Image-based Lesion Classification using Deep Neural Networks

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Abstract: This research explores the topic of moles in cancer using a machine learning approach, with the aim of designing and implementing a system that can determine whether a mole shows a melanoma-like abnormality based on 2D input photographs, and thus whether further examination by a specialist is required. The target system is built around a general-purpose convolutional network, GoogleNet InceptionV3, which has been retrained for the task using a transfer learning technique. In addition to the system, an automated pre-processing phase has been defined to reduce and eliminate anomalies and noise in each sample by means of image processing operations. In conclusion, the system provided 156 correct diagnoses in 180 test cases, indicating a test accuracy of 86.67%, making it an effective melanoma diagnostic tool.

1 INTRODUCTION

Today, according to the National Institute of Oncology, melanoma is the 8th most common type of cancer in Hungary (National Institute of Oncology, 2016).

Melanoma is a malignant lesion of the blackbrown pigment-producing cells in the skin, known as melacytomas, and is one of the most aggressive types of cancer. Although its development is not directly linked to moles, as it can also occur on conventional skin surfaces, they are at higher risk due to their structure. Moles are skin surfaces with a higher concentration of the aforementioned pigmentproducing cells. They are therefore at increased risk; it has been estimated that nearly thirty percent of melanomas develop from pre-existing moles (Howard K., 1991, Balch, 2019).

As an aggressive type of cancer, melanoma not only develops rapidly, but also metastasizes to other organs in a very short period of time. Mainly to the bones, or even to the brain, but also to other more distant organs. Its danger lies precisely in this characteristic. If the underlying disease is diagnosed in time, the chances of cure are almost one hundred percent (~99%), and the treatment consists only of removing the mole and the surrounding tissue. If detected later, at stage two or three, the former survival rate drops dramatically to around fourteen percent, and depending on the different metastases, chemotherapy treatments may be required. Although melanoma accounts for only one percent of all diagnosed skin cancers, it alone is responsible for nearly three quarters of all skin cancer deaths (Rogers, 2015, American Cancer Society, 2016).

Timely detection is therefore key for healing but assessing the lesions on moles is often not an easy task, even for experienced dermatologists. Identifying moles with cancerous lesions is a complex problem that involves many factors:

- Shape (possible asymmetry)
- Irregularity of the edges of the mole
- Color
- Diameter
- Increase over time.

Because of the complexity of the symptoms, an accurate diagnosis can often only be made by biopsy. However, this procedure not only causes pain, but in many cases also scarring, among many other inconveniences. The difficulties associated with the procedure are often unnecessary if the mole is diagnosed as benign.

In the case of software diagnostics, the above factors are not present, so their effective usage could certainly make the screening process less problematic and time-consuming, thus contributing to a raised

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awareness and consciousness to the general public as the system offers a convenient solution to a problem that must not be neglected.

2 A DEEP LEARNING APPROACH

The main complication with the software approach is the decision issue.

Before the excessive development and spread of the field of artificial intelligence and machine learning, the problem of classification was typically solved using traditional methods. These attempts mainly used SVM technology or Logistic Regression. Solutions based on image processing techniques alone were also encountered. A common feature of these approaches is that they have not achieved breakthroughs and have not proved to be more useful in terms of results than flipping a coin.

The low accuracy of these methods is presumably due to the difficulty in identifying the complex set of symptoms of the lesion and the high variability of the photographic samples. Indeed, the identification of the visual aspects listed above requires a complex set of image processing operations and, due to the diversity of photographs and birthmarks, it is almost impossible to produce a generally effective solution.

However, in recent years, the explosion in the field of machine learning has enabled the general and widespread use of different types of neural networks (Jenei, 2021). The emergence of convolutional neural networks, which work well for images and sounds, also promised efficient classification of photographs with a high degree of generalization.

The main strength of neural networks lies in their generalisation ability, which, by their very nature, can ignore irrelevant factors for classification, given a sufficiently large learning database. Since the efficiency of generalisation depends as much on the size and diversity of the training dataset as on the accuracy of classification, neural networks can be considered as an ideal solution when sufficient data are available (Szegedy, 2016).

A schematic process describing the operation of the designed system is shown in Figure 1.

2.1 The ISIC Database

The present research is based on the published and freely available dermatological database of the International Skin Imaging Collaboration (ISIC) melanoma project.

The ISIC gallery consists of approximately 53,000 photographs of lesions with a 1:8 ratio of confirmed melanoma to benign lesions. Although this imbalance may at first seem worrying, using the same number of teaching samples from both diagnostic groups, we can still speak of a sufficient amount of data.

The gallery is characterised by the fact that it includes relatively standardised samples according to a strict set of rules, which helps to use them in scientific projects.

The project's gallery requirements include only and exclusively annotated and biopsy-verified specimens with mostly centrally located lesions of good quality. There is no restriction on the device used to take the photograph. Although this is irrelevant from a medical point of view, it may be



Figure 1: Schematic of the envisaged melanoma diagnostic system (Kalouche, 2016).

difficult to detect differences due to the specificity of the devices when processing the images. Having studied the database, it can be stated that the following anomalies need to be addressed in the preprocessing of photographs (International Skin Imaging Collaboration, 2020):

- Different resolution
- Different image size
- Different illumination
- Different skin color around the lesion
- Presence of vignetting effect in some images
- Presence of hairs in the images.

2.2 Preprocessing of the Data

The ISIC gallery shows a 1:8 bias in favour of benign lesions in terms of number of samples. When the full database is used, this imbalance can severely affect the functioning of the neural network in such a way that it tends to favour the said diagnostic group. To avoid this, an equal number of approximately 6,000 photographs from each output category were used.

In order to maximise the accuracy of the classification, it was necessary to remove anomalies in the photographs and to remove irrelevant parts and noise in order to maximise the accuracy of the classification, given the relatively small number of samples available.

Consequently, a number of custom-made functions were implemented to automate the aforementioned processes (Figure 2). The resulting set of image processing operations can be considered as a complete pre-processing phase, suitable for both the preparation of samples used in training and those diagnosed in real-time. The phase is also responsible for the uniformization of the images to form a suitable input to the neural network.

As a first step in the processing, it is necessary to check for the presence of the so-called vignetting effect in the photo before starting the denoising process. If so, it will need to be removed, which means cropping the photo. This is essentially blacking out the edges of the photo in circles to bring out the essence of the content. However, its presence is counterproductive from an image processing point of view, as increasing the contrast value can also highlight the edge of this circle, consequently fooling the lesion detection algorithm. In order to avoid unnecessary operations and possible loss of data due to cropping, a conditional algorithm iterates over the images in the database and decides whether the effect is detectable by evaluating the conditions. If so, the corners of the sample are clipped along a circle of radius r from the centre of the image.



Figure 2: Pre-processing steps of the samples (from left to right: original image, cropped, blurred, contrast, mask, located, resized).

The next step is to de-noise the images. The algorithm solves noise reduction by Gaussian smoothing and increasing contrast. While the former is responsible for thinning out the hairs present in the sample, the latter helps to separate the edges of the lesion from the background. The size of each dimension of the filter mask and the amount of contrast enhancement are both determined based on the properties of the sample. In practice, this usually means a 5×5 pixel square mask and a 60% contrast enhancement. The latter operation not only increases each pixel value by a multiple, but also increases it by a constant beta value (1.1).

One of the advantages of real-life tests is that the diagnosing specialists know exactly which factors are relevant considering the diagnosis, so they focus only on those. In contrast, convolutional networks are not able to filter out irrelevant content clearly, so we have to do this ourselves during pre-processing. The last step before formatting is therefore the determination of the region of interest. To perform this, a shallow copy of the given photograph is made, and the phase continues to work with it. The ROI is determined based on a thresholding that operates on a run-time value calculated from the sample parameters.

The result of the thresholding is then used to search for each contour, from which the largest is selected and the rest are discarded. Drawing the selected contour line into an array of the same size as the image, initially containing zero values, results in a mask containing binary 1 values only at the location of the pixels representing the lesion. Using a bit-level AND operation, the mask just created is combined with the original photograph to obtain the localized birthmark with a black background color.

In order to use the samples just processed for deep learning purposes, they need to be formatted according to the expected input of the neural network. In practice, this involves two simple steps. The upright orientation photographs are rotated clockwise by 90 degrees to ensure that the orientation differences do not provide false information to the CNN. The need for this operation is checked simply by the ratio of the lengths of the sides. Since the neural network used in this project receives inputs of 248×248 pixels, the last step in the processing is rescaling. To do this, a black background image of the same size as the longest side of the image is created and the contents of the photo to be reduced are copied onto it, starting from the top left corner. In the resulting photo, the content is oriented towards the top left corner, and can therefore be resized easily without loss of data. (Kalouche, 2016)

2.3 The InceptionV3 based CNN Architecture

Since during the preprocessing phase all samples are converted to 248×248 pixels and the network operates with RGB color space photographs, the base model is initialized with input parameters of dimension (248×248×3). In light of the knowledge transfer to be applied, the top layers of the model are not imported. The loaded layers use the original weight values set on the ImageNet database (Russakovsky, 2015).

All the layers of the resulting model are then frozen to ensure that their weight parameters are not altered during the learning process.

In order to use the network as intended, it is necessary to add additional layers: first, a layer with a ReLU activation function of 1024 neurons is added to the last, i.e. output ("mixed7") layer, which is converted to one-dimensional. To obtain the corresponding output, another layer is added, in this case with a single neuron, activated by a softmax function. In between the two layers attached to the network, a dropout regularisation layer with a 20% dropout rate is placed to facilitate higher-level generalisation.

The model uses an RMSProp optimizer to minimize the value of the loss function, which is an

optimizer that operates in a similar way to the momentum-based solutions, but actually works by parameter-level changes. Described by mathematical equations, the operation of RMSProp is as follows:

$$E[g^{2}]_{t} = \beta E[g^{2}]_{t-1} + (1-\beta) \left(\frac{\delta C}{\delta w}\right)^{2}$$

$$w_{t} = w_{t-1} - \frac{\eta}{\sqrt{E[g^{2}]_{t}}} \frac{\delta C}{\delta w}$$
(1)

where $E[g^2]$ is the moving average of squared gradients, *w* is the weight, $\delta C/\delta w$ is the gradient of the cost function with respect to the weight, η is the learning rate and β is the moving average parameter (good default value: 0.9).

The corresponding learning rate is initialized at a lower than usual value of one ten-thousandth.

The actual value of the loss function is calculated using the binary cross-entropy function, which is often used in the deep learning domain. To measure the performance of the resulting network, various metrics are calculated, which are: accuracy, validation accuracy, average absolute error.

As a further regularization step, a callback function implementing Early Stopping was implemented to stop the teaching in time. The idea is that it monitors the value of the validation loss function and monitors the learning process of the network, stopping it if the value of the function seems to increase persistently over more than a predefined number of epochs. In the case of the network, this tolerance value is three epochs. The learning process thus runs until it is stopped, or in other cases for 500 epochs.

The complete network configuration is summarised in Table 1.

Parameters	Values
Learning rate	0.001-0.0001
Epoch count	500
Color mode	RGB, 3 channels
Input format	$(248 \times 248 \times 3)$
Data Augmentation	Yes
Activation function	ReLU, Softmax
Optimizer	RMSprop
Dropout layer	Yes, rate = 0.2

Table 1: Parameter values of the network.

3 RESULTS AND EVALUATION

During the testing phase, we tried to test the constructed network with as many combinations of

parameters and complementary methodologies as possible, with or without them, in order to obtain the most optimal solution. As a consequence, each attempt differs in several aspects.

As a first step, the built model was tested both on the ISIC gallery processed by the demonstrated preprocessing phase and on the raw database, thus testing the need for pre-processing and segmentation. In both cases, the model was instantiated with the same parameterization as presented, so the results can be considered representative. The constructed network produced a segmentation accuracy approximately 6% higher when using the former dataset, indicating that the noise filtering phase does help the classification process.

With this in mind, further experiments were based on the processed data set alone, in some cases supplemented by data augmentation steps. This measure theoretically helps to diversify the database, thereby increasing the number of cases covered and improving the generalisation capability of the network. The results of the two approaches are summarised in Table 2.

From the analysis of the table just seen, an interesting observation can be made: although higher teaching and validation accuracy is observed for the network that does not augment the data, the testing accuracy indicates the performance superiority of the latter. This is presumably due to the better generalisation ability resulting from the increased data set.

	No data augmentation	Data augmentation applied
Color mode	RGB	RGB
Accuracy	83.07%	81.68%
Validation accuracy	77.22%	72%
Correct melanoma prediction	60 / 90	70 / 90
Correct benign prediction	88 / 90	86 / 90
All correct prediction	148 / 180	156 / 180
Total test accuracy	82.22%	86.67%

Table 2: Parameter values of the network.

In addition, it is also noticeable that the first network was more prone to false-negative diagnosis, as 30 out of 90 cases were considered benign, otherwise cancerous lesions. In contrast, the network learning on the augmented dataset made only 20 such diagnostic errors, 33% fewer than the case without data augmentation. It is worth noting that the number of false positive predictions is almost identical, with only a minimal difference. The learning process was also monitored, so that, in addition to the loss function, the evolution of the average absolute error was also observed, with a value of 27.68% by the end of the learning process.

4 CONCLUSIONS AND FUTURE WORK

In summary, a relatively high classification accuracy can be achieved using the InceptionV3 convolutional neural network, even with a relatively small amount of data. However, it is important to highlight that, as shown in Table 1, the model tends to prioritise falsenegative diagnoses, even in cases where it is very likely to be certain of the diagnosis. One possible explanation for this phenomenon is that, when examining the database, it can be stated that photographs showing melanoma lesions contain a higher degree of noise and are also fundamentally less accurately segmented due to their asymmetric shape. This reduced segmentation efficiency, in turn, leads to an increase in the number of training samples that become unusable, which in turn leads to a reduction in the number of photos that can be used in the learning process. Consequently, there is a minimal imbalance in the proportion of samples used, which may explain the phenomenon described.

While the idea of diagnostics relying specifically on software solutions seems utopian for the time being, the results of the system described here clearly indicate the viability of using artificial intelligence in this way, whether in melanoma diagnostics or other medical fields.

The primary objective of the improvement is to increase the classification accuracy achieved. To this end, a number of steps can be formulated, mostly aiming at increasing the number of database, improving the efficiency of the pre-processing phase or modifying the network architecture.

An obvious solution could be to increase the number of cases covered. This could be done by adding another database with similar samples to the current dataset. On the other hand, resolving the imbalance in the database could also lead to a significant improvement, as it would allow the exploitation of the full ISIC gallery. In the latter case, the use of one of the Oversampling and T-link methodologies would seem to be worthwhile.

In terms of the pre-processing phase, the improvement is to maximise efficiency. The bottleneck in processing photographs is to determine the longest contour line needed to locate the lesions. This can be explained by the sensitivity of the formula for calculating the threshold used to determine the contour to certain parameters. For this reason, it would therefore seem worthwhile to find a solution that is less dependent on the average intensity of the photograph and the patient's skin color.

From an architectural point of view, replacing the currently used classification model could lead to an improvement in accuracy. It may be worthwhile to experiment with the VGG-16, a general-purpose convolutional network, instead of the current GoogleNet InceptionV3 model. Furthermore, the use of two convolutional networks in combination, for verification purposes, could be a more far-reaching development direction.

In addition to increasing accuracy, it is also worth focusing on reducing the number of false negative predictions. The tendency of the system to produce false-negative results has been mentioned on several occasions, exposing the user to significant health risks. To overcome this phenomenon, it may be useful to implement a loss function that penalizes falsenegative results more than false-positive ones (International Skin Imaging Collaboration, 2020).

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