

Creating Medical Anomaly Maps with Healthy Reconstruction Models

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Abstract

Identifying medical anomalies is a time-consuming task for physicians, and with the advent of deep-learning models, we show in this paper that we can automate anomaly detection in a visually accessible and effective manner. We compare two different approaches for the creation of these anomaly maps, one using segmentation to recognize the tumor and the other using a healthy reconstruction of a diseased brain. The former of these methods uses SegResNet as the neural network architecture whereas the latter uses a variational auto-encoder for the reconstruction. In both cases, we also apply wavelet denoising to the input images to improve the clarity of the reconstruction. Both of the methods are evaluated on the BRATS2018 dataset for brain tumor detection.

Index Terms

Variational Auto-Encoder, Anomaly Detection, Deep Learning, Segmentation

I. PROBLEM STATEMENT

With the introduction of more powerful hardware, machine learning - and in particular, deep learning - has taken off. We are highly interested in utilizing these deep learning models in the domain of medical imaging. Comparing images and identifying anomalies is a tedious process for physicians, who are already under a great deal of stress. Manual detection also requires significant expertise on the part of physicians. Automating, or at least guiding, this process can help to significantly reduce the chance of human error and incorrect prognoses as well as turnaround time. In this paper, we explore two methods of automating medical anomalies detection through the means of deep learning.

In image processing, anomaly detection is a well-defined and thoroughly studied problem. However, when it comes to medical images, due to the resolution of imaging hardware such as MRI or ultrasound, detection becomes more computationally expensive, as more iterations are needed for models to converge. Currently, there are two main approaches for automatic medical anomaly detection: segmentation and comparing the healthy reconstruction of the region of interest (ROI) with the diseased ROI. Image segmentation involves partitioning the pixels in a given image into different groups. Our specific interest here is to partition the image into healthy and unhealthy sections of the brain. The second approach involves comparing the original scan of a diseased brain with a visualization of a healthy version of the same brain (i.e. without the tumorous region). The difference of these two images is trivially an outline of the diseased region, and this new image is then known as the anomaly map. This method involves using generative neural networks; namely, generative adversarial network (GAN), variational auto-encoder (VAE), and diffusion model, an emergent model that is still being researched and optimized.

In both methods, training data for the models is hard to come by, as it requires pixel-wise labeling of the ground truth, which is extremely time-consuming. However, Wolleb et al. [1] present a novel semi-supervised method, as opposed to the existing weakly-supervised methods, that requires labeling only at

the image-level, significantly decreasing this hurdle. In their paper, the authors propose using diffusion models to create the healthy reconstruction as opposed to VAEs and GANs. As discussed, diffusion models are generative in nature and consist of a forward and backward process. The forward diffusion process takes an input image and iteratively adds Gaussian noise to it until there is only noise, essentially manifesting a Markov chain. If we take $\{x_0, \dots, x_T\}$ to be our set of noisy images, the forward process can then be described by:

$$q(x_{0:T}) = q(x_0)q(x_1|x_0) \cdots q(x_T|x_{T-1}) = q(x_0)N(x_1|\sqrt{\alpha_1}x_0, \beta_1 I) \cdots N(x_T|\sqrt{\alpha_T}x_{T-1}, \beta_T I) \quad (1)$$

with the parameters given by $\beta_1, \dots, \beta_T \in (0, 1)$, $\alpha_t := 1 - \beta_t$, $\bar{\alpha}_t := \alpha_1 \cdots \alpha_t$, $\tilde{\beta}_t := \frac{1-\bar{\alpha}_{t-1}}{1-\bar{\alpha}_t}\beta_t$, and $\tilde{\mu}_t(x_t, x_0) := \frac{\sqrt{\alpha_t}(1-\bar{\alpha}_{t-1})x_t + \sqrt{\bar{\alpha}_{t-1}}(1-\alpha_t)x_0}{1-\bar{\alpha}_t}$

The backward process then attempts to learn the latent representation of the image by iterating backwards, until a satisfactory image can be reconstructed from noise. The backward process is given by:

$$p_\theta(x_T) = N(x_T|0, I) \quad (2)$$

and

$$p_\theta(x_{t-1}|x_t) = N(x_{t-1}|\mu_\theta(x_t, t), \Sigma_\theta(x_t, t)) \quad (3)$$

Their model is then used to generate healthy reconstructions of diseased brains, and finally, an anomaly map is created by subtracting the reconstruction from the input image.

II. NOVEL UPDATES

While Wolleb et al. focus on diffusion models, it is important to note that although novel, they are incredibly computationally expensive to train as compared to other neural network frameworks. We update this framework by implementing SegResNet, introduced by Myronenko [2] and the open-source MONALIO [3]. SegResNet is built off of the well-known ResNet model, and is specifically geared towards segmentation tasks. We will also explore the VAE implementation for anomaly mapping. Finally, we will show how with proper data preprocessing, such as wavelet denoising on the input images, we may achieve similar, if not better, results as the ones achieved by Wolleb et al [1].

III. EXPERIMENTS, RESULTS, ANALYSIS

We will now explore experiments involving data preprocessing and denoising prior to the image reconstruction. The dataset consists of MRI data of 700 subjects, 484 of which are for training and the remaining 218 for validation/testing. Each scan is represented as a 4-dimensional array of the following size $[240, 240, 155, 4]$. Trivially, the first two dimensions represent the length and width axes. The third dimension represents 155 horizontal slices of the brain that are vertically stacked. Finally, the last dimension represents the four channels of the MRI scan, Flair, T1, T1-Contrast Enhanced, T2, each of which captures different structural information. Also provided in the dataset are the ground-truth segmentation labels for the tumorous region. In the following experiments, we use Dice score as the metric of choice, as it is commonly used in image segmentation tasks to evaluate the similarity between the predicted and ground truth segmentation maps. The scoring ranges from 0, indicating no overlap, to 1, indicating perfect overlap between the two images.

To reconstruct a healthy image of a diseased image, we used a pretrained VAE, specifically the KL-Autoencoder which is known for its generative abilities. This model was also used as a benchmark in the original reference paper by Wolleb et al. [1] and was trained on the BraTS 2018 dataset. The VAE was trained for 1500 epochs using Adam optimizer and L1 loss, perceptual loss, KL divergence loss, adversarial loss, and GAN-BCE loss, on a GPU with 32GB memory. We then inferred healthy versions of diseased images and generated the anomaly map.

The other model used in the experiments was SegResNet, an encoder-decoder network based model. We trained the model on for 50 epochs with a batch size of 1, again using DICE loss as a metric for the same. The result generated by it is a 2-D segment of tumor region for the all four MRI channels. The architecture of SegResNet is visualized in Fig. 1

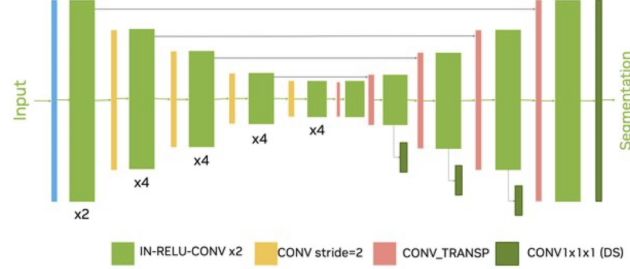


Fig. 1. SegResNet Architecture

In order to improve the performance of both of our models, we added an image denoising step before performing the image reconstruction. We denoised our image using wavelet transformations, in specific bi-orthogonal wavelet transformations. Every image is first transformed using this transformation, filtered with a threshold and then reconstructed back into its original form before passing through encoder network. This helps removing some noise from the original signal. Below we will discuss the improvements from these changes.

In Fig. 2, we show the anomaly map produced using the VAE on one subject, without the denoising process, achieving a 0.299 Dice score. After applying the wavelet denoising, we can see in Fig. 3 that the anomaly map is clearer, indicated by the Dice score improvement to 0.323. Over 50 samples, the VAE scored a mean Dice score of 0.278 and with denoising, it achieved 0.285, showcased in Fig. 4. The VAE benchmarked in the Wolleb et al. [1] achieves only approximately 0.24 as the score; we have clearly shown an improvement here.

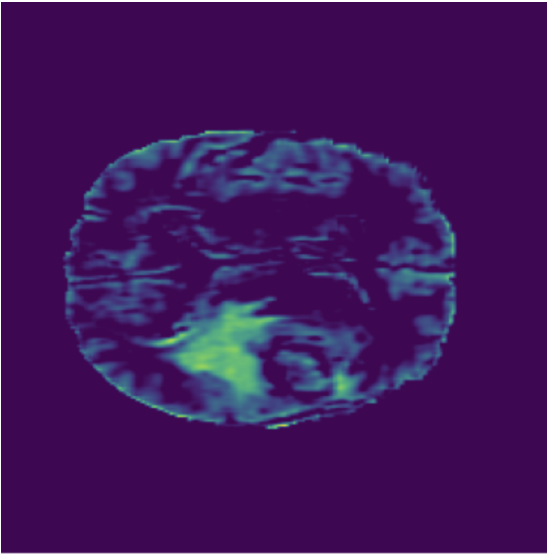


Fig. 2. Anomaly Map with VAE, without denoising

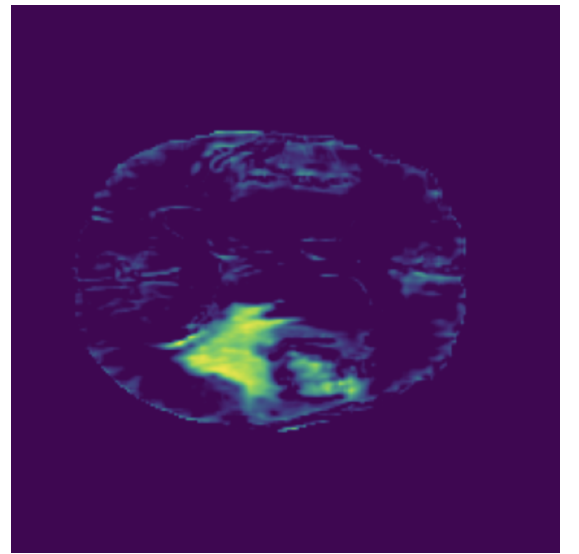


Fig. 3. Anomaly Map with VAE, with Denoising



Fig. 4. DICE Score Comparison - VAE : With and Without Denoising

We trained the SegResNet model for 40 epochs on an NVIDIA 2080ti for approx. 4 hours. The loss decreased from 0.9 to 0.35, as seen in Fig. 5. We also note that we achieved an average Dice score of approximately 0.84 on test data, visualized in Fig. 8. In Fig. 6, we show the anomaly map produced using SegResNet on one subject, without the denoising process, achieving a 0.653 Dice score. After applying the wavelet denoising, we can see in Fig. 2 the Dice score has a negligible decrease to 0.652. Our SegResNet results are comparable to the results achieved by Wolleb et al.'s [1] diffusion model.

In summary, we have shown clear improvements here for the VAE model using denoising compared to the original benchmark done by Wolleb et al. [1]. The same improvements are not shown by SegResNet; however, the key takeaway here is that the computationally expensive diffusion models were not used. The final results are summarized in Table I. We were able to achieve these results with minimal training time as well as computational cost, showing that using either VAE or SegResNet, we are able to achieve accessible anomaly detection results.

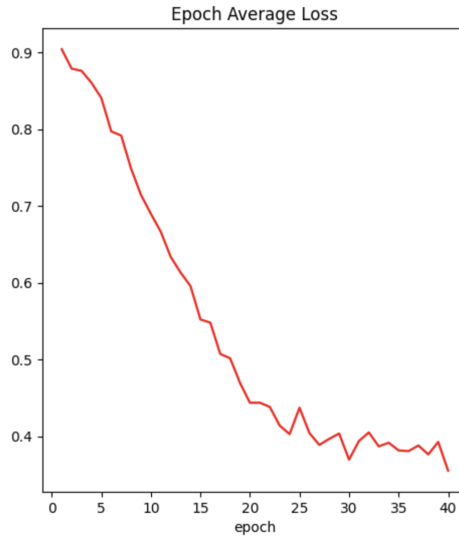


Fig. 5. SegResNet - Loss vs Epoch with Adam Optimizer - batch size = 1

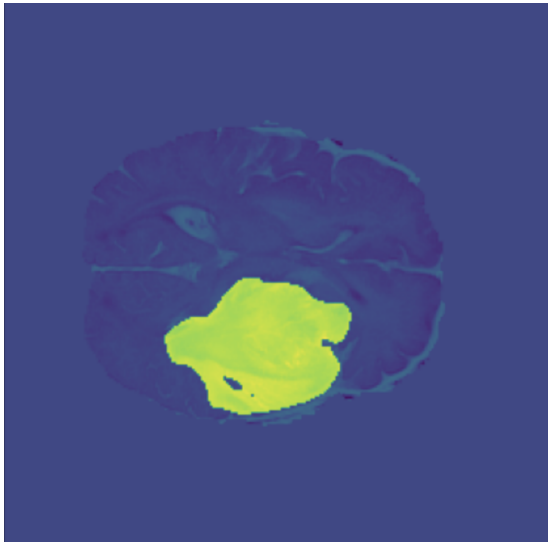


Fig. 6. Anomaly Map with SegResNet, without denoising

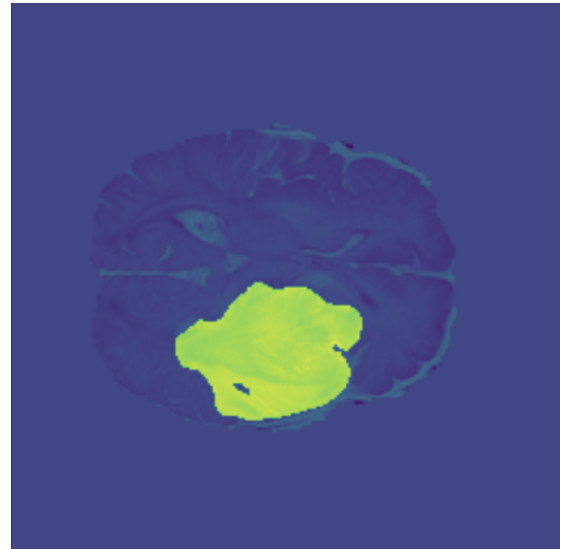


Fig. 7. Anomaly Map with SegResNet, with Denoising

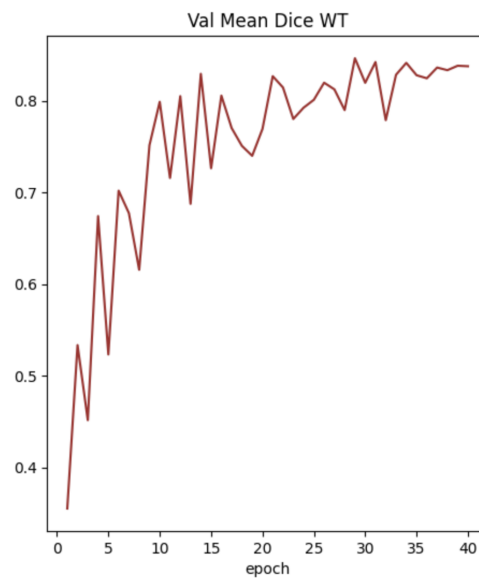


Fig. 8. SegResNet - Dice Score vs Epoch for Adam Optimizer

Model	Dice score
VAE, without denoising	0.298
VAE, with denoising, 100 Epochs	0.322
SegResNet, without denosing	0.653
SegResNet, with denosing	0.652

TABLE I
DICE SCORES FOR THE VARIOUS EXPERIMENTS

REFERENCES

- [1] Wolleb, Julia, et al. "Diffusion models for medical anomaly detection." International Conference on Medical image computing and computer-assisted intervention. Cham: Springer Nature Switzerland, 2022.
- [2] Myronenko, Andriy. '3D MRI brain tumor segmentation using autoencoder regularization.' International MICCAI Brainlesion Workshop. Springer, Cham, 2018.
- [3] Cardoso, M. Jorge, et al. "Monai: An open-source framework for deep learning in healthcare." arXiv preprint arXiv:2211.02701 (2022).