Ira A. Fulton Schools of Engineering
Arizona State University

AnoFPDM: Anomaly Detection with Forward Process of Diffusion Models for Brain MRI

Yiming Che[1,2], Fazle Rafsani[1,2], Jay Shah, Md Mahfuzur Rahman Siddiquee[1,2], and Teresa Wu[1,2]

[1]Arizona State University

[2]ASU-Mayo Center for Innovative Imaging

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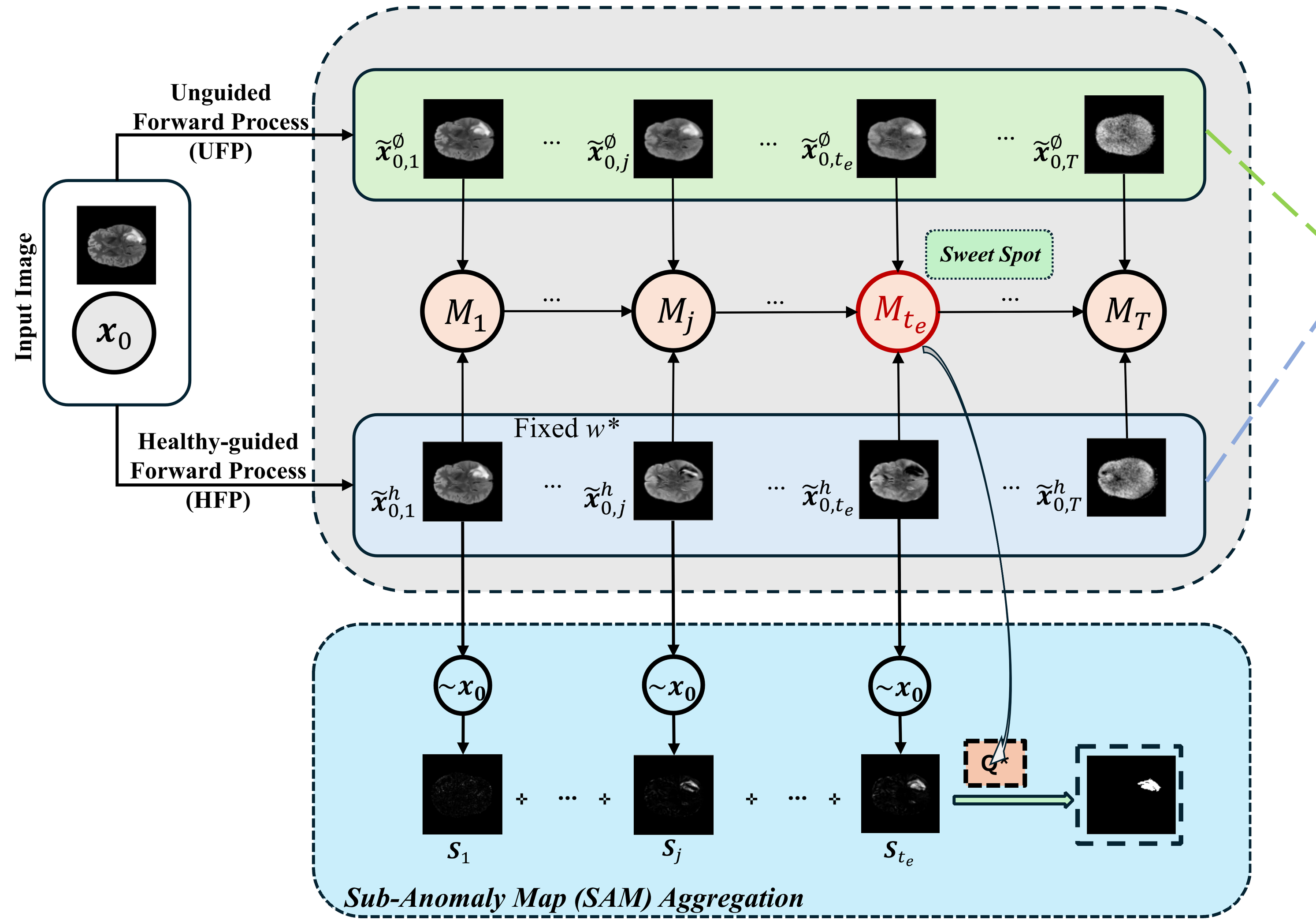
Motivation

- Current weakly-supervised diffusion models for anomaly detection is not fully weakly-supervised.
  - Pixel-level labels is required for hyperparameter tuning in inference!
  - Subject to human annotator bias
  - Costly
- Current hyperparameter selection is fixed
  - All samples are using the same hyperparameters, e.g., noise level and threshold.
- Need a new dynamical hyperparameter selection method.
  - Get rid of pixel-level labels
  - Select hyperparameters individually

Contributions

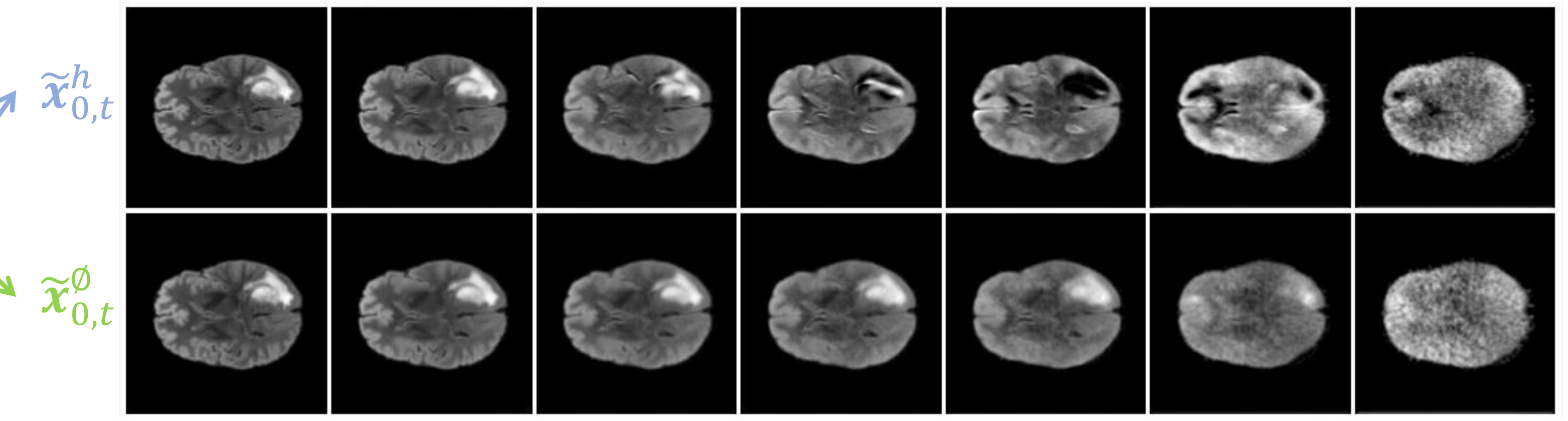
- A fully weakly-supervised anomaly detection framework
- Novel dynamical threshold and noise scale selection and novel fixed guidance strength selection for diffusion models on weakly-supervised anomaly detection
- Novel aggregation strategy combined with dynamical noise scale selection to enhance the signal strength of anomalous regions on anomaly map

Method



- No iterative reconstruction
- Only the forward process
  - Healthy guided
  - Unguided
- Aggregate SAMs until t_e
  - t_e dynamical noise scale
  - Capture 'sweet spot'
  - Determined by max M_t
- Segmentation threshold Q^*
  - Determined by anomaly size
  - Roughly linear related with M_{t_e}
- Optimal fixed guidance strength w^*
  - Determined separately according to classification
  - See Sec. 4.2 in our paper

Healthy-guided Forward Process (HFP)



Unguided Forward Process (UFP)

$$\tilde{\boldsymbol{x}}^h_{0,t} = \frac{\boldsymbol{x}_t - \sqrt{1-\bar{\alpha}_t}\left[(1+w)\boldsymbol{\epsilon}_{\boldsymbol{\theta}}(\boldsymbol{x}_t, t, h) - w\boldsymbol{\epsilon}_{\boldsymbol{\theta}}(\boldsymbol{x}_t, t, \emptyset)\right]}{\sqrt{\bar{\alpha}_t}}$$

$$\tilde{\boldsymbol{x}}^\emptyset_{0,t} = \frac{\boldsymbol{x}_t - \sqrt{1-\bar{\alpha}_t}\boldsymbol{\epsilon}_{\boldsymbol{\theta}}(\boldsymbol{x}_t, t, \emptyset)}{\sqrt{\bar{\alpha}_t}}$$

$$M_t = \frac{\left\|\tilde{\boldsymbol{x}}^h_{0,t} - \tilde{\boldsymbol{x}}^\emptyset_{0,t}\right\|_2^2}{d}$$

$$\frac{B_t^2(1+w)^2}{d}\left\|\nabla_{\boldsymbol{x}_t}\log p_\theta(h|\boldsymbol{x}_t)\right\|_2^2$$

The divergence M_{t_e} is essentially the magnitude of weighted gradient of the log-likelihood of the implicit classifier

$$\boldsymbol{e}^h_t = \tilde{\boldsymbol{x}}^h_{0,t} - \boldsymbol{x}_0$$

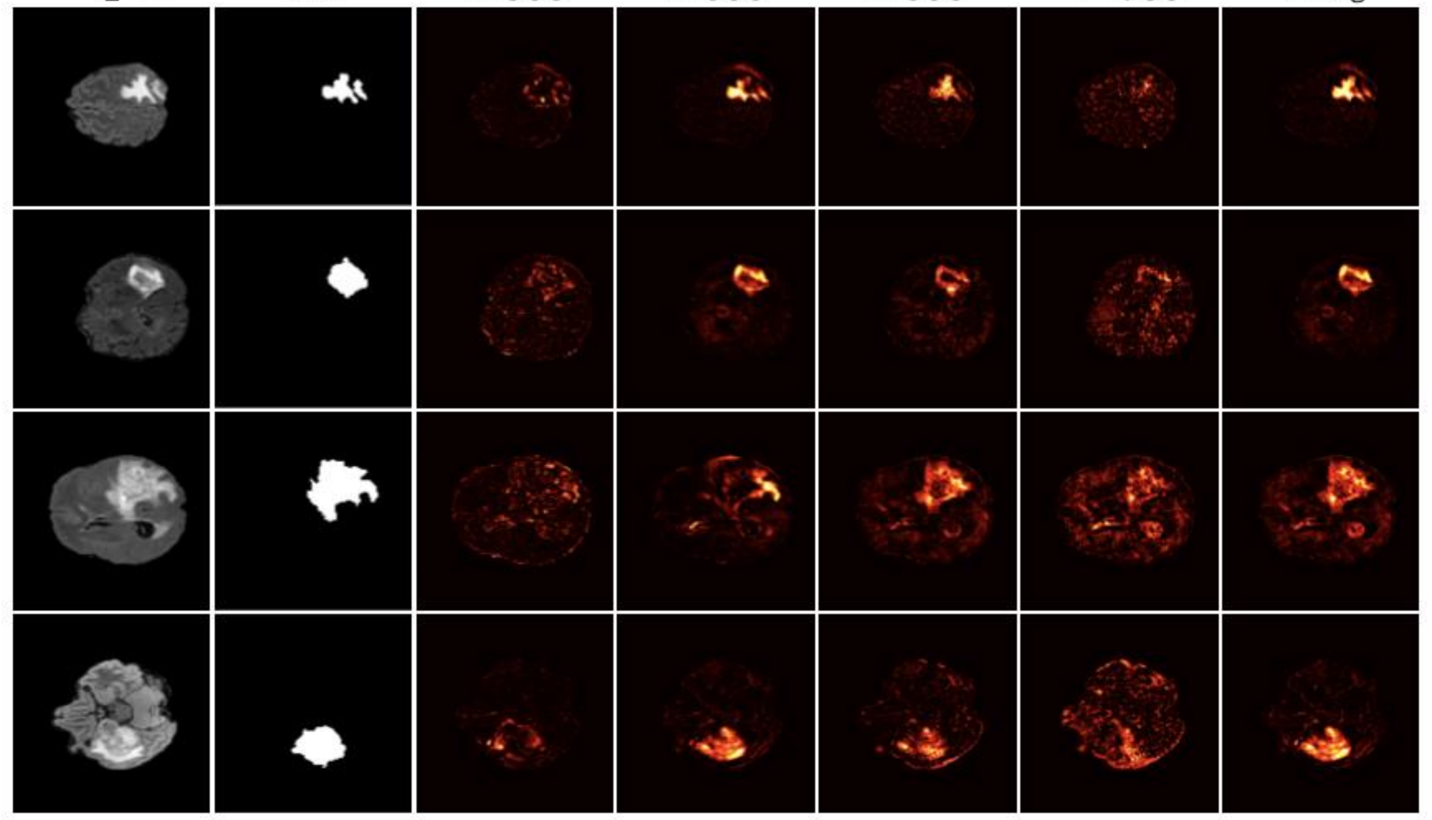
$$\boldsymbol{S}_t = \left(\boldsymbol{e}^h_t\right)^2$$

$$B_t^2\left((1+w)\nabla_{\boldsymbol{x}_t}\log p_\theta(h|\boldsymbol{x}_t) + \Delta\boldsymbol{s}_t\right)^2$$

SAM has similar form but with an extra error term $\Delta\boldsymbol{s}_t$. It achieves better results compared to use the difference between two forward processes.

Sub-anomaly Maps (SAMs)

Input | GT | $\boldsymbol{S}_{300}$ | $\boldsymbol{S}_{500}$ | $\boldsymbol{S}_{600}$ | $\boldsymbol{S}_{700}$ | $\boldsymbol{S}_{t_e}$



How SAMs change?

- Focus: high-frequency to low-frequency components
- The signals from healthy regions appear randomly distributed.
- The signals from anomalous regions exhibit more consistency.
- This consistency is crucial to the effectiveness of the aggregation process.

Experiments

See references in our paper

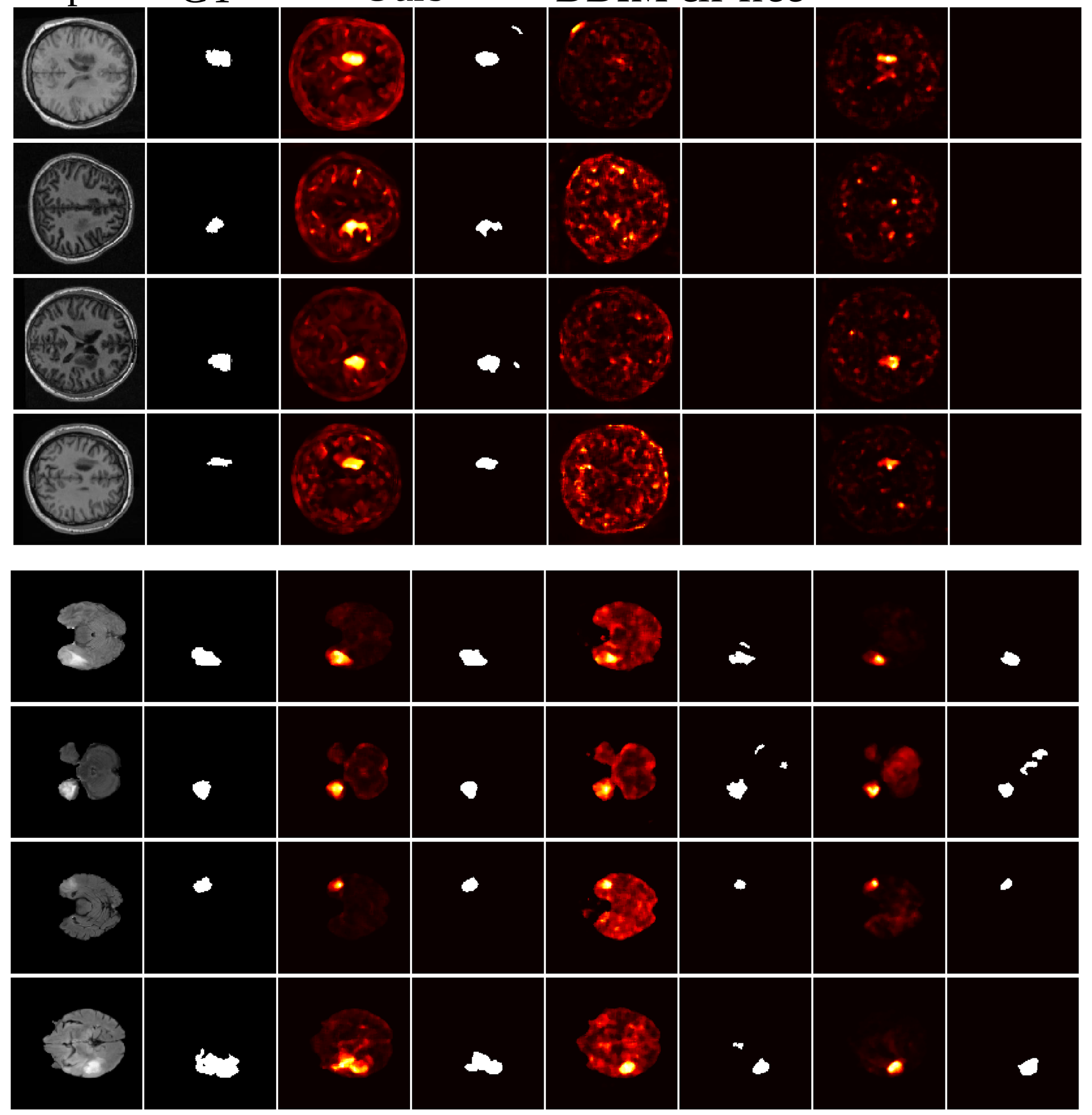
Methods	Mixed DICE	Mixed IoU	Mixed AUPRC	Unhealthy DICE	Unhealthy IoU	Unhealthy AUPRC
AnoDDPM (G) [26]	66.1±0.1	61.7±0.1	51.8±0.1	37.6±0.1	28.1±0.1	61.3±0.1
AnoDDPM (S) [26]	75.1±0.3	69.5±0.2	67.3±0.1	53.7±2.7	45.5±1.3	71.8±0.1
DDIM clf [25]	76.5±0.1	71.0±0.1	58.4±0.3	52.2±0.2	40.4±0.2	61.6±0.2
DDIM clf-free [18]	74.3±0.0	69.1±0.0	59.9±0.0	49.1±0.0	38.1±0.0	61.4±0.0
CG-CDM [9]	-	-	-	44.4±0.3	32.2±0.5	31.2±0.7
AnoFPDM (DDIM)	**77.4±0.0**	**72.5±0.0**	**72.2±0.0**	**61.5±0.0**	**50.0±0.1**	**75.5±0.0**

Segmentation performance on mixed and unhealthy samples from BraTS21 dataset.

Methods	Mixed DICE	Mixed IoU	Mixed AUPRC	Unhealthy DICE	Unhealthy IoU	Unhealthy AUPRC
AnoDDPM (G) [26]	74.8±0.1	74.8±0.1	2.0±0.1	0.4±0.1	0.2±0.1	6.5±0.2
AnoDDPM (S) [26]	74.9±0.1	74.6±0.1	20.8±0.5	3.4±1.0	3.3±0.7	30.9±0.4
DDIM clf [25]	51.5±0.8	50.8±0.7	1.9±0.1	5.8±0.1	3.7±0.1	5.6±0.1
DDIM clf-free [18]	73.5±0.0	73.0±0.0	9.3±0.0	0.1±0.0	0.1±0.0	13.6±0.0
CG-CDM [9]	-	-	-	2.1±0.0	1.1±0.0	1.6±0.0
AnoFPDM (DDIM)	**75.5±0.2**	**75.5±0.2**	**22.5±0.1**	**21.5±0.0**	**15.5±0.0**	**31.2±0.1**

Segmentation performance on mixed slices and unhealthy samples from ATLAS v2.0 dataset.

Input | GT | Ours | DDIM clf-free | Ano DDPM



Qualitative results on (top) ATLAS v2.0 dataset and (bottom) BraTS21 dataset

arXiv: Code: