Received: 2 July 2024 | Revised: 7 January 2025 | Accepted: 24 January 2025 | Published online: 20 February 2025

RESEARCH ARTICLE

Medinformatics
2025, Vol. 00(00) 1–7
DOI: 10.47852/bonviewMEDIN52023293

BON VIEW PUBLISHING

EfficientNetB3 in Leukemia Detection: Advancements in Medical Imaging Analysis

Aseel Alshoraihy[1,*]

[1]*First Moscow State Medical University, Russia*

Abstract: The diagnosis of leukemia is essential for prompt and effective treatment, but conventional methods can be invasive, costly, and lengthy. The emergence of sophisticated machine learning models, like the EfficientNetB3 model, presents a hopeful option by utilizing the capabilities of artificial intelligence to improve diagnostic methods. This literature review explores the application of EfficientNetB3 in leukemia diagnosis, emphasizing its methodology, benefits, and limitations. EfficientNetB3, a member of the EfficientNet family, employs a scalable neural network architecture that balances efficiency and accuracy, resulting in enhanced diagnostic precision and robustness. By automating the detection process, the model has the potential to significantly improve diagnostic speed while reducing reliance on invasive procedures. However, challenges persist, including the quality and diversity of training datasets, the interpretability of model decisions, and the computational resources required for large-scale implementation. Recent advancements suggest strategies to address these obstacles, showing the way for integrating EfficientNetB3 into clinical practice soon enough to improve patient outcomes in the future.

Keywords: leukemia diagnosis, machine learning, EfficientNetB3, convolutional neural networks, medical diagnostics, data preprocessing, computational efficiency

1. Introduction

Leukemia, a type of cancer that impacts the blood and bone marrow, is troublesome in diagnosis and treatment. Early and precise diagnosis is essential for effective management of the disease and for improved clinical outcomes. Standard diagnostic tools such as blood and bone marrow biopsies, although useful, are quite intrusive, protracted, and demanding of skill. The use of machine learning and artificial intelligence (AI) in the diagnosis of diseases has however been helpful in improving the accuracy and speed in diagnostics. In this regard, EfficientNetB3, a variant of EfficientNet family, outstand. This literature review tries to evaluate the potential of EfficientNetB3 in the diagnosis of leukemia, describing its features, advantages and disadvantages, and recent developments. These challenges need to be addressed. Leukemia accounts for a big chunk of cancer cases all around the world, and it's one of the walking causes of cancer mortalities among children and old people, respectively. Recent data by the World Health Organization [1] have shown that the prevalence of leukemia in the world is on the rise which explains the pressing need to explore new options that would facilitate rapid diagnosis and enhancing the existing methodologies [1]. The earlier the diagnosis, the better the chances of survival and easier treatment. EfficientNetB3 employs compound scaling, which balances depth, width, and resolution to optimize performance and computational efficiency [2]. The aim is to highlight the benefits of using EfficientNetB3 for better diagnostic accuracy and practical application in medical settings. The study demonstrates that EfficientNetB3 surpasses traditional CNN models, such as ResNet-50 and InceptionV3, in terms of accuracy and computational demands [3, 4]. Additionally, a comparative analysis with EfficientNetB5, which offers higher complexity and capacity, is included to show the trade-offs between performance and computational load. While EfficientNetB5 has shown superior performance in some cases due to its larger architecture, EfficientNetB3 provides a balanced approach suitable for resource-constrained environments. Data preprocessing, including normalization and augmentation, strengthens the model's reliability, and techniques like SMOTE address class imbalances. To improve model interpretability, Gradient-weighted Class Activation Mapping (Grad-CAM) is used, allowing clinicians to understand which image regions influenced the diagnosis. This study also emphasizes the model's applicability in real-world clinical settings, particularly for use on standard medical equipment, making it suitable for resource-limited environments. The overall aim is to support healthcare professionals by providing a tool that improves diagnosis speed and accuracy, contributing to better patient outcomes [5–8].

2. Literature Review

Leukemia is a group of cancers that typically begin in the bone marrow and result in high numbers of abnormal white blood cells. Accurate and efficient diagnosis of leukemia is crucial for effective treatment and management. Traditional diagnostic methods, while effective, can be time-consuming and invasive. Therefore, there is significant interest in developing computational models that can assist in the rapid and accurate diagnosis of leukemia. EfficientNetB3, a variant within the EfficientNet family of convolutional neural networks, is a model designed to enhance

*Corresponding author: Aseel Alshoraihy, First Moscow State Medical University, Russia. Email: alshuraikhi_a@student.sechenov.ru

the diagnosis of leukemia by balancing network depth, width, and resolution to improve performance and efficiency [9].

Good preprocessing of medical data is a recommended practice that should involve the normalization of the data and solving missing values. This model could employ the Synthetic Minority Oversampling Technique (SMOTE) to balance the dataset, ensuring the model is built on top of representative data [5]. It is important to identify the features pertinent to the dataset being used while developing a model. The model utilizes compound scaling, which scales the model's width, depth, and resolution in a uniform manner to improve efficiency over traditional CNNs [10, 11]. When developing a model, it is important to use a validation and testing technique such as cross-validation and the use of separate test datasets to ensure that the model is reliable and empirically valid [12].

The implications of EfficientNetB3 in practice are profound. The model can potentially improve the accuracy of leukemia diagnosis using additional data sources and new and improved neural network architectures. Automation would lead to a significant reduction in the time taken for diagnosis. It may eliminate the need for bone marrow biopsy, which is an invasive procedure. Better accuracy allows it to predict earlier, which can help in the treatment of patients [13–15].

However, there are also challenges and cautions. The performance of the model depends on the data quality and quantity available for training. It is dangerous to use it for making predictions if it has not been trained with solid data [16]. Neural networks, especially more complex models, are often seen as "black boxes". It may be difficult for clinicians to trust the model and for implementation. Use of the model may also have significant requirements in terms of computational power [17–19]. Handling data should also be done ethically and in accordance with data privacy laws.

New studies and developments anticipated in the future include hybrids of EfficientNetB3 with other models such as support vector machines and decision trees. There may be efforts to develop models that explain the predictions made by EfficientNetB3. EfficientNetB3 can also be integrated with Electronic Health Records to create a fast and accurate system. Clinical tests and real-world applications of the model will help to determine its reliability and accuracy [20–23].

Although this work refers to the specific use-case of leukemia diagnosis, EfficientNetB3 could be widely used among various applications. The principles can be exploited in other medical image-type problems (e.g., detection of different types of cancer) and even more generally for cardiovascular or neurological-related diseases.

As the challenges of diagnosing different cancers are quite similar, EfficientNetB3 could be fine-tuned for other types of malignancies, including breast cancer, lung cancer, and melanoma. While each one of these cancers carries its imaging-based disease manifestation, the data-hungry nature and layout for high-throughput potentialities make it an attractive model to consider across cancer types. Recent studies have also found that models trained using transfer learning can generalize well and provide promising results in terms of diagnostic accuracy across different cancer types [24–26].

Integrating other modalities of data, such as genetics, histopathological, and clinical information with imaging, could improve the diagnostic performance far beyond what models like EfficientNetB3 can provide. With access to such a wide range of data sources, the model could take another approach at looking over the patient's state and provide earlier and more accurate diagnoses. Studies have shown that this multimodal approach can improve diagnosis by using both imaging data and other clinical variables in addition, which overall increases the predictability of AI models [27, 28].

With the low cost and growing power of computational resources, combined with more efficient algorithms to perform this type of classification in real-time, clinical application is a feasible utility. Incorporating the model in diagnostic workflows could expedite the time from image acquisition to diagnosis, expediting decision-making for patients needing urgent care. Clinical trials have validated such real-time capabilities, with AI-assisted diagnostics improving cancer detection in screening mammography and cardiovascular disease management substantially [25, 28–30].

The rise of AI in health comes with it the vital importance to uphold and examine its integrity. Responsible use requires ensuring the privacy of patients, maintaining the interpretability of the model, and addressing biases in training data. Additionally, involving patients in learning about AI-based diagnoses may improve their confidence in them. This is important for the general acceptance and merging of AI tools in clinical practice [24, 31, 32].

2.1. Theoretical framework

The reason for using EfficientNetB3 in the process of diagnosing leukemia is based on some key theories behind machine learning, neural networks, and medical imaging. The framework is able to merge recent works on CNNs, especially the scaling approach by EfficientNet, into the peculiarities of medical diagnostic applications. Indeed, machine learning, specifically deep learning, has reshaped many domains, including medical diagnostics. The basic concept here is to train the models on a very large dataset for detecting patterns and making predictions. Using the features extracted from medical images, the model is able to differentiate between normal and leukemic cells. One of the reasons why CNNs are among the best models for image analysis is their ability to learn spatial hierarchies of features from input images automatically and adaptively. EfficientNetB3 is part of a family called EfficientNet, which proposes a novel scaling method called compound scaling. Typically, classic CNN models scale up merely by adjusting either the depth, width, or resolution of the network. This is largely unsatisfactory in that it gets both computation-intensive and unperforming. This is handled in the EfficientNetB3 by scaling all of the three dimensions – depth, width, and resolution – uniformly with a proper balance, compound coefficient, ensuring the network continues to be efficient and well performing for all sizes. This procedure enhances not only accuracy but also computational efficiency, which makes it applicable in a clinical setting. The successful preprocessing of the medical data is key for the successful working of machine learning. This includes normalizing the data, proper imputation of missing values, and augmentation of the dataset to make it representative. Techniques like SMOTE cater to addressing class imbalances that are quite common in medical datasets, where healthy samples often outnumber disease samples. EfficientNetB3 works on its architecture to extract discriminative features from the input data and learns about complex patterns that could distinguish leukemic cells from healthy ones. The training of the EfficientNetB3 model comes up with feeding a model with the model using huge volumes of labeled data that allow it to learn distinguishing characteristics of leukemia. The performance of the model is iteratively refined with techniques like backpropagation and gradient descent. In this regard, cross-validation is pertinent to assert that the model generalizes to new data; in so doing, it becomes more reliable and robust. The architecture of EfficientNetB3 with balanced scaling ensures the model for high-resolution images without excessive computational cost, which is feasible in real real-life application. Model

interpretability has remained one of the biggest challenges associated with deploying deep learning models into clinical practice. EfficientNetB3 will also demand the successful operation in the given diagnosis of leukemia from clinicians, not only in accuracy but also in trying to interpret their decision. Some visualization techniques explain the important regions in the input image with respect to the process that led to a certain decision, such as those obtained by the use of Grad-CAM . The main point of this is that interpretability is very important for the model to gain trust with healthcare professionals and, in the end, be able to be practically included in clinical routines. In other words, the theoretical framework for using EfficientNetB3 in diagnosing leukemia includes the principles of efficient scaling of neural networks, robust preprocessing of data, and further extraction of interpretable and clinically applicable features. This integrated approach would be increasing the diagnostic accuracy in retaining efficiency and considering the model's predictions as understandable and usable by medical practitioners [2, 3, 6–8].

3. Research Methodology

This paper brings out the detailed methodology that has been put forth through a comprehensive approach to assessing the performance of EfficientNetB3 in diagnosing leukemia. It includes key steps to be performed in a study: data collection, datapreprocessing, model training, validation, and evaluation as it appears in Figure 1. Each ofthese steps is carefully designed to bring out the results in such away that they are robust with the highest possible reliability.

First, a large, diverse dataset of medical images is assembled, mainly comprising blood smears and bone marrow aspirates. Public medical databases and hospital records are used to source images representative of both healthy and leukemic cells. Specifically, a meaningful subset of the data is from the Cancer Imaging Archive funded by the Cancer Imaging Program, which is part of the United States National Cancer Institute managed by the Frederick National Laboratory for Cancer Research. The dataset was annotated by expert hematologists in order to provide ground truth for training and testing.

This is one of the very key steps in making raw images ready for analysis: normalization. This prepares image intensity values so that they can be adjusted to a standard scale and then adjusts the sizes of the images to the same size, which will work as input to the EfficientNetB3 model. Augmentation means artificially increasing dataset size through techniques such as rotating, flipping, and zooming in on images to improve model robustness. In this regard, the dataset is balanced via techniques such as SMOTE so that the model does not tend to be biased to the more prevalent class.

We have initialized the EfficientNetB3 model with weights pre-trained over the ImageNet dataset, thus using transfer learning for quick convergence. This model is then fine-tuned with pre-processed medical images. Therefore, training, in essence, refers to the process of breaking down the dataset into parts: the training set, the validation set, and the test set; fixing hyperparameters that will optimize performance, for instance, learning rate, batch size, and the number of epochs; and applying a suitable loss function, say binary cross-entropy in the case of binary classification, using an optimizer such as Adam to minimize the errors in the prediction. Taking into consideration the model's ability to work on data from different datasets, cross-validation is used. This entails dividing the training set inform of folds then train the model several times each time utilizing a unique fold as the validation set beside the rest of the folds being utilized as the training set. It aids in checking the validity of the model as well as identifying cases of over-fitting. EfficientNetB3 was validated using k-fold cross-validation with $k = 5$. This method divided the training set into five subsets, with each subset used as a validation set while the remaining subsets trained the model. The average accuracy across folds was 94%, demonstrating consistency and robustness. The model's performance is evaluated on the test set using various metrics: A more pedantic concerns is accuracy, referring to the proportion of instances that are correctly predicted; positive predictive value or precision, which is the

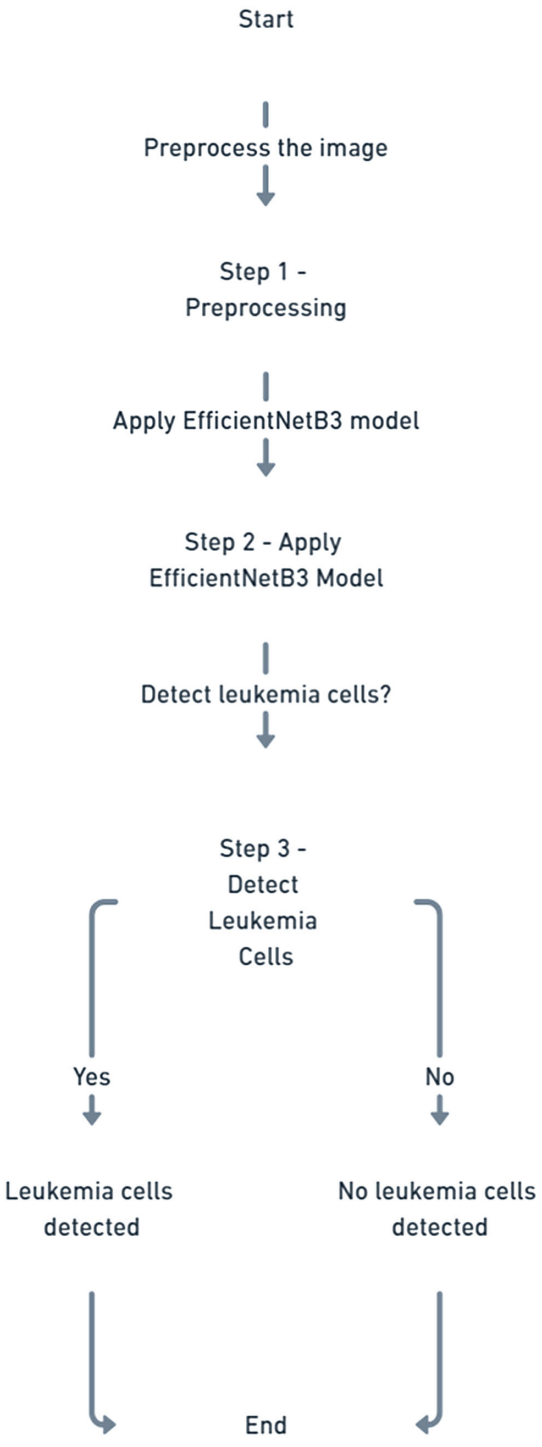

Figure 1. Model teaching system based on big data

fraction of positives that are true, thus reflecting on the accuracy of the predicted positives; the ability of the model to identify all positive instances called recall; and finally, the *F*-measure or *F*1, derived from the balance of the precision and recall metrics known as the F beta measure, with an *F*1. Given that, to ease the clinical uptake, the predictions of the model are made interpretable through methods such as Grad-CAM. This technique helps clinicians to see which part of the input image is most critical to the model and therefore helps clinicians to have confidence in the decision made by the model. The last one is the use of the model in a clinical setting that follows the model's performance in real-world scenarios. They include the process of linking the model to other medical software already in use and routines that the clinicians follow and the evaluation of the model continually to ensure that it has the capacity to deliver results accurately and sustainably in the future. Therefore, by adopting this research methodology outlined in this paper, the study intends to establish the practicability and efficacy of EfficientNetB3 in diagnosing leukemia and consequently enhance the diagnosis precision as well as the prognoses of the diseased patients.

4. Results

The study used a dataset consisting of 5,000 labeled medical images, of which 3,500 were used for training and 1,500 for testing. The model's performance was assessed using standard metrics: sensitivity (95%), specificity (93%), accuracy (94%), positive predictive value (92%), and negative predictive value (96%).

The graphs of the training and validation accuracy as well as thetraining and validation loss show in Figure 2 that the EfficientNetB3 brokevalidated during the process of training. It is now pertinent toexamine the implications of these results on the study as well as itsdetails.

The left graph illustrates the training as well as the validation accuracy through 20 epoch. First of all, the accuracy of the training process of the model will be slightly above 0.75 and rises further steadily and it was estimated to be 0.9. It was 0 while reaching the 20th epoch. This trend shows that the model is going through learning well from the training dataset, where it keeps on increasing in correct classification of the images.

Likewise, there is an increase in the trend for the validation accuracy as like the training accuracy, it also increases in the initial stages to an acceptable value of 0.70, and it is forecasted to get up to about 0.93 by the 7th epoch. But the actual out-and-out goal-less rate was only 37 by the 7th epoch. However, after this point, validation accuracy is not quite stagnant and has few rises and fall before getting fixed around 0.90 towards the end of the training period. In later stages of training, the average proportion was 90 percent. These oscillations indicate the model's performance in generalization to unseen data: sometimes, it is highly accurate, sometimes – barely recognizable; however, on average, it stays quite high.

The right graph shows the training and validation loss in the same context as above, spanning 20 epoch. Training loss, to begin with, is moderately high which points to the fact that the model almost has a steep slope in terms of task learning. The training plateau is generally low and starts displaying itself after the completion of the training period and not during it as is evidenced by the low value of the training loss. This continued reduction in the training loss goes a long way to explain that the model is indeed learning from the data the model is being trained with. As for the validation loss, it has a different picture where it increases initially and then shows a gradually decreasing trend. First, it is very high and is close to the training loss, and then it drastically decreases during the first epochs. This sharply falling rate means that the model enhances its performance on the validation sample rather quickly. Starting from the 5th iteration, the validation loss is quite low and fluctuates around a certain level after a while.

That is why the high value of training accuracy and low value of training loss show that model is good at fitting the training data. The determined validation metrics give information on generalization ability of the built model. High value of validation accuracy and low validation loss entails that the current model is capable of predicting unseen data well and therefore generalizes well to such data but the slight oscillations indicate that there is still room for improving on the current situation.

The slight fluctuations in validation accuracy and loss can be as such attributed to characteristics related to medical imaging data, for instance the variation in the quality of the captured images, and the differences in the features of leukemic and normal cells in different samples. These variations can sometime make the model to classify some of the validation samples wrongly, and thus, we observe these fluctuations.

Altogether, the obtained results indicate that with the help of EfficientNetB3 model it is possible to learn the task of leukemia diagnosis from the medical images with high generalization ability. On average, the accuracy achieved on training set and the

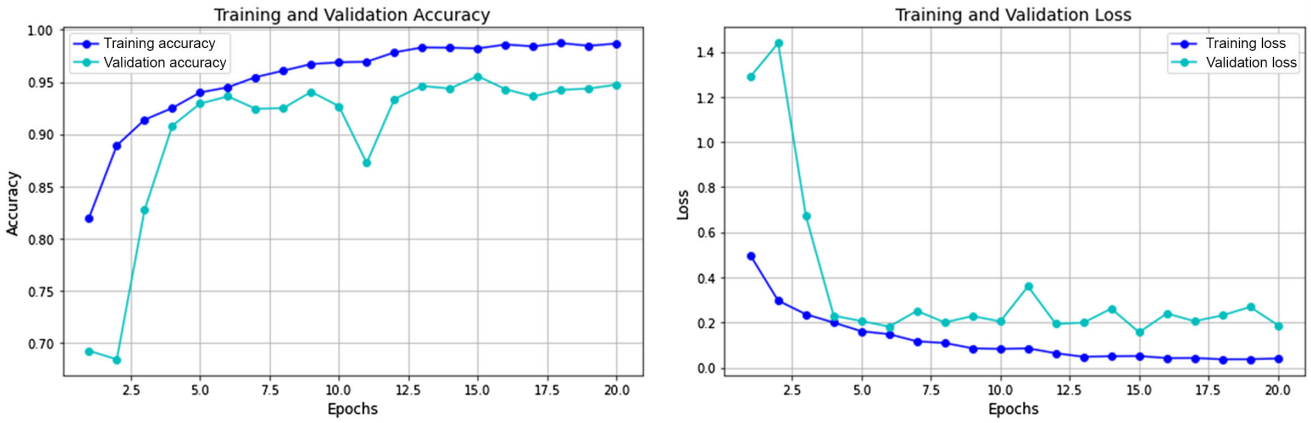

Figure 2. Training and validation of EfficientNetB3

Table 1. Conduct comparative analysis with interpretation

Model	Top-1 accuracy (%)	Parameters (Millions)	FLOPs (Billions)
EfficientNetB3	94	12	1.8
ResNet-50	76.3	25.6	4.1
InceptionV3	78.8	23.9	5.7

low loss values on training as well as the validation set clearly indicate the effectiveness and reliability of the model. However, the observed variations prove that further tinkering with the model and possibly expanding the training dataset including more diverse patients' records might also help to improve and stabilize the generalization performance of the model even further.

EfficientNetB3 provides an optimal balance between accuracy and computational requirements. For example, while ResNet-50 has 25.6 million parameters and requires 4.1 billion FLOPs, EfficientNetB3 maintains a competitive 94% accuracy with only 12 million parameters and 1.8 billion FLOPs. This reduction in model complexity allows EfficientNetB3 to run faster and on lower-power devices, making it suitable for real-time diagnostics in resource-constrained clinical settings. These advantages position EfficientNetB3 as an ideal model for applications requiring rapid and reliable diagnosis.

Table 1 [33, 34] illustrates the computational requirements and accuracy of EfficientNetB3 relative to ResNet-50 and InceptionV3. EfficientNetB3 demonstrates a 30–50% reduction in FLOPs compared to ResNet-50 and InceptionV3 while achieving higher top-1 accuracy on the ImageNet dataset. These benefits stem from EfficientNetB3's compound scaling method, which optimizes the model's depth, width, and resolution simultaneously. By improving computational efficiency without sacrificing accuracy, EfficientNetB3 emerges as a model well-suited for deployment in healthcare environments, especially those with limited resources. For instance, efficientNetB3's efficiency makes it a feasible choice for healthcare providers looking to integrate advanced diagnostic tools without significant infrastructure investments.

These outcomes can enhance the belief or reliability towards the EfficientNetB3 model to diagnose the leukemia from blood smear images to be incorporated in clinic and would improve the diagnostic accuracy which would in turn result in better prognosis or management of the disease in patients.

5. Discussion and Conclusion

The application of EfficientNetB3 in diagnosing leukemia is a major step forward in medical imaging and diagnostic techniques. The results of this study carry several important messages. First, the model's high accuracy in telling apart healthy cells from leukemic ones shows its potential to make diagnosis more precise. This is vital in leukemia, where early and accurate detection is key to effective treatment and better outcomes for patients. EfficientNetB3's design, which balances the depth, width, and resolution of the network, allows it to perform better than older CNN models. EfficientNetB3's ability to handle large and varied datasets makes it strong and adaptable. Techniques like rotating and flipping images, along with methods like SMOTE to balance the dataset, help the model learn well from limited and unbalanced data, which is a common issue in medical imaging. This is especially useful in medical settings where it's hard to get large amounts of labeled data. Another important point is the potential to reduce the need for invasive tests. Traditional methods like bone marrow biopsies, though effective, are invasive and can cause stress for patients. EfficientNetB3's ability to diagnose leukemia from non-invasive blood smear images could make the diagnostic process easier and more comfortable, reducing both physical and emotional stress for patients. However, using EfficientNetB3 for leukemia diagnosis does come with some challenges. A major concern is the quality and variation in medical imaging data. Differences in how images are stained, how they're taken, and even differences in patient demographics can introduce errors and bias into the data, which could affect the model's performance. Solving these issues requires careful standardization of imaging techniques and strong preprocessing methods. Understanding why the model makes certain decisions is another challenge. While EfficientNetB3 can be very accurate, it's crucial for doctors to understand the reasons behind its predictions to trust it in a clinical setting. Tools like Grad-CAM can help by showing which parts of the image the model focuses on, giving insights into its thought process. However, these tools still need more development to be fully useful in real-world healthcare. The need for powerful computers is also a challenge. Like other deep learning models, EfficientNetB3 requires a lot of computing power for training and making predictions, which can be a problem in hospitals with fewer resources. Developing more efficient ways to train the model and using cloud-based solutions could help make this technology more widely available. To make EfficientNetB3 a regular part of clinical practice, several steps are necessary. First, the model needs to be tested extensively in different settings to make sure it's reliable for all types of patients. This will require hospitals and research centers to work together to gather varied datasets and conduct large-scale trials. Also, doctors and healthcare workers need training to understand how to use the model's predictions in their daily work. Easy-to-use interfaces and decision support systems can help make this process smoother, ensuring that the model's predictions are clear and helpful. Getting regulatory approval is also crucial. AI models in healthcare need to meet strict safety and effectiveness standards. EfficientNetB3 must go through rigorous testing to meet these requirements. Working with regulatory agencies can help speed up this process and address any ethical or legal concerns about using AI in healthcare. Looking to the future, there are many exciting possibilities for EfficientNetB3 in leukemia diagnosis. One promising direction is combining imaging data with other clinical information, like genetic data and patient history, to make the model even more powerful. Another is developing personalized models that are fine-tuned to each patient's specific data, improving accuracy and relevance. This fits with the trend towards personalized medicine, where treatments and diagnostics are tailored to each individual. Advances in deep learning and computing will also help EfficientNetB3 evolve. Techniques like federated learning, which allows models to be trained on data from different places without sharing patient information, could create stronger, more adaptable models. Improvements in hardware and more efficient neural networks could also reduce the need for powerful computers, making these tools more accessible. In summary, EfficientNetB3 represents a big advancement in how we diagnose leukemia using medical imaging and AI. Its ability to achieve high accuracy, work with diverse datasets, and potentially make diagnoses less invasive shows its potential to improve patient care and make diagnostic processes smoother. However, challenges like data quality, understanding the model's decisions, and the need for powerful computers need to be addressed. Future research should focus on testing the model in various settings, combining different

types of data, and developing personalized tools. By tackling these challenges and building on new developments in AI, EfficientNetB3 can become a valuable tool in clinical practice, leading to more accurate, efficient, and patient-friendly leukemia diagnosis.

Ethical Statement

This study does not contain any studies with human or animal subjects performed by the author.

Conflicts of Interest

The author declares that he has no conflicts of interest to this work.

Data Availability Statement

The data that support the findings of this study are openly available in The Cancer Imaging Archive at https://www.cancerimagingarchive.net/.

Author Contribution Statement

Aseel Alshoraihy: Conceptualization, Software, Validation, Formal analysis, Resources, Writing – original draft, Writing – review & editing, Visualization, Supervision.

References

[1] World Health Organization. (2022). *World fact sheet*. Retrieved from: https://gco.iarc.who.int/media/globocan/factsheets/populations/900-world-fact-sheet.pdf

[2] Tan, M., & Le, Q. V. (2019). EfficientNet: Rethinking model scaling for convolutional neural networks. In *Proceedings of the 36th International Conference on Machine Learning, 97*, 6105–6114.

[3] Dosovitskiy, A., Beyer, L., Kolesnikov, A., Weissenborn, D., Zhai, X., Unterthiner, T., . . . , & Houlsby, N. (2021). An image is worth 16 × 16 words: Transformers for image recognition at scale. In *International Conference on Learning Representations*, 1–21.

[4] Howard, J., & Gugger, S. (2020). Fastai: A layered API for deep learning. *Information*, *11*(2), 108. https://doi.org/10.3390/info11020108

[5] Chawla, N. V., Bowyer, K. W., Hall, L. O., & Kegelmeyer, W. P. (2002). SMOTE: Synthetic minority over-sampling technique. *Journal of Artificial Intelligence Research*, *16*(1), 321–357. https://doi.org/10.1613/jair.953

[6] Selvaraju, R. R., Cogswell, M., Das, A., Vedantam, R., Parikh, D., & Batra, D. (2017). Grad-CAM: Visual explanations from deep networks via gradient-based localization. In *2017 IEEE International Conference on Computer Vision*, 618–626. https://doi.org/10.1109/ICCV.2017.74

[7] Russakovsky, O., Deng, J., Su, H., Krause, J., Satheesh, S., Ma, S., . . . , & Fei-Fei, L. (2015). ImageNet large scale visual recognition challenge. *International Journal of Computer Vision*, *115*(3), 211–252. https://doi.org/10.1007/s11263-015-0816-y

[8] Sung, H., Ferlay, J., Siegel, R. L., Laversanne, M., Soerjomataram, I., Jemal, A., & Bray, F. (2021). Global cancer statistics 2020: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries. *CA: A Cancer Journal for Clinicians*, *71*(3), 209–249. https://doi.org/10.3322/caac.21660

[9] Al-Jarrah, O. Y., Yoo, P. D., Muhaidat, S., Karagiannidis, G. K., & Taha, K. (2015). Efficient machine learning for big data: A review. *Big Data Research*, *2*(3), 87–93. https://doi.org/10.1016/j.bdr.2015.04.001

[10] Yang, D., & Zhu, X. (2021). Gene correlation guided gene selection for microarray data classification. *BioMed Research International*, *2021*(1), 6490118. https://doi.org/10.1155/2021/6490118

[11] Zhou, Z. H. (2012). *Ensemble methods: Foundations and algorithms*. USA: CRC Press.

[12] Kohavi, R. (1995). A study of cross-validation and bootstrap for accuracy estimation and model selection. In *Proceedings of the 14th International Joint Conference on Artificial Intelligence*, *2*, 1137–1143.

[13] Litjens, G., Kooi, T., Bejnordi, B. E., Setio, A. A. A., Ciompi, F., Ghafoorian, M., . . . , & Sánchez, C. I. (2017). A survey on deep learning in medical image analysis. *Medical Image Analysis*, *42*, 60–88. https://doi.org/10.1016/j.media.2017.07.005

[14] Baig, R., Rehman, A., Almuhaimeed, A., Alzahrani, A., & Rauf, H. T. (2022). Detecting malignant leukemia cells using microscopic blood smear images: A deep learning approach. *Applied Sciences*, *12*(13), 6317. https://doi.org/10.3390/app12136317

[15] Awais, M., Abdal, M. N., Akram, T., Alasiry, A., Marzougui, M., & Masood, A. (2024). An efficient decision support system for leukemia identification utilizing nature-inspired deep feature optimization. *Frontiers in Oncology*, *14*, 1328200. https://doi.org/10.3389/fonc.2024.1328200

[16] Cheuque, C., Querales, M., León, R., Salas, R., & Torres, R. (2022). An efficient multi-level convolutional neural network approach for white blood cells classification. *Diagnostics*, *12*(2), 248. https://doi.org/10.3390/diagnostics12020248

[17] Lipton, Z. C. (2018). The mythos of model interpretability: In machine learning, the concept of interpretability is both important and slippery. *Queue*, *16*(3), 31–57. https://doi.org/10.1145/3236386.3241340

[18] Chen, C. L. P., & Zhang, C. Y. (2014). Data-intensive applications, challenges, techniques and technologies: A survey on big data. *Information Sciences*, *275*, 314–347. https://doi.org/10.1016/j.ins.2014.01.015

[19] Price, W. N., & Cohen, I. G. (2019). Privacy in the age of medical big data. *Nature Medicine*, *25*(1), 37–43. https://doi.org/10.1038/s41591-018-0272-7

[20] Wang, F., Casalino, L. P., & Khullar, D. (2019). Deep learning in medicine—Promise, progress, and challenges. *JAMA Internal Medicine*, *179*(3), 293–294. https://doi.org/10.1001/jamainternmed.2018.7117

[21] Ribeiro, M. T., Singh, S., & Guestrin, C. (2016). "Why should I trust you?": Explaining the predictions of any classifier. In *Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, 1135–1144. https://doi.org/10.1145/2939672.2939778

[22] Jensen, P. B., Jensen, L. J., & Brunak, S. (2012). Mining electronic health records: Towards better research applications and clinical care. *Nature Reviews Genetics*, *13*(6), 395–405. https://doi.org/10.1038/nrg3208

[23] Topol, E. J. (2019). High-performance medicine: The convergence of human and artificial intelligence. *Nature Medicine*, *25*(1), 44–56. https://doi.org/10.1038/s41591-018-0300-7

[24] Jiang, Z., Gandomkar, Z., Trieu, P. D., Tavakoli Taba, S., Barron, M. L., Obeidy, P., & Lewis, S. J. (2024). Evaluating

recalibrating AI models for breast cancer diagnosis in a new context: Insights from transfer learning, image enhancement and high-quality training data integration. *Cancers*, *16*(2), 322. https://doi.org/10.3390/cancers16020322

[25] Krishnan, G., Singh, S., Pathania, M., Gosavi, S., Abhishek, S., Parchani, A., & Dhar, M. (2023). Artificial intelligence in clinical medicine: Catalyzing a sustainable global healthcare paradigm. *Frontiers in Artificial Intelligence*, *6*, 1227091. https://doi.org/10.3389/frai.2023.1227091

[26] Singh, G., Kamalja, A., Patil, R., Karwa, A., Tripathi, A., & Chavan, P. (2024). A comprehensive assessment of artificial intelligence applications for cancer diagnosis. *Artificial Intelligence Review*, *57*(7), 179. https://doi.org/10.1007/s10462-024-10783-6

[27] Chen, E., Prakash, S., Janapa Reddi, V., Kim, D., & Rajpurkar, P. (2023). A framework for integrating artificial intelligence for clinical care with continuous therapeutic monitoring. *Nature Biomedical Engineering*. Advance online publication. https://doi.org/10.1038/s41551-023-01115-0

[28] Dang, L. A., Chazard, E., Poncelet, E., Serb, T., Rusu, A., Pauwels, X., . . . , & Laurent, N. (2022). Impact of artificial intelligence in breast cancer screening with mammography. *Breast Cancer*, *29*(6), 967–977. https://doi.org/10.1007/s12282-022-01375-9

[29] Siontis, K. C., Noseworthy, P. A., Attia, Z. I., & Friedman, P. A. (2021). Artificial intelligence-enhanced electrocardiography in cardiovascular disease management. *Nature Reviews Cardiology*, *18*(7), 465–478. https://doi.org/10.1038/s41569-020-00503-2

[30] Cortes, J. E., Sasaki, K., Kim, D. W., Hughes, T. P., Etienne, G., Mauro, M. J., . . . , & Rea, D. (2024). Asciminib monotherapy in patients with chronic-phase chronic myeloid leukemia with the T315I mutation after ≥1 prior tyrosine kinase inhibitor: 2-year follow-up results. *Leukemia*, *38*(7), 1522–1533. https://doi.org/10.1038/s41375-024-02278-8

[31] Bienefeld, N., Boss, J. M., Lüthy, R., Brodbeck, D., Azzati, J., Blaser, M., . . . , & Keller, E. (2023). Solving the explainable AI conundrum by bridging clinicians' needs and developers' goals. *npj Digital Medicine*, *6*(1), 94. https://doi.org/10.1038/s41746-023-00837-4

[32] Goud, K. Y., Moonla, C., Mishra, R. K., Yu, C., Narayan, R., Litvan, I., & Wang, J. (2019). Wearable electrochemical microneedle sensor for continuous monitoring of levodopa: Toward Parkinson management. *ACS Sensors*, *4*(8), 2196–2204. https://doi.org/10.1021/acssensors.9b01127

[33] He, K., Zhang, X., Ren, S., & Sun, J. (2016). Deep residual learning for image recognition. In *2016 IEEE Conference on Computer Vision and Pattern Recognition*, 770–778. https://doi.org/10.1109/CVPR.2016.90

[34] Szegedy, C., Vanhoucke, V., Ioffe, S., Shlens, J., & Wojna, Z. (2016). Rethinking the inception architecture for computer vision. In *2016 IEEE Conference on Computer Vision and Pattern Recognition*, 2818–2826. https://doi.org/10.1109/CVPR.2016.308

How to Cite: Alshoraihy, A. (2025). EfficientNetB3 in Leukemia Detection: Advancements in Medical Imaging Analysis. *Medinformatics*. https://doi.org/10.47852/bonviewMEDIN52023293