Weakly-Supervised Midline Shift Quantification through Simulating the Reversed Disease Progression

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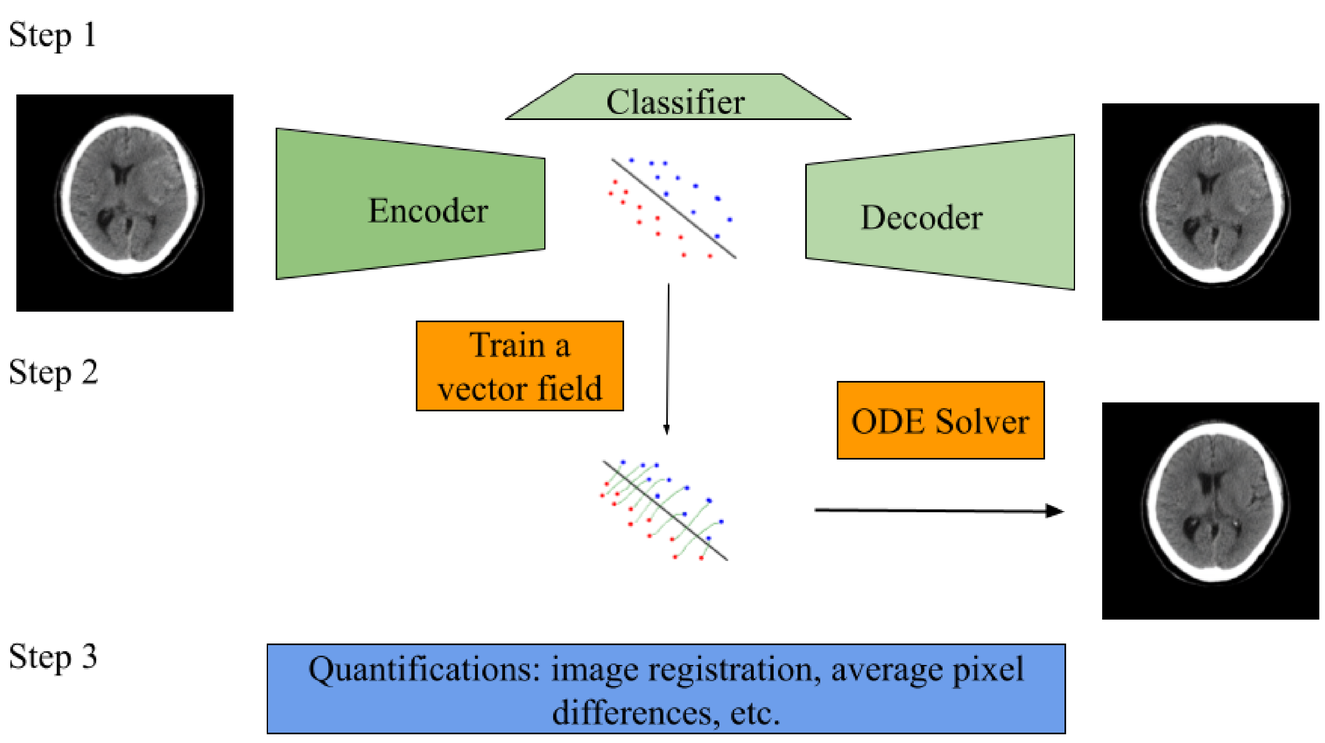
Abstract

Medical segmentation masks are often scarce. To get visual and quantitative information, we propose constructing trajectories from anomaly data to normal data using conditional flow matching on an autoencoder, augmented with an auxiliary classification head in the latent space. This allows both visualization and estimation of MLS using only classification labels, avoiding the need for segmentation masks. Displacement between the original and transformed images is used to approximate MLS distance.

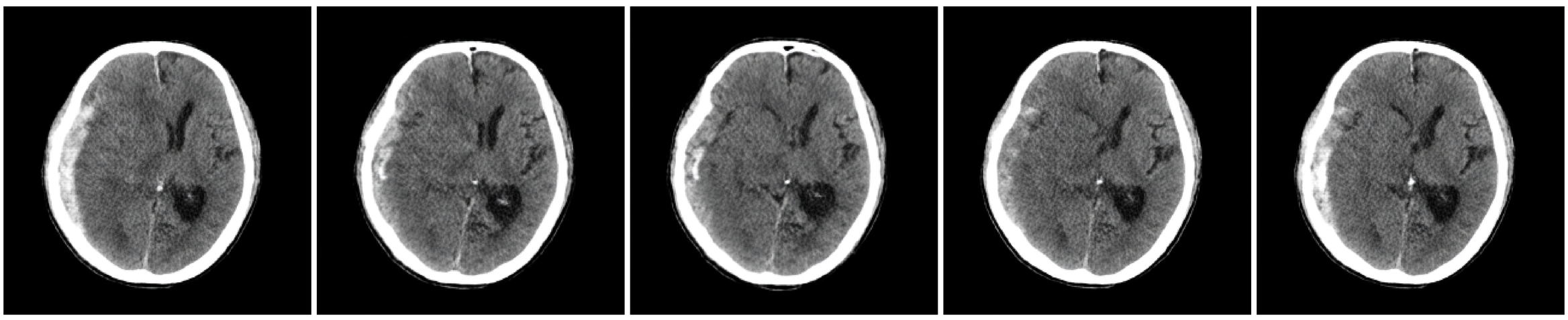
Data and Method



Our method is illustrated in the left figure. We want to reverse the disease process with minimal metamorphosis. Therefore, we propose training a flow matching network in the latent spaces of an autoencoder. We utilized VQGAN with an auxiliary linear classification head operating in the latent space. To further quantify our results, we apply diffeomorphic registration to measure the displacement between the original and transformed images, which serves as an estimate of the midline shift distance of the original image.

The training and testing datasets were from the Chang Gung Research Database (CGRD). For the training data, we used 1177 slices with midline shifts and 2221 normal slices from 907 Brain CT images. During the training of the flow matching network, the slices are further rigid registered to ensure minimal rotation are involved in the reversed disease progression path. For testing data, we used 294 normal slices, 287 slices with midline shift distances ranging from 2mm and 5mm, and 160 slices with midline shift distances greater than 5mm.

Result



Step 0 Step 40 Step 60 Step 80 Step 99

MLS (mm)	# of slices	MAE (mm)	Mean of disp. (mm)	STD of disp. (mm)
$[0, 2)$	294	1.19	1.54	1.98
$[2, 5)$	287	2.59	3.96	3.08
> 5	160	4.23	5.94	2.64
All	741	2.38	3.42	1.98

The visualization of our generated reversed disease progression is shown in the above figure. We were surprised to find that the generated paths appear very realistic. The mean absolute errors (MAE) between the ground truths and measured displacements are presented in the left table. We empirically observed that our model tends to underestimate cases with large midline shifts. We believe the phenomenon may be attributed to the training data size not being large enough for effective generalization of the flow matching/diffusion models and can be improved by incorporating more data with larger midline shift distances.

Conclusion

When training a neural network with only classification labels, it can be challenging to incor- porate more meaningful information. In this study, we propose to reinterpret the network's predictions. Specifically, we construct reversed disease paths within the latent space of the classifier. Additionally, we measure the displacements between the original and generated images to estimate midline shift distances. Our findings indicate a strong correlation between these displacements and the actual midline shift dis- tances.

So far the results may not be as precise as those obtained through fully supervised segmentation methods. In the future, we plan to explore methods to improve our results, such as increasing the batch size, expanding the training dataset, and making other careful adjustments. One possible direction is to enhance our framework's data effectiveness for application in various clinical scenarios.

The poster can be downloaded using the QR code on the right.