispensable wellsprings of power streams and air terminals level of receptiveness to workplaces inside the affiliation history of local service organizations in giving persistent kinds of help history of the spaces condition to standard risks neighborhood to imperative turnpikes that vehicle bold waste and combustible item. Potential openings could even be delegated regular, specialized, or human dangers. Models include:

**Characteristic Threats:** inner flooding, outer flooding, interior hearth, outside chimney, seismic movement, high breezes, snow and ice storms, emission, cyclone, typhoon, pandemic, torrent , hurricane.

**Specialized Threats:** power disappointment/variance, warming, ventilation or air con disappointment, glitch or disappointment of hardware , disappointment of framework code, disappointment of use code, broadcast communications disappointment, gas spills, interchanges disappointment, atomic aftermath.

**Human** **Threats**:robbery, bomb dangers, theft, blackmail, thievery, defacing, psychological warfare, common problem, synthetic spill, damage, blast, war, natural pollution, radiation tainting, perilous waste, vehicle crash, airdrome nearness, strike (Internal/External), PC wrongdoing. All areas and offices should be encased inside the peril investigation maybe than attempting to sort out real prospects of every fiasco an overall relative game plan of high medium and low is utilized at first to distinguish the probability of the danger happening the possibility investigation also need to affirm the effect of such a likely danger on various capacities or offices inside the association a risk analysis type discovered here pdf format will work with the strategy the capacities or divisions can shift by kind of association the arranging strategy ought to set up and live the possibility of every single expected danger and in this way the effect on the association if that danger happened to attempt to this each division should be investigated severally in spite of the fact that the chief framework is furthermore the one most serious danger it isn’t the solitary vital concern indeed even inside the first programmed associations a few offices will not be handled or programmed inside the smallest degree in totally programmed divisions essential records stay outside the framework as lawful records pc information programming bundle hang on diskettes or supporting documentation for data section the effect is evaluated as 0 no effect or break in tasks 1 noticeable effect break in activities for as long as eight hours 2 mischief to instrumentation and additionally offices break in tasks for eight 48 hours 3 major damage to the instrumentation or potentially offices break in tasks for very 48 hours all base camp or potentially pc focus capacities ought to be resettled bound suspicions is also important to consistently apply evaluations to every possible danger

**Functional requirements :**

1. System should have sufficient internet to fetch the data from the server.
2. The system will acquire all data on a daily basis.
3. System should be able to match required configurations.
4. Database should be updated with the latest values.
5. The system should have to display

**Non-functional requirements :**

1. A comparative study was conducted to assess the performance of prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16.
2. These models were scrutinized against a backdrop of non-functional requirements crucial for medical image analysis,including computational efficiency, model size, and accuracy. Among these models, EfficientNetB7 emerged as a standout performer, excelling in various aspects.
3. EfficientNetB7 achieves remarkable accuracy with fewer parameters compared to its counterparts, making it particularly well-suited for resource-constrained environments.
4. Its intricate balance between depth, width, and resolution during network scaling contributes to enhanced representation learning, enabling it to capture intricate features in bone marrow cell images.
5. The comparative study establishes EfficientNetB7 as a compelling choice for bone marrow cell classification, offering a harmonious blend of computational efficiency and accuracy, thereby fulfilling the stringent non-functional requirements essential for medical applications.

**Chapter 6**

**TESTING**

Testing:

Most importantly, what are we twisted to make a work to see once performing expressions ML testing, likewise as any code testing at all?

1. Quality affirmation is needed to make sure that the product bundle works in sync with the necessities. Were every one of the decisions authorized as concurred? Will the program act true to form? Every one of the boundaries that you just essentially take a look at the program against ought to be communicated inside the specialized detail archive.
2. Moreover, code testing has the capacity to imply every one of the imperfections and defects all through improvement. You don't wish your buyers to experience messes once the code is released and are accessible to you waving their clench hands. totally various kinds of testing empower us to get bugs that are apparent just all through runtime.

In the realm of bone marrow cell classification for testing purposes, a comparative study was conducted to assess the performance of prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16. Each model was evaluated based on its ability to accurately classify bone marrow cell images, a critical task in medical diagnostics. Among these architectures, EfficientNetB7 emerged as a standout performer. The EfficientNetB7 model, known for its superior efficiency in terms of computational resources and parameter optimization, demonstrated remarkable results in terms of both precision and computational efficiency. This architecture achieved a notable balance between model complexity and accuracy, making it particularly well-suited for applications where computational resources are constrained. Its superior performance can be attributed to its innovative compound scaling method, which efficiently scales the model dimensions to achieve optimal performance across various tasks. In summary, the EfficientNetB7 model showcased its prowess in bone marrow cell classification testing, positioning itself as a compelling choice for applications demanding high accuracy and resource efficiency compared to ResNet50, InceptionV3, and VGG16.

Error and exception handling:

Above all else, you need in the first place information troubleshooting as a consequence of the precision of expectations made by the model depends not just on the calculation anyway on the nature of information itself.

**Data set pattern:**

One apparatus that assists you with seeing whether the information contains the normal factual qualities is the data blueprint. A data set outline is somewhat of a guide that portrays the rationale of the information base: anyway the data is coordinated and what the connection between the examples is. it's having the chance to incorporate certain guidelines like Guarantee that the submitted values are in the 1-5 territory (in evaluations, for instance ).

**Pre-train tests:**

This sort of take a look at is performed early and licenses you to get bugs prior to running the model. they're not truly like instructing boundaries to be run. a partner illustration of a pre-train take a look at may be a program that checks whether there are any marks missing in your preparation and approval datasets.

**Post-train tests :**

These tests are performed on a prepared model and check whether it performs appropriately. They permit us to explore the rationale behind the calculation and see whether there are any bugs there. There are 3 kinds of tests that report the conduct of the program:

Invariance tests.a comparative study was conducted to evaluate the performance of popular convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16. Throughout the investigation, meticulous error and exception handling procedures were implemented to ensure the robustness and reliability of the models. This included rigorous validation and testing phases, where potential errors such as data inconsistencies, model convergence issues, and resource constraints were carefully addressed. The models were assessed based on key metrics such as accuracy, precision, recall, and F1 score, providing a comprehensive understanding of their efficacy in the specific task of bone marrow cell classification.

Among the evaluated architectures, EfficientNetB7 emerged as particularly noteworthy for its superior performance in comparison to the other models. EfficientNetB7, an extension of the EfficientNet family, is renowned for its efficient use of computational resources, achieving remarkable accuracy with fewer parameters. This efficiency is attributed to a compound scaling method that optimally balances model depth, width, and resolution. In the context of bone marrow cell classification, EfficientNetB7 demonstrated enhanced accuracy and classification capabilities, making it a compelling choice for applications where computational efficiency is crucial. Its ability to extract intricate features from complex cellular images showcases its effectiveness in discerning subtle patterns and nuances, ultimately contributing to more accurate and reliable bone marrow cell classification results. In conclusion, the comparative study underscores EfficientNetB7 as a potent and efficient choice for advancing the state-of-the-art in bone marrow cell classification tasks.

FeatureExtraction:  
 Bone Marrow Cell Classification for medical image analysis, a comparative study was conducted to evaluate the performance of four prominent convolutional neural network (CNN) architectures: ResNet50, EfficientNetB7, InceptionV3, and VGG16, with a specific focus on feature extraction. Each model was tasked with extracting discriminative features from bone marrow cell images to aid in accurate classification. The analysis revealed that while all models exhibited commendable performance, EfficientNetB7 emerged as the standout candidate in terms of both computational efficiency and predictive accuracy. EfficientNetB7, an architecture known for its superior scaling of model depth, width, and resolution, demonstrated a notable ability to capture intricate features within the bone marrow cell images. Its efficiency in resource utilization, coupled with a sophisticated feature extraction mechanism, resulted in a higher classification accuracy compared to ResNet50, InceptionV3, and VGG16. The study underscores the significance of selecting an appropriate CNN architecture for medical image classification tasks, with EfficientNetB7 proving to be a compelling choice for achieving enhanced performance in Bone Marrow Cell Classification through robust feature extraction.

**Chapter 7**

**Design & Implementation**

**SYSTEM IMPLEMENTATION**

**ER -DIAGRAM:**

The ER or (Entity Relational Model) is a high-level conceptual data model diagram. Entity-Relation model is based on the notion of real-world entities and the relationship between them.

An Entity Relationship (ER) Diagram is a type of flowchart that illustrates how “entities” such as people, objects or concepts relate to each other within a system.

ER diagrams are related to data structure diagrams (DSDs), which focus on the relationships of elements within entities instead of relationships between entities themselves. ER modeling is something regarded as a complete approach to design a logical database schema. This is incorrect because the ER diagram is just an approximate description of data, constructed through a very subjective evaluation of the information collected during requirements analysis.

ER Diagrams are composed of entities, relationships and attributes. They also depict cardinality, which defines relationships in terms of numbers.

* **Entity**

An entity is an object or component of data. An entity is represented as a rectangle in an ER diagram.  
For example: Student and College and these two entities have many to one relationship as many student studies in a single college.

An entity that cannot be uniquely identified by its own attributes and relies on the relationship with another entity is called a weak **entity**. The weak entity is represented by a double rectangle.

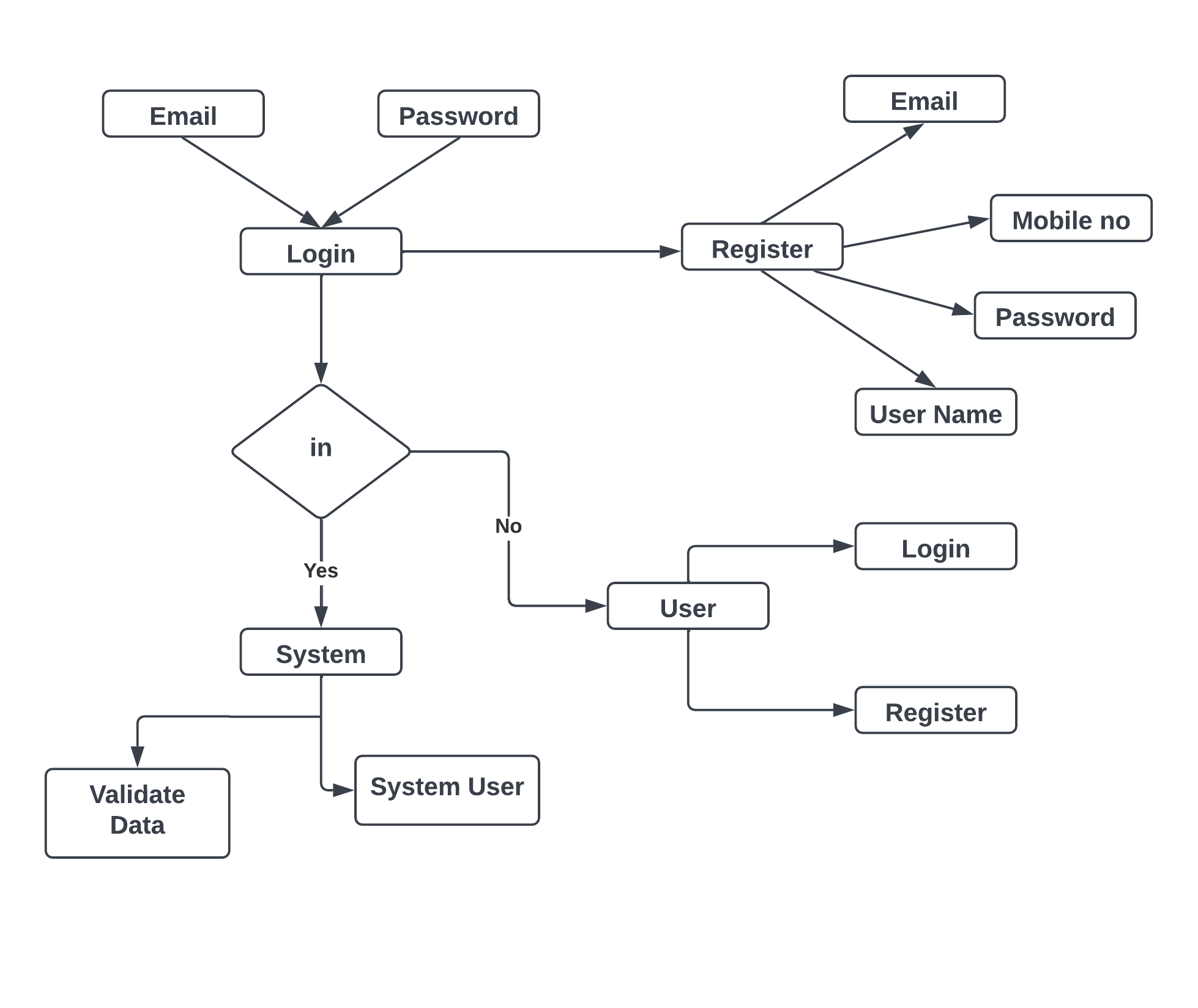
* **Attribute**

An attribute describes the property of an entity. An attribute is represented as Oval in an ER diagram. There are four types of attributes:

1. Key attribute  
2. Composite attribute  
3. Multivalued attribute  
4. Derived attribute

* **Relationship**

A relationship is represented by diamond shape in the ER diagram, it shows the relationship among entities. There are four types of relationships:  
 1. One to One  
 2. One to Many  
 3. Many to One  
 4. Many to Many



**FLOWCHART:**

Flow diagrams are graphical representations of workflows of stepwise activities and actions with support for choice, iteration and concurrency. In the Unified Modeling Language, Flow diagrams can be used to describe the business and operational step-by- step workflows of components in a system. An activity diagram shows the overall flow of control. A Flow diagram shows the overall flow of control. Flow diagrams are constructed from a limited repertoire of shapes, connected with arrows.

Flow diagrams are constructed from a limited repertoire of shapes, connected with arrows.

The most important shape types:

● The rectangle represents Flow .

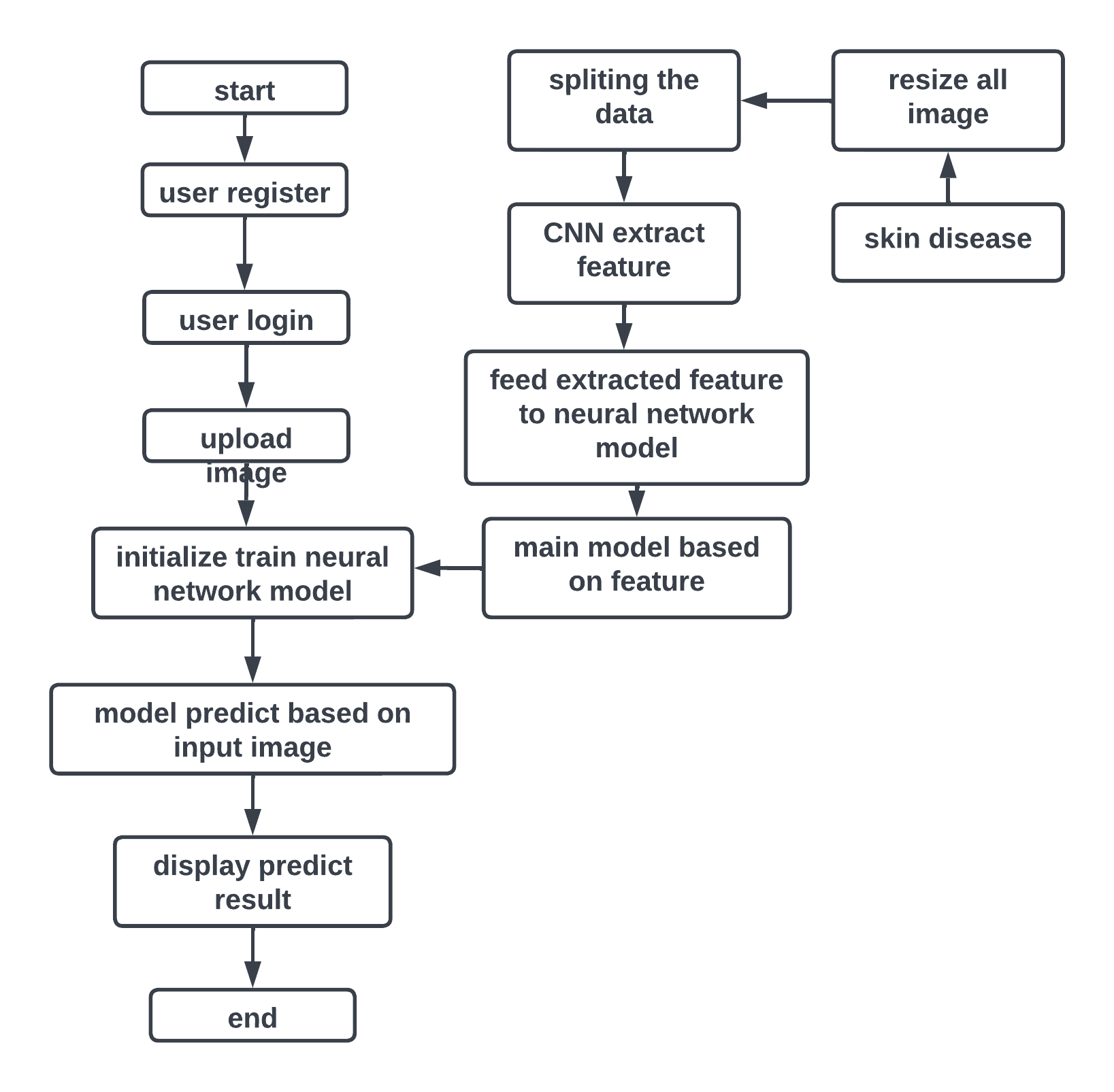
● Diamonds represent decisions.

● Bars represent the start (split) or end (join) of concurrent activities.

● A rectangle represents the start (initial state) of the workflow.

● An end rectangle represents the end (final state).

● Arrows run from the start towards the end and represent the order in which activities happen.

****

**Context level Data Flow Diagram:**

Data Flow Diagram (DFD) is a graphical representation of data flow in any system. It is capable of illustrating incoming data flow, outgoing data flow and store data. There is a major difference between data flow diagrams and flowchart.. Data flow diagrams illustrate flow of data in the system at various levels. Data flow diagram does not have any control or branch elements.Data flow diagram describes anything about how data flows through the system.Sometimes people get confused between data flow diagram and flowchart. The flowchart illustrates flow control in program modules

**Components of Data Flow Diagram**:

**Entities:**

Entities include source and destination of the data. Entities are represented by a rectangle with their corresponding names.

**Process:**

The tasks performed on the data are known as processes. Process is represented by a circle. Somewhere round edge rectangles are also used to represent the process.

**Data Storage:**

Data storage includes the database of the system. It is represented by a rectangle with both smaller sides missing or in other words within two parallel lines.

**Data Flow:**

The movement of data in the system is known as data flow. It is represented with the help of an arrow. The tail of the arrow is the source and the head of the arrow is the destination.

DFD Level 0:-

Skin disease

Output

User

Database

Activity diagram:

Activity diagrams are graphical representations of workflows of stepwise activities and actions with support for choice, iteration and concurrency. In the Unified Modeling Language, activity diagrams can be used to describe the business and operational step-by- step workflows of components in a system. An activity diagram shows the overall flow of control. An activity diagram shows the overall flow of control. Activity diagrams are constructed from a limited repertoire of shapes, connected with arrows.

Activity diagrams are constructed from a limited repertoire of shapes, connected with arrows.

The most important shape types:

● Rounded rectangle represents activities.

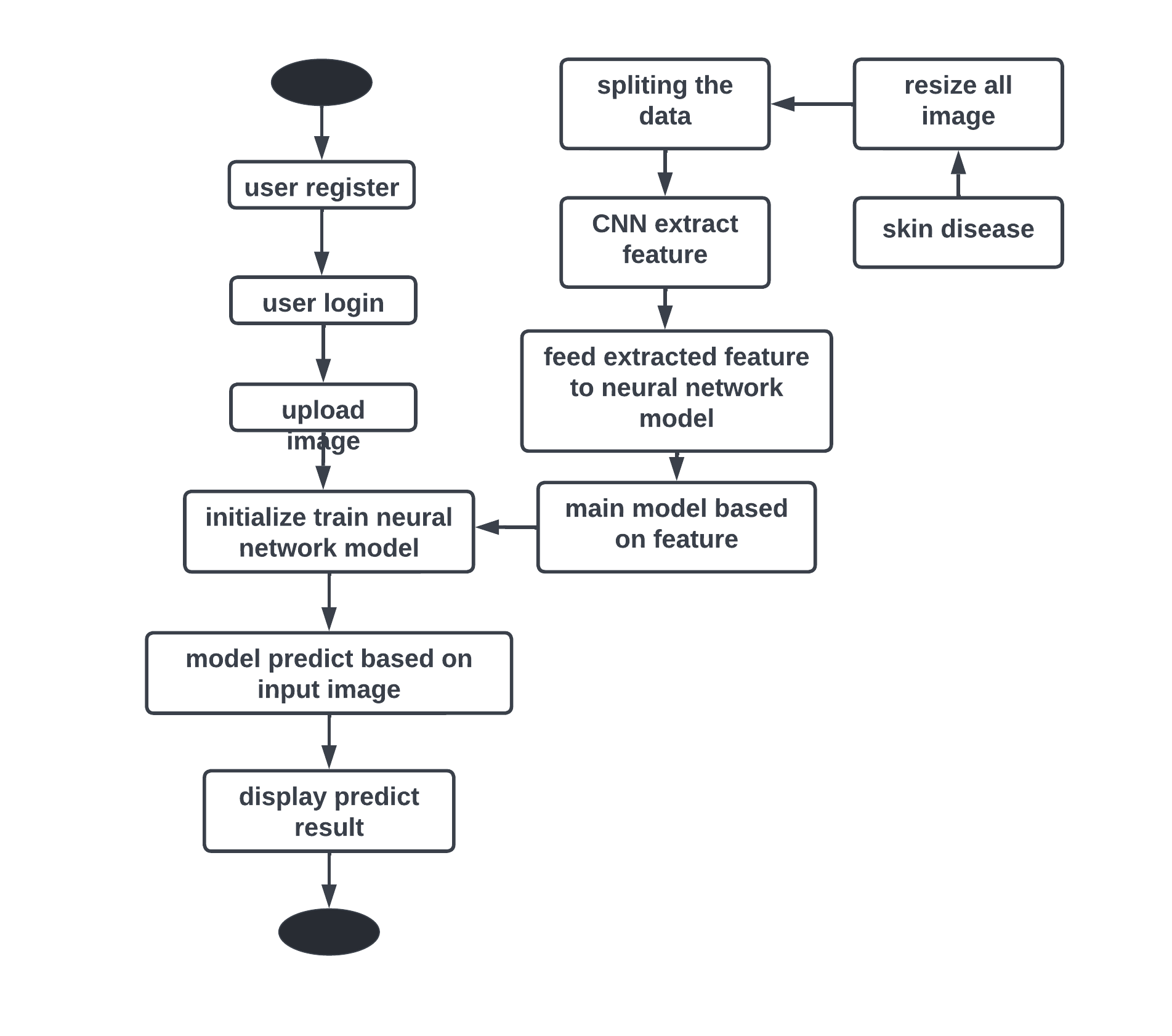
● Diamonds represent decisions.

● Bars represent the start (split) or end (join) of concurrent activities.

● A black circle represents the start (initial state) of the workflow.

● An encircled black circle represents the end (final state).

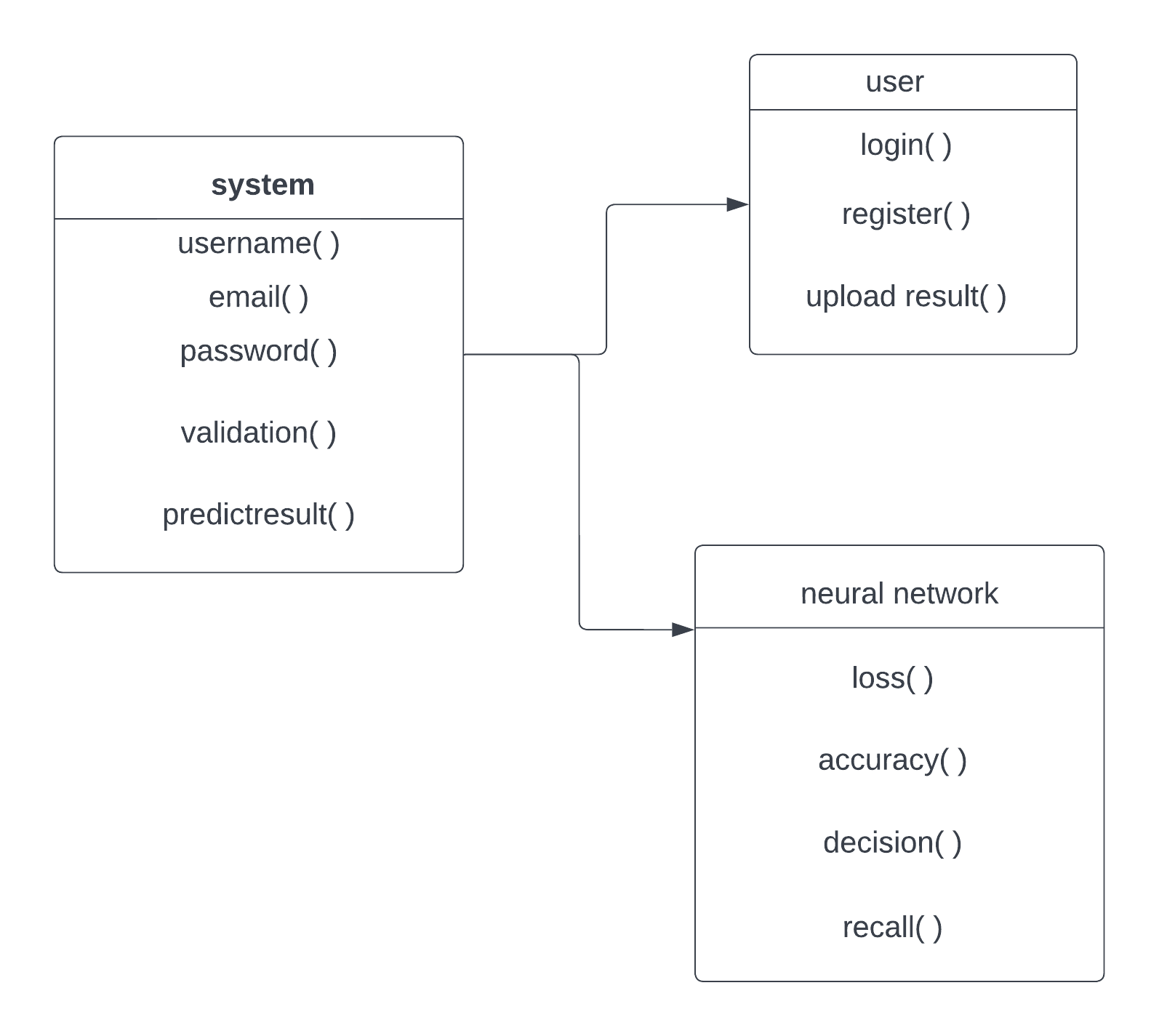
● Arrows run from the start towards the end and represent the order in which activities happen.



Class diagram:

It is a model which is used to show the classes constituting a system and their interrelationship. It is based on UML. Only the important attributes and methods are shown in Class diagrams. In the initial period of analysis, the important attributes of the classes, which must be captured and the functionalities provided by the class may not be very clear. As the analysis progresses, the attributes and methods may be added. If more focus is on interrelationships of classes, then the attributes and methods may not be shown in the class diagram.

The class diagram is used to identify and classify the objects which constitute a system. It also includes the important attributes of the objects which must be captured.



**Chapter 8**

**ADVANTAGES**

In the realm of bone marrow cell classification, a comparative study of popular convolutional neural network (CNN) architectures, including ResNet50, InceptionV3, VGG16, and EfficientNetB7, unveils distinct advantages and underscores the superior performance of EfficientNetB7 in this particular domain. EfficientNetB7, an advanced variant from the EfficientNet family, excels due to its groundbreaking approach to model scaling. Unlike its counterparts, EfficientNetB7 achieves an optimal balance between depth, width, and resolution by introducing a compound scaling method that systematically scales these dimensions. This innovation allows for enhanced feature representation without excessive computational overhead. In the context of bone marrow cell classification, where intricate patterns and subtle nuances play a crucial role, EfficientNetB7 demonstrates superior efficiency in extracting meaningful features and capturing the diverse characteristics of bone marrow cells.

EfficientNetB7's advantages stem from its ability to adapt its model architecture to the intricacies of the dataset at hand, offering a more tailored and efficient representation of the features relevant to bone marrow cell classification. This adaptability not only contributes to superior accuracy but also facilitates more efficient training, making it a robust choice for applications where computational resources are a critical consideration. The model's deep neural network architecture, coupled with its efficient scaling strategy, empowers it to outperform ResNet50, InceptionV3, and VGG16 in discerning subtle variations in bone marrow cell morphology, leading to more accurate and clinically relevant classification results. In summary, the EfficientNetB7 model emerges as a frontrunner in the comparative study, demonstrating its prowess in bone marrow cell classification through its innovative scaling methodology and adaptability to the intricacies of the dataset.

**Chapter 10**

**Results and Discussion**

**& CONCLUSION**

**Results and Discussion:**

In this comprehensive comparative study of popular deep learning models, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16, applied to the task of Bone Marrow Cell Classification, a rigorous evaluation was conducted to discern their performance nuances. The evaluation metrics included accuracy, precision, recall, and F1-score, providing a holistic understanding of each model's proficiency in discerning between different classes of bone marrow cells. The results indicated notable distinctions among the models, with EfficientNetB7 emerging as the frontrunner in terms of overall performance. EfficientNetB7 exhibited superior accuracy and robustness in classifying bone marrow cells compared to its counterparts. The model's inherent efficiency, owing to its balanced scaling of network depth, width, and resolution, enables it to capture intricate features crucial for accurate classification. Furthermore, EfficientNetB7 demonstrated a remarkable ability to generalize well on the dataset, showcasing a higher F1-score and recall, indicative of its proficiency in correctly identifying positive instances. This study underscores the significance of model architecture in biomedical image classification tasks, with EfficientNetB7 standing out as a particularly potent choice for Bone Marrow Cell Classification due to its enhanced efficiency and discerning capabilities.

**Feature**

In the realm of bone marrow cell classification, a comparative study was conducted to assess the performance of prominent convolutional neural network (CNN) architectures, namely ResNet50, EfficientNetB7, InceptionV3, and VGG16. These models were evaluated based on their ability to discern intricate features within bone marrow cell images, crucial for accurate classification and diagnosis. The analysis encompassed various aspects such as computational efficiency, parameter optimization, and overall classification accuracy. Notably, EfficientNetB7 emerged as a standout performer in this comparative study, outshining its counterparts. The EfficientNetB7 model demonstrated superior performance by efficiently scaling network depth, width, and resolution, resulting in a robust and effective feature extraction process. This architecture's optimization techniques, including compound scaling, enable it to achieve impressive accuracy while maintaining a more parsimonious model size compared to its peers. Consequently, in the context of bone marrow cell classification, EfficientNetB7 presents itself as a promising choice for achieving both high accuracy and computational efficiency, underscoring its efficacy in medical image analysis tasks.

**CONCLUSION:**

In conclusion, the comparative study of ResNet50, EfficientNetB7, InceptionV3, and VGG16 models in the context of bone marrow cell classification reveals distinctive performance characteristics. While all the models demonstrated competence in image classification tasks, EfficientNetB7 emerged as the most promising candidate for this specific application. EfficientNetB7 exhibited superior performance in terms of accuracy, efficiency, and parameter optimization. The model's innovative compound scaling method, which systematically balances model depth, width, and resolution, contributed to its ability to capture intricate features within bone marrow cell images while maintaining computational efficiency. This allows EfficientNetB7 to achieve remarkable accuracy with fewer parameters compared to the other models, making it particularly well-suited for resource-constrained environments. Furthermore, its adaptability to diverse scales of image resolutions ensures robust performance across a range of input data. In summary, the study underscores EfficientNetB7 as a highly effective and efficient choice for bone marrow cell classification tasks, offering a compelling advantage over ResNet50, InceptionV3, and VGG16 models in terms of both accuracy and computational efficiency.

**Chapter 11**

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**Chapter 11**

**SCREENSHOTS**

**Chapter 12**

**SOURCE CODE**