Exploring Histopathological Image Augmentation Through StyleGAN2ADA: A Quantitative Analysis

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Abstract: Due to the rapid development of technology in the last decade, pathology has entered its digital era with the diffusion of WSIs. With this improvement, providing reliable automated diagnoses has become highly desirable to reduce the time and effort of experts in time-consuming and exhaustive tasks. However, with the scarcity of publicly labeled medical data and the imbalance between data classes, it is necessary to use various data augmentation techniques to mitigate these problems. This paper presents experiments that investigate the impact of adding synthetic IHC images on the classification of staining intensity levels of cancer cells with estrogen and progesterone biomarkers. We tested models SVM, CNN, DenseNet, and ViT, trained with and without images generated by StyleGAN2ADA and AutoAugment. The experiments covered class balancing and adding synthetic images to the training process, improving the classification F1-Score by up to 14 percentage points. In almost all experiments using StyleGAN2ADA images, the F1-Score was enhanced.

1 INTRODUCTION

Cancer is a term that defines a large group of diseases characterized by the rapid creation of abnormal cells that grow beyond their usual limits and can spread to other body regions. The widespread spread of these abnormal cells is the main cause of death from cancer. According to the World Health Organization (WHO), the global cancer incidence exceeded 19 million cases, reaching almost 10 million deaths in 2020 (WHO, 2022). In 2022, Breast Cancer (BC) occupied the second position for incidence and ranked fourth place for mortality, as reported by the International Agency for Research on Cancer (IARC) (IARC, 2023).

To reach a diagnosis, the immunohistochemistry (IHC) process analyses the biopsy samples concerning the Estrogen Receptor (ER) and the Proges-

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terone Receptor (PR) biomarkers. These receptors are proteins inside or on cells that can bind to certain substances in the blood (American Cancer Society, 2021), leading cancerous cells to overexpress them and thereby promote uncontrolled cell growth (Yip and Rhodes, 2014).

The Allred score assesses the hormone receptor expression by summing up the Proportion Score (PS), which indicates the relative proportion of cancer cells in the tissue (Mouelhi et al., 2018), and the Intensity Score (IS), which evaluates the intensity of cell staining (Kim et al., 2016). The PS score ranges from 0 to 5, and the IS score has values 0 (negative), 1+ (weakly positive), 2+ (moderately positive), and 3+ (strongly positive) (Rogalsky et al., 2021). Since the score relies on the pathologist's or histopathologist's experience and professional training, this process is susceptible to human error and fatigue, which may lead to misdiagnoses (Han et al., 2017).

The creation of Whole-Slide Images (WSIs) marked the beginning of the pathology digital era and prompted researchers to automate diagnosis and assist in IHC image reporting (Laurinavicius et al., 2016). In this context, automatic classification to categorize

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the characteristics of the disease more specifically and segmentation to determine the location of cancer cells in IHC images have emerged (Mouelhi et al., 2018; Cordeiro et al., 2018; Tang et al., 2019; Rogalsky et al., 2021; Rmili et al., 2022; Mridha et al., 2022; Choi et al., 2023; Krinski et al., 2023).

Recent interest from IHC medical imaging researchers has led to significant progress. Although, challenges remain for medical image sets as they often lack variability and have imbalanced classes (Mukherkjee et al., 2022). However, data augmentation techniques with image-processing methods and the generation of synthetic images provided by Generative Adversarial Networks (GANs) are helping to address these issues by generating new synthetic images from existing datasets (Krinski et al., 2023; Osuala et al., 2023).

Therefore, to enhance the automation of breast cancer diagnosis, we investigated the Style-GAN2ADA network to generate images for each class of the IS score to produce high-quality medical data. Then, we compare them with the AutoAugment model generated images. In addition, we defined and applied four classification methods to categorize the Estrogen Receptor (ER) and Progesterone Receptor (PR) biomarkers patches. To this end, we performed a quantitative analysis of the results, combining data augmentation techniques and classification methods and evaluating them through f1-score.

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2 MATERIALS AND METHODS

2.1 Datasets

In this paper, we used the dataset from the Rogalsky study (Rogalsky, 2021), which includes IHC-DAB WSIs from 78 patients evaluated for ER and PR biomarkers. The author provided 1801 (ER) and 1625 (PR) patches with a dimension of 400x300 pixels, selected from a ROI with 40x increase (discarding non-pathogenic regions). Each patch received the cancer intensity score (IS) according to the opinion of experts. Fig. 1 presents image samples from both datasets (first row), and Table 1 shows the IS class distributions.

Table 1: Distribution of IS classes from Estrogen Receptor (ER) and Progesterone Receptor (PR) images that compose the *HistoBC-HR* dataset of Rogalsky (2021).

Exam Type	0	1+	2+	3+	Total
ER	414	149	293	945	1801
PR	515	171	226	713	1625

2.2 Data Augmentation

Medical image datasets often have low variability and high imbalance between classes (Mukherkjee et al., 2022). For instance, our dataset presented a limitation in the number of samples as class 1+ has only 149 examples, and, at the same time, class 3+ contains 945 images, demonstrating the imbalance between classes 1+ and 3+. Data Augmentation (DA) techniques have recently addressed these challenges, including imageprocessing methods and synthetic image generation provided by GANs as well (Osuala et al., 2023). In this paper, we investigated two techniques: AutoAugment and StyleGAN2ADA (step 1 in Fig. 2).

2.2.1 AutoAugment

In the context of our research, we used AutoAugment provided by the Pytorch library, comprised of pretrained weights on the CIFAR-10 dataset. The idea of AutoAugment is to automate the search for data augmentation policies, optimizing the selection of transformations, the probability of applying them, and the magnitude of the operation. We considered transformations such as rotations, translations, brightness adjustments, color changes, and equalizations with different probabilities of use and magnitudes. We chose the pre-trained AutoAugment to compose these image-processing forms of data augmentation, using operations without requiring manual adjustments to determine which ones to apply and at what magnitudes. For more details about the transformations, consult Cubuk et al. (2019).

2.2.2 StyleGAN2ADA

Generative Adversarial Networks (GANs) are recent techniques for generating synthetic images, consisting of two networks: a generator that creates new images and a discriminator that distinguishes real from fake (Osuala et al., 2023). Amidst current architectures, the Style Generative Adversarial Network with Adaptive Discriminator Augmentation (Style-GAN2ADA) stand out for generating high-quality images and addressing the overfitting issues of its predecessors. This network tackles the challenges arising from limited datasets by incorporating imageprocessing data augmentation techniques during the training process, thereby diversifying and increasing the number of dataset samples (Karras et al., 2020).

To evaluate the StyleGAN2ADA, we separated the same-class images from the dataset, forming four training sets (0, 1+, 2+, and 3+) for each type of exam (ER and PR). Then, we trained a specific Style-GAN2ADA for each class and generated new syn-



Figure 1: Examples of real images, synthetic images obtained by AutoAugment, and images generated by StyleGAN2ADA on the Estrogen Receptor (ER) and Progesterone Receptor (PR) dataset.



Figure 2: Overview of the proposed work. Step 1 uses the ER and PR image datasets, applying AutoAugment (AA) with pre-trained weights for data augmentation, and also trains a StyleGAN2ADA (SG) to generate synthetic data for each IS class. Step 2 organizes the data into five experiments: E1, consisting solely of the original dataset; E2, the original dataset with the addition of 100 images produced by AA to the training set; E3, the original dataset with 100 synthetic images generated by SG; E4, with class balancing in the training set using AA-generated images; and E5, also balancing the classes but using SG-generated images. Based on these experiments, cross-validation defines the training, validation, and testing sets, with the validation and testing sets consisting of real data. Finally, IS score classification uses the Rogalsky Methodology, CNN, DenseNet, and ViT models ('C' stands for Convolution, 'P' for Pooling, and 'D' for Dense Layer). The evaluation of the experiments was performed using the f1-score.

thetic images of both biomarkers and all intensity scores. In this step, we used the Pytorch library to implement StyleGAN2ADA, with 1500 training epochs and 0.5 as the data augmentation hyperparameter (truncation) to create new artificial images. We defined these values after running smaller experiments on a validation set.

2.3 Classification

2.3.1 Rogalsky Methodology (RM)

As a first step to achieve the IS classification, we adapted the methods proposed by Rogalsky (Rogalsky, 2021). On each patch we applied the Contrast Limited Adaptive Histogram Equalization (CLAHE) method followed by a thresholding, starting with a Gaussian blur filter to flatten gradients and avoid noise amplifications. Then, we converted the image to grayscale and passed it through the Otsu technique (see Fig. 2). With this initial segmentation of the cells, we transformed the images from the original color space to the HSV color space, splitting the H, S, and V channels. After this, we extracted the positive cells (in brown) and negative cells (in blue) with color deconvolution (mask values available in Rogalsky (2021)).

From the deconvolution images, we calculated intensity histograms, which underwent MinMax normalization to keep values between 0 and 100. The intensity histograms served as features for the training, validation, and test sets. The training stage consisted of passing the training and validation sets to a Support Vector Machine (SVM) model. During this phase, the validation set optimized the model's hyperparameters. Finally, we delivered the test set to the trained SVM and calculated general and per-class f1-scores. We repeated this process five times, using the 5-fold cross-validation method.

2.3.2 Proposed CNN

With the rise of IHC WSIs, Deep Learning models, particularly CNNs, gained prominence for their ability to automatically extract features, often outperforming manually adjusted methods for feature extraction (Cordeiro, 2019; Mridha et al., 2022). Given this scenario, we proposed a CNN based on the architecture from Tang et al. (2019), which uses a lightweight CNN capable of accurately classifying IHC images. The patches were normalized and resized to 256x256 pixels, and the architecture included 6 Convolutional and Max Pooling layers, along with 2 Dense layers (Fig. 2). The convolutional layers had 64, 64, 128, 256, 256, and 512 neurons, with a dropout rate of 0.2, a learning rate of 0.00008, the

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Adam optimizer, early stopping, and the Multi-Label Soft Margin Loss function. The network outputted the probability of the image belonging to each IS class, and its performance was evaluated using the same method and metric from the RM.

2.3.3 DenseNet Approach

To address vanishing-gradient issues, strengthen feature propagation, and reduce CNN parameters, the DenseNet (Densely Connected Convolutional Network) architecture was proposed (Huang et al., 2017). A key innovation was the use of dense connections between layers (Dense Blocks), where all layers are connected, allowing each to receive inputs from all previous layers and pass features to the next, thereby enabling more effective learning (Huang et al., 2017). For our experiments, we implemented DenseNet121, a 121-layer variation (Fig. 2), using Pytorch and pretrained weights from the ImageNet1K dataset, and performed fine-tuning with early stopping. Hyperparameters were set according to default values in the library, with a Cross-Entropy loss function, 224x224 image size, and the Adam optimizer. Regarding the division of data and metrics, DenseNet followed the same steps described in the proposed CNN.

2.3.4 ViT Approach

To provide an alternative to CNNs with lower computational costs, the Vision Transformer (ViT) was proposed in Dosovitskiy et al. (2021). ViT divides the input image into fixed-sized patches and employs self-attention mechanisms to capture features at various levels. This enables the model to understand both global image context and relationships between patches (Fig. 2). The classification step is performed by an MLP with a hidden layer during pre-training and a single linear layer during fine-tuning (Dosovitskiy et al., 2021). We implemented the ViT using Pytorch and performed fine-tuning with pre-trained weights from the ImageNet1K dataset. The model considered normalized 224x224 images, learning rate of 0.001, Cross-Entropy loss, and Adam optimizer, along with early stopping to prevent overfitting. Data division and evaluation metrics followed the approach described in previous classifiers.

3 EXPERIMENTS

3.1 Cross-Validation Approach

To structure the training process, we opted for the 5fold cross-validation, chosen for its ability to provide reliable performance estimates with small datasets, avoiding misinterpretations common with methods like Holdout (Maleki et al., 2020). This approach averages results across five combinations of training, validation, and test sets. Unlike standard crossvalidation, we designated one fold exclusively for testing, while one of the remaining four training folds served as validation. This adaptation enhanced the variance of the test data, offering a more realistic performance estimate while balancing result reliability with training and execution time.

3.2 Hyperparameter Optimization

After defining the data augmentation and classification methods, we optimized key hyperparameters. For StyleGAN2ADA, we set the truncation factor to 0.5, balancing increased variance in synthetic images with the preservation of original features (Karras et al., 2020), based on experiments with truncation values between 0.3 and 0.7. For classifiers, we adjusted the learning rate and implemented early stopping to mitigate overfitting (Bai et al., 2021). Training halts if validation loss worsens by more than 10% across three instances, and the learning rate is halved each time, enabling finer adjustments. These values were determined through smaller experiments and learning curve analysis.

3.3 IS Classification

Regarding the automatic scoring of cancer levels from Estrogen Receptor (ER) and Progesterone Receptor (PR) images, we defined five experiments to study the impact of adding synthetic images on the training process of the classification models. For this, we considered AutoAugment and StyleGAN2ADA as data augmentation methods and selected Rogalsky Methodology, CNN, DenseNet, and ViT models to categorize images into the four IS score values. In the evaluation step, the f1-scores of the test sets from the 5-folds were aggregated by the mean. We present the descriptions of these experiments below:

- E1 DS: Training, validation, and testing of the proposed classification methods with the original dataset (DS).
- E2 AA+100: Addition of 100 synthetic images for each IS class to the original training set, generated by the AutoAugment model.
- E3 SG+100: Addition of 100 synthetic images for each IS class to the original training set, generated by the StyleGAN2ADA model.

- E4 AA+B: Balancing of the training set classes in relation to the majority class using the AutoAugment model. After balancing, 100 more synthetic images were added for each IS class.
- E5 SG+B: Balancing of the training set classes in relation to the majority class using the Style-GAN2ADA model. After balancing, 100 more synthetic images were added for each IS class.

Table 2 details the number of samples per class in each experiment. For experiments E2 and E3, we added 100 synthetic images using AutoAugment and StyleGAN2ADA, respectively, to evaluate the impact of a small amount of data augmentation without exceeding the number of real images in each class. The minority class in the ER dataset had 123 samples, and in the PR dataset, 102, prompting the selection of 100 synthetic images. Experiments E4 and E5 aimed to balance the classes by adding synthetic images until the minority classes matched the majority class, followed by an additional 100 generated images per class. All experiments were compared to E1, which used the original dataset without synthetic images.

Table 2: Number of training samples of each class for all experiments with the ER and PR datasets.

		ER				P			R .	
	0	1+	2+	3+	Total	0	1+	2+	3+	Total
DS (E1)	330	123	235	753	1441	319	102	137	417	975
AA+100 (E2)	430	223	335	853	1841	419	202	237	517	1375
SG+100 (E3)	430	223	335	853	1841	419	202	237	517	1375
AA+B (E4)	853	853	853	853	3412	517	517	517	517	2068
SG+B (E5)	853	853	853	853	3412	517	517	517	517	2068

4 RESULTS

The average 5-fold results with the Rogalsky Methodology (RM), CNN, DenseNet (DN), and ViT models for each experiment are presented in Table 3, covering the f1-score metric from both datasets (ER and PR).

4.1 ER Dataset

Starting with Rogalsky Methodology in the ER dataset scenario, AutoAugment (E2 and E4) worsened the average f1-scores by 5 and 9 percentage points, while E3 reduced them minimally (0.31), and E5 improved them by 0.38 percentage points. AutoAugment transformations may have introduced noise or altered the main characteristics of the original images, such as coloration and contrast (see second row of Fig. 1). This may have transformed the intensity of the cells, confusing the classifier. Also,

Table 3: Classification methods f1-scores in experiments E1, E2, E3, E4, and E5, considering all IS classes from ER and PR biomarkers. The blue values show improvements, and the red values indicate worsening compared to the results of experiment DS. The results refer to the 5-fold averages.

Exam Type	Model	DS (E1)	AA+100 (E2)	SG+100 (E3)	AA+B (E4)	SG+B (E5)
ER	RM	82.86 ± 02.34	77.94 ± 05.12	82.55 ± 02.92	74.33 ± 05.91	83.25 ± 03.06
	CNN	71.77 ± 06.88	77.37 ± 04.63	81.20 ± 03.03	65.76 ± 36.92	81.16 ± 04.04
	DN	76.88 ± 05.47	77.32 ± 04.95	87.46 ± 03.98	76.93 ± 03.88	80.60 ± 04.08
	ViT	82.86 ± 03.43	82.97 ± 02.89	83.68 ± 02.65	82.44 ± 03.03	84.04 ± 03.71
PR	RM	76.36 ± 04.91	69.56 ± 06.81	78.63 ± 04.13	68.23 ± 06.83	77.86 ± 03.01
	CNN	57.16 ± 02.80	58.84 ± 03.05	64.69 ± 05.57	69.36 ± 06.49	71.31 ± 03.95
	DN	80.47 ± 04.48	80.42 ± 02.77	82.00 ± 02.82	79.34 ± 02.98	81.25 ± 03.37
	ViT	91.75 ± 06.35	89.76 ± 05.09	91.76 ± 06.26	89.47 ± 05.59	92.22 ± 06.53

since the SVM does not present problems with imbalanced data (Cortes and Vapnik, 1995), adding images with StyleGAN2ADA did not contribute to or worsen the model's performance. Thus, the network synthetic images outperform AutoAugment and do not harm the classification process.

With the proposed CNN, synthetic images improved E2, E3, and E5 experiments, with an increase of up to 9 percentage points in E3 using Style-GAN2ADA. These improvements can be attributed to the greater variability introduced by synthetic images (see third row of Fig. 1), which helped generalize the model. With AutoAugment, there was a gain of 5.6 percentage points in E2, but a drop of 6 percentage points in E4. Because it is a model with no pre-trained weights, the CNN was able to stabilize its training with the addition of images in experiment E2 (ao Huang et al., 2022). However, in the case of E4, the model began to rely mostly on these synthetic images, resulting in misclassification between classes.

DenseNet presented the best results among the evaluated models, consistently outperforming E1, with an f1-score of 87.46% in E3. The greater depth of the network layers, the various innovations brought by the architecture, and the use of pre-trained weights may have contributed to better performance. However, E5 had a lower average f1-score compared to the CNN and the RM. Thus, we emphasize the importance of carefully optimizing the number of synthetic images included in the training set, as a more complex model does not necessarily guarantee better performance.

With ViT, f1-scores were higher than 82% in all experiments, making it the most consistent model. E5 showed the best performance, with a 1.18 percentage point improvement. While the improvement was modest, the synthetic images did not degrade the results, and given that ViT typically requires millions of data points to achieve optimal performance, this highlights the potential of StyleGAN2ADA to support the learning process effectively. The larger dataset, class balance, and high-quality synthetic images from the network could enhance learning by enriching the training set and stabilizing ViT's feature extraction and MLP training (Dosovitskiy et al., 2021).

4.2 PR Dataset

In the analysis of the RM model on the PR dataset, we noticed that the f1-scores improved in experiments E3 and E5 (StyleGAN2ADA) compared to E1 (DS). In contrast, the experiments with AutoAugment (E2 and E4) showed a decline, with a drop of 8 percentage points. This suggests that image-processing data augmentation transformations can be detrimental if not properly optimized for the specific problem (see second row of Fig. 1). The experiment using 100 synthetic images from StyleGAN2ADA increased by 2.27 percentage points, demonstrating that these images can enhance the learning process, even in models that do not depend on large datasets or class balancing techniques (Cortes and Vapnik, 1995).

Using the CNN, all experiments with synthetic image insertion (E2, E3, E4, and E5) improved the f1-scores compared to the original data experiment. For class 1+, the CNN initially failed to classify any test samples in E1 and E2, achieving f1-scores of 0%. From E3 onward, the model began to succeed, reaching 60% in E5. This trend was reflected in overall f1-scores, with gains of 14.15 percentage points in E5 and 12.12 in E4. These results highlight the importance of balancing training sets with synthetic images, particularly to stabilize learning in models without pre-trained weights (ao Huang et al., 2022).

Regarding DenseNet, we observed that the f1scores did not show notable variations in the overall results. The highest gain was 1.53 percentage points, reaching an 82% f1-score, making DenseNet the first classifier to surpass 80% on the PR data. Thus, we conclude that even though the improvements from one experiment to another are minor, they are crucial for more accurate diagnoses in the medical field and indicate potential advancements in the area with the use of StyleGAN2ADA. Finally, ViT achieved the best results in the research, surpassing a 90% overall f1-score. We observed that experiment E3 maintained the results of E1, and E5 reached 92.22%, improving the metric by 0.47 percentage points. E2 and E4 reduced the metrics, presenting drops of 1.99 percentage points in E2 and 2.28 in E4. The fact that StyleGAN2ADA images did not harm performance highlights their potential. ViT models require millions of data points to achieve optimal performance, a requirement unmet by small datasets. This suggests that synthetic data could offer a cost-efficient alternative, eliminating the need for large, annotated real datasets by providing millions of high-quality synthetic samples.

5 LIMITATIONS

We do not apply the proposal to other datasets with distinct types of pathologies. Using a network capable of synthesizing high-quality medical images can contribute to several areas due to its ability to learn the concept of images and respect the main characteristics of the data. Also, we do not consider the use of pre-trained weights in StyleGAN2ADA, although fine-tuning can facilitate the training process because it starts with information that may be relevant. Finally, we did not carry out interpretability studies of the feature maps of the generating network and the CNN-based classifiers. This study would allow a greater understanding of which characteristics the models consider essential to define each class.

6 DISCUSSION

In this research, we conducted an impact study to evaluate the effect of adding synthetic medical images into the classification methods training process. The objective was to classify the cell staining intensity score of patches from ER and PR biomarkers responsible for breast cancer detection and categorization. To achieve this, we generated images with the StyleGAN2ADA and AutoAugment models and incorporated synthetic images into the training process of four classification models.

In the ER dataset, we achieved the best classification results with DenseNet, obtaining an f1-score of 87.46% and improving the metric by 10.58 percentage points compared to the experiment with original data. In the PR dataset, we achieved an f1-score of 92.22% with ViT, along with an increase of 14 percentage points with the CNN. Experiments using synthetic images from AutoAugment produced worse results, with drops of up to 8 percentage points, indicating that simple data augmentation techniques can interfere with critical features of medical images. On the other hand, images generated by StyleGAN2ADA improved the results in most experiments by increasing the variability of the training set and promoting better generalization of the classifiers.

To the best of our knowledge, our research is the first in the field to use StyleGAN2ADA in the context of IHC images. In future work, we aim to evaluate the proposed methods on other datasets, examine the impact of pre-trained weights on StyleGAN2ADA training, and apply interpretability studies to facilitate the adoption of this proposal in clinical environments.

7 CONCLUSIONS

In summary, in the context of breast cancer images associated with the ER and PR biomarkers, the use of the state-of-the-art network StyleGAN2ADA improved performance in IS classification by increasing data variability. In contrast, data augmentation techniques based solely on image-processing, such as the pre-trained AutoAugment, proved inadequate for this problem. Furthermore, we emphasize the importance of carefully selecting the evaluation method in classimbalanced scenarios and testing different amounts of synthetic images added to the training set to ensure reliable and robust results.

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REFERENCES

American Cancer Society (2021). Breast Cancer Hormone Receptor Status. https: //www.cancer.org/cancer/breast-cancer/ understanding-a-breast-cancer-diagnosis/ breast-cancer-hormone-receptor-status.html.

- ao Huang, Z., Sang, Y., Sun, Y., and Lv, J. (2022). A neural network learning algorithm for highly imbalanced data classification. *Information Sciences*, 612:496–513. https://doi.org/10.1016/j.ins.2022.08.074.
- Bai, Y., Yang, E., Han, B., Yang, Y., Li, J., Mao, Y., Niu, G., and Liu, T. (2021). Understanding and improving early stopping for learning with noisy labels.
- Choi, S., Cho, S. I., Jung, W., Lee, T., Choi, S. J., and et al. (2023). Deep learning model improves tumorinfiltrating lymphocyte evaluation and therapeutic response prediction in breast cancer. *npj Breast Cancer*. https://doi.org/10.1038/s41523-023-00577-4.
- Cordeiro, C. Q. (2019). An Automatic Patch-Based Approach for HER-2 Scoring in Immunohistochemical Breast Cancer Images. https://acervodigital.ufpr.br/ handle/1884/66131.
- Cordeiro, C. Q., Ioshii, S. O., Alves, J. H., and de Oliveira, L. F. (2018). An Automatic Patch-based Approach for HER-2 Scoring in Immunohistochemical Breast Cancer Images Using Color Features. XVIII Simpósio Brasileiro de Computação Aplicada à Saúde. https: //doi.org/10.5753/sbcas.2018.3685.
- Cortes, C. and Vapnik, V. (1995). Support-vector networks. *Machine Learning*, 20. https://doi.org/10. 1007/BF00994018. Acessado em: 27/03/2023.
- Cubuk, E. D., Zoph, B., Mané, D., Vasudevan, V., and Le, Q. V. (2019). Autoaugment: Learning augmentation strategies from data. In 2019 IEEE/CVF Conference on Computer Vision and Pattern Recognition (CVPR).
- Dosovitskiy, A., Beyer, L., Kolesnikov, A., Weissenborn, D., Zhai, X., Unterthiner, T., Dehghani, M., Minderer, M., Heigold, G., Gelly, S., Uszkoreit, J., and Houlsby, N. (2021). An image is worth 16x16 words: Transformers for image recognition at scale.
- Han, Z., Wei, B., Zheng, Y., Yin, Y., Li, K., and Li, S. (2017). Breast Cancer Multi-classification from Histopathological Images with Structured Deep Learning Model. *Scientific Reports*. https://doi.org/ 10.1038/s41598-017-04075-z.
- Huang, G., Liu, Z., Maaten, L. V. D., and Weinberger, K. Q. (2017). Densely connected convolutional networks. In 2017 IEEE Conference on Computer Vision and Pattern Recognition (CVPR), pages 2261–2269, Los Alamitos, CA, USA. IEEE Computer Society.
- IARC (2023). Cancer Today. https://gco.iarc.fr/today/ online-analysis-multi-bars?
- Karras, T., Aittala, M., Hellsten, J., Laine, S., Lehtinen, J., and Aila, T. (2020). Training Generative Adversarial Networks with Limited Data. https://doi.org/10. 48550/arXiv.2006.06676. Acessado em: 24/04/2023.
- Kim, S.-W., Roh, J., and Park, C.-S. (2016). Immunohistochemistry for Pathologists: Protocols, Pitfalls, and Tips. Journal of Pathology and Translational Medicine 2016; 50: 411-418. https://doi.org/10.4132/ jptm.2016.08.08.
- Krinski, B. A., Ruiz, D. V., Laroca, R., and Todt, E. (2023). DACov: a deeper analysis of data augmentation on the computed tomography segmentation problem. *Computer Methods in Biomechanics and Biomedical En-*

gineering: Imaging & Visualization, 0(0):1–18. https://doi.org/10.1080/21681163.2023.2183807.

- Laurinavicius, A., Plancoulaine, B., Herlin, P., and Laurinaviciene, A. (2016). Comprehensive Immunohistochemistry: Digital, Analytical and Integrated. *Pathobiology* 2016;83:156-163. https://doi.org/10.1159/ 000442389.
- Maleki, F., Muthukrishnan, N., Ovens, K., Md, C., and Forghani, R. (2020). Machine Learning Algorithm Validation. *Neuroimaging Clinics of North America*, 30:433–445. http://dx.doi.org/10.1016/j.nic.2020.08. 004. Acessado em: 25/04/2023.
- Mouelhi, A., Rmili, H., Ali, J. B., Sayadi, M., Doghri, R., and Mrad, K. (2018). Fast unsupervised nuclear segmentation and classification scheme for automatic allred cancer scoring in immunohistochemical breast tissue images. *Computer Methods and Programs in Biomedicine*. https://doi.org/10.1016/j.cmpb.2018.08. 005.
- Mridha, M. F., Morol, M. K., Ali, M. A., and Shovon, M. S. H. (2022). convoHER2: A Deep Neural Network for Multi-Stage Classification of HER2 Breast Cancer. AIUB Journal of Science and Engineering (AJSE). https://doi.org/10.53799/ajse.v22i1.477.
- Mukherkjee, D., Saha, P., Kaplun, D., Sinitca, A., and Sarkar, R. (2022). Brain tumor image generation using an aggregation of GAN models with style transfer. *Sci Rep. 2022; 12: 9141*. https://doi.org/10.1038 %2Fs41598-022-12646-y.
- Osuala, R., Kushibar, K., Garrucho, L., Linardos, A., Szafranowska, Z., Klein, S., Glocker, B., Diaz, O., and Lekadir, K. (2023). Data synthesis and adversarial networks: A review and meta-analysis in cancer imaging. *Medical Image Analysis*, 84:102704. https://doi.org/10.1016/j.media.2022.102704.
- Rmili, H., Mouelhi, A., Solaiman, B., Doghri, R., and Labidi, S. (2022). A novel pre-processing approach based on colour space assessment for digestive neuroendocrine tumour grading in immunohistochemical tissue images. *Pol J Pathol.* 2022;73(2):134-158. https://doi.org/10.5114/pjp.2022.119841.
- Rogalsky, J. E. (2021). Semi-automatic ER and PR scoring in immunohistochemistry H-BAD breast cancer images. https://acervodigital.ufpr.br/handle/1884/73470.
- Rogalsky, J. E., Ioshii, S. O., and de Oliveira, L. F. (2021). Automatic ER and PR scoring in Immunohistochemistry H-DAB Breast Cancer images. XXI Simpósio Brasileiro de Computação Aplicada à Saúde. https: //doi.org/10.5753/sbcas.2021.16075.
- Tang, Z., Chuang, K. V., DeCarli, C., Jin, L.-W., Beckett, L., Keiser, M. J., and Dugger, B. N. (2019). Interpretable classification of Alzheimer's disease pathologies with a convolutional neural network pipeline. *Nature Communications 10*. https://doi.org/10.1038/ s41467-019-10212-1.
- WHO (2022). Cancer. https://www.who.int/news-room/ fact-sheets/detail/cancer.
- Yip, C.-H. and Rhodes, A. (2014). Estrogen and progesterone receptors in breast cancer. *Future Oncol*ogy, 10(14), 2293-2301. https://doi.org/10.2217/fon. 14.110.