# Automated diagnosis of breast cancer using deep learning

**Iustin FLOROIU, Daniela TIMISICĂ, Radu Marius BONCEA**

National Institute for Research & Development in Informatics – ICI Bucharest

iustin.floroiu@ici.ro, daniela.timisica@ici.ro, radu.boncea@ici.ro

**Abstract:** Breast cancer is one of the most common types of cancer in recent years. Therefore, effective diagnostic methods are essential to reduce complications and the risk of metastasis. Using histopathological analysis with the naked eye is not efficient in preventing cancer because most malignant tumors exhibit genetic instability due to repeated and abnormal mitosis. This leads to the formation of immature cells with varying membrane properties and different protein receptors. The purpose of this article is to present an analysis of the current stage in the field of breast cancer, as well as the biomedical applications of deep learning. By using convolutional neural network architectures, artificial intelligence enables automatic diagnosis through the recognition of patterns and features from histopathological samples.

**Keywords:** Breast Carcinoma, Automated Diagnosis, Artificial Intelligence, Convolutional Networks.

# Diagnosticul automatizat al cancerului mamar utilizând algoritmi de învățare profundă

**Rezumat:** În ultimii ani, cancerul mamar a devenit una dintre cele mai frecvente patologii oncologice. Din acest motiv, metodele eficiente de diagnostic sunt esențiale pentru a minimiza complicațiile și riscul de metastaze. Cu toate acestea, utilizarea analizei histopatologice cu ochiul liber nu este o măsură eficientă de prevenire a cancerului. Acest lucru se datorează, în principal, instabilității genetice observate în majoritatea tumorilor maligne, cauzată de cicluri mitotice repetate și anormale. Prin urmare, această instabilitate duce la formarea de corpuri celulare imature cu proprietăți membranare distincte, inclusiv receptori proteici diferiți. Scopul acestui articol este de a prezenta analiza stadiului actual în domeniul cancerului mamar, precum și aplicațiile biomedicale ale învățării profunde. Prin utilizarea arhitecturilor de tip rețele convoluționale, inteligența artificială permite diagnosticarea automată prin recunoașterea formelor și trăsăturilor din probe histopatologice.

**Cuvinte cheie:** carcinom mamar, diagnostic automatizat, inteligență artificială, rețele convoluționale.

## 1. Introduction

Breast cancer is one of the most challenging type of cancers because of its peculiarity of tissue behaviour, as well as its prevalence. It is estimated that breast cancer will become one of the most common, if not the most common type of cancer in humans. Due to the fact that it is a type of cancer that largely affects epithelial tissue, it is known as carcinoma. Given the nature of carcinomas, it is common for cancer cells to form mineralisation of tissues. However, due to the nature of breast tissue, mineralisation is common in this given tissue, which makes identification more difficult (Sharma et al., 2010) (Paraschiv et al., 2020).

The purpose of this study case is to showcase the biomedical applications of deep learning and not to make medical inferences regarding the nature of carcinomas.

There are multiple ways to study and identify breast carcinomas. The most usual one is based on histopathological analysis of the stained tissue using optical microscopy. Other types of analysis involve more complex techniques, such as positron emission tomography, X-ray imaging and magnetic resonance imaging.

## 2. Histopathological notions about carcinoma

Cellular division is faster in cancer cells than in healthy, normal cells, which makes it easier, from a genetic standpoint, for mutations to occur. Breast cancer is one of the most common oncological pathologies in recent years (Sharma et al., 2010). For this reason, effective diagnostic

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methods are needed to reduce the factors that can lead to serious complications or the development of metastases in the body. Thus, one method effective method to prevent cancer using histopathological analysis by the naked eye is not effective for the reason that most malignant tumours, through their genetic instability, mainly caused by repeated and cyclically abnormal mitosis, lead to the formation of immature cell bodies with different membrane properties, including different protein receptors (Waks et al., 2019). Genetic mutations caused by infantile mitosis can easily lead to the formation of metastases that lead to cell vectors forming tumour subtypes that are less likely to of responding to treatments applied to initially identified metastases. Therefore, any type of cancer, depending on the tumour aggressiveness present, can mutate through formation of secondary metastases, indicating that very few people affected by cancers end up with only one subtype of cancer in the body, so treatments quickly become ineffective and more than histopathological analysis is needed. Most biomarker tests have very large errors in sensitivity and accuracy in targeting tumour targeting, and most of the subtypes of cancers that can arise from mutations are genomically and proteomically unknown. Thus, analyses that can lead to identification of mutations can be obtained by machine learning and computer vision techniques, by identifying cell morphologies and extracellular matrix. Because of this particularity, a specific carcinoma type is more susceptible to evolve into multiple subtypes inside the body. Unfortunately, for many cancer subtypes, there is still no biochemical component found to identify them. It is estimated that there are thousands subtypes of cancer that are not identifiable by any standard of detection and this is why computer vision techniques and artificial intelligence solutions are useful (Huttunen et al., 2020). It is known that different mutations influence how the morphology of the cells and the cellular organelles inside of them. Even though there is no molecular marker in detecting more cancer subtypes, morphological changes regarding the form of the cell and particularities in the nucleus represent an accurate way of identifying possible changes of a cancer type.

Biochemically, cancer cells are cells that grow and multiply uncontrolled. They are formed by faulty transcriptomic mechanisms, leading to misreading of the DNA information, which is necessary for mitosis. The formation of these cell types is common in the body, but in very rare cases these cells are not destroyed by the body's immune system. This leads to the formation of metastases through excessive division of tumour cells. In order to grow, these cells also secrete molecular factors of a protein molecules that interfere with the molecular cascades that lead to cell signalling and communication. between cells to elicit specific responses from the environment. One such example is the modification of cell signalling pathways at the fibroblast level. Fibroblasts are cells that produce the cellular matrix. The cellular matrix is a polymeric system in mainly of collagen and elastin, found in all cells, which have the property of creating a substrate mechanically and biochemically stable substrate on which cells grow. By modifying the secretion of fibroblasts by tumour cells, the collagen secreted by fibroblasts will be produced differently from the way it is normally produced (Fahad Ullah et al., 2019).

Regarding different imaging techniques necessary for the identification and analysis of carcinoma, optical microscopy is the most common of the techniques from a histopathological standpoint. Optical microscopy involves an electromagnetic radiation illuminating a stained specimen. The stains are used to identify different parts of a tissue. Usually, haematoxylin and eosin are the most common stains, highlighting the collagen fibres, cellular bodies and cell nucleus. The collagen fibres from the extracellular matrix of a tissue are very important in the identification of cancer because malignity produces changes in the distribution of the fibres. The tumoral cells communicate directly with the collagen fibres and with the cells that are responsible for the creation of lysis of the fibres, more specifically with fibroblasts and adipocytes, through cellular signalling, with the purpose of macromolecular structural alteration and changes in the ways the collagen is oriented and localised in the specimen. These alterations are most commonly associated with a series of specific norms, called TACS (tumour associated collagen signatures) which showcase a classification of collagen distributions in malign tissue. Haematoxylin and eosin staining highlight the cell distribution inside the tissue, which shows the formation of a primal cancer or a metastasis based on the number of cells, the form of the cells and the percentage of tissue lysis and necrosis presented (Hristu et al., 2021), (Xi et al., 2021).

## 3. Artificial Intelligence aspects and architectures

From a computational point of view, learning techniques are useful through automated diagnosis, and existing computer vision techniques can lead to segmentation of the tumour surface and collagen fibres. Artificial intelligence is naturally inspired and enables automated diagnosis through pattern recognition in the data to be analysed (Huttunen et al., 2020), (Vrejoiu, 2019).

MobileNetV3 base is a convolutional neural network model developed by Google, which is optimized for computational efficiency and performance on devices. It is part of a series of MobileNet models, with its previous version being MobileNetV2. MobileNetV3 base is based on a looped convolutional neural network architecture and advanced non-linear activation features, giving it superior performance in comparison to its predecessors. By using convolution, MobileNetV3 base can significantly reduce the number of parameters and computational operations required without sacrificing much performance. The model has a modular design and can be configured to suit different usage scenarios. For example, it can be adjusted for maximum computational efficiency or for higher accuracy, depending on the application requirements. MobileNetV3 base has been trained on large and diverse data sets to learn to recognize a wide range of objects and visual features. It can therefore be used for image classification in a variety of applications, such as real-time object recognition, image classification on mobile devices and other deep learning tasks involving image analysis (Koonce, 2021).

EfficientNetB0 base is another convolutional neural network model developed researchers at Google, which stands out for its computational efficiency and performance. It is part of a series of EfficientNet models, with larger variants and more complex models. EfficientNetB0 base uses an innovative architecture that combines different components to achieve an optimal balance between accuracy and efficiency. The model uses a technology called compound scaling, which simultaneously adjusts the depth, width and resolution to achieve superior performance in an efficient way. By adapting the model dimensions to the requirements of the application, EfficientNetB0 base can be used on a wide range of devices and applications, from resource-constrained mobile devices to more powerful machine learning systems. Model efficiency is achieved through the use of special building blocks, such as convolution layers with block filters, skip connections and channel optimisation. These techniques reduce the total number of parameters and calculations required, without affecting the accuracy of the model. It can be used for image classification, object detection, segmentation semantic segmentation and other deep learning tasks involving image analysis, being a powerful and efficient option for machine learning tasks, offering a balanced trade-off between performance and efficiency (Clement et al., 2022).

VGG16 base is a convolutional neural network model that is part of the family of Visual Geometry Group (VGG) models developed by researchers at the University of Oxford University. This model is known for its deep architecture and excellent performance in image classification. VGG16 base is characterised by the use of a large number of convolutional layers and fully connected layers, 16 in total. This deep architecture allows the model to learn complex and abstract image representations. The model uses small (3x3) convolutional filters and pooling layers to extract features from images in a progressive way. These filters are applied repeatedly to capture information at different levels of detail. VGG16 base has been trained on a massive and varied dataset, such as ImageNet, which contains millions of tagged images to learn to recognise a wide range of objects and visual features. However, the VGG16 base has a very deep architecture, which means it requires more computational resources and time for training and inference than more recent models and more efficient models. It is more suitable for systems with more powerful resources or uses in where computational time is not a critical issue (Albashish et al., 2021).

VGG19 is a convolutional neural network model developed by researchers at University of Oxford, known for its depth and excellent performance in classifying images. VGG19 is based on a deep architecture with a total of 19 layers, including layers convolutional layers and fully connected layers. This deep design allows the model to capture complex and abstract image features. The VGG19 architecture is characterised by the repeated use of convolutional filters of and pooling layers, which progressively extract information from the image. The small filters help

capture fine details, while the pooling layers reduce the size of the extracted features. It uses back propagation and gradient descent, to adjust the weights and improve its performance. Although VGG19 is a powerful and accurate model for image classification, it has one drawback in terms of computational efficiency. Having a deep architecture, it requires more resources for training and inference than newer and more optimized models (Shallu et al., 2018).

ResNet50v2 base is a convolutional neural network model that is part of the family of ResNet (Residual Network) models developed by Microsoft Research. This model is based on the innovative idea of using residue blocks to facilitate training deep networks. ResNet50v2 base is notable for its use of residue blocks, which allow the model to learn more accurate image representations. These blocks contain skip connections, which allow direct passage of unaltered information from one layer to another. This helps to avoid performance degradation problems when additional layers are added to the network. The ResNet50v2 base consists of 50 layers, making it deeper than other simpler models. Its architecture is based on the use of convolutional layers, followed by batch normalization layers and non-linear activation functions, such as ReLU. ResNet50v2 base has been trained on large and diverse datasets such as ImageNet, to learn to recognize a wide range of objects and visual features. Thus, the model is suitable for image classification, object detection and other deep learning tasks that involve image analysis. Although ResNet50v2 base is a powerful model, it is more complex and requires more computational resources for training and inference than simpler models. However, it offers superior performance in terms of accuracy and learning ability (Mangeri et al., 2021).

The ReLU (Rectified Linear Unit) activation function is used in machine learning, especially in neural networks, to introduce non-linearity in the learning process. The ReLU activation function is defined as follows: for each element $x$ in the input of the function, ReLU($x$) will be equal to $x$ if $x$ is greater than or equal to zero, and otherwise, it will be zero. This function transforms negative scores into zero and keeps positive scores unchanged. Therefore, the ReLU function has a linear characteristic for positive scores and total inactivity for negative scores. The ReLU function is preferred in neural networks due to its simplicity and its ability to solve the vanishing gradients problem that can occur in deep neural networks. The ReLU activation function is frequently used in the hidden layers of neural networks, helping in learning complex representations and extracting relevant features from data. Additionally, ReLU can be combined with other activation functions or regularization techniques to achieve improved results in various machine learning tasks, such as classification, object recognition, or natural language processing (Zhang et al., 2021).

The GELU (Gaussian Error Linear Unit) activation function is a type of non-linear activation function that has gained popularity in deep learning and neural network architectures. It was introduced as an alternative to traditional activation functions like ReLU (Rectified Linear Unit) and Sigmoid, aiming to address certain limitations and improve network performance. The GELU activation function combines the characteristics of the Sigmoid and ReLU functions. It exhibits Sigmoid-like behaviour for small input values, allowing gradients to flow even for inputs far from zero, which helps mitigate the vanishing gradient problem. For larger positive input values, it approaches the identity function, acting similar to ReLU. This combination of properties makes GELU well-suited for deeper neural networks. One of the key advantages of GELU is its smoothness, which can lead to more stable training and improved generalization performance compared to some other activation functions. However, it's worth noting that GELU may not always outperform other activation functions in all scenarios and should be evaluated alongside other options based on the specific characteristics of the task and the architecture being used. GELU has been widely adopted in various deep learning applications and has contributed to advancements in the field (Zhang et al., 2021).

## 4. Dataset and image acquisition

The database chosen is the BreaKHis dataset, containing both malign and benign, labelled and cleaned data. The images are haematoxylin and eosin stained tissue specimens acquired through optical microscopy. It is composed of over 9000 images of breast tumour from 82 patients,

using different magnifying factors, 40X, 100X, 200X and 400X, containing 2480 benign specimens and 5429 malignant samples. The images are 3 channel RGB, 700X460 pixels, 8-bit depth in each channel and are of PNG format (Spanhol et al., 2016).

Benign is a term that refers to tumours that do not match the criteria of malignancy, usually growing slow and being localized. Malignant tumours are carcinomas presented in the breast tissue, that are capable of invading other biological structures and metastasize in other body parts.

The samples were collected through partial mastectomy (excisional biopsy), which removes a large size of tissue sample and is done with general anesthesia (Spanhol et al., 2016).

## 5. Algorithm implementation and results

The first step towards a binary classification of malignant samples and healthy breast tissue is image redimensioning. Because the images are 700x460, we will transpose them to be 700x700. However, this procedure will create distortions that should be avoided. Because of this aspect, the image padding is used to maintain the rapport of the images (Figure 1).

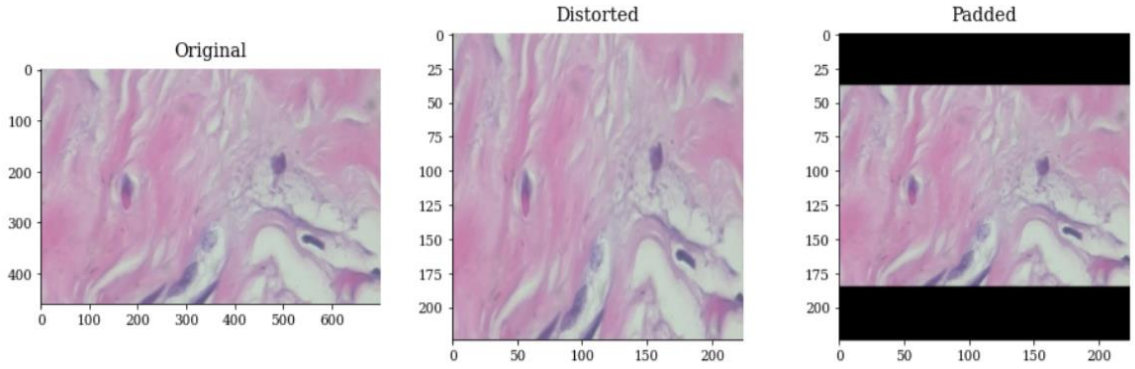


**Figure 1.** The initial image, the redimensioned image and the padded image

The objective is to implement the pretrained architectures discussed above and a custom original one. The purpose is to evaluate them using specific metrics.

Because of the collagen fibres in the images, it is desirable a local analysis of the fibre variability and distribution, thus making convolutional networks the most useful.

50 epochs were used for the automated diagnosis and an original convolutional network that contains 4 convolutional layers, 4 dense layers and multiple maxpooling and global max pooling was suggested, as presented in Figure 2.

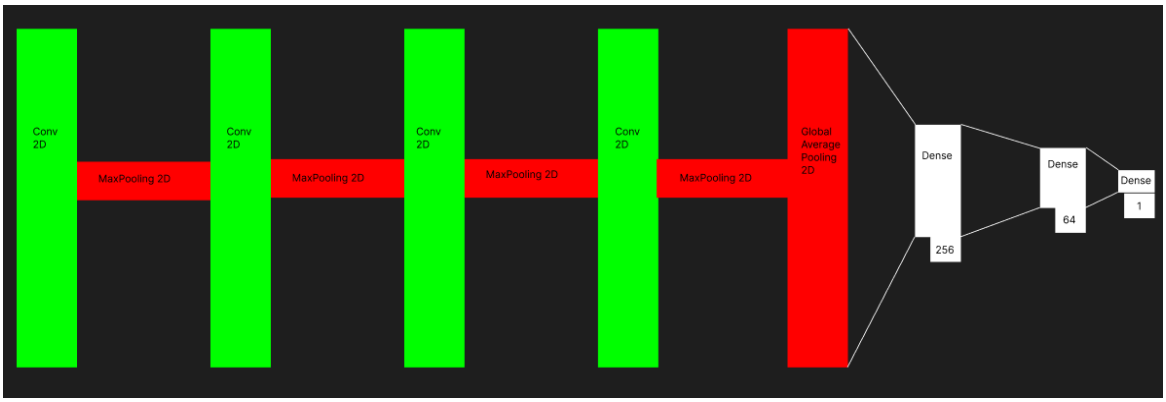


**Figure 2.** The graphical representation of the custom neural model

Multiple activation functions were chosen to analyse all of the possible outcomes and the optimal one was selected.

Using ReLU, an accuracy of 85.505% and a loss of 0.3198 are obtained. Following the results, the precision-recall curve of the model is presented in Figure 3.

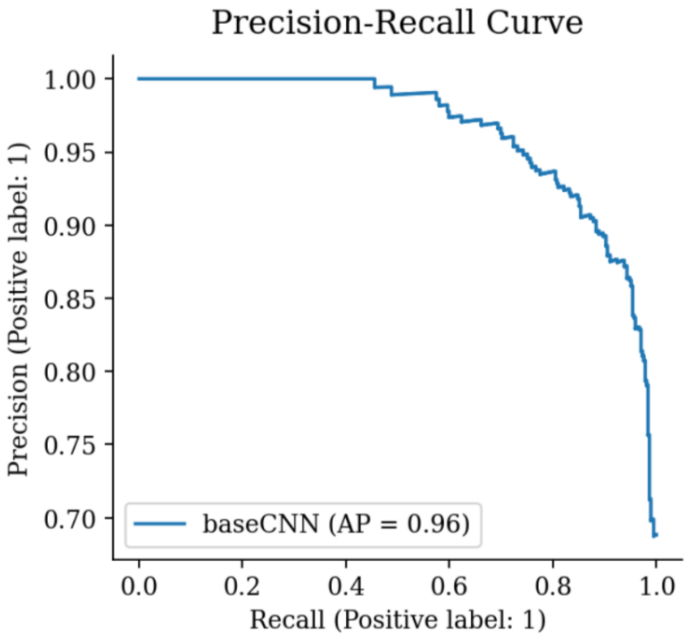


**Figure 3.** The Precision-Recall curve for the base convolutional model with ReLU activation

Using GeLU, a slightly better accuracy, of 86.972% and a slightly higher loss of 0.34 were obtained. For this model, the precision-recall curve is shown in Figure 4.

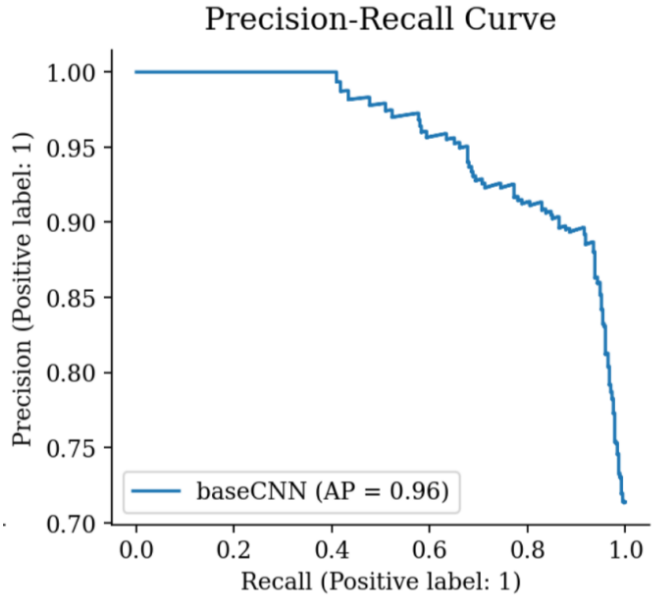


**Figure 4.** The Precision-Recall Curve for the base convolutional model with GeLU activation

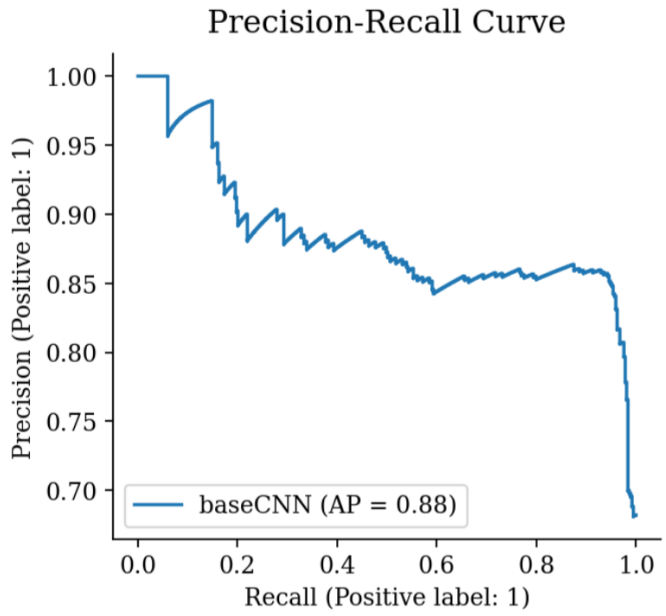


**Figure 5.** The Precision-Recall Curve for the base convolutional model with Swish activation

The Swish activation function for the model was implemented, with an accuracy lower than the GeLU model, of 85.321%, and a high loss function of 0.43840. Also, the precision-recall curve is an indicator of the fact that the model is not doing better than the models described above (Figure 5).

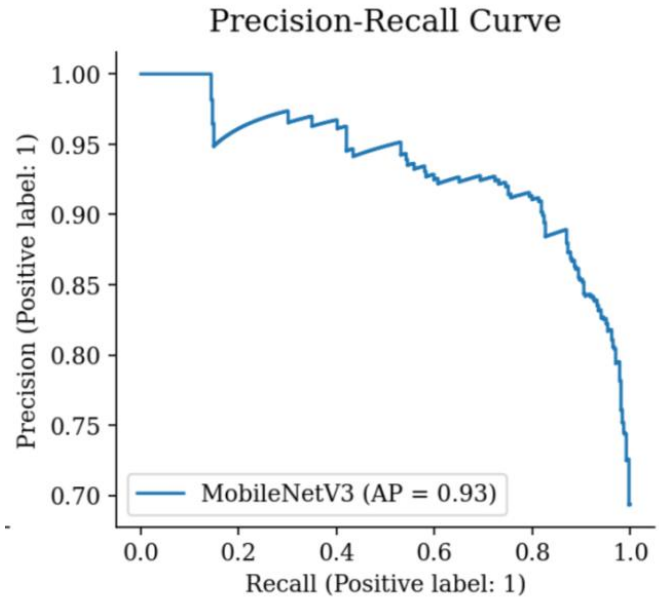


**Figure 6.** The Precision-Recall Curve for the MobileNetV3 model

For MobileNet, the accuracy is lower than the accuracy shown in the custom model, of 82.385%, while the loss is 0.38596. The precision-recall curve highlights the GeLU base model does better than this pretrained one. This model is shown in Figure 6.

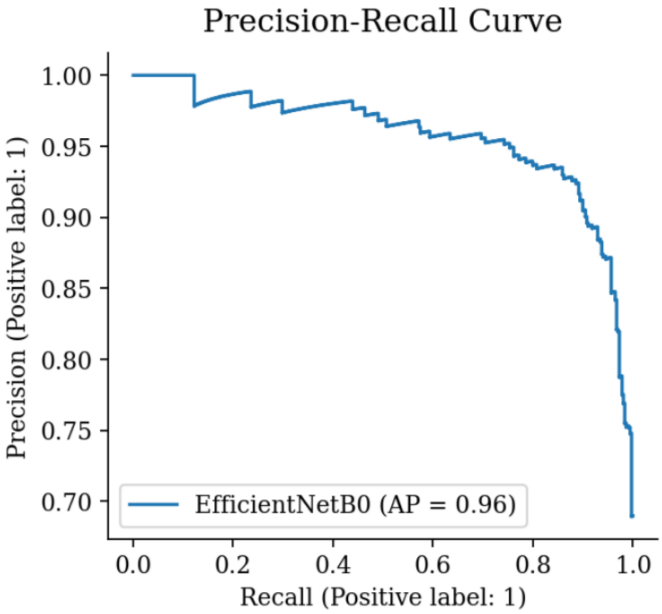


**Figure 7.** The Precision-Recall Curve for the EfficientNetB0 model

For the EfficientNet, the accuracy is 85.505%, which, even though is higher than the MobileNet model, it is still lower than the custom model utilizing the GeLU activation function, and the loss is 0.3424, with a precision-recall curve shown in Figure 7.

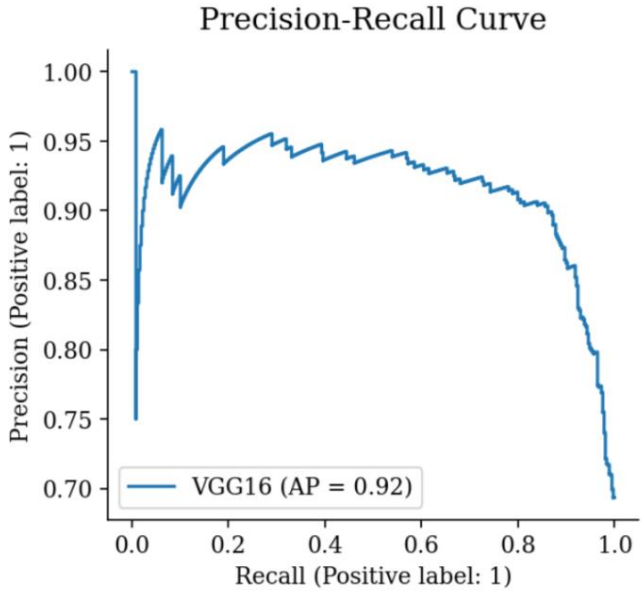


**Figure 8.** The Precision-Recall Curve for the VGG-16 model

Regarding the VGG16 model, the accuracy obtained is just of 83.853%, while the loss attains a high value of 0.43, with a precision-recall curve as in Figure 8.

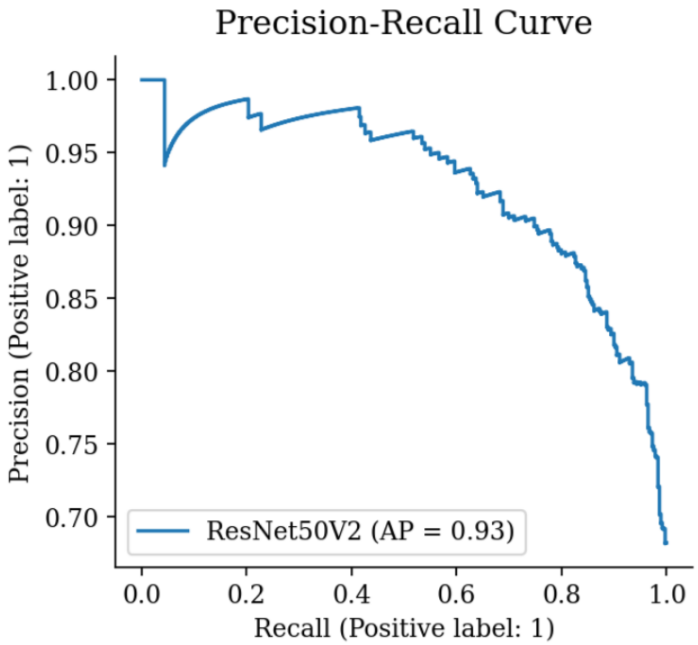


**Figure 9.** The Precision-Recall Curve for the ResNet model

The lowest accuracy was obtained by using the ResNet model, of just 80.183%, while the loss function still remains high, with a value of 0.42, with the following precision-recall curve, as depicted in Figure 9.

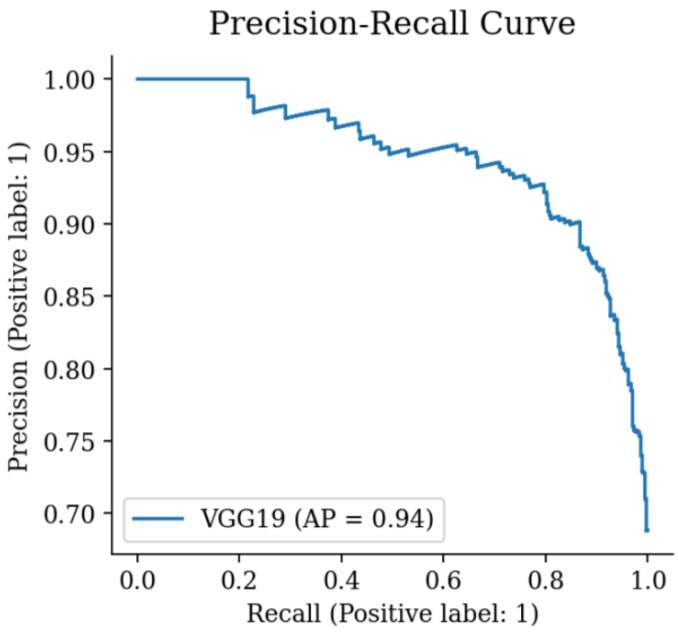


**Figure 10.** The Precision-Recall Curve for the VGG-19 model

Figure 10 shows the VGG19 model that reached an accuracy of 83.119%, similar to the VGG16 model, with a lower loss function as 0.396, as expected, and a precision-recall curve.

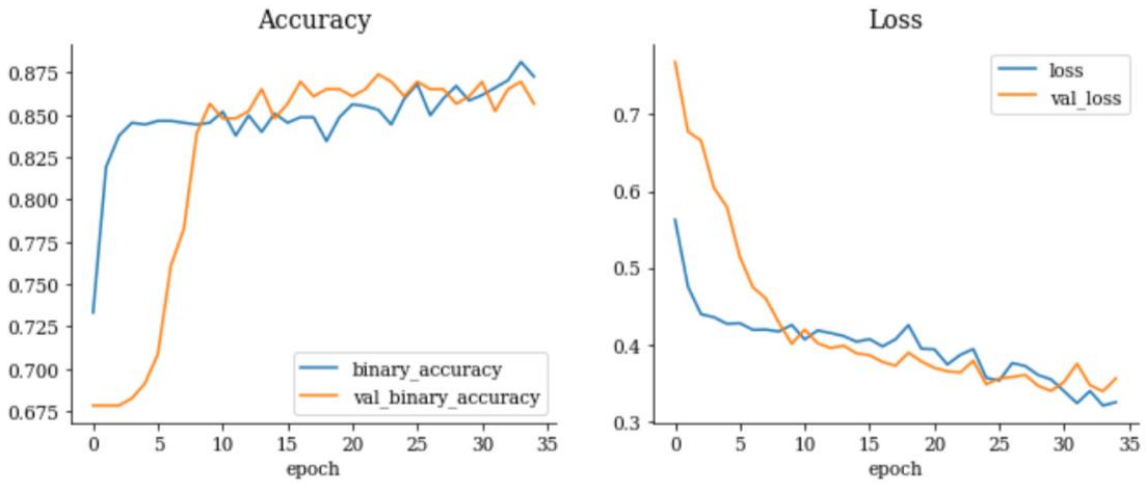


**Figure 11.** The Accuracy and Loss obtained based on the epoch numbers selected for the network testing

It is shown that the custom model has the highest accuracy with the aid of GeLU activation function. Based on this regard, the custom model shows the following characteristics of loss and accuracy by the number of epochs used (Figure 11).

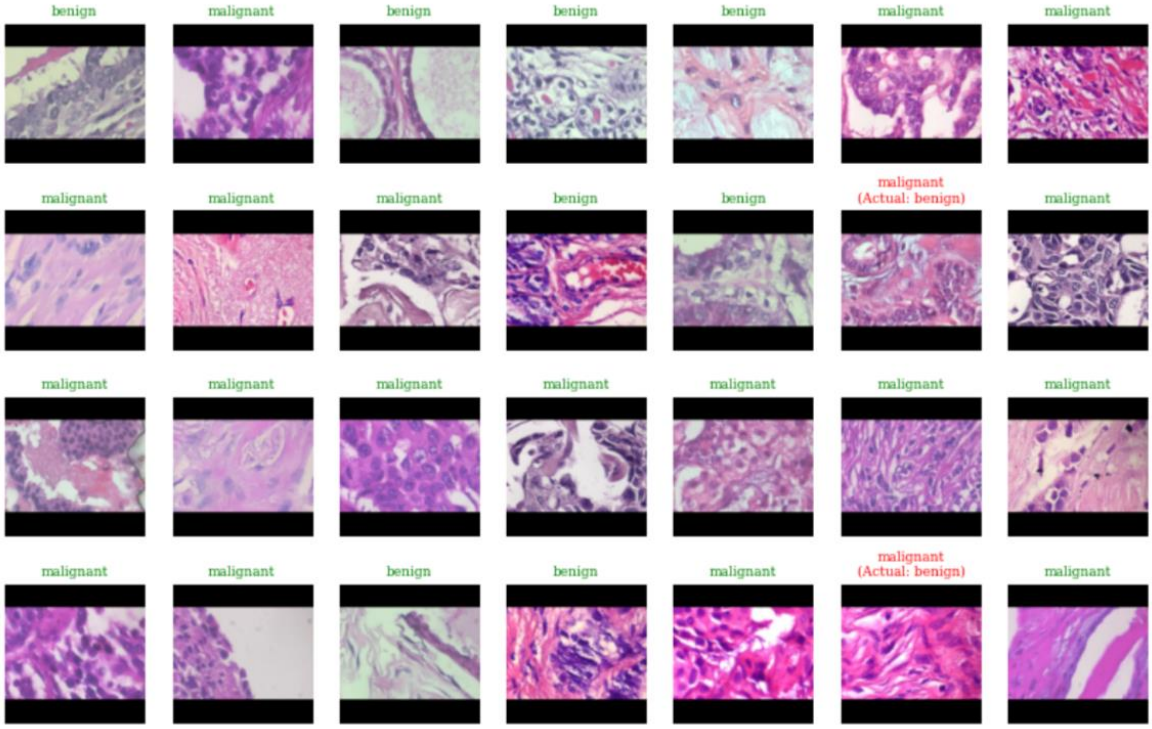


**Figure 12.** BreaKHis images labelled after the training, with green labels if the images were labelled correctly and red labels if the images were incorrectly labelled

Some of the predicted images were be highlighted, where the green coloured text was used for the images correctly predicted and red coloured text for the images incorrectly predicted (Figure 12).

To put the models into perspective, the following table will aid the comparison between the models used, as shown in Table 1.

**Table 1.** The models used and the highest accuracy and loss obtained for each one of them

| Name of the model | Accuracy | Loss |
|---|---|---|
| Custom Model (with ReLU activation) | 0.85505 | 0.3198 |
| Custom Model (with GeLU activation) | 0.86972 | 0.34 |
| Custom Model (with Swish activation) | 0.85321 | 0.43840 |
| MobileNetV3 | 0.82385 | 0.38596 |
| EfficientNetB0 | 0.85505 | 0.3424 |
| VGG-16 | 0.83853 | 0.3424 |
| ResNet | 0.80183 | 0.42 |
| VGG-19 | 0.83119 | 0.396 |

## 6. Conclusions

In conclusion, even though with a slightly higher loss value, the custom convolutional model using GeLU activation is the optimal choice in handling this problem of image classification.

Possible error sources could be from the different resolutions of the images presented in the dataset. While a linear filter could have been useful in blurring the low magnification images with the purpose of bringing them to a similar resolution as the higher magnification ones, this kind of process is imbued with information loss, which could negatively affect the automated diagnosis. Another possible error source could come from the present mineralisation of tissue. While already discussed that malignant tumours aid to the formation of mineralization in the tissue, the breast tissue gained an adaptation from the environment to form mineralization even if in a healthy state. The presence of mineralization in both classes in some images could have been a possible error source in this regard.

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**Iustin FLOROIU** is an engineer with a bachelor's degree in biomedical engineering, obtained at the Polytechnic University of Bucharest in 2022. Currently, he is pursuing a master's degree in information technology, specializing in intelligent systems and artificial vision, at the same university. Over the past four years, he has been involved in biomedical research, working on scientific topics related to cancer research, biomolecular machinery characterization, biophotonics, and image processing. His primary research interests include computational intelligence and artificial vision. He is the author and co-author of four scientific articles published in international journals and conferences.

**Iustin FLOROIU** este inginer cu diplomă de licență în ingineria biomedicală, obținută în cadrul Universității Politehnica din București în anul 2022. În prezent urmează studii universitare de master în tehnologia informației, specializarea în sisteme inteligente și viziune artificială, în

cadrul aceleiași universități. În ultimii patru ani a lucrat în cercetarea biomedicală, implicându-se în teme științifice legate de cercetarea cancerului, caracterizarea mașinăriilor biomoleculare, biofotonica și prelucrarea imaginilor. Principalele sale domenii de interes pentru cercetare includ inteligența computațională și vederea artificială. Este autor și coautor a patru articole științifice care au fost publicate în reviste și conferințe științifice internaționale.

**Daniela TIMISICĂ** is a graduate of the Faculty of Management at the Bucharest University of Economic Studies and holds a master's degree in "Management Consulting" obtained from the same institution. She currently works as a Scientific Researcher at the National Institute for Research and Development in Informatics - ICI Bucharest. Her main areas of interest and research activity include the Internet of Things (IoT), web programming, cybersecurity, and blockchain technology. She is also interested in the study of Artificial Intelligence, the application of 5G technology, and their implementation in emerging digital ecosystems.

**Daniela TIMISICĂ** este absolventă a Facultății de Management din cadrul Academiei de Studii Economice din București și deține o diplomă de master în „Consultanță în Management”, obținută în cadrul aceleiași academii. În prezent este Cercetător Științific în cadrul Institutului Național de Cercetare-Dezvoltare în Informatică – ICI București. Principalele sale domenii de interes și activitate pentru cercetare sunt: Internetul Obiectelor (IoT – Internet of Things), programare web, securitatea cibernetică și tehnologia Blockchain. De asemenea, este interesată de studiul Inteligenței Artificiale, aplicarea tehnologiei 5G și implementarea acestora în noile ecosisteme digitale emergente.

**Radu Marius BONCEA** is a Scientific Researcher Grade II and currently holds the position of Head of the "Software Engineering and Complex Systems" Department at the National Institute for Research and Development in Informatics - ICI Bucharest. His areas of expertise and interest include the Internet of Things (IoT), machine learning, cloud computing, software architectures, and distributed computing. He has been involved as a Project Director in numerous national projects, including research programs under the Core Program of the Operational Competitiveness Program (POC), and has led working teams for European projects such as SPOCS, eSENS, and Cloud for Europe. Additionally, he oversees the research, development, and innovation activities of the IoT innovation laboratory at ICI Bucharest, where he has established a team of young researchers and modern computing infrastructure.

**Radu Marius BONCEA** este Cercetător Științific gradul II și ocupă funcția de Șef al Departamentului „Ingineria Software și a Sistemelor Complexe” în cadrul Institutului Național de

Cercetare-Dezvoltare în Informatică – ICI București. Domeniile sale de expertiză și interes includ: Internetul Obiectelor (IoT – Internet of Things), învățarea automată, cloud computing, arhitecturile software și calculul distribuit. Acesta a fost implicat ca Director de Proiect în numeroase proiecte naționale, inclusiv programe de cercetare din cadrul Programului Nucleu din Programul Operațional COMPETITIVITATE (POC), și a condus echipe de lucru în cadrul proiectelor proiecte europene, cum ar fi: SPOCS, eSENS și Cloud for Europe. De asemenea, conduce activitățile de cercetare, dezvoltare și inovare ale laboratorului de inovare în IoT din cadrul ICI București, unde a pus bazele formării unei echipe de tineri cercetători și a unei infrastructuri moderne de calcul.