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Research Article

A hybrid meta-heuristic approach for brain abnormalities detection using CNN Deep Learning Network

Yahya shaheen bresem[1], Dr. Saeed Shaerbaf[2]

[1]Research scholar Imam Reza international University Iraq
[2]Professor Imam Reza international University Iran
[1]alk48975@gmail.com, [2]shaerbaf@imamreza.ac.ir

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Abstract: Brain tumor is the most common brain abnormalities in children and adults. Brain tumors are the reason for one-third of all cancer deaths in the world. Image processing techniques and algorithms help a lot to perform this research and presented a second idea for analysis improvement and accuracy detection of radiologists. Deep Learning (DL) has achieved a huge number of gaps in various image processing and computer vision problems such as classification, segmentation, excellent resolution and so on. CNNs have been used in the field of computer vision for decades. However, the use of conventional CNNs has shown significant performance, there is still a lot to do for improvement. Like most artificial neural networks, CNN is prone to multiple local optimum states. In order to avoid trapping in the local optimum state, local optimization algorithms are required. In this paper, sine-cosine algorithm (SCA) and artificial bee colony (ABC) methods, two well-known metaheuristic algorithms, are proposed as an alternative approach to optimize CNN performance and they are also applied for image segmentation in order to detect brain anomalies. The simulation results of the proposed method show that the accuracy of the proposed method has improved by 5% compared to the base paper. This is due to the optimal selection of CNN parameters.

Keywords: Detection of brain abnormalities, image segmentation, Deep learning (DL), Artificial bee colony (ABC), Sine-cosine algorithm (SCA), convolutional neural networks (CNN).

1. Introduction

Medical imaging enhances the awareness of the original image by denoising, repairing, or highlighting information in the image to segment the organs and favorite tissues in quantitative analysis. However, there are many types of medical image segmentation methods, medical image segmentation methods are basically divided into the following five groups: threshold-based medical image section, medical image section based on growing area account, and medical image section based on transformation model, medical image section based on graph theory and medical image section based on machine learning [1].

Image recognition is a classic machine learning problem. This is a challenging task for object recognition or image recognition from a video or digital image. Image recognition is applicable in various fields of computer vision, some of which include face recognition, biometric systems, autonomous car, emotion recognition, image restoration, robotics, and so on. Deep learning algorithms have acquired great improvement in the field of computer vision. Deep learning is the implementation of artificial neural networks with several hidden layers with the aim of imitating the function of human brain membrane. Deep neural network layers extract several features and provide several levels of perception. In comparison with shallow networks, this cannot extract or work on multiple features. Convolutional neural networks are a powerful deep learning algorithm that is able to control millions of parameters and save computational costs by inserting a two-dimensional image and solving it with filters / cores as well as generating output values [2]. CNNs have been used in the field of computer vision for several decades. Although the use of conventional CNNs has shown significant performance, there is still a lot to do for improvement. Like most artificial neural networks, CNN is prone to several local optimum states. In order to avoid getting trapped in the local optimal state, global optimization algorithms are needed [3].

Brain tumors are the reason for one-third of cancer deaths in the world. A brain tumor is a group of cells growing randomly inside or around the brain. Basically, these two groups of tumors, the first one is non-cancerous tumor (benign) and the second is cancerous tumor (malignant). Another brain abnormality is brain inflammation related to brain tumor, which is very common and can occur and surround the brain tumor. Image processing techniques and algorithms have contributed a lot in this field of research and have provided a second idea for development of the analysis and accurate diagnosis of radiologists. In the literature, many researchers proposed different methods of BMRI image in order to achieve the diagnosis of brain abnormalities with the least human interaction [3].

In this project, sine-cosine algorithm (SCA) and artificial bee colony (ABC) methods, two well-known metaheuristic algorithms, are proposed as an alternative approach to optimize CNN performance and they are also applied image segmentation for detecting brain abnormalities.

In the following of this paper in section 2, previous works will be reviewed. In section 3, the proposed method is provided. In section 4, experiments' results are discussed and in the last section, the conclusion of paper is provided.

2. Related Work

In this section, we study the works done in the field of convolutional neural networks for medical images.

In [4], the authors propose a multi-class diagnostic framework based on a set of deep hybrid convolution neural networks (CNNs) using the most informative images from three-dimensional MRI of three data planes to detect patients with Alzheimer's disease (AD), mild cognitive impairment (MCI), and clinical condition in terms of normal cognitive (CN). They employ three different pipelines that learn features from different point of views on MRI data and obtain more complete spatial information. Experimental results are achieved using a combination of voting from these hybrid CNN pipelines in the OASIS neuroimaging dataset, using the 10-fold cross-validation technique, so it provides superior performance than some modern methods. If CNN structures are deeper, the accuracy is higher. Because the proposed method uses predetermined weights and selects the most informative training data instead of a complete randomized initialization training, it is also more efficient in terms of computation.

In [5], the authors propose a new method using genetic algorithms to complete structures and values' initialization of connection weight from a deep convolution neural network for solving image classification problems. In the proposed algorithm, an effective gene encoding strategy with variable length is designed to show the different blocks of structure and the potentially optimal depth in convolutional neural networks. Furthermore, a new fit representation scheme is proposed to speed up metaheuristic search with significantly less computing resources. Experimental results show the significant superiority of the proposed algorithm in comparison with advanced schemes in terms of classification error rate and number of parameters (weights).

In [6], the authors examined the use of convolutional neural networks to divide three-dimensional vessels in vivo in vivo microscopic images that are achieved by multi-photon microscope. In order to investigate the effect of aging and Alzheimer's disease on capillaries, they applied DeepVess models in three-dimensional images of cortical blood vessels in young and old models of rats suffering from Alzheimer and wild type of baby mice. They did not see much difference in capillary diameter distribution or inflamation between these groups, but found a reduction in the number of longer capillary sections (> 75μm) in older animals compared to younger animals in mouse models of Alzheimer's disease as well as wild types of mice.

In [7], the first step is to examine the performance of three deep CNN deep structures (VGG16, ResNet50, InceptionV3) in terms of mass and non-mass classification in a general set of digital mammography (CBIS-DDSM). Secondly, the best performance of CNN is used to classify mass and non-mass sections in other small public datasets (INbreast). Here, a study is performed to detect mass in mammography and it compares the results during transfer learning between images of similar sections (i.e., digitized and digital mammography) against the obtained results when transfer learning is performed between images of different sections (mammography and natural images). The classification results are evaluated using test accuracy, while the diagnostic results are evaluated using the free-response receiver operating characteristic (FROC) 34.

In [8], the authors have proposed a deep transfer learning-based method using chest X-ray images obtained from COVID-19 patients and normal individuals to automatically diagnose COVID-19 patients. The performance results show that the ResNet50 pre-trained model achieved the highest accuracy equals to 98% among the three models. According to the findings, it is believed that because of its high performance, it helps physicians to make the necessary decisions about clinical performance. In order to identify COVID-19 in its early stages, this study provides insight into how deep transfer learning techniques can be used.

In [3], the authors propose a monitored MRI diagnosis method based on the diagnosis of brain abnormalities using the K-Means algorithm to segment brain components in order to extract gray and white material of image where brain abnormalities are concentrated in these two main components. A CNN-based deep learning method was used to detect these abnormalities to create a deep learning network to classify brain abnormalities based on the applied training database. According to the results obtained from the diagnosis of abnormalities using the K-

Means algorithm and deep learning network, the proposed method in the diagnosis of brain abnormalities achieves a detection accuracy of about 95%.

3. The proposed method

In this research, we present a supervised and effective method of detecting brain abnormalities using image segmentation by integrating both ABC and SCA algorithms in order to extract the image of the two main brain elements and classify them as normal and abnormal brain elements. We suggest using CNN Deep Learning Network. The adoption of ABCSCA for CNN progress is shown in Figure 1.

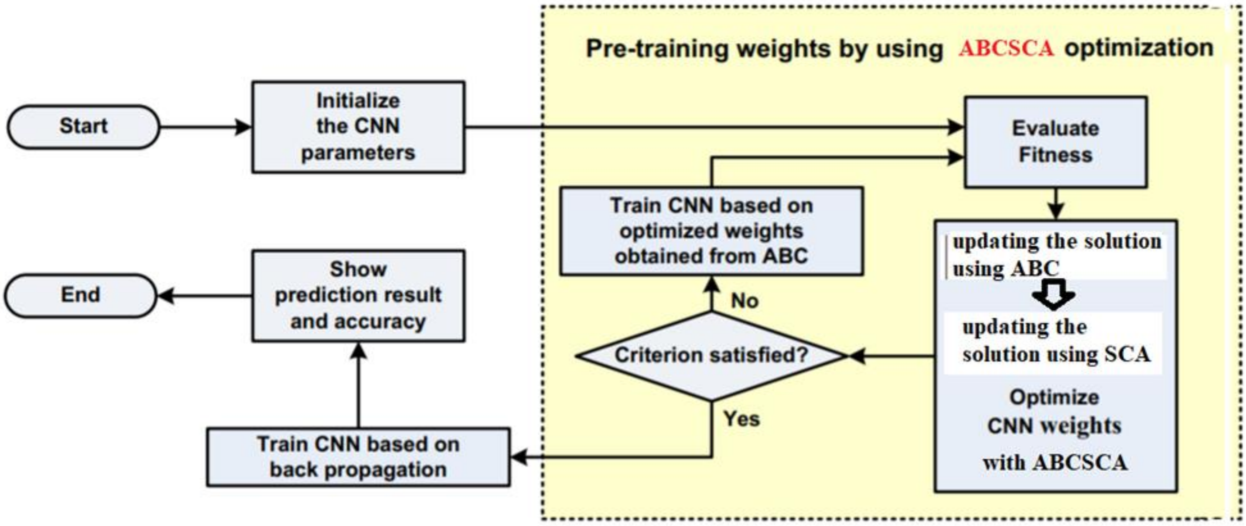

Figure 1- The Flowchart of the proposed method

We use the ABCSCA algorithm to optimize CNN weights and image sections.

First, in this study, we intend to apply the ABCSCA algorithm to find the optimal weight set from different initial weight sets. On the other hand, we try to find the optimal weight set minimizing the total error. Then, in image segmentation, ABC is used to reduce the search area by determining the best solution, after that SCA searches in the reduced area. Thus, the ABCSCA algorithm is started by calculating the input image histogram and then it generates a random population of N solutions (displaying threshold values). After that, ABC updates the population with three groups of honeybees. Then, the best solution of the population is determined based on the best solutions of the ABC algorithm. The SCA begins to determine the optimal value of the threshold using the ABC output (best solution) and updates the population solutions through the strategy. The optimal global solution is determined and all previous steps are repeated until justified by the same conditions.

3-1- Artificial bee colony (ABC)

ABC is an optimization algorithm inspired by the colony behavior of real honeybees [9]. It consists of three groups. The first group is employed bees. This group is looking for new food sources and information about this group is transferred to the next group (onlooker bees). Onlooker bees use this information to find new food source. The third group (scout bees) is randomly looking for a food source. The ABC algorithm generates a random population of N solutions that describe the employed bee, $x_i \in R^d$, i = 1, 2, . . . ,N. The new solution vi produced based on xi is as follows:

$$v_{ij}=x_{ij}+\phi_{ij}(x_{ij}-x_{kj}), \quad k=int(rand*N),\ j=1,\ldots,d \tag{1}$$

That xk is the employed bee next to xi, $\varphi_{ij} \in [-1, 1]$ and this is generated in a random behavior. Objective functions for F_{xi} and F_{vi} are computed for xi and vi, respectively; then, if $F_{xi} \le F_{vi}$, the solution xi is removed from the first group memory and vi is added. The objective function F_{xi} obtained from employed bees is transmitted to onlooker bees. Then, the roulette wheel transfer method is used to determine xi, which is more likely to have an objective function (P_i), which is calculated as follows:

$$P_i = \frac{fit_i}{\sum_{i=1}^{N} fit_i}, \quad fit_i = \begin{cases} \dfrac{1}{1+Fx_i} & if\ Fx_i > 0 \\ 1 + abs(Fx_i) & otherwise \end{cases} \tag{2}$$

Each onlooker bee updates its solution through a process used by employed bees. The onlooker bee tests both new and old solutions to decide whether the old solution has been removed from memory. If no difference is found in solutions after a certain number of iterations, these solutions are discarded; Then, the scout bee group discovers a new solution to update xi, such as:

$$x_{ij} = x_j^{min} + (x_j^{max} - x_j^{min}) \times \delta \tag{3}$$

Where x_{ij} is the optimized parameter for the i^th employed bee, x_j^{min} and x_j^{max} are upper and lower bounds of x_{ij} respectively, and δ is a random number. After a new solution, x_{ij} is produced, it becomes an employed bee.

3-2- Sine-Cosine Algorithm (SCA)

SCA is a metaheuristic algorithm. It uses sine and cosine mathematical shapes for applying optimization problems [9]. SCA starts the optimization process by generating different random solutions and then it initializes the iterations for achieving the best solution. The best solution is defined as the target point. Continuing the iterative process, the sine and cosine range are adjusted based on their mathematical shapes to make better use of the search space. If the fixed conditions are satisfied, the iterations will stop. The following equation specifies the mathematical form of SCA:

$$A_k^{t+1} = \begin{cases} A_k^t + n_1 \times sin(n_2) \times |n_3 P_k^t - A_k^t|, & n_4 < 0.5 \\ A_k^t + n_1 \times cos(n_2) \times |n_3 P_k^t - A_{kk}^t|, & n_4 \geqslant 0.5 \end{cases} \tag{4}$$

Where A_k^{t+1} is the state of the current solution in the kth dimension, t determines the current iteration, n1, n2 and n3 are random numbers, P_k is the state of the target point in the kth dimension, n4 is the random number in {1 and 0}. The sine and cosine range in Equation (4) are reduced by the value of n1 (in such a way that n1 = c - t × c / T, which T is the length of the iteration and C is constant).

4. Result evaluation

4-1- Dataset

In this study, we used a brain tumor dataset [10] that included 3064 images with increased T1 weight contrast from 233 patients with three types of brain tumors: meningioma (708 crops), glioma (1426 crops) and pituitary tumor (930 crops).

These data are organized in the form of Matlab data (mat file). Each file stores a structure containing the fields in Table 1 for an image.

Table 1- Data set description

Field	Description
cjdata.label	1 for meningioma, 2 for glioma, 3 for pituitary tumor
cjdata.PID	Patient ID
cjdata.image	Image data
cjdata.tumorBorder	It is a vector that saves the coordinates of discrete points at the tumor border.
cjdata.tumorMask	A binary image with 1s that shows the tumor area

Images have a screen resolution of 512 × 512 with a pixel size of 0.49 × 0.49 square millimeter. The crop thickness is 6 mm and the crop gap is 1 mm. Tumor borders were determined manually by three professional radiologists. The four figures are shown in Figure 2.

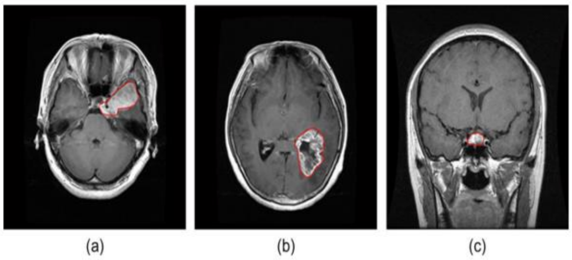

Figure 2- The images of three brain tumors: (a) meningioma. (Be) glioma; And (c) pituitary tumor. The red lines show the tumor border.

4-2- The simulation environment

Implementation process was performed by MATLAB 2018b on a 2.1 GHz Pentium CORE i7 with 8 GB RAM. This section discusses the evaluation of the proposed algorithm using computational experiments. The tests are performed using a brain tumor dataset. In order to evaluate the efficiency, the proposed method is compared with the basic paper algorithm. The proposed algorithm is implemented in Matlab 2018b environment. This environment includes facilities for managing variables in the workspace and a tool for developing, managing, debugging and creating M files in MATLAB programs.

4-3- Parameters' initialization

Bone cancer is classified using the MANFIS classifier. Artificial bee colony (ABC) is a widely swarm-based technique to search for optimal solutions because it uses quantitative adjustment parameters. This research uses the ABCSCA algorithm for CNN optimization. In this study, the initial parameters for the ABCSCA bee colony algorithm for CNN are given in Tables 2 and 3, respectively.

Table 1- Initial values for parameters in ABCSCA

Parameters	Initial values
The number of parameters	11
The maximum repetition	100
The percentage of train data	0.80
The percentage of test data	0.20
limit	10

Table 2- Initial values for parameters on CNN

parameters	Initial values
Learning rate	0.01
The maximum repetition	100
The percentage of train data	0.80
The percentage of test data	0.20
MaxEpochs	20

4-4- The evaluation criteria

In this paper, accuracy criteria have been measured in order to evaluate the accuracy of the proposed method.

Choosing a criterion for evaluating the effectiveness of the method depends on the problem we are trying to solve. Suppose a number of data samples are available. These data are given to the model individually and one class is received as output for each of them. The class predicted by the model and the actual data class can be displayed in a table. This table is called the confusion matrix.

Table 3- Confusion table

	The label of predicted class		
	predicted real	Healthy	Sick
The label of real class	Healthy	*True negative (TN)*	*False positive (FP)*
	Sick	*False negative (FN)*	*True positive (TP)*

True positive: Samples that have been correctly detected as patient by the test.
False Positive: Samples that have been mistakenly detected as patient by the test.
True negative: Samples that have been correctly detected as healthy by the test.
False negative: Samples that have been mistakenly detected as healthy by the test.

4-4-1- Accuracy criteria

The ability of a test to differentiate correctly between sick and healthy cases from other cases is called accuracy. To calculate the accuracy of a test, the ratio of the sum of true positive and negative samples to the total of tested items must be obtained. Mathematically, this ratio can be expressed as follows:

$$Accuracy = \frac{TP+TN}{TP+FP+FN+TN} \qquad (5)$$

4-4-2- Sensitivity criteria

The sensitivity parameter is another type of criterion for displaying the efficiency of rules. It calculates the percentage of accuracy in diagnosing the rules of illness. If this value is higher, the rules have more capability for detection.

$$Sensitivity = \frac{TP}{TP+FN} \qquad (6)$$

4-4-3- Specificity criteria

The ability of a test to find healthy items is called specificity. To calculate the specificity of a test, the ratio of true negatives to the sum of true negatives and false positives must be obtained. Mathematically, this ratio can be expressed as follows:

$$Specificity = \frac{TN}{FP+TN} \qquad (7)$$

4-5- The Evaluation of results

Accuracy and loss for the deep learning network with the aim of anomalies detection during training for 20 courses are described according to the training database in subsection 4.1, the 100% accuracy and very little level loss were obtained. Figure 5 and 6 show the progress of learning during training.

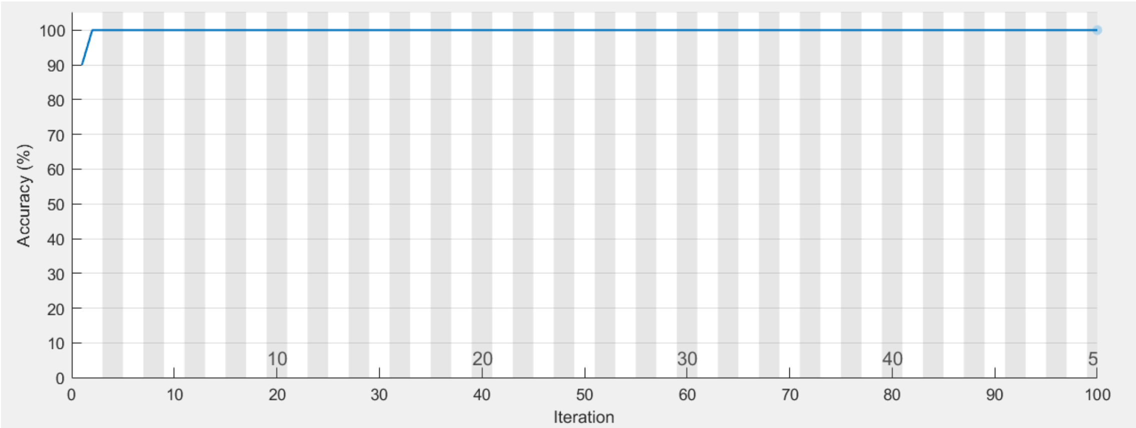

Figure 5- Improving accuracy in the training phase

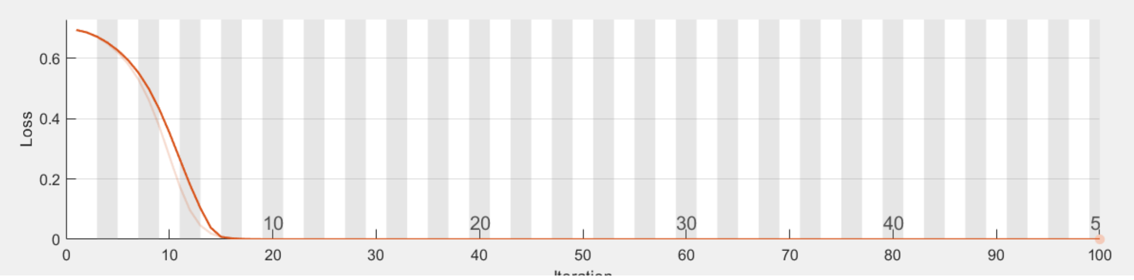

Figure 6- Progress of loss during the training phase

In this work, we used an experimental database including 3064 MRI scans of the brain with a 512 × 512 resolution with a pixel size of 0.49 × 0.49 square millimeter. All images of the skull are removed and only parts of the brain are available. The experimental results of brain segmentation are presented in Figure 7 below. All brain segmentation results are classified as normal or abnormal components of the brain using a created deep learning network.

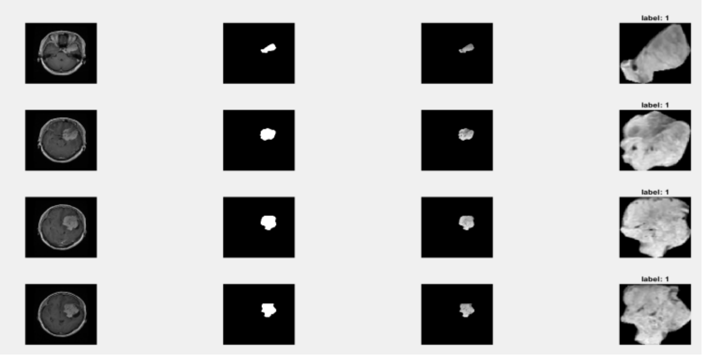

Figure7- An example of brain segmentation

The evaluation of proposed method for the diagnosis of brain abnormalities is based on the parameters of sensitivity, specificity and accuracy. According to the results presented in Table 5, it shows all parametric evaluations such as sensitivity, specificity and accuracy, strength and effectiveness of the proposed method using the deep learning network in order to realize the classification of brain components as normal or abnormal cases of brain with 100% sensitivity, 100% specificity and 100% accuracy detection of brain abnormalities. The results of the proposed method are compared with the base paper and the results are shown in Table 5. As you can see from the results, the accuracy of the proposed method has improved by 5% compared to the base paper. This is due to the optimal selection of CNN parameters.

Table 5- The results of proposed method and the base paper method

	Accuracy	sensitivity	**Specificity**
Base paper [3]	95%	93%	100%
Proposed method	100%	100%	100%

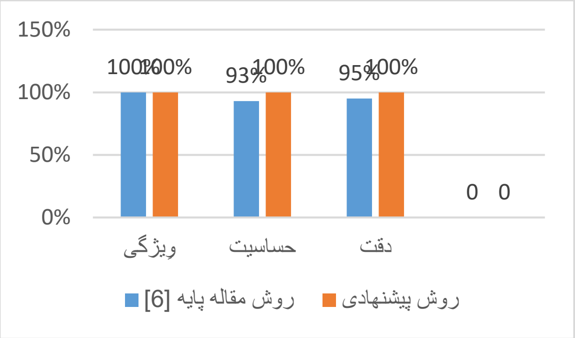

Figure 8- The Comparison of proposed method and the base paper method

5. Conclusion

In this paper, sine-cosine algorithm (SCA) and artificial bee colony (ABC) methods, two well-known metaheuristic algorithms, are proposed as an alternative approach for optimizing CNN performance and also it is applied for image segmentation in order to detect brain anomalies. In this work, we used an experimental database including 3064 MRI scans of the brain with a 512 × 512 resolution with a pixel size of 0.49 × 0.49 square millimeter. All images of the skull are removed and just parts of the brain are available. The simulation results of the proposed method show that the accuracy of the proposed method has improved by 5% compared to the base paper. This is due to the optimal selection of CNN parameters.

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