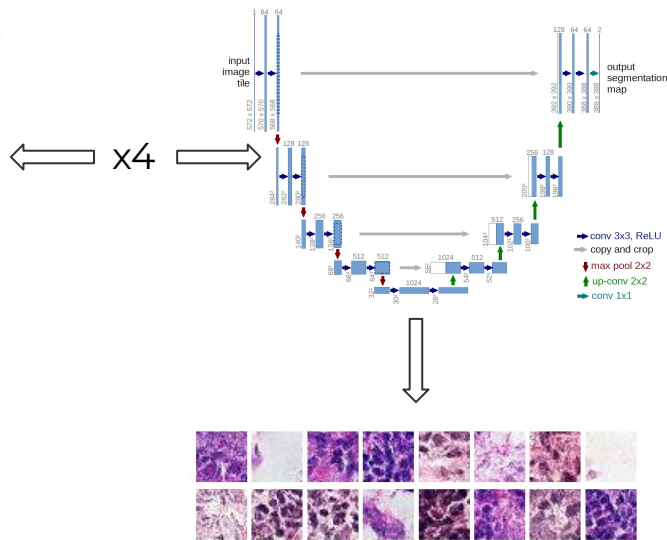
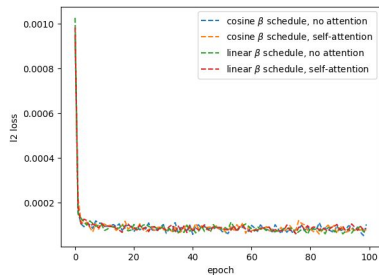
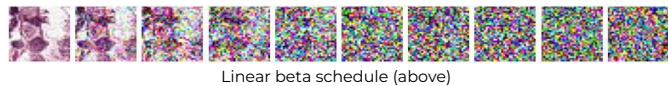
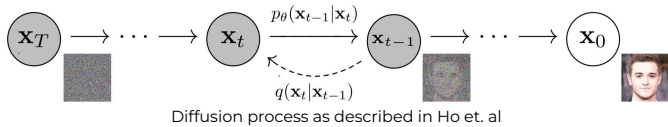




Denoising Diffusion Probabilistic Models for Synthetic Histopathologic Image Generation

Sunny Son
sons01



Algorithm 1 Training

```

1: repeat
2:    $\mathbf{x}_0 \sim q(\mathbf{x}_0)$ 
3:    $t \sim \text{Uniform}(\{1, \dots, T\})$ 
4:    $\epsilon \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$ 
5:   Take gradient descent step on
6:    $\nabla_{\theta} \|\epsilon - \epsilon_{\theta}(\sqrt{\bar{\alpha}}\mathbf{x}_0 + \sqrt{1 - \bar{\alpha}_t}\epsilon, t)\|^2$ 
7: until converged
  
```

Algorithm 2 Sampling

```

1:  $\mathbf{x}_T \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$ 
2: for  $t = T, \dots, 1$  do
3:    $\mathbf{z} \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$  if  $t > 1$ , else  $\mathbf{z} = \mathbf{0}$ 
4:    $\mathbf{x}_{t-1} = \frac{1}{\sqrt{\alpha_t}} \left( \mathbf{x}_t - \frac{1 - \alpha_t}{\sqrt{1 - \alpha_t}} \epsilon_{\theta}(\mathbf{x}_t, t) \right) + \sigma_t \mathbf{z}$ 
5: end for
6: return  $\mathbf{x}_0$ 
  
```

$$\mathcal{L}_{\text{simple}} = \mathbb{E}_{t, \mathbf{x}_0, \epsilon} \left[\left\| \epsilon - \epsilon_{\theta}(\mathbf{x}_t, t) \right\|^2 \right]$$

$$= \mathbb{E}_{t, \mathbf{x}_0, \epsilon} \left[\left\| \epsilon - \epsilon_{\theta}(\sqrt{\bar{\alpha}}\mathbf{x}_0 + \sqrt{1 - \bar{\alpha}_t}\epsilon, t) \right\|^2 \right]$$

Table 2. Average SSIM & Maximum Likelihood Results

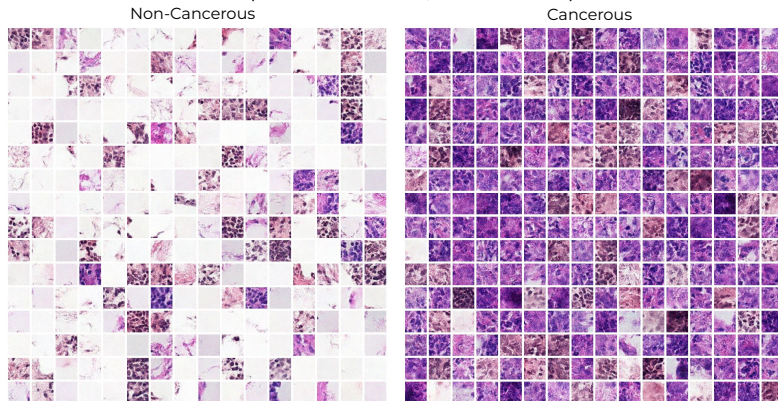
Sched.	Attn.	SSIM (\uparrow)	Log. Likelihood (\downarrow)
linear	none	0.00013885	0.01569078
linear	self	0.00010798	0.01568433
cosine	none	0.00026722	0.01448672
cosine	self	0.00015712	0.01710702

$$\text{BCE} = - \sum_{s,b} [y \times \log(p) + (1 - y) \times \log(1 - p)]$$

$$\text{SSIM}(\mathbf{x}, \mathbf{y}) = [l(\mathbf{x}, \mathbf{y})]^\alpha \cdot [c(\mathbf{x}, \mathbf{y})]^\beta \cdot [s(\mathbf{x}, \mathbf{y})]^\gamma$$

x2 Models Cancerous/ Non-Cancerous

Generate 512 images of each class using selected architecture
(cosine schedule, no attention)



Visual inspection for 16
images from each class

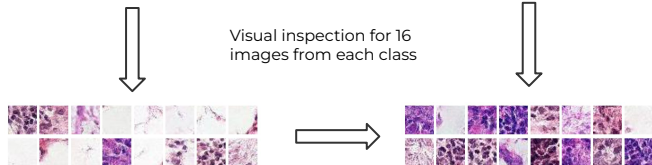


Table 3. *Four Questions of +/- Class Matching*

Correct (%)	Incorrect (%)
25 (69.4%)	11 (30.6%)

Table 4. *Four Questions of +/- Class Identification*

Class	Correct (%)	Incorrect (%)
+	15 (83.3%)	3 (16.7%)
-	11 (61.1%)	7 (38.9%)

Table 5. *Four Questions of Generated/Ground-Truth Matching*

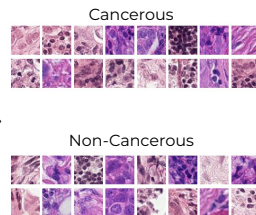
Class	Correct (%)	Incorrect (%)
+	8 (44.4%)	10 (55.6%)
-	8 (44.4%)	10 (55.6%)

Table 6. *Four Questions of Generated/Ground-Truth Identification*

Class	Correct (%)	Incorrect (%)
GT +	4 (44.4%)	5 (55.6%)
GT -	2 (22.2%)	7 (77.8%)
Gen +	2 (22.2%)	7 (77.8%)
Gen -	3 (33.3%)	6 (66.7%)

Table 7. *Two Questions of Overall Quality (Scores range from 1 to 5)*

Class	Cellularity	Atypia	Color	Overall
+	3.89	4.22	3.67	4.33
-	4.33	4.00	3.67	4.11



Combine to
create

In addition to 16 positive/16 negative class
ground truth samples