Deep CNNs for Peripheral Blood Cell Classification

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Abstract

The application of machine learning techniques to the medical domain is especially challenging due to the required level of precision and the incurrence of huge risks of minute errors. Employing these techniques to a more complex subdomain of hematological diagnosis seems quite promising, with automatic identification of blood cell types, which can help in detection of hematologic disorders. In this paper, we benchmark 27 popular deep convolutional neural network architectures on the microscopic peripheral blood cell images dataset. The dataset is publicly available, with large number of normal peripheral blood cells acquired using the CellaVision DM96 analyzer and identified by expert pathologists into eight different cell types. We fine-tune the state-of-the-art image classification models pre-trained on the ImageNet dataset for blood cell classification. We exploit data augmentation techniques during training to avoid overfitting and achieve generalization. An ensemble of the top performing models obtains significant improvements over past published works, achieving the state-of-the-art results with a classification accuracy of 99.51%. Our work provides empirical baselines and benchmarks on standard deep-learning architectures for microscopic peripheral blood cell recognition task.

Keywords: Blood Cell Classification, Transfer Learning, Medical Imaging, Convolutional Neural Networks, Deep Learning.

1. Introduction

Blood carries oxygen and nutrients to living cells in different organs and tissues. It carries away the waste for detoxification. It transports hormones to the desired site of action to fight infections and regulates body temperature. The ability to classify blood constituents can be critical in assessing the patient’s health. Plasma, which constitutes 55% of blood, is a colored liquid comprising mainly water (about 90%) and other essential substances such as proteins (albumin, clotting factors, antibodies, enzymes, and hormones), glucose, and fats. Rest 45% of blood is composed of white blood cells (WBCs/leukocytes), platelets (thrombocytes), and red blood cells (RBCs/erythrocytes), which float in the plasma (Fathima and Syeda, 2017; L., 2005). All these cells are associated with different functionalities. RBCs are responsible for transporting gases ($O_2, CO_2$) from lungs to tissues and maintaining systemic acid/base equilibria. Damage of red cell integrity, defined as hemolysis, has been shown to significantly contribute to severe pathologies, including endothelial dysfunction (Kuhn et al., 2017).

Based on the presence of visible granules in the microscopic view, WBCs can be classified into two broad categories: granulocytes and agranulocytes (nongranulocytes). Neutrophils, eosinophils, and basophils belong to the granulocytes category, while lymphocytes...
and monocytes belong to the agranulocytes category (Almezhghwi and Serte, 2020; Acevedo et al., 2019). Various types of WBCs play a role in immune response (L., 2005) and act as a defense mechanism in the body against illness-causing agents. Immature granulocytes (IG) are under-developed WBCs released from the bone marrow into the blood. Except for blood from newborn children or pregnant women, the appearance of IG (promyelocytes, myelocytes, and metamyelocytes) (Acevedo et al., 2019) in the peripheral blood (PB) indicates an early-stage response to infection, inflammation, or other stimuli of the bone marrow. Similarly, erythroblasts are nucleated immature RBCs or erythroid precursors not seen after the neonatal period. Their appearance in PB of children and adults can signify bone marrow damage, stress, malignant neoplasms, or other potentially serious diseases (Constantino and Cogioniis, 2000). Platelets are anucleated cells in blood and get activated at the site of injury to form a blood clot. Besides, they play an important role in innate immunity and regulation of tumor growth and extravasations in the vessel (Holinstat, 2017). They make up less than 1% of blood volume. Usually, the typical percentages of neutrophils in the blood are 0-6%. Eosinophils constitute 1–3%, basophils 0–1%, lymphocytes 25–33%, and monocytes 3–10% of the leukocytes circulating in the blood (Acevedo et al., 2019).

Recognition of various blood cell types can reveal anomalous blood cell populations like immature cells (IG or erythroblasts). On accurate identification, differential blood cell count can suggest any possible abnormalities in the blood, or help diagnose an infection, inflammation, leukemia (Shafique and Tehsin, 2018; Mathur et al., 2013), or any immune system disorder. Analyzing the blood cell morphology is the outset for the diagnosis of 80% of hematological diseases (Acevedo et al., 2019). Quantitative morphological analysis can thus, help cytologists assess blood samples and conclude about the patient’s blood conditions. However, the above processes are complex and time-consuming, involving a specialist meticulously examining the blood smear under a microscope, subjecting it to human errors. For the past few years, several attempts have been made to automate these processes using image processing techniques and machine learning, making them time and cost-effective and substantially reducing the workload in laboratories.

Convolutional neural networks (CNNs) are known to show excellent results on image recognition tasks, and hence, there has been an extensive research for applying them in the medical domain. In this paper, we explore various deep CNNs for blood cell classification task with peripheral blood cell (PBC) images dataset containing samples of eight different cell types: neutrophils, eosinophils, basophils, lymphocytes, monocytes, IG, erythroblasts, and platelets (Acevedo et al., 2020). Our work provides state-of-the-art results on the PBC classification task without the need of manual feature extraction or designing complex and hybrid architectures. The main contributions of this paper are as follows:

1. Train and evaluate an end-to-end deep learning-based classification system to recognize eight different blood cell types in peripheral blood smear.

2. Explore and benchmark 27 standard deep CNN architectures for blood cell classification using transfer learning.

3. Exploit data augmentation and ensembling techniques to further improve the model performance. Our model achieves state-of-the-art performance over previously published works.
2. Related Work

Computer-aided PBC classification is a challenging problem, and it has been studied extensively for the last few decades. Its solution can be used to develop tools and software that can assist doctors and radiologists in examining and diagnosing many blood-related diseases. Early attempts at this include designing the handcrafted features by experts, which can be further used to perform classification with the pattern recognition algorithms. The application of morphological analysis, including but not limited to morphological operators for PBC segmentation and classification, is the research area that has been explored in great detail (Kim et al., 2001; Di Ruberto et al., 2002; Piuri and Scotti, 2004; Scotti, 2005; Dorini et al., 2007; Theera-Umpoon and Dhomponsa, 2007; Taherisadr et al., 2013; Lee and Chen, 2014; Rodellar et al., 2018) before the deep learning-based approach became popular. There has been a significant increase in the studies on the deep learning-based WBC classification approaches (Su et al., 2014; Othman et al., 2017; Jiang et al., 2018; Macawile et al., 2018; Throngnumchait et al., 2019; Sharma et al., 2019; Banik et al., 2019; Shahin et al., 2019; Almezghawi and Serte, 2020; Baydilli and Atila, 2020; Sahlol et al., 2020) in the last decade, especially after the successful application of CNNs on other computer vision problems. The works (Saraswat and Arya, 2014; Rawat et al., 2015; Al-Dulaimi et al., 2018; Patodia et al., 2020), provide a review of the state-of-the-art methods of leukocyte segmentation, feature extraction, and classification published in the last two decades. The authors identified scope for improvement in several aspects compared to the classical approach involving image preprocessing and manual feature extraction, which achieved low performance and required expertise for labeling and handcrafting features. The usage of deep learning based techniques in the medical field has become popular due to the development of more efficient algorithms (Kumar et al., 2016; Ravì et al., 2016; Cabitza and Banfi, 2018). There has also been a wide array of research in the area of RBC segmentation and classification (Tomari et al., 2014; Tyas et al., 2017; Xu et al., 2017; Alzubaidi et al., 2020) for diagnosis of many blood-related diseases. There are many different PBC sub-types; however, most studies in this direction focus only on the major types like leukocyte or RBC. Recently, there are attempts at blood cell analysis, encapsulating all different blood cells classes with the same model (Acevedo et al., 2019; Ucar, 2020), and it can be more useful, having a large number of applications. Our models outperform the previously published works by successfully applying various standard deep CNN architectures on the large dataset (Acevedo et al., 2020) of microscopic images of peripheral blood cells.

3. Methodology

3.1. Overview

In this work, our primary goal is to develop a deep learning-based end-to-end system to perform PBC recognition. We apply transfer learning to fine-tune standard state-of-the-art deep CNN architectures pre-trained on the ImageNet dataset for the PBC classification task. This approach leverages the already learned features and fine-tunes the models to learn specialized features of microscopic blood cell images. After fine-tuning these models, we apply ensemble techniques to improve the system’s overall performance utilizing the
knowledge of all trained models, wherein our voting-based ensemble outperforms all other models and previously published works.

3.2. CNN Architectures

Deep CNNs have been demonstrated to outperform all other traditional machine learning algorithms for a variety of computer vision tasks in the last decade. Some of the exciting CNN application areas include Image Classification and Segmentation, Face Recognition, Object Detection, Video Processing, Natural Language Processing, and Speech Recognition. The powerful learning ability of deep CNNs is primarily due to multiple feature extraction stages that can automatically learn representations from the data. The CNN architecture generally consists of a feature extractor - containing several convolutional and pooling layers followed by a classifier - containing one or more fully connected layers where the last layer has softmax activation for classification. Depending upon the type of architectural modifications, CNNs can be broadly divided into seven different categories: spatial exploitation, depth, multi-path, width, feature-map exploitation, channel boosting, and attention-based CNNs (Khan et al., 2020b). We utilize 27 standard CNN architectures and analyze their performance for the blood cell classification task. The details about these models can be found in Appendix B. For our experiments, we use the Python implementation of these architectures available in the PyTorch model zoo.

3.3. Transfer learning

In machine learning, transfer learning (TL) is a technique where the knowledge gained solving one problem is applied to a different but related problem (Ventura and Warnick, 2007). In the last few years, several transfer learning techniques have been developed and successfully applied using deep neural networks in domains like computer vision, reinforcement learning and natural language processing (Shao et al., 2015; Weiss et al., 2016; Csurka, 2017; Tan et al., 2018; Zhuang et al., 2021; Taylor and Stone, 2009). We employ transfer learning to solve the blood cell classification problem by fine-tuning 27 different standard deep CNN architectures pre-trained on the ImageNet dataset. As the size of our dataset is not as huge as ImageNet, transfer learning is a suitable choice for our use-case. We use the feature extractor from the pre-trained models and pass the extracted features through a single layer fully connected classifier with eight output units. The fine-tuning of the feature extractor allows us to take advantage of the learned knowledge to further learn new specialized features from blood cell images. This makes the end-to-end training process easier and faster compared to training the whole model from scratch.

4. Experiments

This section presents the details of the experiments performed along with the results for peripheral blood cell classification. All the experiments were performed using Google’s Colaboratory platform with GPU backend. The code is written in Python using Pytorch deep learning framework.
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4.1. Dataset

For the classification of blood cells, peripheral blood cells dataset (Acevedo et al., 2020) was used which contains a total of 17,092 RGB images of normal blood cells, acquired using the analyser CellaVision DM96. The images are 360x363 dimensions each and were labelled by expert clinical pathologists at the Hospital Clinic of Barcelona. The traceability to the patient data was removed, resulting in an anonymized dataset. It is to be noted that the subjects were individuals without infection, hematologic or oncologic disease and free of any pharmacologic treatment at the moment of blood collection. No further filtering or image processing techniques were performed to the images in the dataset. Figure 1 shows a few sample images from the dataset. Number of instances in each class are presented in the Table 1. We split the dataset retaining 64% samples in each class as training samples, 24% as validation, and the rest 12% as testing samples while maintaining the sample per class ratio in all the sets as the original dataset.

4.2. Training Configuration

We perform our experiments with 27 different deep CNN models pre-trained on the ImageNet dataset. We use the stochastic gradient descent optimizer with momentum of 0.9, and adopt the weight initialization for classifier as in (He et al., 2015). These models are trained with a minibatch size of 32 on 1 GPU. We start with a learning rate of 0.001 and decay it by a factor of 0.1 every 7 epochs, and terminate training at 25 iterations as model converges. We use data augmentation techniques during training to deal with the limited amount of data which would help the model to generalize well on the unseen samples. The training set is augmented using common image transformations like random vertical and horizontal flips and rotating image by 60 degrees. At this stage, the images are also resized and centered-cropped to dimensions 299x299 for InceptionV3 model and 224x224 for rest of the architectures. For testing, we only evaluate the single view of the original 360x363
image. We use the softmax activation function at the output layer of the classifier and categorical cross-entropy as a loss function. We evaluate the performance of our models by calculating the confusion matrix and reporting evaluation metrics like accuracy, precision, sensitivity and specificity. The formulae of the parameters can be found in Appendix A.

4.3. Results

Table 2 presents the class-wise and overall test accuracy metrics for all the models. The four top performing models are highlighted in bold which we use further for ensembling. We observe a minute difference (<1%) in overall accuracies of all the models. The lowest accuracy of 98.39% is reported on AlexNet and the highest accuracy is reported as 99.32% on Wide ResNet-50-2. The confusion matrices and training plots for the top models are presented in Appendix C.

To further improve the performance, we employ voting-based ensemble by combining the top performing four models namely, Wide ResNet-50-2, VGG-19, Wide ResNet-101-2, and ResNet-34. For each instance in the test set, the class predicted by majority of the four classifiers is considered. This method improves the overall classification performance, achieving 99.51% overall accuracy, compared to the best model, Wide ResNet-50-2. It should be noted that there are five other models with overall accuracy equal to that of ResNet-34 that is, 99.17%, but we pick ResNet-34 over them because the validation performance of ensemble is highest with ResNet-34. Figure 2 shows the confusion matrix for the ensemble model. Table 3 reports the accuracy, precision, sensitivity and specificity metrics denoting that our ensemble outperforms the previously published works as well as the top performing models.

Figure 2: Confusion matrix for the Ensemble model on the test data
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| Architecture | Basophil | Eosinophil | Erythroblast | IG | Lymphocyte | Monocyte | Neutrophil | Platelet | Overall |
|--------------|----------|-------------|--------------|----|------------|----------|------------|----------|--------|
| AlexNet      | 0.9864   | 0.9973      | 0.9893       | 0.9483 | 0.9932     | 0.9766   | 0.9875     | 1.0000   | 0.9839 |
| DenseNet-121 | 0.9932   | 0.9973      | 0.9893       | 0.9713 | 0.9932     | 0.9942   | 0.9850     | 1.0000   | 0.9935 |
| DenseNet-161 | 1.0000   | 0.9973      | 0.9947       | 0.9770 | 0.9863     | 0.9942   | 0.9755     | 1.0000   | 0.9988 |
| DenseNet-169 | 1.0000   | 0.9973      | 0.9893       | 0.9885 | 0.9863     | 0.9942   | 0.9775     | 1.0000   | 0.9908 |
| DenseNet-201 | 0.9864   | 0.9973      | 0.9947       | 0.9885 | 0.9863     | 0.9942   | 0.9775     | 1.0000   | 0.9903 |
| VGG-11bn     | 0.9932   | 0.9973      | 0.9786       | 0.9799 | 0.9932     | 0.9825   | 0.9800     | 1.0000   | 0.9878 |
| VGG-11       | 1.0000   | 0.9947      | 0.9947       | 0.9684 | 0.9932     | 0.9708   | 0.9875     | 1.0000   | 0.9932 |
| VGG-13       | 1.0000   | 0.9973      | 0.9893       | 0.9770 | 0.9932     | 0.9708   | 0.9875     | 1.0000   | 0.9932 |
| VGG-13bn     | 1.0000   | 0.9973      | 0.9893       | 0.9914 | 0.9932     | 0.9883   | 0.9800     | 1.0000   | 0.9917 |
| VGG-16bn     | 1.0000   | 1.0000      | 0.9947       | 0.9856 | 0.9863     | 0.9825   | 0.9725     | 1.0000   | 0.9938 |
| VGG-16       | 0.9932   | 0.9973      | 0.9786       | 0.9828 | 0.9932     | 0.9825   | 0.9775     | 0.9965   | 0.9874 |
| VGG-19       | 1.0000   | 1.0000      | 1.0000       | 0.9799 | 0.9932     | 0.9883   | 0.9875     | 1.0000   | **0.9927** |
| VGG-19bn     | 0.9864   | 0.9973      | 0.9893       | 0.9828 | 0.9795     | 0.9883   | 0.9775     | 1.0000   | 0.9878 |
| ResNet-18    | 1.0000   | 1.0000      | 0.9947       | 0.9856 | 0.9932     | 0.9883   | 0.9800     | 1.0000   | 0.9917 |
| ResNet-34    | 1.0000   | 0.9973      | 0.9947       | 0.9885 | 0.9932     | 0.9883   | 0.9800     | 1.0000   | **0.9917** |
| ResNet-50    | 1.0000   | 0.9973      | 0.9947       | 0.9856 | 0.9932     | 0.9942   | 0.9775     | 1.0000   | 0.9912 |
| ResNet-101   | 0.9932   | 1.0000      | 1.0000       | 0.9828 | 0.9863     | 0.9825   | 0.9875     | 1.0000   | 0.9917 |
| ResNet-152   | 1.0000   | 0.9973      | 0.9893       | 0.9856 | 0.9863     | 0.9942   | 0.9750     | 1.0000   | 0.9898 |
| ResNetX-30-32x4d | 0.9932  | 1.0000      | 0.9947       | 0.9770 | 0.9863     | 0.9942   | 0.9825     | 1.0000   | 0.9903 |
| ResNetXt-101-32x8d | 0.9864 | 0.9973 | 1.0000  | 0.9914 | 0.9863 | 0.9942 | 0.9800 | 1.0000 | 0.9917 |
| SqueezeNet 1.0 | 0.9932 | 0.9973 | 0.9893 | 0.9799 | 0.9932 | 0.9708 | 0.9825 | 1.0000 | 0.9883 |
| SqueezeNet 1.1 | 0.9932 | 0.9973 | 0.9786 | 0.9540 | 0.9932 | 0.9591 | 0.9925 | 1.0000 | 0.9839 |
| Wide ResNet-50-2 | 0.9932 | 1.0000 | 0.9947 | 0.9856 | 0.9932 | 0.9942 | 0.9875 | 1.0000 | **0.9932** |
| Wide ResNet-101-2 | 1.0000 | 1.0000 | 1.0000 | 0.9799 | 0.9932 | 0.9942 | 0.9825 | 1.0000 | **0.9922** |
| GoogLeNet    | 0.9864   | 0.9973      | 0.9947       | 0.9856 | 0.9832     | 0.9825   | 0.9775     | 0.9965   | 0.9898 |
| Inception-v3 | 1.0000   | 0.9973      | 1.0000       | 0.9828 | 0.9932     | 0.9825   | 0.9850     | 1.0000   | 0.9917 |
| MobileNet-v2 | 0.9932   | 0.9973      | 1.0000       | 0.9856 | 0.9932     | 0.9883   | 0.9800     | 1.0000   | 0.9912 |

Table 2: Class-wise & Overall Test Accuracy values after fine-tuning various Deep CNN models for Peripheral Blood Cell Classification Task

| Method                  | Accuracy | Precision | Sensitivity | Specificity |
|-------------------------|----------|-----------|-------------|-------------|
| (Acevedo et al., 2019)  | 96.20    | 97.00     | 96.00       | 97.00       |
| (Ucar, 2020)            | 97.94    | 97.94     | 97.94       | 99.71       |
| (Long et al., 2021)     | 99.30    | 99.17     | 99.16       | 99.88       |
| ResNet-34 (Ours)        | 99.17    | 99.20     | 99.27       | 99.88       |
| Wide ResNet-101-2 (Ours)| 99.22    | 99.24     | 99.37       | 99.89       |
| VGG-19 (Ours)           | 99.27    | 99.17     | 99.36       | 99.89       |
| Wide ResNet-50-2 (Ours) | 99.32    | 99.29     | 99.35       | 99.90       |

Table 3: Comparison of Overall Classification Performance metrics (in %) of previous published works with our approach on test set of PBC image dataset

5. Discussion

The automatic peripheral blood cell classification is an interesting problem studied widely in recent decades, which can help in the diagnosis of several blood-related diseases.
Early attempts to solve this problem involved applying traditional machine learning algorithms with manual feature extraction and morphological analysis. In recent years, deep learning techniques, especially CNNs, are employed extensively in this direction. In this work, we solve this problem using deep CNNs, wherein we finetune 27 standard CNN architectures pre-trained on the ImageNet dataset. We further improve the overall performance using the voting-based ensemble of the top four models. Table 3 shows the comparison of our work with the previously published works where our ensemble model outperforms all of them, achieving a classification accuracy of 99.51%. It is worth noting that our model achieves a true positive rate (TPR) of 100% on basophils, eosinophil, erythroblasts, and platelets, 99.42% on monocytes, 99.32% on lymphocytes, 99.14% on IG, and 98.75% on neutrophil. From the confusion matrix in Figure 2, we can see that 1.25% of neutrophils are classified as IG. This may be due to the morphological similarities between the two classes, mainly in the nucleus shape. Moreover, single instances, each from classes lymphocyte and monocyte, are misclassified, which may be the anomalies in dataset.

In addition to our ensemble model, our finetuned CNN models AlexNet (98.39%), ResNet-18 (99.17%), VGG-16 (98.74%), InceptionV3 (99.17%) show considerable improvement in performance over the corresponding models in the past related works. (Acevedo et al., 2019) achieve overall accuracy 96.2% on VGG-16 and 95% on InceptionV3 and (Long et al., 2021) achieve overall accuracies of 81.5%, 95.9%, 97.8% and 98.4% on AlexNet, ResNet-18, VGG-16 and InceptionV3 respectively, which is considerably lower than our reported values. Such a significant difference in performance may be due to our careful selection of hyperparameters and weight initialization. Moreover, we notice that even with different architectures with varying configurations of depth, number of parameters, layers, or branches, models don't show a vast difference in the overall performance. The reason behind it may be the simplicity and the smaller size of the PBC dataset compared to the ImageNet which has 1000 classes with over 14 million images making it a much harder dataset wherein the changes in architecture produce notable performance differences. It is noteworthy that the standard CNN architectures we fine-tuned, outperform the specialized architectures and techniques designed (Almezhghwi and Serte, 2020; Long et al., 2021) for the peripheral blood cell classification.

6. Conclusion

In this work, we solve peripheral blood cell classification problem by fine-tuning standard deep CNN architectures pre-trained on ImageNet dataset. We employ transfer learning to utilize features already learned by state-of-the-art deep learning models and fine-tune them to learn new specialized features of blood cells. In our experiments, all 27 models achieve ≥ 98% accuracy and 14 of them achieve ≥ 99% accuracy, showing significant improvements over past works. The Wide ResNet-50-2 achieves the highest accuracy of 99.32% and the VGG-19 achieves the second highest accuracy of 99.27%. An ensemble of the top performing models outperforms all other models, achieving state-of-the-art results with a classification accuracy of 99.51%. Our work provides an empirical baselines for deep learning-based blood cell classification against which the future works with specialized architectures and techniques can be compared. We think that our findings will help further advances in research in deep learning-based automatic blood cell classification.
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Appendix A. Evaluation Metrics Formulae

Below are the performance metrics used to evaluate the classification model on PCB dataset.

\[
\text{Overall Accuracy} = \frac{\text{Total Number of Correct Predictions}}{\text{Total Number of Samples}}
\]

\[
\text{Precision} = \frac{TP}{TP + FP}, \quad \text{Sensitivity} = \frac{TP}{TP + FN}, \quad \text{Specificity} = \frac{TN}{TN + FP}
\]

where TP (True Positive) is the value of principal diagonal of target class in confusion matrix, TN (True Negative) is the sum of all the elements except the row and column of target class, FP (False Positive) is the sum of all column elements of target class excluding its TP, and FN (False Negative) is the sum of all row elements of target class excluding its TP. For this multi-class classification problem, we considered one-vs-all approach for calculating specificity, sensitivity and precision from the confusion matrix.

Appendix B. More details on CNN Architectures

The evolution of the CNN architectures in the last decade has been remarkable. Initially, different ideas such as information gating mechanism across multiple layers, skip connections, and cross-layer channel connectivity were introduced (Srivastava et al., 2015; He et al., 2016; Huang et al., 2017). Then, the focus of research shifted mainly on designing of generic blocks that can be inserted at any learning stage in CNN architecture to improve the network representation (Peng et al., 2015) and can be used to assign attention to spatial and feature map information (Wang et al., 2017; Roy et al., 2017; Woo et al., 2018). In 2018, an idea of channel boosting was introduced by Khan et al. (Khan et al., 2020a) to boost the performance of a CNN by learning distinct features and utilizing the already learned features using the TL. Some of the salient improvements involve knowledge distillation and compression or squeezing of pre-trained networks (Chen et al., 2015; Han et al., 2015; Wu et al., 2016; Frosst and Hinton, 2017). GoogleNet replaced the conventional convolution operation with point-wise group convolution operation to make it small and computationally efficient (Szegedy et al., 2015). ShuffleNet also used the point-wise group convolution but with a new idea of channel shuffle that reduced the number of operations significantly without impacting the performance (Zhang et al., 2018). For our experiments we used 27 standard CNN architectures, details of which are presented in Table 4.
| Architecture | Top-1 Error | Top-5 Error | Depth | #Params (millions) | Main Contribution |
|--------------|-------------|-------------|-------|--------------------|-------------------|
| AlexNet (Krizhevsky, 2014) | 43.45 | 20.91 | 5 | 61 | - Deeper and wider than the LeNet - Uses Relu, dropout and overlap Pooling - GPUs NVIDIA GTX 580 |
| VGG-11 | 30.98 | 11.37 | 11 | 133 | - Analysis with different depths |
| VGG-13 | 30.07 | 10.75 | 13 | 133 | - Homogenous topology |
| VGG-16 | 28.41 | 9.62 | 16 | 138 | - Uses small size kernels |
| VGG-19 | 27.62 | 9.12 | 19 | 144 | |
| VGG-11 bn (Simonyan and Zisserman, 2014) | | | | | - Homogenous topology |
| VGG-13 bn | 29.62 | 10.19 | 11 | 133 | |
| VGG-16 bn | 26.63 | 8.5 | 16 | 138 | |
| VGG-19 bn | 25.76 | 8.15 | 19 | 144 | |
| ResNet-18 | 30.24 | 10.92 | 18 | 11 | - Residual learning framework |
| ResNet-34 | 26.7 | 8.58 | 34 | 21 | |
| ResNet-50 | 23.85 | 7.13 | 50 | 25 | - Identity mapping based skip connections |
| ResNet-101 | 22.63 | 6.44 | 101 | 44 | - Ease the training of deeper networks |
| ResNet-152 (He et al., 2016) | 21.69 | 5.94 | 152 | 60 | |
| SqueezeNet 1.0 (Iandola et al., 2016) | 41.9 | 19.58 | 18 | 1.24 | - 50x reduction in model size of AlexNet |
| SqueezeNet 1.1 | 41.81 | 19.38 | 18 | 1.23 | - Deep compression with 8-bit quantization |
| Densenet-121 (Huang et al., 2017) | 25.35 | 7.83 | 121 | 8 | - Cross-layer information flow |
| Densenet-169 | 24 | 7 | 169 | 14 | - Alleviate the vanishing-gradient problem |
| Densenet-201 | 22.8 | 6.43 | 201 | 20 | - Reduced number of parameters |
| Densenet-161 | 22.35 | 6.2 | 161 | 28 | - Encourage Feature Reuse |
| Inception v3 (Szegedy et al., 2016) | 22.55 | 6.44 | 48 | 24 | - Handles representational bottleneck |
| MobileNet V2 (Sandler et al., 2018) | 30.22 | 10.47 | 22 | 6 | - Replace large size filters with small filters |
| MobileNet (Szegedy et al., 2015) | 28.12 | 9.71 | 53 | 3 | - Introduced block concept |
| MobileNet V2 (Sandler et al., 2018) | 28.12 | 9.71 | 53 | 3 | - Split transform and merge idea |
| ResNet-50-32x4d | 22.38 | 6.3 | 50 | 25 | - Inverted residual structure |
| ResNet-101-32x8d (Xie et al., 2017) | 20.69 | 5.47 | 101 | 88 | - Non-linearities in narrow layers removed |
| ResNeXt-50-32x4d | 22.38 | 6.3 | 50 | 25 | - Cardinality |
| ResNeXt-101-32x8d | 20.69 | 5.47 | 101 | 88 | - Homogeneous topology |
| ResNeXt-101-32x8d (Xie et al., 2017) | 22.38 | 6.3 | 50 | 25 | - Grouped convolution |
| Wide ResNet-50-2 | 21.49 | 5.91 | 50 | 68 | - Feature Reuse and Fast training |
| Wide ResNet-101-2 (Zagoruyko and Komodakis, 2016) | 21.16 | 5.72 | 101 | 126 | - Width is increased and depth is decreased |

Table 4: Overview of CNN model architectures. Error rates (%) on ImageNet dataset as reported in Pytorch documentation.

Appendix C. Additional Evaluation Results

In this section, the training and validation plots for accuracy (Figures 8, 10, 12, 14), and loss (Figures 7, 9, 11, 13) are presented along with the confusion matrices (Figures 3, 4, 5, 6) of our four top performing models are presented.
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Figure 3: Confusion Matrix for Wide ResNet-50_2

Figure 4: Confusion Matrix for VGG-19

Figure 5: Confusion Matrix for Wide ResNet-101_2

Figure 6: Confusion Matrix for ResNet-34
Figure 7: Loss vs Epochs plot for Wide ResNet-50_2

Figure 8: Accuracy vs Epochs plot for Wide ResNet-50_2

Figure 9: Loss vs Epochs Plot for VGG-19

Figure 10: Accuracy vs Epochs Plot for VGG-19
Figure 11: Loss vs Epochs Plot for Wide ResNet-101_2

Figure 12: Accuracy vs Epochs Plot for Wide ResNet-101_2

Figure 13: Loss vs Epochs Plot for ResNet-34

Figure 14: Accuracy vs Epochs Plot for ResNet-34
