Assessing the Impact of Deep End-to-End Architectures in Ensemble Learning for Histopathological Breast Cancer Classification

Hasnae Zerouaoui¹¹^a, Ali Idri^{1,2}^b and Omar El Alaoui²⁶

¹Modeling, Simulation and Data Analysis, Mohammed VI Polytechnic University, Benguerir, Morocco ²Software Project Management Research Team, ENSIAS, Mohammed V University in Rabat, Morocco

- Keywords: Deep Learning, Machine Learning, Ensemble Learning, Computer Vision, Breast Cancer, Whole Slide Images.
- Abstract: One of the most significant public health issues in the world and a major factor in women's mortality is breast cancer (BC). Early diagnosis and detection can significantly improve the likelihood of survival. Therefore, this study suggests a deep end-to-end heterogeneous ensemble approach by using deep learning (DL) models for breast histological images classification tested on the BreakHis dataset. The proposed approach showed a significant increase of performances compared to their base learners. Thus, seven DL architectures (VGG16, VGG19, ResNet50, Inception_V3, Inception_ResNet_V2, Xception, and MobileNet) were trained using 5-fold cross-validation. Thereafter, deep end-to-end heterogeneous ensembles of two up to seven base learners were constructed based on accuracy using majority and weighted voting. Results showed the effectiveness of deep end-to-end ensemble learning techniques for breast cancer images classification into malignant or benign. The ensembles designed with weighted voting method exceeded the others with an accuracy value reaching 93.8%, 93.4%, 93.3%, and 91.8% through the BreakHis dataset's four magnification factors: 40X, 100X, 200X, and 400X respectively.

1 INTRODUCTION

Cancer is considered among the most serious health issues in the world. In 2020, more than 19.3 million new cancer cases are diagnosed and nearly 10 million deaths are declared (Sung et al., 2021). By far the most eminent and leading cause of death in women worldwide is breast cancer (BC), with 2.3 million women affected by it in 2020 (Sung et al., 2021). Early detection and diagnosis of this disease are essential to minimise morbidity in women. Even though X-ray, MRI (Magnetic Resonance Imaging), ultrasound, and other imaging techniques have been used for more than 40 years to detect breast cancer (Stenkvist et al., 1978), biopsy techniques have always been the most commonly used method for correctly diagnosing breast cancer. The procedure entails collecting tissue samples, mounting them on microscopic glass slides, and staining them for visualization purposes (Mitko Veta, 2014). Pathologists then examine and diagnose the histopathological images to affirm the diagnosis of breast cancer. (Mitko Veta, 2014). Manual examination of large-scale histological images, however, is a difficult process due to changes in appearance, structure, and textures(Li *et al.*, 2019), it is time-consuming, and usually depends on human subjective interpretation since the level of experience of the pathologists involved may have an impact on the results of the analysis. Therefore, computer-aided (Aswathy and Jagannath, 2017) analysis of histological images are crucial in the diagnosis of breast cancer.

Deep learning (DL) has recently outperformed a variety of machine learning (ML) models for the medical image analysis tasks, such as classification (Mardanisamani *et al.*, 2019), detection (Herent *et al.*, 2019), and segmentation (Lateef and Ruichek, 2019). When compared to other types of ML classifiers, DL has the advantage of being able to achieve results that are similar or better than human performance. DL techniques have been used in computer vision (Xie *et*

Zerouaoui, H., Idri, A. and El Alaoui, O.

DOI: 10.5220/0011574400003335

^a https://orcid.org/0000-0001-7268-8404

^b https://orcid.org/0000-0002-4586-4158

^c https://orcid.org/0000-0002-4395-9989

Assessing the Impact of Deep End-to-End Architectures in Ensemble Learning for Histopathological Breast Cancer Classification.

In Proceedings of the 14th International Joint Conference on Knowledge Discovery, Knowledge Engineering and Knowledge Management (IC3K 2022) - Volume 1: KDIR, pages 109-118 ISBN: 978-989-758-614-9; ISSN: 2184-3228

Copyright © 2022 by SCITEPRESS – Science and Technology Publications, Lda. All rights reserved

al., 2018), biological science (Gulshan *et al.*, 2016), and many other domains to solve problems of traditional feature extraction. More specifically the Deep convolutional neural networks (DCNNs) have been widely recognized as one of the most efficient tools for image classification since they provide numerous advantages over traditional solutions, including an end-to-end architecture that relieves users from hand-crafted feature extraction tasks. (Jia *et al.*, 2020).

Despite its popularity, a single DCNNs model can only extract a limited amount of discriminative features, resulting in suboptimal classification performance. To improve classification accuracy, ensembles of DCNN architectures have been designed to learn the representation of histopathological images from various perspectives. Since then, many researchers started investigating deep ensemble learning techniques to ameliorate the performances. For instance, the study (El Ouassif et al., 2021), proposed multiple heterogeneous ensembles for breast cancer classification on three datasets (WDBC, Wisconsin, WPBC). From seven classifiers (KNN, Decision Three, MLP, SVM, SVM-PUK, SVM-RBF, S-LK, SVM-NP), the authors, selected and constructed ensembles based on two selection strategies: (1) selection by accuracy and diversity, and (2) selection by only accuracy. Then, the constructed ensembles were combined using the majority voting method. According to the findings of this study, investigating both accuracy and diversity to select ensemble members often resulted in better performance than designing and building ensembles without member selection. In (Vo et al., 2019), authors proposed an ensemble constructed with three DL models for breast cancer classification tested on the BreakHis and Bioimaging-205 datasets. Inception ResNet V2 was used to extract features and gradient boosting trees for classification. the classifiers were combined using the majority voting strategy to improve the performance. The accuracy values reached: 95.1%, 96.3%, 96.9%, 93.8% and 86.75% for the magnification factors (MF) MFs of the BreakHis dataset and bioimaging dataset respectively. Some limitations have been revealed in the studies(Idri et al., 2020),(Vo et al., 2019): (1) the design of heterogenous ensemble using only one combination method, (2) except of the study (El Ouassif et al., 2021), a lack of statistical analysis to select the outperforming proposed model is noticeable.

To elevate the burden of those limitations, this study proposes a deep end-to-end heterogenous ensemble technique (DEHtE) using seven end-to-end DL models as base learners for breast histopathological images classification over the BreakHis dataset. The proposed approach consists of combing seven DL techniques of two up to seven DL models as base learners, based on accuracy using two voting methods: majority voting by taking the mode of the distribution of predicted labels, and weighted voting by taking the average of predicted probabilities. The seven DL techniques were based on fine-tunned VGG16, VGG19, ResNet50, Inception_V3, Inception_ResNet_V2, Xception, and MobileNet, using a 5-fold cross-validation evaluation technique.

The performance of the proposed approach was evaluated using four classification performance measures (Hosni *et al.*, 2019; Zerouaoui and Idri, 2021a) (accuracy, precision, recall, and F1-score), Scott Knott (SK) statistical test to group the proposed ensembles and identify the best cluster, and the Borda Count voting method to sort and identify the best performing ensemble. So far as we are knowledgeable, this study is the first to construct DEHtE of DL models as base learners based on accuracy and combined with two voting methods for histopathological BC classification.

The current study focuses on two research questions. (RQs):

- (RQ1): Does the deep end-to-end heterogenous ensembles using voting methods outperform their base learners?
- (RQ2): What are the suitable number of base learners to design the deep end-to-end heterogenous ensembles and the suitable voting combination method used?

The following are the study's main contributions:

- 1. Assessing and comparing the performance of the seven fine-tunned DL end-to-end architectures over the BreakHis dataset.
- 2. Constructing DEHtE using one selection criteria: selection by accuracy.
- 3. Combining the constructed ensembles using majority and weighted voting methods.
- 4. Assessing and comparing the performance of the designed DEHtE with their base learners over the BreakHis dataset.

The remainder of this paper is structured as follows: Section 2 provides an overview of the deep learning models and ensemble learning techniques used to develop the proposed approach. Section 3 presents data preparation process. Section 4 provides the details of the experiment configuration, the empirical methodology and the abbreviations followed in this empirical study. Section 5 reports and discusses the empirical results. Section 6 covers the threats of validity of this study. Lastly, Section 7 Outlines the conclusion and ongoing work.

2 BACKGROUND

This section delves into some of the key principles used in this empirical study, starting with the concept underlying the experiment's various DCNN architectures, then discussing ensemble learning techniques.

2.1 DCNNS Architectures

This subsection introduces and defines the different DCNNs used in this proposal.

VGGNet (2014): VGGNet finished first in the 2014 ImageNet Challenge (Simonyan and Zisserman, 2015). There is a total of six VGGNet architectures. The most common are VGG-16 and VGG-19. The VGG architectures are made up of convolutional layers with the ReLU, one max pooling layer, and multiple fully connected layers.

ResNet (2015): Resnet was designed to avoid the vanishing gradient problem that previous deep learning models had. (He and Sun, 2016). ResNet is built with a variety of layer counts: 34, 50, 101, 152, and 1202. ResNet50. The most popular ResNet have 49 convolution layers and one fully connected layer at the end.

Inception_V3: Inception V3 is a member of the Inception deep architectures, has the same architecture as InceptionV1 and InceptionV2 with a few changes. Inception V3 has 42 layers anwithd a fixed input size of 299x299 by default (Szegedy *et al.*, 2014). It has a parallel convolutional layer block with three different filter sizes (1x1, 3x3, 5x5).

Inception_ResNet_V2: Inception ResNet V2 is a convolutional neural network with 164 layers and an input size of 299x299. It is based on a combination of the Inception architecture and the Residual connection. Multiple convolutional filters are combined with residual connections in this architecture(Szegedy *et al.*, n.d.).

MobileNet_V2: As a source of non-linearity, MobileNet V2 filters features using lightweight depthwise convolution layers. It begins with a fully convolutional layer with 32 filters, then proceeds to 19 residual bottleneck layers(Sandler *et al.*, 2018).

Xception: Xception is an architecture with 36 convolutional layers that serve as the network's feature extraction foundation. It consists of a linear stack of separable depth-wise convolution layers with residual connections. This makes it very simple to define and modify the architecture. Xception has a

total of 22.8 million trainable parameters. (Chollet, 2017).

2.2 Ensemble Learning

In 1965, Ensemble Learning was proposed for classification tasks(Nilsson, 1965). It is based on the concept of training several base learners as ensemble members and combining their predictions into a single output that should outperform any other ensemble member with uncorrelated error on the target dataset on average(Zhou, 2012). An ensemble is composed of several base learners. A base learning algorithm, which can be a decision tree, a neural network, or another type of learning algorithm, is typically used to generate base learners from training data. Learners of the same type, leads to homogeneous ensembles, and learner of different algorithms are leading to heterogenous ensembles. An ensemble's generalization ability is commonly much higher than that of base learners.

The current study uses heterogenous ensembles with majority and weighted voting methods to combine predictions of the DL base learners. Every classifier vote for one class label in majority voting, and the final output class label is the one that receives more than half of the votes. Weighted voting, on the other hand, takes into account the probabilities thrown by each classifier; these probabilities are weighted and averaged, and the winning class is the one with the highest weighted and averaged probability. (Zhou, 2012)

3 DATA PREPARATION

In this section, we will present the process to prepare the histological BreakHis dataset consisting of five steps: data acquisition, data pre-processing using Contrast Limited Adaptive Histogram Equalization (CLAHE), intensity normalization and data augmentation. Since the same process was followed in the studies (Zerouaoui *et al.*, 2021; Zerouaoui and Idri, 2022), we therefore summarize it as described below.

The BreakHis dataset contains haematoxylin-eosinstained breast histological slides which refer to microscopic examination of a biopsy to study the appearances of the cancer. It is constituted of 7,909 breast histopathological images collected from 82 patients at different magnification factors (MF) such as 40X, 100X, 200X, and 400X with effective pixel sizes of 0.49 m, 0.20 m, 0.10 m, and 0.05 m All images are stored in TrueColor (24-bit colour depth, 8 bits per colour channel) three channel format (RGB). A pathologist examined the images and identified the most relevant region of interest, excluding out-of-focus images and images with undesirable areas such as black borders or text annotations. Each image's final size is 700x460 pixels in PNG format (Gandomkar *et al.*, 2018)(Spanhol *et al.*, 2016). The dataset is divided into benign tumor (adenosis, fibroadenoma, phyllodes tumor, and tubular adenoma) and malignant tumor (ductal carcinoma, lobular carcinoma, mucinous carcinoma, and papillary carcinoma) (Zhu *et al.*, 2019). One of the benefits of the BreakHis dataset is the use of four magnification factors, which allows for the detection of various cancer types and subtypes (Alom *et al.*, 2019).

We used intensity normalization and CLAHE (Zerouaoui and Idri, 2021b, 2022) to improve the image quality. The data augmentation was used to deal with the imbalanced data by incorporating geometric transformations (Jiang *et al.*, 2019)(Hosni *et al.*, 2019) since the number of images in each category non-cancerous (2480 images) and cancerous (5429 images) are imbalanced with 70% of the images represent the malignant class.

4 EMPIRICAL DESIGN

In this section, the empirical design proposed to build the DEHtE is provided, starting with the process tailed to construct and evaluate the designed proposed approach including the experiment configuration and the statistical tests such as Scott Knott (SK) and borda count voting method (Bhering *et al.*, 2008; Black, 1976). Next, the abbreviations employed to refer to the designed ensembles and their base learners are given. At last, a framework of the experiment and the empirical design will be described.

4.1 Experiment Configuration

After preprocessing, the data is divided into two sets (train and test sets) with partitions of (80%, 20%), respectively. Then, using transfer learning for fine-tunning, seven DL techniques (VGG16, VGG19, ResNet50, Inception V3, Inception ResNet V2, Xception, and MobileNet) were trained for each MF of the BreakHis dataset (Nguyen *et al.*, 2020). The models were trained on the train set and tested on the test set using stratified K-fold cross validation with k=5.

The seven DL techniques were trained using the following configurations:

- 1. The histological images were resized to 224x224 pixels for all DL architectures except for both Inception_V3 and Inception-ResNet_V2 that was resized to 299x299 pixels.
- 2. The transfer learning technique for fine tuning was used for the training of the seven DL models. The pre-trained architecture's top convolutional layers were frozen (ImageNet weights were used) and the extracted features were fed to an Artificial neural network (ANN) classifier.
- 3. The ANN classifier used is built with a fully connected layer of 256 neurons with RELU activation function. To avoid overfitting, we added a dropout layer with rate set to 50%, a dense layer of two neurons with SoftMax activation function, and a dense layer of two neurons with SoftMax activation function. The batch size was set to 32 and the number of epochs to 200. As for the optimization, we used the Adam optimizer with a learning rate of 0.0001 that decreases during training. Finally, we added L2 regularization to penalize large weight values and reducing model overfitting.

The end-to-end architectures of this experiment are trained and tested in Python using the Keras and Tensorflow deep learning frameworks and run on a TPU processing unit with 8 cores, 35 GB of RAM, and a Linux-based OS provided by Google in Colab Notebook. The training process of the seven DL models is depicted in Figure 1.



Figure 1: Training process of the seven DL techniques.

4.2 Statistical Tests

Scott Knott (SK) is a hierarchical clustering algorithm proposed by Scott and Knott in 1974 (Idri *et al.*, 2018). It is a quick and efficient way to perform multiple comparisons with no ambiguity (Bhering *et al.*, 2008). Because of its simplicity and robustness, the SK test is the most commonly used hierarchical clustering algorithm when compared to other statistical tests (Spanhol *et al.*, 2016)(Hamza and Larocque, 2005). The SK test was used in this study

to cluster the base learners and DEHtE techniques based on accuracy to see if there was a significant difference between them.

Borda count is a single-winner election method in which candidates are assigned points in descending order based on their ranking. The point values for all ranks and votes are added up, and the candidate with the most points is declared the winner (Emerson, 2013). The Borda count method was used in this study to find the best performing DEHtE based on four classification performance measures with equal weights (accuracy, precision, recall, and f1-score).

4.3 Abbreviation

To help the reader and abbreviate the names of the various techniques used in this research, we shorten the names of each DL technique as described in Table 1:

Table 1: The abbreviation of the DL architectures

DL architecture	Abbreviations
Xception	XCEP
ResNet50	RES50
MobileNet	MOBN
Inception_ResNet_V2	INRESV2
Inception_V3	INV3

As for the DEHtE names the following abbreviations were chosen:

EnHVA: Ensemble of size n combined with hard voting method and constructed with selection by accuracy strategy.

EnWVA: Ensemble of size n combined with weighted voting method and constructed with selection by accuracy strategy.

Exemple: Ensemble of 6 base learners using weighted voting with the selection by accuracy strategy is E6WVA

4.4 Empirical Design

This subsection describes the methodology followed for the DEHtE method. This experiment consists of the following seven steps:

- *Step 1:* evaluating the performance of the seven deep learning techniques based on accuracy.
- *Step 2:* Constructing for each MF, DEHtE of 2 up to 7 DL models used as base learners (combinations of 2, 3, 4, 5, 6, and 7) following the selection by accuracy strategy which consists of ranking the seven DL techniques with Borda count in terms of accuracy, precision, recall and fl-score, then from top to down constructing

combinations of two, four, five, six and seven. At the end of this step, we obtain 6 DEHtE for each MF.

- *Step 3:* For each MF, apply the majority and weighted voting methods on all combinations obtained in step 2, to obtain then, 12 ensembles for each MF (6 DL end-to-end architecture x 2 voting methods). Then, evaluate their performance in term of accuracy.
- *Step 4:* For each MF, apply the SK test on each 12-ensemble obtained in step 3 with the seven DL end-to-end architectures based on accuracy.
- *Step 5:* This step entails using Borda count to rank the variants of the best clusters (obtained in step 4) based on accuracy, precision, recall, and F1-score.

Figure 2 describes the process to design the DEHtE, it consists of three main steps: 1) data preprocessing, 2) DL models training for both feature extraction and classification and 3) combining the DEHtE using the selection by accuracy strategy and using the two com bination rules: majority (Idri *et al.*, 2020) and weighted voting.



Figure 2: The main steps to design the deep ent-to-end heterogenous ensemble.

5 RESULTS AND DISCUSSION

This section describes and compares the performance of the DEHtE designed using the selection by accuracy strategy and their base learners over the four MFs of the BreakHis dataset (40X, 100X, 200X and 400X) and defines the suitable number of base learners and voting combination methods. To do so, (1) the performances were analyzed and compared based on accuracy of all DEHtE, then (2) the difference of performances was observed using SK statistical test, (3) the best clusters obtained using SK test were ranked using Borda count voting method.

5.1 Performance of Deep End-to-End Heterogenous Ensembles

In a previous study (Alaoui *et al.*, 2022), the seven DL architectures including VGG16, VGG19, ResNet50, Inception_V3, Inception_ResNet_V2, Xception, and MobileNet were evaluated and compared using the BreakHis dataset. The main results have showed that the DL end-to-end architecture XCEP achieved the highest accuracy using the 40X MF with a value of 90.91 %, the DL end-to-end architecture VGG16 achieved 90.43 % on 100X MF, and the DL end-to-end architecture MOBN performed best on 200X and 400X with accuracy values of 90.90 % and 89.91 %, respectively. Furthermore, it is noticeable that the DL model RES50 underperformed compared to the other architectures regardless the MF used.

To assess and compare the performances of DEHtE constructed based on the selection by accuracy strategy and combined using two voting techniques (majority and weighted voting), we first rank the seven DL architectures based on accuracy and then combine them using majority and weighted voting following the ranking presented in Table 2. As results we obtained DEHtE of 2, 3, 4, 5, 6 and 7 DL models as base learners.

Table 2: The ranking of the seven DL models to design the DEHtE based on the selection by accuracy strategy.

Rank	40X	100X	200X	400X
1	XCEP	VGG16	MOBN	MOBN
2	MOBN	MOBN	XCEP	INRES
3	INRES	XCEP	VGG16	VGG16
4	VGG16	INV3	VGG19	XCEP
5	INV3	INRES	INRES	INV3
6	VGG19	VGG19	INV3	VGG19
7	RES50	RES50	RES50	RES50

Table 3 indicates the accuracy values of the DEHtE selected by accuracy using majority and weighted voting methods over the BreakHis dataset four MFs. It is revealed that:

For 40X MF, the best accuracy value obtained using majority voting was 93.5% reached by ensemble of size six, and the best accuracy obtained using weighted voting was 93.8% reached by ensembles of size six and seven. Moreover, ensemble of size two shows the worst accuracy value in both voting methods: majority and weighted voting with values: 90.9% and 92%, respectively.

- For 100X MF, the best accuracy value obtained using majority voting was 92.8% reached by ensemble of size six, and the best accuracy value obtained using weighted voting was 93.4% reached by ensemble of size four. Moreover, the worst accuracy value obtained using majority voting was 90.4% reached by ensemble of size two, and the worst accuracy value obtained using weighted voting was 92.5% reached by ensemble of size three.
- For 200X MF, ensemble of size seven shows the best accuracy value in both voting methods: majority and weighted voting with values: 93.1% and 93.3%, respectively. Moreover, ensemble of size two shows the worst accuracy value in both voting methods: majority and weighted voting with values: 90.9% and 92.3%, respectively.
- For 400X MF, the best accuracy value obtained using majority voting was 91.5% reached by ensemble of size six, and the best accuracy obtained using weighted voting was 91.8% reached by ensembles of size four and seven. Moreover, ensemble of size two shows the worst accuracy value in both voting methods: majority and weighted voting with values: 89.9% and 90.9%, respectively.

Table 3: Results based on accuracy of DEHtE selected	by
accuracy over the BreakHis dataset.	

	40X	100X	200X	400X
E2HVA	90.90 %	90.40%	90.90%	89.90%
E3HVA	93.20%	92.50%	92.80%	91.30%
E4HVA	93.30%	92.50%	92.70%	91.40%
E5HVA	93.40%	91.80%	93.00%	91.30%
E6HVA	93.50%	92.80%	93.00%	91.50%
E7HVA	93.00%	92.10%	93.10%	91.40%
E2WVA	92.00%	93.00%	92.30%	90.90%
E3WVA	93.20%	92.70%	92.90%	91.50%
E4WVA	93.50%	93.40%	93.00%	91.80%
E5WVA	93.70%	92.90%	93.20%	91.40%
E6WVA	93.80%	93.00%	93.20%	91.60%
E7WVA	93.80%	93.10%	93.30%	91.80%

In order to determine whether the DEHtE outperform their singles, we clustered the constructed ensembles following the selection by accuracy strategy and using two voting methods (majority and weighted voting) with their seven DL models used as base learners. Figure 3 illustrates the outcomes of the SK statistical test on the BreakHis dataset. It is observed that:

 For 40X MF, 6 SK clusters were obtained. The best cluster includes 10 ensembles out of 12 (all ensembles except E2WVA which belongs to the second cluster, and E2HVA which belongs to the third cluster with the DL model XCEP). The fourth cluster contains VGG16, INRES, MOBN and INV3. Moreover, the fifth and the last clusters contain VGG19 and ResNe50, respectively.

- For 100X MF, 6 SK clusters were obtained. The best cluster involves 7 ensembles out of 12 (E7WVA, E6WVA, E5WVA, E4WVA, E3WVA, E2WVA, E6HVA). The second cluster contains 4 ensembles (E7HVA, E5HVA, E4HVA, and E3HVA). E2HVA belongs to the third cluster with VGG16 and MOBN, the fourth cluster contains XCEP and INV3. Moreover, INRES and VGG19 belong to the fifth cluster, and the last cluster contains RES50.
- For 200X MF, 5 SK clusters were obtained. The best SK cluster groups 11 ensembles out of 12 (all ensembles except E2HVA which was shown in the second cluster with MOBN and XCEP). The third cluster contains VGG16. The fourth cluster contains VGG19, INRES and INV3. Lately, RES50 was presented in the last cluster.
 For 400X MF, 6 SK clusters were obtained. The best SK cluster comprises 11 ensembles out of 12 (all ensembles except E2HVA which was shown in the second cluster with MOBN). The third
 - cluster contains INRES. The fourth cluster contains VGG16, XCEP and INV3. The fifth and the last clusters contain VGG19 and ResNe50, respectively.





Figure 3: The SK test of ensembles selected by accuracy over BreakHis dataset.

To sum up the obtained results, the SK test showed that:

- For 40X, 10 out of 12 ensembles gave significant results compared to their base learners (all ensembles except E2HVA and E2WVA).
- For 100X, 7 out 12 ensembles gave significant results compared to their base learners (E7WVA, E6WVA, E5WVA, E6HVA, E4WVA, E3WVA, E2WVA).
- For 200X and 400X MFs, all ensembles except E2HVA gave significant results compared to singles.

The analysis above proves that the designed DEHtE significantly outperformed their base learners since they almost always belong to the best or second-best SK cluster. As results it is recommended to use the proposed approach to ameliorate the performances.

5.2 Number of Base Learners and Combination Rule to Use

This subsection is to determine the suitable number of base learners and combination rule to use in the design of the DEHtE. To do so, Borda Count voting method was applied on the basis of the four performance measures to rank the ensembles belonging to the best SK cluster. Table 4 displays the ranking results for the BreakHis dataset.

Ensembles	40X	100X	200X	400X
E7WVA	1	2	1	1
E6WVA	2	3	2	3
E5WVA	3	5	3	6
E6HVA	4	6	4	5
E4WVA	4	1	5	2
E4HVA	5		8	7
E5HVA	6		5	10
E7HVA	7		4	8
E3WVA	7	7	6	4
E3HVA	8		7	9
E2WVA		4	9	11

Table 4: Borda Count Ranking of Ensembles Selected by Accuracy on Breakhis.

As a summary, the Borda count voting method showed that E7WVA outperformed all other DEHtE over the BreakHis dataset MFs, since it was ranked top one on the three dataset MF (40X, 200X, and 400X) and ranked second for the 100X MF. As results this study has shown the importance of designing DEHtE to ameliorate the performances of the histopathological classification for BC diagnosis compared to the 7 DL models used as base learners. Furthermore, it showed that the number of base learners to design DEHtE plays a significant role since the ensemble of 7 base learners outperformed the others, and the ensembles of two base learners underperformed compared to the others.

Finally, the best combination rule to design the DEHtE is the weighted voting since the ensemble E7WVA outperformed the others and achieved an accuracy of 93.8%, 93.3%, 93.1%, and 91.8% over the MFS values 40X, 100X, 200X and 400X, respectively of the BreakHis dataset.

6 THREATS OF VALIDITY

Internal Validity: This study applied a 5-fold cross validation evaluation technique, which is commonly used in machine learning to assess a model's ability to predict new data points(Hosni *et al.*, 2019). Another internal threat is the use of transfer learning for fine tuning, which involves freezing all convolutional base layers with ImageNet weights. Freezing or tuning some convolutional layers may affect the performance of classifiers.

External Validity: The external threat's aim is to see if the study's findings are applicable to other contexts(Idri *et al.*, 2016). Since this study used only one dataset of histological images with four magnification factors, we cannot generalize the results to all datasets of the same image type. As a consequence, it is essential to test this study on other public or private datasets in order to confirm or refute the study's findings.

Construct Validity: The construct validity seeks to provide an answer to the measurement validity question(Hosni *et al.*, 2018), or, more precisely, the reliability of the measurements chosen to assess the performance of the proposed techniques. As a result, this study employs four performance measures (accuracy, precision, recall, and F1-score), the SK test to cluster statistically indifferent models and the Borda count voting technique, which takes into account the four-evaluation metrics, ensures that no performance metric is favored over another.

7 CONCLUSION

This paper addresses the problem of breast histopathological images binary classification over the BreakHis dataset. It designed and proposed a deep end-to-end heterogenous ensemble learning approach based on seven DL models using fine-tuned VGG16, VGG19, RES50, INV3, INRESV2, XCEP, and MOBN. The proposed approach consists of using two voting methods (majority and weighted voting) and constructing DEHtE of two up to seven models based on the selection by accuracy strategy. The following evaluation techniques were used to assess and rank the proposed ensembles over the BreakHis dataset: four classification performance criteria (accuracy, precision, recall, and F1-score), SK statistical test, and Borda Count. The following are the study's main findings:

(RQ1): Does the heterogenous ensembles using voting methods outperform the singles?

The deep end-to-end heterogeneous ensembles outperformed the DL base learners in all dataset MFs, with the accuracy value increasing from 90.91 % (the best accuracy value achieved on 40X by XCEP) to 93.8 % when using weighted voting. For 100X MF, the accuracy value increased by 3.07% (from 90.43% to 93.5% achieved by ensemble of six when using weighted voting). For 200X and 400X MFs, the accuracy value increased from 90.9%, 89.91% to 93.3%, 91.8%, respectively. As a result, the DEHtE outperformed their base learners significantly.

(RQ2): What are the suitable number of base learners to design the deep end-to-end heterogenous ensembles and the suitable voting combination method used?

The results have proved that the deep end-to-end heterogenous ensemble designed using the weighted voting combination rule outperformed the ones with majority voting. In addition to that, the increase of number of base learners to design the DEHtE plays an important role in the amelioration of the performances since the best performing designed DEHtE is the E7WVA across the BreakHis Mf values.

Ongoing works will focus on proposing DEHtE techniques using different selection strategies such as selection by diversity and selection by both accuracy and diversity, in order to determine the best criteria to select the base learners in order to propose the most performing DEHtE.

ACKNOWLEDGEMENTS

This work was conducted under the research project "Machine Learning based Breast Cancer Diagnosis and Treatment", 2020-2023. The authors would like to thank the Moroccan Ministry of Higher Education and Scientific Research, Digital Development Agency (ADD), CNRST, and UM6P for their support.

This study was funded by Mohammed VI polytechnic university at Ben Guerir Morocco.

Compliance with ethical standards.

Conflicts of interest/competing interests Not applicable.

Code availability not applicable.

REFERENCES

- Alaoui, O. El, Zerouaoui, H. and Idri, A. (n.d.). "Deep stacked ensemble for breast cancer diagnosis", pp. 1– 10.
- Alom, M.Z., Yakopcic, C., Nasrin, M.S., Taha, T.M. and Asari, V.K. (2019), "Breast Cancer Classification from Histopathological Images with Inception Recurrent Residual Convolutional Neural Network", *Journal of Digital Imaging*, Journal of Digital Imaging, available at:https://doi.org/10.1007/s10278-019-00182-7.
- Aswathy, M.A. and Jagannath, M. (2017), "Detection of breast cancer on digital histopathology images: Present status and future possibilities", *Informatics in Medicine Unlocked*, Elsevier Ltd, Vol. 8 No. October 2016, pp. 74–79.
- Bhering, L.L., Cruz, C.D., De Vasconcelos, E.S., Ferreira, A. and De Resende, M.F.R. (2008), "Alternative methodology for Scott-Knott test", *Crop Breeding and Applied Biotechnology*, Vol. 8 No. 1, available at:https://doi.org/10.12702/1984-7033.v08n01a02.
- Black, D. (1976), "Partial justification of the Borda count", Public Choice, Vol. 28 No. 1, pp. 1–15.
- Chollet, F. (2017), "Xception: Deep learning with depthwise separable convolutions", *Proceedings - 30th IEEE Conference on Computer Vision and Pattern Recognition, CVPR 2017*, Vol. 2017-Janua, available at:https://doi.org/10.1109/CVPR.2017.195.

- Emerson, P. (2013), "The original Borda count and partial voting", *Social Choice and Welfare*, Vol. 40 No. 2, pp. 353–358.
- Gandomkar, Z., Brennan, P.C. and Mello-Thoms, C. (2018), "MuDeRN: Multi-category classification of breast histopathological image using deep residual networks", *Artificial Intelligence in Medicine*, Elsevier B.V., Vol. 88, pp. 14–24.
- Gulshan, V., Peng, L., Coram, M., Stumpe, M.C., Wu, D., Narayanaswamy, A., Venugopalan, S., et al. (2016), "Development and validation of a deep learning algorithm for detection of diabetic retinopathy in retinal fundus photographs", *JAMA - Journal of the American Medical Association*, Vol. 316 No. 22, available at:https://doi.org/10.1001/jama.2016.17216.
- Hamza, M. and Larocque, D. (2005), "An empirical comparison of ensemble methods based on classification trees", *Journal of Statistical Computation* and Simulation, Vol. 75 No. 8, pp. 629–643.
- He, K. and Sun, J. (2016), "Deep Residual Learning for Image Recognition", available at:https://doi.org/10.1109/CVPR.2016.90.
- Herent, P., Schmauch, B., Jehanno, P., Dehaene, O., Saillard, C., Balleyguier, C., Arfi-Rouche, J., et al. (2019), "Detection and characterization of MRI breast lesions using deep learning", *Diagnostic and Interventional Imaging*, Société française de radiologie, Vol. 100 No. 4, pp. 219–225.
- Hosni, M., Abnane, I., Idri, A., Carrillo de Gea, J.M. and Fernández Alemán, J.L. (2019), "Reviewing ensemble classification methods in breast cancer", *Computer Methods and Programs in Biomedicine*, Vol. 177, pp. 89–112.
- Hosni, M., Idri, A., Abran, A. and Nassif, A.B. (2018), "On the value of parameter tuning in heterogeneous ensembles effort estimation", *Soft Computing*, Vol. 22 No. 18, available at:https://doi.org/10.1007/s00500-017-2945-4.
- Idri, A., Abnane, I. and Abran, A. (2018), "Evaluating Pred(p) and standardized accuracy criteria in software development effort estimation", *Journal of Software: Evolution and Process*, Vol. 30 No. 4, pp. 1–15.
- Idri, A., Bouchra, E.O., Hosni, M. and Abnane, I. (2020), "Assessing the impact of parameters tuning in ensemble based breast Cancer classification", *Health and Technology*, Health and Technology, Vol. 10 No. 5, pp. 1239–1255.
- Idri, A., Hosni, M. and Abran, A. (2016), "Improved estimation of software development effort using Classical and Fuzzy Analogy ensembles", *Applied Soft Computing Journal*, Elsevier B.V., Vol. 49, pp. 990– 1019.
- Jia, H., Xia, Y., Song, Y., Zhang, D., Huang, H., Zhang, Y. and Cai, W. (2020), "3D APA-Net: 3D Adversarial Pyramid Anisotropic Convolutional Network for Prostate Segmentation in MR Images", *IEEE Transactions on Medical Imaging*, Vol. 39 No. 2, available atkittan//doi.org/10.1100/TMI.2010.2028056

- Jiang, Y., Chen, L., Zhang, H. and Xiao, X. (2019), "Breast cancer histopathological image classification using convolutional neural networks with small SE-ResNet module", *PLoS ONE*, Vol. 14 No. 3, pp. 1–21.
- Lateef, F. and Ruichek, Y. (2019), "Survey on semantic segmentation using deep learning techniques", *Neurocomputing*, Vol. 338, available at:https://doi.org/10.1016/j.neucom.2019.02.003.
- Li, C., Wang, X., Liu, W., Latecki, L.J., Wang, B. and Huang, J. (2019), "Weakly supervised mitosis detection in breast histopathology images using concentric loss", *Medical Image Analysis*, Elsevier B.V., Vol. 53, pp. 165–178.
- Mardanisamani, S., Maleki, F., Kassani, S.H., Rajapaksa, S., Duddu, H., Wang, M., Shirtliffe, S., et al. (2019), "Crop lodging prediction from UAV-acquired images of wheat and canola using a DCNN augmented with handcrafted texture features", *IEEE Computer Society Conference on Computer Vision and Pattern Recognition Workshops*, Vol. 2019-June, available at:https://doi.org/10.1109/CVPRW.2019.00322.
- Mendel, K., Li, H., Sheth, D. and Giger, M. (2019), "Transfer Learning From Convolutional Neural Networks for Computer-Aided Diagnosis: A Comparison of Digital Breast Tomosynthesis and Full-Field Digital Mammography", *Academic Radiology*, Elsevier Inc., Vol. 26 No. 6, pp. 735–743.
- Mitko Veta. (2014), Breast Cancer Histopathology Image Analysis, Vol. 6.
- Nguyen, M.-T., Le, D.T., Son, N.H., Minh, B.C., Duong, D.H.T. and Linh, L.T. (2020), "Understanding Transformers for Information Extraction with Limited Data", *Proceedings of the 34th Pacific Asia Conference* on Language, Information and Computation, No. October, pp. 478–487.
- Nilsson, N.J. (1965), "Learning machines; foundations of trainable pattern-classifying systems", *McGraw-Hill Series in Systems Science*.
- El Ouassif, B., Idri, A. and Hosni, M. (2021), "Investigating Accuracy and Diversity in Heterogeneous Ensembles for Breast Cancer Classification", pp. 263–281.
- Sandler, M., Howard, A., Zhu, M., Zhmoginov, A. and Chen, L.C. (2018), "MobileNetV2: Inverted Residuals and Linear Bottlenecks", *Proceedings of the IEEE Computer Society Conference on Computer Vision and Pattern Recognition*, IEEE, pp. 4510–4520.
- Simonyan, K. and Zisserman, A. (2015), "Very deep convolutional networks for large-scale image recognition", 3rd International Conference on Learning Representations, ICLR 2015 - Conference Track Proceedings, pp. 1–14.
- Spanhol, F.A., Oliveira, L.S., Petitjean, C. and Heutte, L. (2016), "A Dataset for Breast Cancer Histopathological Image Classification", *IEEE Transactions on Biomedical Engineering*, Vol. 63 No. 7, pp. 1455–1462.
- Stenkvist, B., Westman-Naeser, S., Holmquist, J., Nordin, B., Bengtsson, E., Veaelius, J., Eriksson, O., *et al.* (1978), "Computerized Nuclear Morphometry as an Objective Method for Characterizing Human Cancer

Cell Populations", *Cancer Research*, Vol. 38 No. 12, pp. 4688–4697.

- Sung, H., Ferlay, J., Siegel, R.L., Laversanne, M., Soerjomataram, I., Jemal, A. and 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*, Vol. 71 No. 3, pp. 209–249.
- Szegedy, C., Ioffe, S., Vanhoucke, V. and Alemi, A.A. (n.d.). "the Impact of Residual Connections on Learning", pp. 4278–4284.
- Szegedy, C., Vanhoucke, V., Shlens, J. and Wojna, Z. (2014), "Rethinking the Inception Architecture for Computer Vision".
- Vo, D.M., Nguyen, N.Q. and Lee, S.W. (2019), "Classification of breast cancer histology images using incremental boosting convolution networks", *Information Sciences*, Vol. 482, available at:https://doi.org/10.1016/j.ins.2018.12.089.
- Xie, J., Hou, Q., Shi, Y., Lü, P., Jing, L., Zhuang, F., Zhang, J., et al. (2018), "The Automatic Identification of Butterfly Species", Jisuanji Yanjiu Yu Fazhan/Computer Research and Development, Vol. 55 No. 8, available at:https://doi.org/10.7544/issn1000-1239.2018.20180181.
- Zerouaoui, H. and Idri, A. (2021a), "Reviewing Machine Learning and Image Processing Based Decision-Making Systems for Breast Cancer Imaging", Journal of Medical Systems.
- Zerouaoui, H. and Idri, A. (2021b), "Reviewing Machine Learning and Image Processing Based Decision-Making Systems for Breast Cancer Imaging", *Journal* of Medical Systems, Vol. 45 No. 1, p. 8.
- Zerouaoui, H. and Idri, A. (2022), "Biomedical Signal Processing and Control Deep hybrid architectures for binary classification of medical breast cancer images", *Biomedical Signal Processing and Control*, Elsevier Ltd, Vol. 71 No. PB, p. 103226.
- Zerouaoui, H., Idri, A., Nakach, F.Z. and Hadri, R. El. (2021), "Breast Fine Needle Cytological Classification Using Deep Hybrid Architectures BT - Computational Science and Its Applications – ICCSA 2021", in Gervasi, O., Murgante, B., Misra, S., Garau, C., Blečić, I., Taniar, D., Apduhan, B.O., et al. (Eds.), , Springer International Publishing, Cham, pp. 186–202.
- Zhou, Z.H. (2012), Ensemble Methods: Foundations and Algorithms, Ensemble Methods: Foundations and Algorithms, available at:https://doi.org/10.1201/b12207.
- Zhu, C., Song, F., Wang, Y., Dong, H., Guo, Y. and Liu, J. (2019), "Breast cancer histopathology image classification through assembling multiple compact CNNs", *BMC Medical Informatics and Decision Making*, Vol. 19 No. 1, pp. 1–17.