AUTOMATIC ACTIVE LESION TRACKING USING DIFFUSION PROBABILISTIC MODELS

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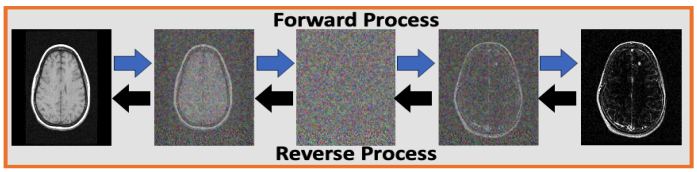

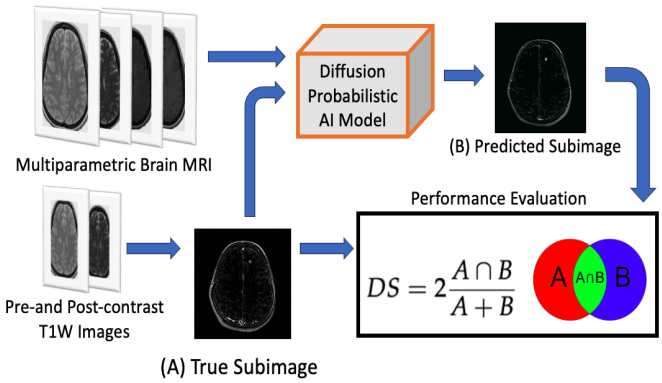

Fig. 1. Multiparametric brain MRI framework for active lesion identification using diffusion probabilistic AI model. Dice similarity (DS) was used to compare predicted and true active multiple sclerosis lesions.

1. INTRODUCTION

Identifying active lesions on magnetic resonance imaging (MRI) is crucial for diagnosis and management of Multiple Sclerosis (MS) patients [1]. Active lesions are detected with gadolinium based contrast agents (GBCAs) and appear hyperintense on post-contrast T1-weighted (T1-post) images. Recent studies have raised concerns with GBCA due to potential patient side effects and increased scan cost [**?**]. Therefore, identifying active lesions without GBCAs is highly desirable. We propose using a Diffusion Probabilistic Model (DPM) for automatic active lesion identification.

2. MATERIAL AND METHOD

Deidentified MRI from 20 MS patients were used in this work. MRI scans included Fluid Attenuated Inversion Recovery, Proton Density Weighted, T2-weighted, pre-contrast T1 (T1-pre), and T1-post. We employed FLAIR, PDW, T2w, and T1-pre as our input images and subtracted T1-pre and T1-post image as our ground truth (subimage). All true subimage lesion were labeled by experts as active.

We used a DPM, Brownian Bridge Diffusion Model (BBDM) [2] to predict active lesions in multiparametric brain MRI. We used dice similarity (DS) to compare predicted and true active lesions and performed subject level leave-one-out-cross-validation with 20 patients.

3. RESULTS

We applied BBDM on 20 MS subjects and achieved a median DS score of 0.80. Using true subimages, BBDM method achieved great active lesion prediction performance.

4. CONCLUSION

We demonstrated a generative approach for predicting active MS lesions on non-enhanced images. To best of our knowledge, this is one of the implementations of DPM for active lesion prediction. However, these results need to be validated on a larger sample size. We believe our method has the potential to predict MS lesions and be extended to longitudinal data to track disease activity.

5. REFERENCES

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