MedAI AnomalyPro: Advancing Unsupervised Anomaly Detection in Medical Imaging

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Abstract. Automated anomaly detection in medical imaging, encompassing modalities like MRIs and X-rays, plays a crucial role in accelerating disease diagnosis processes. While existing methods often rely on models trained solely on healthy images, they may struggle with real-world datasets containing a mix of healthy and diseased individuals. Our study introduces "MedAI AnomalyPro," a novel unidirectional image-to-image translation approach. Unlike traditional techniques, MedAI AnomalyPro focuses on translating images from diverse datasets into representations akin to those of healthy subjects, overcoming challenges associated with unpaired and mixed data. Leveraging the generated disparity maps from translated outputs, the system accurately identifies potential anomalies. Remarkably, MedAI AnomalyPro outperforms conventional methods across various benchmarks, including datasets related to COVID-19, NIH ChestX-ray14, and an institutional dataset. In Covid 19 detection, MedAI AnomalyPro achieved an AUC of 0.84, surpassing all competitors, with precision, specificity, and F1 scores of 0.76. MedAI AnomalyPro achieved the highest detection AUC score of 0.56 in Chest X-ray 14, outperforming its closest competitor, with precision, recall, specificity, and F1 scores of 0.55. With an impressive AUC value of 0.75, MedAI AnomalyPro demonstrated its superiority in migraine detection over the leading traditional approach, with recall, accuracy, specificity, and F1 scores of 0.79, 0.71, 0.81, and 0.74, respectively.

Keywords: Automated anomaly detection · Medical imaging · Unsupervised learning · Image-to-image translation · Disease diagnosis · GAN

1 Introduction

In the ever-evolving landscape of medical image analysis, the strides made with supervised learning through deep neural networks have reshaped the field, particularly in scenarios rich with annotations. However, tackling anomaly detection in the realm of rare diseases poses a formidable challenge, as the procure-

ment of large annotated datasets becomes increasingly impractical. Recent initiatives have primarily focused on models trained exclusively on images portraying healthy subjects, inadvertently sidelining the existence of unannotated anomalous samples within real-world datasets. To address this oversight, our research endeavors to fortify anomaly detection capabilities by harnessing the potential of unannotated mixed datasets alongside images depicting normal cases.

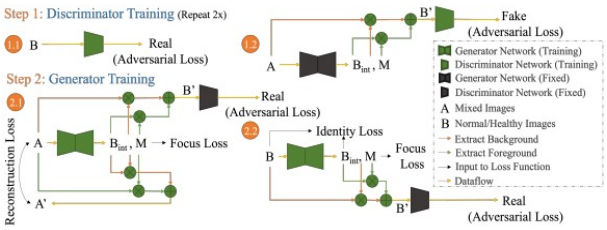

Fig. 1. Single iteration of MedAI AnomalyPro Method

Central to our efforts is the introduction of "MedAI AnomalyPro," a groundbreaking unidirectional unpaired image-to-image translation network firmly rooted in the foundational principles of Generative Adversarial Networks (GANs). What sets MedAI AnomalyPro apart is its remarkable ability to seamlessly transform images from diverse datasets into representations akin to those illustrating normal cases, thereby facilitating the discernment of abnormalities based on salient disparities between input and output images. Conventional unpaired image-to-image translation methodologies often fall short in our specific problem domain, often necessitating bi-directional transformations or reliance on prior image annotations. In contrast, MedAI AnomalyPro introduces pivotal attributes: unpairedness and one-directionality in its image-to-image translation process. Furthermore, a novel reconstruction loss mechanism has been devised to ensure the preservation of effective cycle-consistency without the need for annotated inputs. The efficacy of MedAI AnomalyPro is substantiated through rigorous experimentation, where it consistently outperforms existing methods, yielding substantial performance enhancements across various benchmarks such as COVID-19, National Institutes of Health ChestX-ray14, and a proprietary institute dataset focused on migraine detection.

Our contributions transcend mere algorithmic innovations; they encompass the development of a revolutionary one-directional unpaired image-to-image translation methodology, the introduction of a novel reconstruction loss mechanism enabling cycle-consistency without annotated inputs, and extensive experimentation that propels anomaly detection in medical imaging to unprecedented heights.

2 Literature Review

Author Changhee Han et al[1] proposed the MADGAN method, utilizing unsupervised learning on large-scale unannotated medical images. Trained on healthy T1 and T1c brain MRI datasets, MADGAN obtained substantial accuracies in detecting early-stage Alzheimer's disease (AUC 0.727 for MCI, AUC 0.894 for late-stage AD) and brain metastases (AUC 0.921), demonstrating its potential for disease detection on multi-sequence MRI images.

Baur et al[2] proposed an unsupervised deep learning approach utilizing spatial autoencoders with skip-connections to detect anomalies in brain MR images. The model trained on 100 normal MR images outperformed thresholding approaches in lesion diagnosis, with mean F1 scores ranging from 17% to 62% across different datasets. Furthermore, the model performed similarly to a supervised U-Net classifier (20% to 64% F1 scores) across varied pathologic situations, underscoring its usefulness in automated anomaly identification.

Author Hasan Iqbal [3] proposed a novel method called the masked-denoising diffusion probabilistic model (mDDPM) for identifying brain MRI anomalies.This study used datasets with malignancies and multiple sclerosis lesions. The mDDPM technique, which incorporates Masked Image Modeling (MIM) and Masked Frequency Modeling (MFM), outperformed existing fully/weakly supervised baselines for unsupervised anomaly identification.

Cosmin I. Bercea's [4] study proposed the use of reversed auto-encoders (RA) for unsupervised anomaly detection in T1w brain MRIs. The approach addressed the limitations of current auto-encoders in recognizing non-hyperintense abnormalities such brain shrinkage, edema, and resections. Their technique improved global anomaly detection (AUROC from 73.1 to 89.4) and local pathology localization (detection rate from 52.6% to 86.0%) on the T1w brain MRI dataset.

Finn Behrendt et al [5] proposed a novel approach for brain MRI pathology detection using unsupervised anomaly detection. They utilized a dataset containing brain MRI scans with tumors and multiple sclerosis lesions. Their solution reconstructed the generation job with patch-based estimate and spatial context guidance, resulting in a 25.1% relative improvement over current baselines. The study used diffusion models to produce anatomically consistent MRI images of healthy brains.

Jai Shah's [11] Deep neural networks (DNNs) in medical imaging faced challenges due to limited annotated data for rare diseases. They proposed Brainomaly, a GAN-based method tailored for neurologic disease detection. By leveraging unannotated mixed data, Brainomaly outperforms existing methods in detecting Alzheimer's and headaches. Their novel pseudo-AUC metric aids model selection in the absence of annotated samples. Access our code at

3 MedAI AnomalyPro : Proposed Method

3.1 Framework

The proposed MedAI AnomalyPro is made up of a discriminator and a generator network. Following the PatchGAN design, our discriminator seeks to distinguish between authentic medical pictures and synthetically manufactured anomaly-free images, as shown in Figure 1.

The generator network, which functions without label information, is in charge of translating input medical pictures into anomaly-free representations. Our training technique makes use of a composite dataset (Set A) that includes both anomaly-free and anomaly-containing photos, as well as another dataset (Set B) that only contains anomaly-free images. The produced photos from these sets are denoted as A0 and B0, respectively.

The generator network processes images without prior knowledge of their classifications and transforms them into images categorized as healthy. During the training phase, we utilize two datasets: Set A, comprising both diseased and healthy images, and Set B, consisting solely of healthy images. The resultant images from these sets are labeled as A0 and B0 respectively.

$$A_0 = A \odot M + B_{\text{int}} \odot (1 - M) \tag{1}$$

Instead of directly generating A0 and B0 images, the generator produces intermediate healthy images, denoted as Bint, along with masks represented by M. These masks have values ranging from 0 to 1, where 0 signifies background pixels and 1 denotes foreground pixels. The final generated images, B0, and A0 are then produced according to equations 1 and 2 below respectively. However, the A0 and B0 pictures are not created directly by the generator. Instead, it generates intermediate anomaly-free pictures labeled as Bint and corresponding masks indicated as M. These masks range. The final generated image B0 is then computed using Eq. 2, while A0 follows Eq. 1.

$$B_0 = B_{\text{int}} \odot M + A \odot (1 - M) \tag{2}$$

In instances where an image from Set A depicts a disease, we anticipate the mask M to highlight the diseased area as foreground. Conversely, if the image is healthy, we expect the mask M to remain empty or zero.

In cases when the image is from Set A and contains anomalies, we predict that the mask M will highlight the anomaly regions as foreground. In contrast, if the image has no anomalies, we anticipate M to stay empty or zero. Notably, Eq. 2 contains analogies to the cycle-consistency idea established in [39]. Given that our technique partially governs picture formation via the mask M, there is no requirement for labels or an extra generator network to generate A0 (see Fig. 2). Because the generator only supports the translation of input pictures in one direction, we classify it as a one-way image-to-image translator.

3.2 Discriminator Objective

The discriminator aims to distinguish genuine healthy images from those generated by the generator. It utilizes an adversarial loss function, inspired by the Wasserstein GAN framework, which consists of three components:

1. **Adversarial Loss**: It Measures the ability of the discriminator to differentiate between real and generated images. It encourages the discriminator to assign higher probabilities to real images and lower probabilities to generated ones.
2. **Gradient Penalty Term:** It enhances training stability by penalizing the gradients of the discriminator's output concerning its input. Helps to maintain the Lipschitz constraint.

The discriminator's adversarial loss function is represented by

$$\mathcal{L}_{\text{adv}} = \mathbb{E}_{x\in A}\left[D_{\text{real/fake}}(G(x))\right] - \mathbb{E}_{x\in B}\left[D_{\text{real/fake}}(x)\right] + \lambda_{\text{gp}}\mathbb{E}_{\hat{x}}\left[\left(||\mathcal{O}_{\hat{x}}D_{\text{real/fake}}(\hat{x})||^2 - 1\right)^2\right] \tag{3}$$

In this context, G(x) represents the generator's output. Dreal/fake(x) signifies the output of the discriminator network. The discriminator undergoes training to distinguish real healthy images in set B as genuine and perceives any images generated by the generator as counterfeit, employing an adversarial loss.

3.3 Generator Objective

The generator aims to transform input images into their corresponding healthy counterparts. For healthy input images, it behaves like an autoencoder, while for diseased input images, it aims to eliminate anomalies and produce a healthy output. The generator's objective consists of several loss terms:

- Adversarial Loss which measures the ability of the generator to produce images that are classified as genuine by the discriminator.
- Identity Loss which ensures that the generator preserves the identity of healthy input images.
- Reconstruction Loss which Encourages the generator to produce outputs that are close to the input images
- Focus Loss which Controls the alignment of mask values to ensure they are closer to 0 or 1

The final objective functions for the discriminator and generator are the sum of their respective loss components, each weighted by a coefficient that determines their relative importance:
For the discriminator:

$$L_D = L_{\text{adv}} \tag{4}$$

For the generator:

$$L_G = L_{\text{adv}} + \lambda_{\text{rec}}L_{\text{rec}} + \lambda_{\text{id}}L_{\text{id}} + \lambda_f L_f \tag{5}$$

Terms of rec, id, and f determine the relative importance of the reconstruction loss, identity loss, and focus loss, respectively.

Automated anomaly identification in medical imaging, including MRI and X-ray modalities, is extremely important for accelerating the diagnosis of illness. Modern approaches mostly rely on models that are created only from photographs of healthy individuals, assuming that these models can identify images of patients as abnormalities. Nevertheless, unannotated mixtures of both healthy and sick people are a common problem in real-world datasets. Our study clarifies the introduction of "MedAI AnomalyPro", a novel technique to unidirectional image-to-image translation. Unlike existing methods, MedAI AnomalyPro translates photos from heterogeneous datasets into representations that look like they belong to healthy patients, overcoming the difficulties that come with unpaired and mixed data compositions. Through the utilization of disparity maps that are produced from the translated outputs, possible anomalies can be precisely identified.

If the input picture is healthy, we expect the difference image to contain mostly pixels with a value near to zero; if the input image is diseased, we expect the ensuing difference images to indicate diseased regions. Consequently, by looking at the mean value of the differential photographs, the existence of sickness is found. Not only can the difference pictures show if a sickness or abnormality exists, but they also help identify the specific image regions that are linked to the conditions. It is essential to recognize, nonetheless, that despite MedAI AnomalyPro's impressive capabilities, it might not be able to detect every trait unique to a certain condition. For the purposes of this study, however, identifying a subset of disease-specific features is adequate.

4 Experiments and Results

In our pursuit for anomaly detection perfection, we compared MedAI AnomalyPro against six cutting-edge anomaly detection approaches, including ALAD, ALOCC, f-AnoGAN, Ganomaly, PaDiM, and PatchCore. We have chose these strategies based on their recent significance. Notably, ALAD, f-AnoGAN, and Ganomaly are methodologically related to MedAI AnomalyPro, although PatchCore and PaDiM, while methodologically unique, are recognized as state-of-the-art for novelty identification in natural image datasets such as MVTec AD.

We utilized the receiver operating characteristic (ROC) curve's Area Under the Curve (AUC) score to compare MedAI AnomalyPro's efficacy with traditional techniques. For a thorough analysis, precision, recall, specificity, and F1 scores were also provided. Calculating the mean value of the absolute difference between the input and translated pictures is part of the MedAI AnomalyPro prediction score. It has been demonstrated that this method is more reliable than applying the maximum difference. Conventional approaches followed the anomalous score creation techniques of their individual authors.

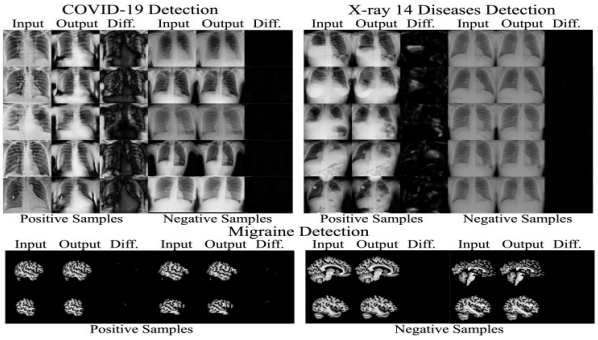

Fig. 2. MedAI AnomalyPro's results for detecting COVID-19, Chest X-ray 14 illnesses, and migraines

5 Covid 19 Recognition

- **Dataset:**The COVID-x dataset was employed, with 200 Chest X-rays in the testing set (100 positives, 100 healthy) and 15,464 in the training set (1,670 COVID-19 positives, 13,794 healthy). A mixed unannotated training set included 1,570 COVID-19 positive and 3,663 healthy photographs.
- **Results:** MedAI AnomalyPro outperformed conventional methods in COVID-19 detection, achieving an AUC of 0.84, surpassing all competitors. Precision, specificity, and F1 scores of 0.76 were also notably superior.

6 Chest X-ray 14: Identification of Diseases

- **Dataset:** Focusing solely on Posterior Anterior (PA) images from the ChestX-ray14 collection, which includes images associated with 14 thoracic disorders.
- **Results:** MedAI AnomalyPro achieved the highest detection AUC score of 0.56, outperforming its closest competitor, f-AnoGAN, which scored 0.55. Both methods exhibited precision, recall, specificity, and F1 scores of 0.55

7 Migraine Detection for Migrane

- **Dataset:** Our migraine dataset, including 104 people who were in good health and 96 brain MRIs of migraine sufferers.
- **Results:** With an impressive AUC value of 0.75, MedAI AnomalyPro demonstrated its superiority over the leading traditional approach, Ganomaly, with a score of 0.70. Further evidence of its superiority came from recall, accuracy and specificity combined with F1 scores of 0.79, 0.71, 0.81, and 0.74, respectively.

Table 1. Summary of Results

Method	Dataset	AUC	Precision/Specificity	F1 Score
Covid 19 Recognition	COVID-x	0.84	0.76	0.80
Chest X-ray 14	ChestX-ray14	0.56	0.55	0.55
Migraine Detection	Migraine	0.75	0.81	0.74

8 Conclusion

In conclusion, MedAI AnomalyPro represents a pivotal advancement in medical image analysis, offering unparalleled capabilities in automated anomaly detection. Through its innovative approach leveraging unpaired image-to-image translation and novel reconstruction loss mechanisms, MedAI AnomalyPro surpasses conventional methods, particularly in scenarios with limited annotated data.

Extensive experimentation across diverse medical imaging datasets demonstrates MedAI AnomalyPro's superior performance, underscoring its potential to revolutionize disease diagnosis processes and enhance patient care standards. As we continue to refine and integrate this technology into clinical workflows, it holds promise for improving diagnostic precision and streamlining healthcare practices. In summary, MedAI AnomalyPro heralds a new era in medical diagnostics, leveraging artificial intelligence to address complex challenges and advance patient care with unprecedented efficiency and accuracy.

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