# Fusing of Deep Learning, Transfer Learning and GAN for Breast Cancer Histopathological Image Classification

Mai Bui Huynh Thuy and Vinh Truong Hoang(✉)

Faculty of Information Technology, Ho Chi Minh City Open University, Ho Chi Minh City, Vietnam
{maibht.178i,vinh.th}@ou.edu.vn

**Abstract.** Biomedical image classification often deals with limited training sample due to the cost of labeling data. In this paper, we propose to combine deep learning, transfer learning and generative adversarial network to improve the classification performance. Fine-tuning on VGG16 and VGG19 network are used to extract the good discriminated cancer features from histopathological image before feeding into neuron network for classification. Experimental results show that the proposed approaches outperform the previous works in the state-of-the-art on breast cancer images dataset (BreaKHis).

**Keywords:** Deep learning · Transfer learning · BreaKHis dataset · Breast cancer · Histopathological image classification · GAN

## 1 Introduction

Breast cancer is the most common invasive cancer in women and have a significant impact to 2.1 million people yearly. In 2018, the World Health Organization (WHO) estimated 627,000 death cases because of breast cancer, be getting 15% death causes. Early cancer detection might help to treat and increase survival rate for patients. WHO finds that there are the effective diagnostic methods such as X-ray, Clinical Breast Exam but it needs to have the professional physicians or experts. In fact, the diagnostic result is not always 100% accuracy because of some reasons such as subjective experiments, expertise, emotional state. There are several applications of computer vision for Computer-Aided Diagnosis (CADx) have been proposed and implemented [6,7]. The breast cancer can be diagnosed via histopathological microscopy imaging, for which image analysis can aid physicians and technical expert effectively [7,12].

Moreover, the CADx system for breast cancer diagnosis is still challenging until now due to the complexity of the histopathological images. In the last decade, many works have been proposed to enhance the recognition performance of breast cancer image. They can be categorized into three groups:


H. A. Le Thi et al. (Eds.): ICCSAMA 2019, AISC 1121, pp. 255–266, 2020.
https://doi.org/10.1007/978-3-030-38364-0_23

- **Handcrafted-feature or deep feature**: Spanhol and Badejo [3,28] compare several handcrafted features extracted from Local Binary Patterns, Local Phase Quantization, Gray Level Co-Occurrence Matrices, Free Threshold Adjacency Statistic, Oriented FAST and Rotated BRIEF based on 1-NN, SVM and Random forest classifiers. Alom et al. [2] combine the strength of Inception, ResNet and Recurrent Convolutional Neural Network with and without augmentation for 4 magnification factors. Zhang et al. [34] propose a method to use skip connection in Resnet in order to solve the optimization issues when network becomes deeper. Roy et al. [21] propose a patch-based classifier using CNN network consisting of 6CONV-5POOL-3FC.
- **Transfer learning approach**: Weiss et al. [32] evaluate different features extracted from VGG, ResNet and Xception with a limited training samples and achieved a good result in the state-of-the-art on BACH dataset. This method downsized BACH image into $1024 \times 768$ in order to build the classification model. Vo et al. [31] apply the augmentation techniques as rotate, cut, transform image to increase the training data before extracting deep feature from Inception-ResNet-v2 model in order to avoid the over-fitting. Vo trained the model with multi-scale input images $600 \times 600$, $450 \times 450$, $300 \times 300$ to extract local and global feature. Then Gradient Boosting Trees model again was trained to detect breast cancer. Fusion model will vote the higher accuracy classifier. The accuracy rate archived to 93.8%–96.9% at low cost computation. Murtaza et al. [18] use Alexnet as feature extraction hierarchical classification model by combination of 6 classifiers to reduce the feature space and increase the performance.
- **Generative Adversarial Network (GAN) method**: Shin et al. [24] apply Image-to-Image Conditional GAN mode (pix2pix) to generate synthesis data and discriminate T1 brain tumor class on ADNI dataset. They then use this model on other dataset namely, BRATS to classify T1 brain tumor. This GAN model can increase accuracy compared to train on the real image dataset. Iqbal et al. [8] propose a new GAN model for Medical Imaging (MI-GAN) to generate synthetic retinal vessel images for STARE and DRIVE dataset. This method generated precise segmented image better than existing techniques. Author declared that synthetic image contained the content and structure from original images. Senaras et al. [22] employ a conditional GAN (cGAN) to generate synthetic histopathological breast cancer images. Six readers (three pathologists and image analysts) tried to differentiate 15 real from 15 synthetic images and the probability that average reader would be able to correctly classify an image as synthetic or real more than 50% of the time was only 44.7%. Mahapatra et al [15] propose a P-GANs network to generate a high-resolution image of defined scaling factors from a low-resolution image.

Both handcrafted and deep feature demonstrate the good cancer detection capability. Various researches combine numerous color features and local texture descriptors to improve the performance [1,16]. Modak et al. [16] did comparative analysis of several multi-biometric fusions consisting levels of feature-mostly feature concatenation, score or rules/algorithms level. Authors statistically

analyzed that fusion approach represents many advantages than single mode such as accuracy improvement, noise data and spoof attack reduction, more convenience. Fotso Kamga Guy et al. [1] exploited the powerful transfer-learning technique from popular models such as Alexnet, VGGNet-16, VGGNet-19, GoogleNet and ResNet to design the fusion schema at feature level for satellite images classification. It is said that fusion from many ConvNet layers are better than feature extracted from single layer. Features extracted from CNN network is less effected by different conditions such as edge of view, color space; it is an invariant feature and getting the better generalization. Thus data augmentation methods might affect the accuracy if it is applied inadequately. In order to save low computation cost from scratch, transfer learning technique can be considered to employ in medical field. It needs to be retrained or fine-tuning in some layers so that these networks can detect the cancer features. Furthermore, GAN is the effective data augmentation method in computer vision but GAN training process is still a difficult problem. These method have been investigated intensively for common data and rarely for medical data. To overcome this limitation, we propose a composition method of three techniques to be boosting the breast cancer classification accuracy in a limited training data.

The rest of this paper is organized as follows. Section 2 introduces our proposed approach by combining three methods such as transfer learning, deep learning and GAN. The experimental results are then introduced in Sect. 3. Finally, the conclusion is given in Sect. 4.

## 2 Proposed Approach

In the recent years, Convolutional Neural Network (CNN) proved as an efficient approach in computer vision and have significantly improved in cancer classification. Both VGG16 and VGG19 are proven to be a good candidate in transfer-learning technique. To get the discriminated benign and malignant from the tumor features, the base networks have to retrained on BreaKHis dataset and then be used as an input for CNN network.

A combination of different feature extraction methods can increase the classification accuracy. This work uses VGG16 network and then both VGG16 & VGG19 to extract the features. The proposed architecture is summarized in Fig. 1 and can be described in the following steps:

- **Input layer**: the input layer has three channels of $256 \times 256$ pixels which normalized from RGB patch images.
- **Fine-tuning VGG16 and VGG16 & VGG19 feature extraction**: the first 17 layers of VGG16 and VGG19 has primitive low-level spatial characteristic learned on ImageNet dataset which can be transferred to medical dataset. To later higher convolutional layer, they are trained according to BreaKHis dataset.
- **Batch normalization**: layer to normalize a number of activations in combination layer of VGG16 & VGG19's output layer to reduce overfitting from ImageNet's original weight.

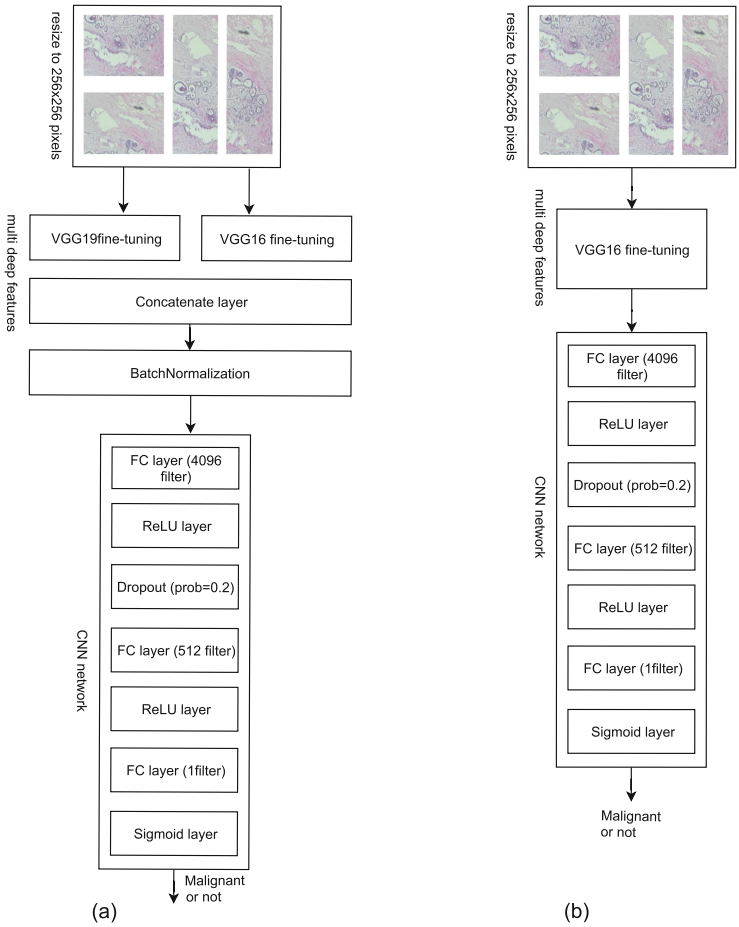


**Fig. 1.** (a) Fine-tuning VGG16 and CNN, (b) Fine-tuning VGG16 & VGG19 and CNN

- **Full connected layer**: all neurons in this layer have full connections to previous layer's neurons.
- **Rectified Linear Units (ReLU) layer**: ReLU activation layer

$$f(x) = \max(0, x) \tag{1}$$

will output previous layer value if it is positive, otherwise it will output zero. So ReLU layer is used many in deep learning because it helps the network to be trained easily and achieve the better performance.
- **Dropout layer**: is a regularization technique which removes some neurons randomly out network with probability 0.2 during forward or backward propagation process.

– **Output layer**: the layer uses a non-linear activation - sigmoid function.

$$h_\theta(x) = \frac{1}{1 + e^{-\theta^T x}} \tag{2}$$

Furthermore, three voting methods are applied to compute the model accuracy based on the patch image for two malignant or benign class. We define the so called method A is to select a majority predicted accuracy of the 4 patch images as final result of orginal image. Method B is a similar to A however, if 2 patch images is correctly predicted and 2 patch images is wrongly predicted, the final results of original image will be assigned as correct. Otherwise, method C is defined as at least one patch image is correct, orginal image is predicted as correct.

## 3 Experiments

### 3.1 Dataset Description

We propose to evaluate the proposed approach on one real histopathological image database (BreaKHis) and two generated databases from BreaKHis by GAN. The following subsection describes theses datasets.

**The BreaKHis Dataset.** [28] is a recent benchmark database proposed by Spanhol et al. to study the automated classification problem for breast cancer. This dataset contains 7,909 images (see Fig. 2) of 82 patients using 4 magnifying factors (40×, 100×, 200×, 400×). It is divided into 2 main groups: benign and malignant tumors, 8 sub cancer type as well totally size is 4 GB. It is publicly available from https://web.inf.ufpr.br/vri/databases/breast-cancer-histopathological-database-breakhis

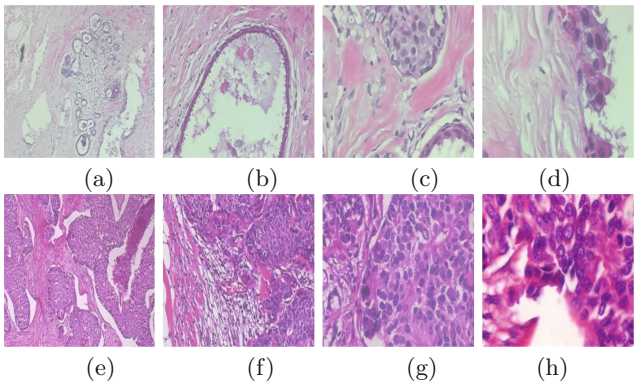


**Fig. 2.** Illustration of BreaKHis database at different magnification factors of benign cell 40× (a), 100× (b), 200× (c), 400× (d) and malignant cell 40× (e), 100× (f), 200× (g), 400× (h).

**The Fake BreaKHis.** images generated from StyleGAN transfers [11] the style image to input latent space $z$ by using mapping network $f$ to create an immediate feature space $w$. The adaptive instance normalization (AdaIN) technique is applied to control the style transferred image. We use StylgeGAN to generate the fake benign and malignant image for each scale of 40×, 100×, 200×, 400× (Fig. 3). StyleGAN is trained with $256 \times 256$ BreaKHis image for the independent scale and type on a PC with NVIDIA Tesla P100 1GPU during 8 h.

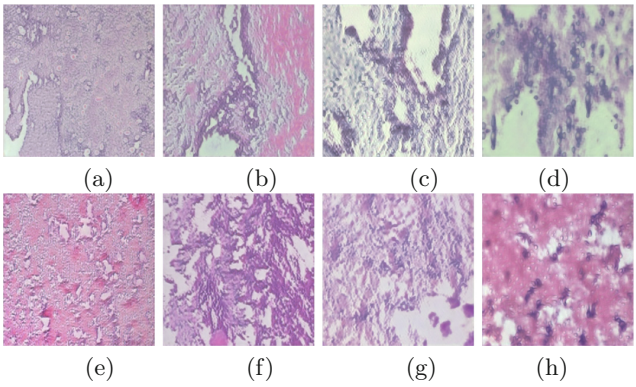


**Fig. 3.** Illustration of generated database by StyleGAN at different magnification factors of benign cell 40× (a), 100× (b), 200× (c), 400× (d) and malignant cell 40× (e), 100× (f), 200× (g), 400× (h).

**The Fake BreaKHis.** generated by Pix2Pix which is a conditional GAN network proposed by Isola et al. [9]. This framework applies U-Net model and skip connector technique as proposed generator network and discriminator architecture from PatchGAN to penalize structure at patch scale. To synthesize cancer image at each rate, we trained Pix2Pix network by using conditional image as the generated magnification rate image and the rest of magnification rates as input image. Benign 40× rate image will be conditional image and Begnign 100×, 200×, 400× rate images will be used as input image. Because of complex cancer structure, most of latent space from other magnification rate images can be transferred to the target image and might maintain original feature (Fig. 4).

### 3.2 Experimental Setup

The accuracy was estimated by a cross validation method through 5 iterations while the ratio of training and testing set ratio of each class are 70% and 30%, respectively. The reason that we choose this ration because it is the most common decomposition (be applied in more than 20 papers) in the literature on BreaKHis dataset. We train the proposed approach with BreaKHis dataset mentioned in a previous section. Firstly, the histopathological image will be divided into 2

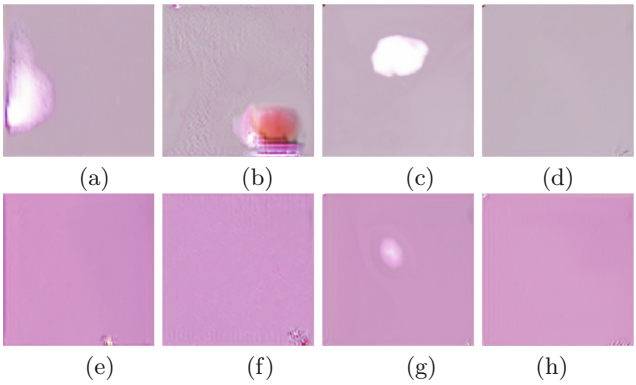


**Fig. 4.** Magnification factor of fake benign cell 40× (a), 100× (b), 200× (c), 400× (d) and fake malignant cell 40× (e), 100× (f), 200× (g), 400× (h) from Pix2Pix model.

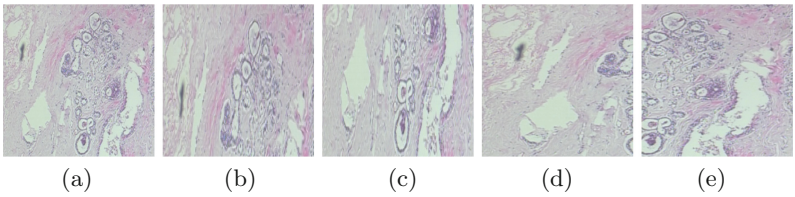


**Fig. 5.** Magnification factor of 40× benign image (a), top half (b), a bottom half (c), a left half (d) a right half (e)

patches by horizontal (resulting in Fig. 5b and c) and vertical direction (resulting in Fig. 5d and e).

The image patch size is $700 \times 230$ pixels in horizontal direction and $350 \times 460$ pixels in vertical direction. In stead of extracting small patch size as $32 \times 32$ pixels or $64 \times 64$ pixels, the approach can keep not only the textural and geometrical features but increase data's complexity and dimension. Most of discriminated features are twice stronger if it is at a central of images. After extracting all patch images needed, image pixel in each channel is normalized to the range of $[0, 1]$ in order to decrease the colored intensive rate. Then patch image is resized to $256 \times 256$ pixels, using the bilinear interpolation method. Each image in train comprises the 4 patches of an original image so that our network can learn the multi deep features and increase the performance.

Secondly, the discriminated features extracted from fine-tuning VGG16 and concatenated of fine-tuning VGG16 & VGG19 transfer learning is classified by our novel approach. In this work, all layers before $17^{th}$ layer of VGG16 & VGG19 is freezed and the rest of layers is re-trained. The loss function is a binary cross-entropy and the Adam optimizer is applied. All experiments are implemented in TensorFlow-GPU version 2 on 16 CPU, 64 GB RAM Tesla P4.

### 3.3 Results

Table 1 shows that the concatenation of many transfer learning features can increase the recognition accuracy of breast cancer. To train the deep networks efficiently, a large enough dataset is needed so apply the transfer learning is nominated approach nowadays. This technique shared the low feature space but have many differences about textural and geometrical features between ImageNet and BreaKHis. So our approach suggest to train some top layers of VGG16 & VGG19 network and achieved the averaged accuracy from 91.7% to 95.0%.

Both of evaluation method B & C get the average accuracy from 94.9% to 99.2% which can be applied to quickly detect the cancer if patients present any potential signs before doing many costly medical examinations. In order to compare our results, we carefully select the works (Table 1) in the state-of-the-art with the same decomposition and experimental condition. We can observe that the proposed approach clearly outperforms all the previous works. Additionally, the local image descriptors based approach does not give a good results compared with deep learning based method. Our work is "a plus" since we apply GAN to generate more medical images and apply deep learning method to classify images (Table 2).

**Table 1.** The experimental results of two proposed approaches on BreaKHis dataset.

| Model | Evaluation method | 40× | 100× | 200× | 400× | Average |
|---|---|---|---|---|---|---|
| VGG16 ft + CNN | Method C | 97.5±1.6 | 98.3±0.8 | 97.3±1.7 | 96.8±1.5 | 97.5±1.4 |
| | Method B | 95.0±1.5 | 95.6±1.8 | 95.4±1.8 | 94.0±1.6 | 95.0±1.6 |
| | Method A | 91.6±2.4 | 92.2±2.6 | 92.7±2.2 | 89.6±2.2 | 91.6±2.2 |
| VGG16 ft + CNN + StyleGAN | Method C | 97.3±1.3 | 98.0±1.3 | 97.4±1.2 | 95.3±2.1 | 97.1±1.4 |
| | Method B | 94.7±1.9 | 95.7±1.9 | 95.0±1.9 | 93.0±2.4 | 94.6±1.9 |
| | Method A | 90.9±2.0 | 92.0±2.0 | 92.2±1.7 | 89.2±1.5 | 91.1±1.7 |
| VGG16 ft + CNN + Pix2Pix | Method C | 97.5±1.5 | 98.5±1.0 | 97.4±2.1 | 95.3±1.5 | 97.2±1.5 |
| | Method B | 94.9±2.9 | 96.2±1.6 | 95.4±2.2 | 92.8±1.9 | 94.9±2.1 |
| | Method A | 91.4±3.4 | 92.9±1.8 | 92.8±2.5 | 89.3±1.9 | 91.7±2.3 |
| VGG16 &VGG19 ft + CNN | Method C | 99.2±1.0 | 99.5±0.6 | 99.2±1.1 | 99.1±1.3 | 99.2±1.0 |
| | Method B | 98.2±1.6 | 98.3±1.3 | 98.2±1.3 | 97.5±2.1 | 98.1±1.5 |
| | Method A | 95.1±3.0 | 95.2±2.4 | 95.2±1.7 | 94.6±2.9 | 95.0±2.4 |
| VGG16 &VGG19 ft + CNN + StyleGAN | Method C | 98.6±0.8 | 99.0±1.3 | 99.0±1.0 | 98.1±1.8 | 98.7±1.2 |
| | Method B | 96.7±0.8 | 97.9±1.8 | 97.8±1.9 | 96.1±2.5 | 97.1±2.0 |
| | Method A | 93.5±3.2 | 95.2±3.0 | 94.4±2.7 | 92.6±3.5 | 94.0±3.0 |
| VGG16 &VGG19 ft + CNN + Pix2Pix | Method C | 98.8±1.4 | 98.8±1.4 | 98.7±1.6 | 97.8±1.7 | 98.6±1.5 |
| | Method B | 97.0±2.6 | 97.3±2.3 | 97.3±2.0 | 95.5±2.0 | 96.8±2.2 |
| | Method A | 93.8±3.4 | 94.4±3.1 | 94.2±2.7 | 91.8±2.8 | 93.6±2.9 |

**Table 2.** Comparison of the proposed approach with previous works in the state-of-the-art on BreaKHis dataset.

| Ref,Year | Method | 40x | 100x | 200x | 400x | 2 classes |
|---|---|---|---|---|---|---|
| [2] 2019 | IRRCNN + augmentation | 97.9 | 97.5 | 97.3 | 97.4 | - |
| [31] 2019 | Inception & Boosting & Fusion | 95.1 | 96.3 | 96.9 | 93.8 | - |
| [34] 2019 | ResNet50 + CBAM | 91.2 | 91.7 | 92.6 | 88.9 | - |
| [23] 2018 | VGG16 (finetuning) + LR | - | - | - | - | 91.7 |
| [19] 2018 | Active learning | 89.4 | 90.9 | 91.6 | 90.4 | - |
| [25] 2018 | CSE (Fish vector) | 87.5 | 88.6 | 85.5 | 85.0 | - |
| [26] 2017 | Intra-embedding algorithm | 87.7 | 87.6 | 86.5 | 83.9 | - |
| [30] 2019 | Non parametric | 87.8 | 85.6 | 80.8 | 82.9 | - |
| [27] 2017 | DeCaf feature | 84.6 | 84.8 | 84.2 | 81.6 | - |
| [29] 2016 | CNN | 85.6 | 83.5 | 83.1 | 80.8 | - |
| [28] 2016 | PFTAS | 83.8 | 82.1 | 85.1 | 82.3 | - |
| [18]2019 | BMIC Net | - | - | - | - | 95.5 |
| [5] 2018 | DMAE | 89.8 | 88.0 | 91.5 | 89.2 | - |
| [10] 2018 | MVPNet+NuView data | - | - | - | - | 92.2 |
| [3] 2018 | Texture Descriptor | 91.1 | 90.7 | 87.2 | 87 | - |
| [13] 2018 | CNN | 82.0 | 86.2 | 84.6 | 84.0 | - |
| [17] 2018 | PCANet | 96.1 | 97.4 | 90.9 | 85.9 | - |
| [14] 2018 | Multi-task deep learning | 94.8 | 94.0 | 93.8 | 90.7 | - |
| [4] 2018 | Deep VGG16 & Reduction | 86.3 | 84.9 | 84.7 | 81.0 | - |
| [33] 2018 | Domain Knowledge | - | - | - | - | 81.2 |
| [20] 2018 | CNN + Over-sampling | - | - | - | - | 86.8 |
| Our - A | VGG16 & VGG19 & CNN | 95.1 | 95.2 | 95.2 | 94.6 | 95.0 |
| Our - B | VGG16 & VGG19 & CNN | **98.2** | **98.3** | **98.2** | **97.5** | **98.1** |

## 4 Conclusion

We proposed a composition method of three techniques, transfer learning, deep learning and GAN to be boosting the breast cancer classification accuracy in a limited training dataset. We studied two GAN models such as StyleGAN and Pix2Pix to boost the medical train dataset. At each training iteration, we combine the additional fake images of 4,800 generated StyleGAN and 2,912 generated Pix2Pix images. The experiments show that GAN images created much noise and effected to classification accuracy. Although GAN network can not generate the similar structure as original images but it can synthesize some features from medical images which proved not to be different accuracy. The future of this work is to adjust the U-Net generator in Pix2Pix network to increase a volumes of training set and improve the classification performance.

## References


1. Fotso Kamga Guy, A., Akram, T., Laurent, B., Naqvi, S.R., Alex, M.M., Muhammad, N.: A deep heterogeneous feature fusion approach for automatic land-use classification. Inf. Sci. **467**, 199–218 (2018)
2. Alom, M.Z., Yakopcic, C., Nasrin, M.S., Taha, T.M., Asari, V.K.: Breast cancer classification from histopathological images with inception recurrent residual convolutional neural network. J. Digital Imaging, 1–15 (2019)
3. Badejo, J.A., Adetiba, E., Akinrinmade, A., Akanle, M.B.: Medical image classification with hand-designed or machine-designed texture descriptors: a performance evaluation. In: Rojas, I., Ortuño, F. (eds.) Bioinformatics and Biomedical Engineering, vol. 10814, pp. 266–275. Springer, Cham (2018)
4. Cascianelli, S., Bello-Cerezo, R., Bianconi, F., Fravolini, M.L., Belal, M., Palumbo, B., Kather, J.N.: Dimensionality reduction strategies for CNN-based classification of histopathological images. In: De Pietro, G., Gallo, L., Howlett, R.J., Jain, L.C. (eds.) Intelligent Interactive Multimedia Systems and Services 2017, vol. 76, pp. 21–30. Springer, Cham (2018)
5. Feng, Y., Zhang, L., Mo, J.: Deep manifold preserving autoencoder for classifying breast cancer histopathological images. IEEE/ACM Trans. Comput. Biol. Bioinf. 1 (2018)
6. Guillén-Rondon, P., Robinson, M., Ebalunode, J.: Breast cancer classification: a deep learning approach for digital pathology. In: Meneses, E., Castro, H., Hernández, C.J.B., Ramos-Pollan, R. (eds.) High Performance Computing, vol. 979, pp. 33–40. Springer, Cham (2019)
7. Zilong, H., Tang, J., Wang, Z., Zhang, K., Zhang, L., Sun, Q.: Deep learning for image-based cancer detection and diagnosis - a survey. Pattern Recogn. **83**, 134–149 (2018)
8. Iqbal, T., Ali, H.: Generative adversarial network for medical images (MI-GAN). J. Med. Syst. **42**(11), 231 (2018)
9. Isola, P., Zhu, J.-Y., Zhou, T., Efros, A.A.: Image-to-Image Translation with Conditional Adversarial Networks. arXiv:1611.07004 [cs]
10. Jonnalagedda, P., Schmolze, D., Bhanu, B.: [Regular Paper] MVPNets: multi-viewing path deep learning neural networks for magnification invariant diagnosis in breast cancer. In: 2018 IEEE 18th International Conference on Bioinformatics and Bioengineering (BIBE), pp. 189–194. IEEE, Taichung, October 2018
11. Karras, T., Laine, S., Aila, T.: A Style-Based Generator Architecture for Generative Adversarial Networks. arXiv:1812.04948 [cs, stat], December 2018
12. Komura, D., Ishikawa, S.: Machine learning methods for histopathological image analysis. Comput. Struct. Biotechnol. J. **16**, 34–42 (2018)
13. Kumar, K., Rao, A.C.S.: Breast cancer classification of image using convolutional neural network. In: 2018 4th International Conference on Recent Advances in Information Technology (RAIT), pp. 1–6. IEEE, Dhanbad, March 2018
14. Li, L., Pan, X., Yang, H., Liu, Z., He, Y., Li, Z., Fan, Y., Cao, Z., Zhang, L.: Multi-task deep learning for fine-grained classification and grading in breast cancer histopathological images. In: Multimedia Tools and Applications, December 2018
15. Mahapatra, D., Bozorgtabar, B., Garnavi, R.: Image super-resolution using progressive generative adversarial networks for medical image analysis. Comput. Med. Imaging Graph. **71**, 30–39 (2019)
16. Modak, S.K.S., Jha, V.K.: Multibiometric fusion strategy and its applications: a review. Inf. Fusion **49**, 174–204 (2019)

17. Mukkamala, R., Neeraja, P.S., Pamidi, S., Babu, T., Singh, T.: Deep PCANet framework for the binary categorization of breast histopathology images. In: 2018 International Conference on Advances in Computing, Communications and Informatics (ICACCI), pp. 105–110. IEEE, Bangalore, September 2018
18. Murtaza, G., Shuib, L., Mujtaba, G., Raza, G.: Breast cancer multi-classification through deep neural network and hierarchical classification approach. Multimed. Tools Appl. 1–31 (2019)
19. Qi, Q., Li, Y., Wang, J., Zheng, H., Huang, Y., Ding, X., Rohde, G.: Label-efficient breast cancer histopathological image classification. IEEE J. Biomed. Health Inf. **23**, 1 (2018)
20. Reza, M.S., Ma, J.: Imbalanced histopathological breast cancer image classification with convolutional neural network. In: 2018 14th IEEE International Conference on Signal Processing (ICSP), pp. 619–624. IEEE, Beijing, China, August 2018
21. Roy, K., Banik, D., Bhattacharjee, D., Nasipuri, M.: Patch-based system for classification of breast histology images using deep learning. Comput. Med. Imaging Graph. **71**, 90–103 (2019)
22. Senaras, C., Niazi, M.K.K., Sahiner, B., Pennell, M.P., Tozbikian, G., Lozanski, G., Gurcan, M.N.: Optimized generation of high-resolution phantom images using cGAN: application to quantification of Ki67 breast cancer images. PLoS ONE **13**(5), e0196846 (2018)
23. Shallu, Mehra, R.: Breast cancer histology images classification: training from scratch or transfer learning? ICT Express **4**(4), 247–254 (2018)
24. Shin, H.-C., Tenenholtz, N.A., Rogers, J.K., Schwarz, C.G., Senjem, M.L., Gunter, J.L., Andriole, K.P., Michalski, M.: Medical image synthesis for data augmentation and anonymization using generative adversarial networks. In: Gooya, A., Goksel, O., Oguz, I., Burgos, N. (eds.) Simulation and Synthesis in Medical Imaging, vol. 11037, pp. 1–11. Springer, Cham (2018)
25. Song, Y., Chang, H., Gao, Y., Liu, S., Zhang, D., Yao, J., Chrzanowski, W., Cai, W.: Feature learning with component selective encoding for histopathology image classification. In: 2018 IEEE 15th International Symposium on Biomedical Imaging (ISBI 2018) (2018)
26. Song, Y., Chang, H., Huang, H., Cai, W.: Supervised Intra-embedding of fisher vectors for histopathology image classification. In: Han, Y. (ed.) Physics and Engineering of Metallic Materials, vol. 217, pp. 99–106. Springer, Singapore (2017)
27. Spanhol, F.A., Oliveira, L.S., Cavalin, P.R., Petitjean, C., Heutte, L.: Deep features for breast cancer histopathological image classification. In: 2017 IEEE International Conference on Systems, Man, and Cybernetics (SMC), pp. 1868–1873. IEEE, Banff, AB, October 2017
28. Spanhol, F.A., Oliveira, L.S., Petitjean, C., Heutte, L.: A dataset for breast cancer histopathological image classification. IEEE Trans. Biomed. Eng. **63**(7), 1455–1462 (2016)
29. Spanhol, F.A., Oliveira, L.S., Petitjean, C., Heutte, L.: Breast cancer histopathological image classification using Convolutional Neural Networks. In: 2016 International Joint Conference on Neural Networks (IJCNN), pp. 2560–2567. IEEE, Vancouver, BC, Canada, July 2016
30. Sudharshan, P.J., Petitjean, C., Spanhol, F., Oliveira, L.E., Heutte, L., Honeine, P.: Multiple instance learning for histopathological breast cancer image classification. Expert Syst. Appl. **117**, 103–111 (2019)
31. Vo, D.M., Nguyen, N.-Q., Lee, S.-W.: Classification of breast cancer histology images using incremental boosting convolution networks. Inf. Sci. **482**, 123–138 (2019)

32. Weiss, N., Kost, H., Homeyer, A.: Towards interactive breast tumor classification using transfer learning. In: Campilho, A., Karray, F., Romeny, B.H. (eds.) Image Analysis and Recognition, vol. 10882, pp. 727–736. Springer, Cham (2018)
33. Zhang, G., Xiao, M., Huang,Y.-H.: Histopathological image recognition with domain knowledge based deep features. In: Huang, D.-S., Gromiha, M.M., Han, K., Hussain, A. (eds.), Intelligent Computing Methodologies, vol. 10956, pp. 349–359. Springer, Cham (2018)
34. Zhang, X., Zhang, Y., Qian, B., Liu, X., Li, X., Wang, X., Yin, C., Lv, X., Song, L., Wang, L.: Classifying breast cancer histopathological images using a robust artificial neural network architecture. In: Rojas, I., Valenzuela, O., Rojas, F., Ortuño, F. (eds.) Bioinformatics and Biomedical Engineering, vol. 11466, pp. 204–215. Springer, Cham (2019)