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AnoDDPM: Anomaly Detection with Denoising Diffusion Probabilistic Models using Simplex Noise

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Github repository and project page available at: https://julianwyatt.co.uk/anoddpm

Background

Unsupervised anomaly detection is the process of determining whether a datapoint has some abnormality. For example, examining whether an MR scan contains a tumour. Typically, models train on **solely healthy samples** to reconstruct a query image and imagine what it would look like if it was normal. However, it is regarded a notoriously difficult problem to reconstruct high quality images with small datasets [3].

We utilise **D**enoising **D**iffusion **P**robabilistic **M**odels (**DDPMs**) [1], a state-of-the-art generative model for small datasets and sample quality. **DDPMs** learn a parameterised noise approximation function:

$$p_\theta(x_{t-1}|x_t) = \mathcal{N}(x_{t-1}|\mu_\theta(x_t,t), \tilde{\beta}_t\mathbf{I}),$$

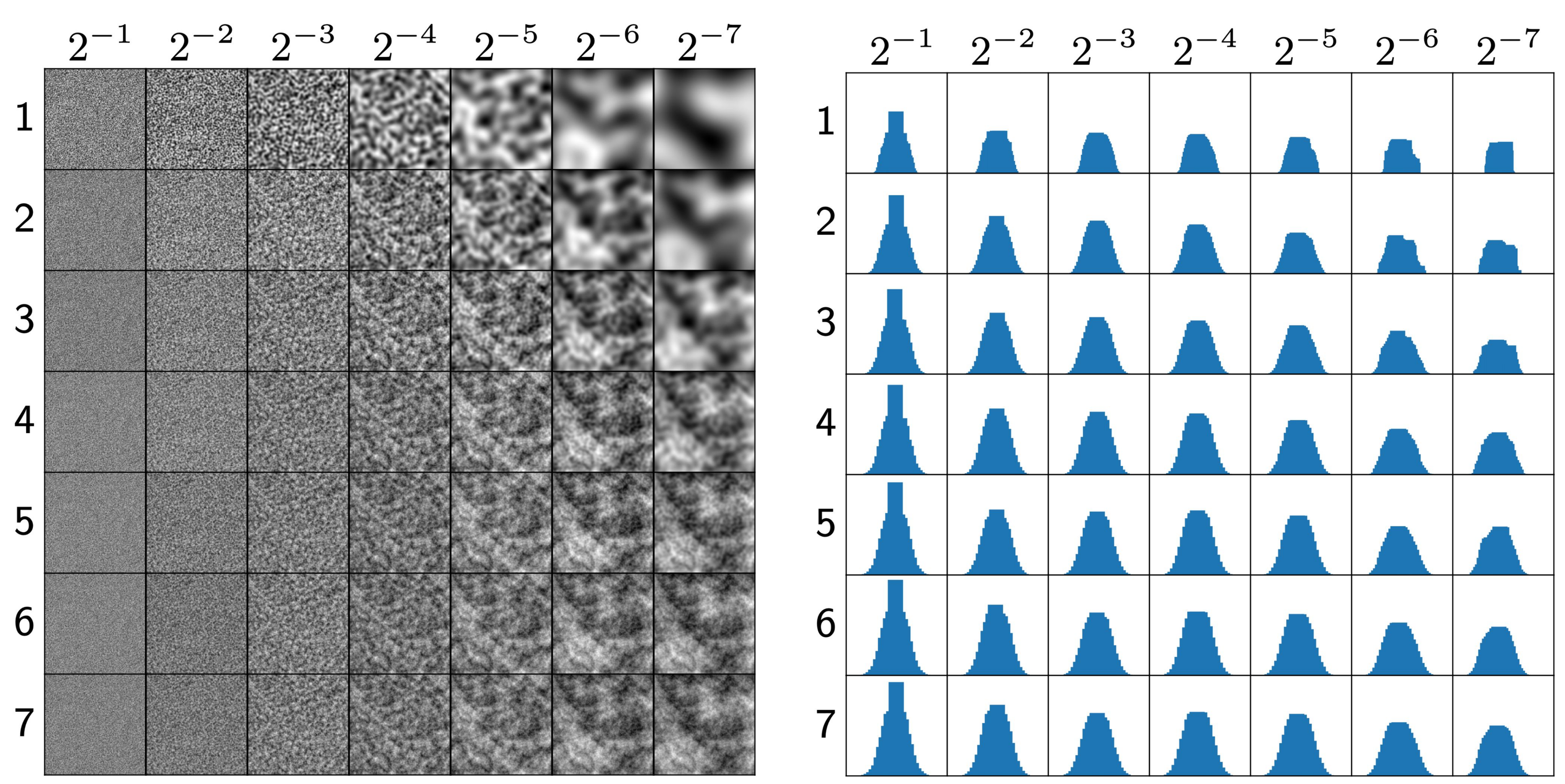
which removes noise from an image and is optimised by minimising the loss function:

$$\mathcal{L}_s = \mathbb{E}_{t\sim[1-T], x_0\sim q(x_0), \epsilon\sim\mathcal{N}(0,\mathbf{I})}[||\epsilon - \epsilon_\theta(x_t,t)||^2].$$

New samples are then generated by iteratively applying: $p_\theta(x_{t-1}|x_t)$, for $t = T, ..., 0$, where the initial sample at T is an isotropic Gaussian distribution.

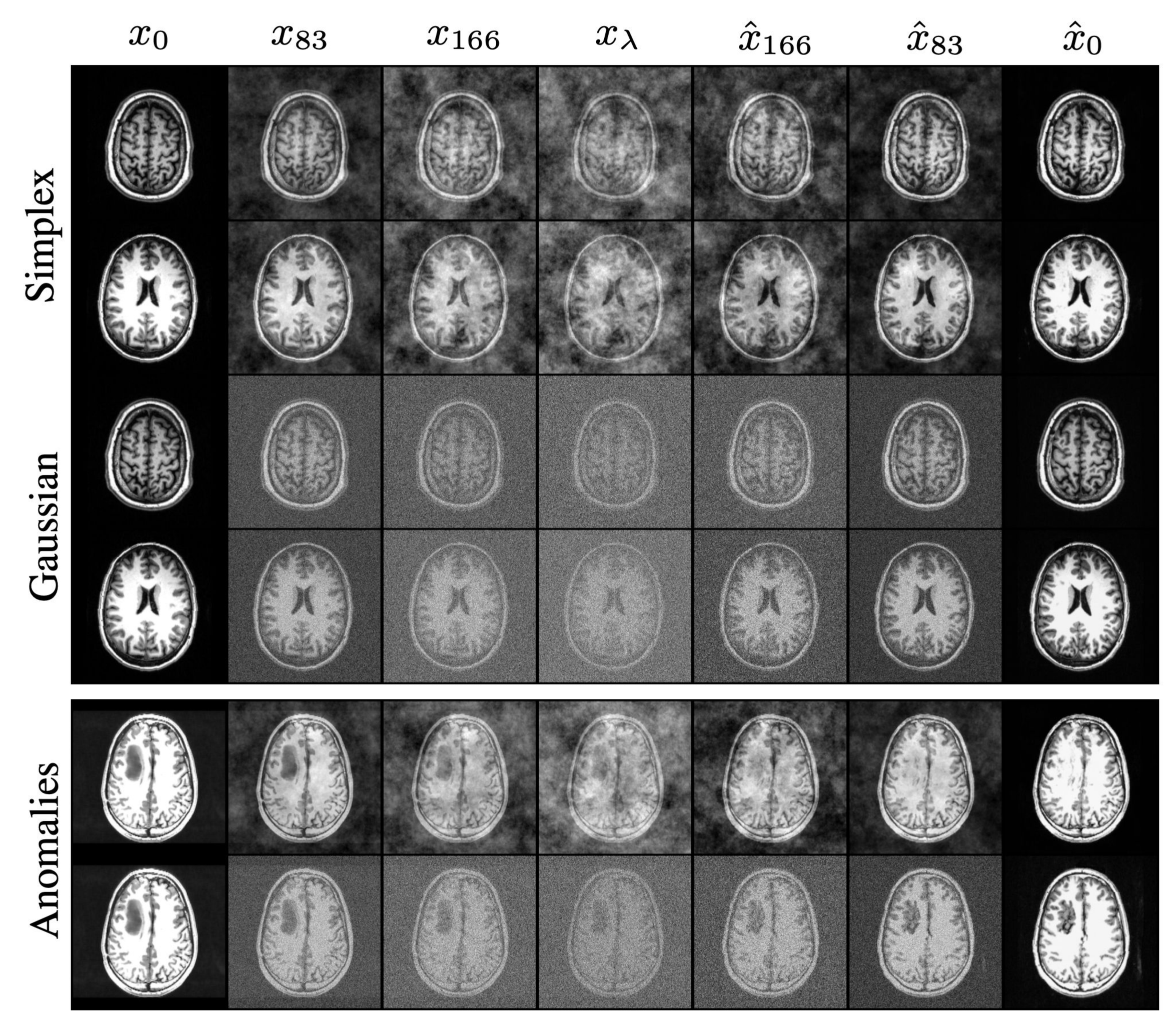
Structured noise functions such as simplex [2] and Perlin noise stochastically generate smooth structured noise by interpolating random gradients on an N-dimensional grid.

Multiple frequencies of simplex noise can be applied to approximate the Gaussian distribution used in DDPMs:



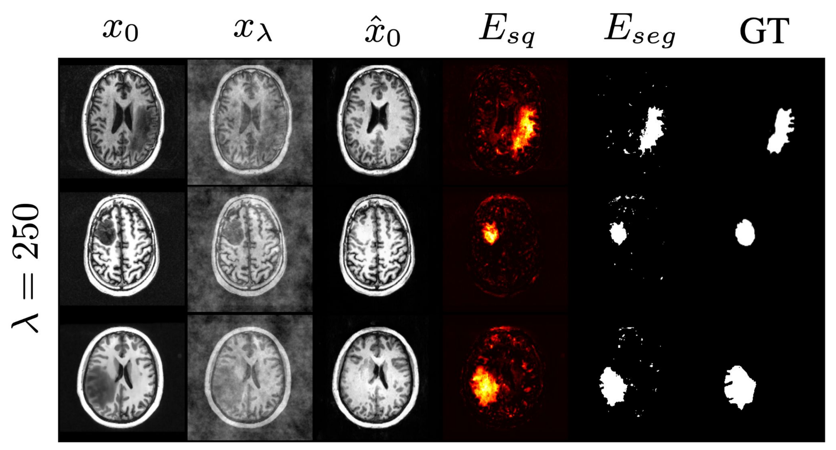
Methodology

We observe that the full sampling **markov chain** is not required for reconstruction and propose a novel partial diffusion strategy, by gradually adding noise to λ and denoising from this step:

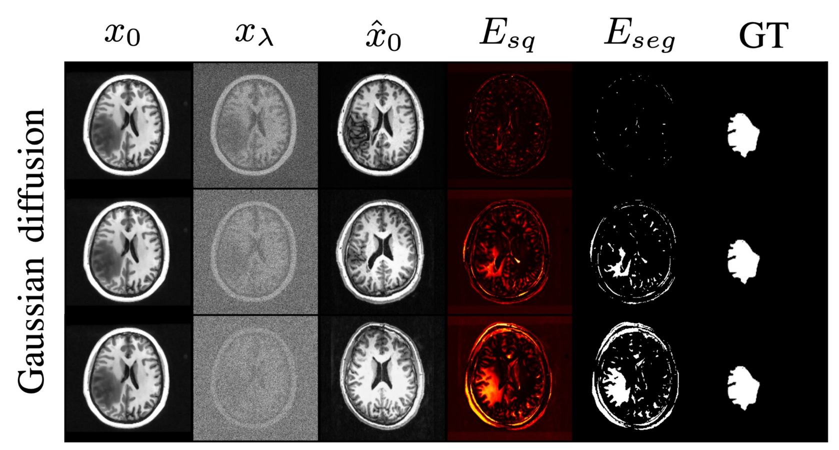


AnoDDPM

As above, **Gaussian** diffusion was unable to capture larger anomalies, so we propose the use of a multi-scale structured noise function like simplex noise.
Simplex noise enables a heuristic denoising approach which is able to remove anomalous structures that are far from the learned healthy distribution. We then make our anomalous segmentation prediction via the **square error** between the initial and reconstructed images. To separate anomalous vs. normal regions in the segmentation, we take a naïve threshold of 0.5.



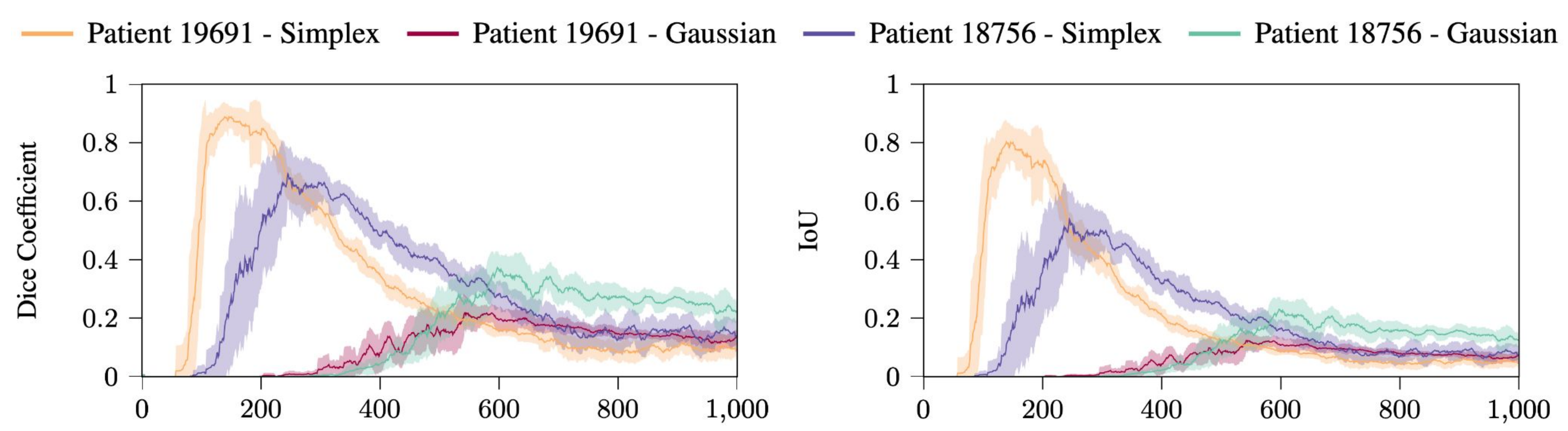
AnoDDPM simplex curated samples



AnoDDPM Gaussian with $\lambda = 250, 500, 750$.

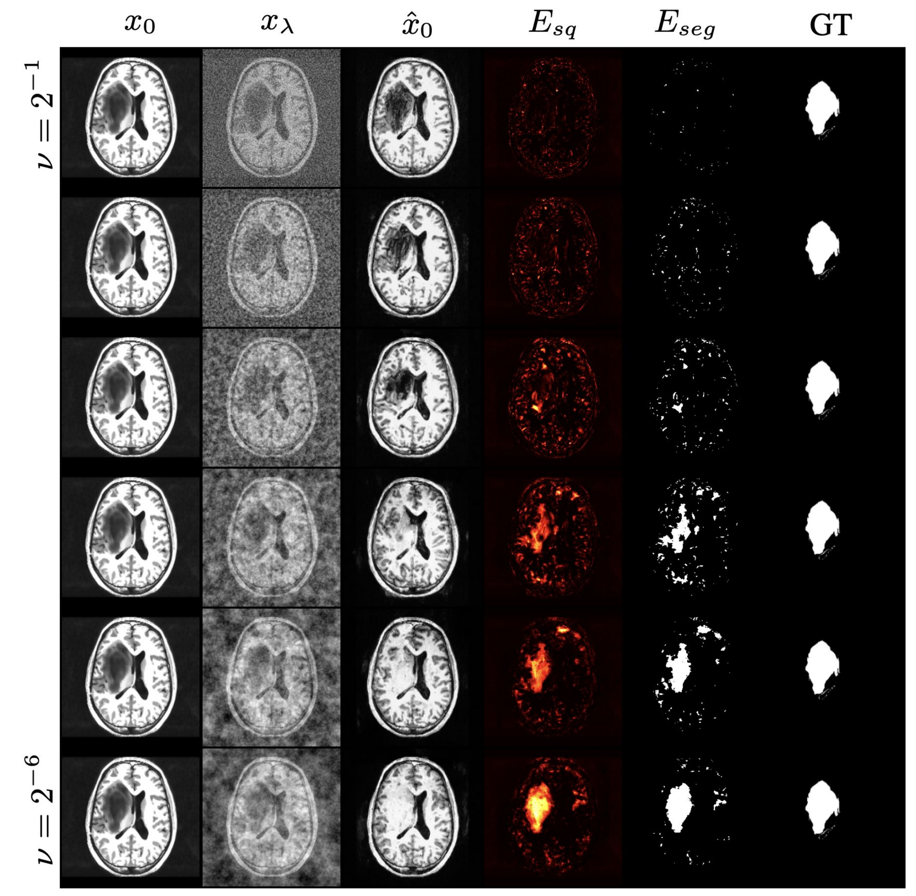
Results

We evaluate the qualitative and quantitative performance of AnoDDPM using 5 metrics: **dice**, **IoU**, precision, recall and **AUC**. Dice and IoU asses the quality of the segmentation for the given threshold. However, as AUC is robust to the selection of threshold values, it provides a better comparison with alternative models.



Summary

For MRI brain tumour detection, our proposed solution AnoDDPM (simplex) **outperforms** anomaly detection technique: f-AnoGAN [4]. Alternatively, AnoDDPM (Gauss) produces **high quality samples** but struggles to segment anomalies.



AnoDDPM simplex with increasing frequency.

	Dice ↑	IoU ↑	Precision ↑	Recall ↑	AUC ↑
Context Encoder [5]	0.252 ± 0.209	0.162 ± 0.149	0.258 ± 0.223	0.279 ± 0.234	0.707 ± 0.150
f-AnoGAN [4]	0.128 ± 0.001	0.093 ± 0.003	0.362 ± 0.009	0.080 ± 0.003	0.789 ± 0.001
AnoDDPM - Gauss (Ours)	0.009 ± 0.012	0.004 ± 0.006	0.006 ± 0.009	0.032 ± 0.044	0.601 ± 0.074
AnoDDPM $\mathcal{L}_s$ (Ours)	**0.383 ± 0.258**	**0.269 ± 0.204**	**0.373 ± 0.269**	**0.468 ± 0.283**	**0.863 ± 0.107**

References

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