



Latent Space Diffusion Models of Cryo-EM Structures

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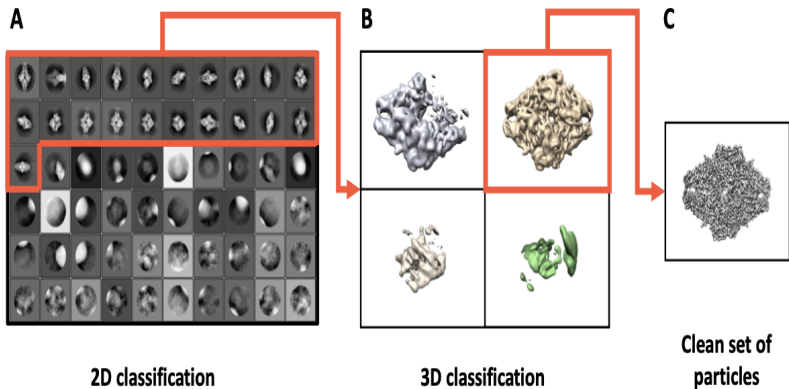
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June, 2024

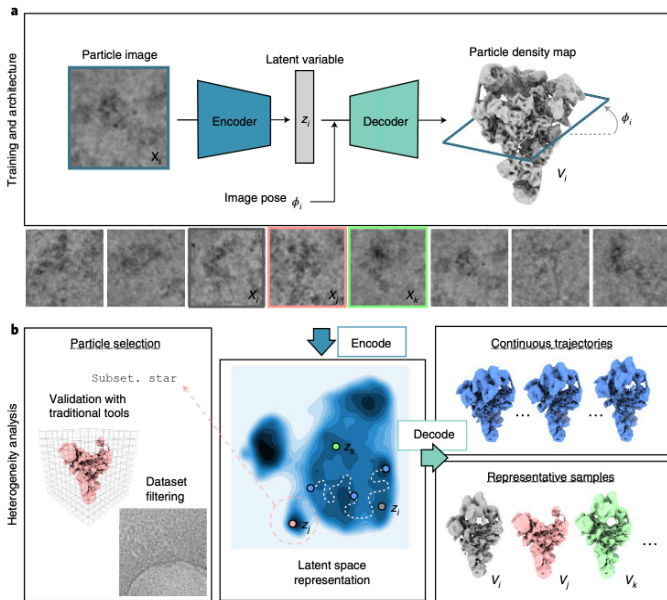
Background of cryo-EM

- Formulation of cryo-EM:

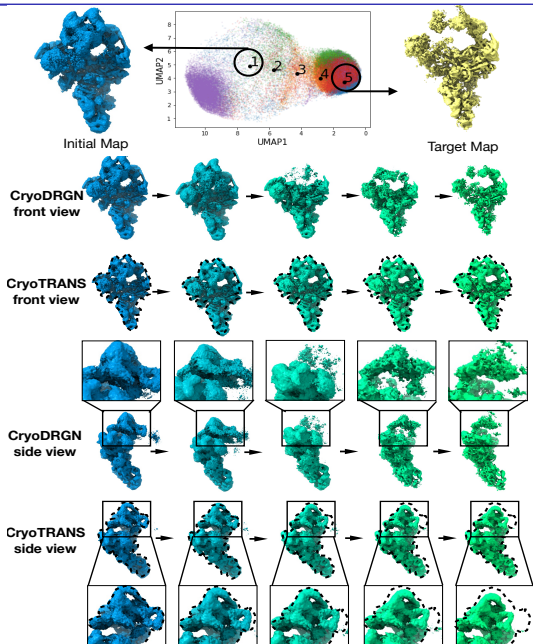
$$X_i = \text{CTF}_i * (P_i^\phi \circ V) + N_i \quad i = 1, 2 \dots N$$



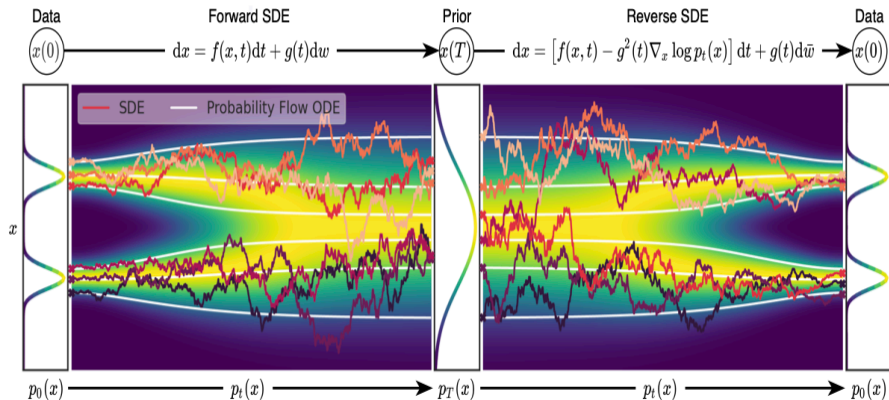
Background of CryoDRGN



Background of CryoDRGN



Background of Diffusion Model



Background of DDPM

- Suppose that $x_0 \sim q_{\text{data}}(x_0)$, the reverse process is defined as a Markov chain:

$$p_{\theta}(\mathbf{x}_{0:T}) := p(\mathbf{x}_T) \prod_{t=1}^T p_{\theta}(\mathbf{x}_{t-1} \mid \mathbf{x}_t)$$

$$p_{\theta}(\mathbf{x}_{t-1} \mid \mathbf{x}_t) := \mathcal{N}(\mathbf{x}_{t-1}; \boldsymbol{\mu}_{\theta}(\mathbf{x}_t, t), \boldsymbol{\Sigma}_{\theta}(\mathbf{x}_t, t))$$

- The forward process is fixed to a Markov chain that gradually adds Gaussian noise to the data:

$$q(\mathbf{x}_{1:T} \mid \mathbf{x}_0) := \prod_{t=1}^T q(\mathbf{x}_t \mid \mathbf{x}_{t-1})$$

$$q(\mathbf{x}_t \mid \mathbf{x}_{t-1}) := \mathcal{N}(\mathbf{x}_t; \sqrt{1 - \beta_t} \mathbf{x}_{t-1}, \beta_t \mathbf{I})$$

- Define $\alpha_t = 1 - \beta_t$ and $\bar{\alpha}_t := \prod_{s=1}^t \alpha_s$, we have

$$q(\mathbf{x}_t \mid \mathbf{x}_0) = \mathcal{N}(\mathbf{x}_t; \sqrt{\bar{\alpha}_t} \mathbf{x}_0, (1 - \bar{\alpha}_t) \mathbf{I})$$

Background of DDPM

- ▶ maximize the ELBO:

$$\mathbb{E}_q \left[\underbrace{D_{\text{KL}}(q(\mathbf{x}_T | \mathbf{x}_0) \| p(\mathbf{x}_T))}_{L_T} + \sum_{t>1} \underbrace{D_{\text{KL}}(q(\mathbf{x}_{t-1} | \mathbf{x}_t, \mathbf{x}_0) \| p_\theta(\mathbf{x}_{t-1} | \mathbf{x}_t))}_{L_{t-1}} - \underbrace{\log p_\theta(\mathbf{x}_0 | \mathbf{x}_1)}_{L_0} \right]$$

- ▶ Here

$$q(\mathbf{x}_{t-1} | \mathbf{x}_t, \mathbf{x}_0) = \mathcal{N}(\mathbf{x}_{t-1}; \tilde{\boldsymbol{\mu}}_t(\mathbf{x}_t, \mathbf{x}_0), \tilde{\beta}_t \mathbf{I})$$

where $\tilde{\boldsymbol{\mu}}_t(\mathbf{x}_t, \mathbf{x}_0) := \frac{\sqrt{\bar{\alpha}_{t-1}}\beta_t}{1-\bar{\alpha}_t}\mathbf{x}_0 + \frac{\sqrt{\alpha_t}(1-\bar{\alpha}_{t-1})}{1-\bar{\alpha}_t}\mathbf{x}_t$ and $\tilde{\beta}_t := \frac{1-\bar{\alpha}_{t-1}}{1-\bar{\alpha}_t}\beta_t$

- ▶ Suppose that $p_\theta(\mathbf{x}_{t-1} | \mathbf{x}_t) = \mathcal{N}(\mathbf{x}_{t-1}; \boldsymbol{\mu}_\theta(\mathbf{x}_t, t), \sigma_t^2 \mathbf{I})$, we can write

$$L_{t-1} = \mathbb{E}_q \left[\frac{1}{2\sigma_t^2} \|\tilde{\boldsymbol{\mu}}_t(\mathbf{x}_t, \mathbf{x}_0) - \boldsymbol{\mu}_\theta(\mathbf{x}_t, t)\|^2 \right] + C$$

Background of DDPM

- ▶ We choose the parameterization

$$\mu_{\theta}(\mathbf{x}_t, t) = \frac{1}{\sqrt{\alpha_t}} \left(\mathbf{x}_t - \frac{\beta_t}{\sqrt{1 - \bar{\alpha}_t}} \epsilon_{\theta}(\mathbf{x}_t, t) \right)$$

- ▶ The equation simplifies to

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

- ▶ Simplified variational bound:

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

Background of DDPM

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  
        $\nabla_{\theta} \left\| \epsilon - \epsilon_{\theta}(\sqrt{\bar{\alpha}_t} \mathbf{x}_0 + \sqrt{1 - \bar{\alpha}_t} \epsilon, t) \right\|^2$   
6: 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:    $\mathbf{x}_{t-1} = \frac{1}{\sqrt{\alpha_t}} \left( \mathbf{x}_t - \frac{1 - \alpha_t}{\sqrt{1 - \bar{\alpha}_t}} \epsilon_{\theta}(\mathbf{x}_t, t) \right) + \sigma_t \mathbf{z}$   
5: end for  
6: return  $\mathbf{x}_0$ 
```

Background of DDPM

- ▶ Define $\beta(\frac{t}{T}) = T\beta_t$, as $T \rightarrow \infty$, the forward process of DDPM converges to the following SDE:

$$d\mathbf{x} = -\frac{1}{2}\beta(t)\mathbf{x}dt + \sqrt{\beta(t)}d\mathbf{w}$$

- ▶ For a general forward SDE:

$$d\mathbf{x} = \mathbf{f}(\mathbf{x}, t)dt + \mathbf{G}(t)d\mathbf{w}$$

there exists a probability flow ODE corresponding to its backward form:

$$d\mathbf{x} = \left\{ \mathbf{f}(\mathbf{x}, t) - \frac{1}{2}\mathbf{G}(t)\mathbf{G}(t)^\top \nabla_{\mathbf{x}} \log p_t(\mathbf{x}) \right\} dt$$

Background of SMLD

- ▶ In SMLD, the process $\{\mathbf{x}(t)\}_{t=0}^1$ is given by the following SDE:

$$d\mathbf{x} = \sqrt{\frac{d[\sigma^2(t)]}{dt}} d\mathbf{w}$$

- ▶ The probability flow ODE is formulated as:

$$d\mathbf{x} = -\dot{\sigma}(t)\sigma(t)\nabla_{\mathbf{x}} \log p(\mathbf{x}; \sigma(t))dt$$

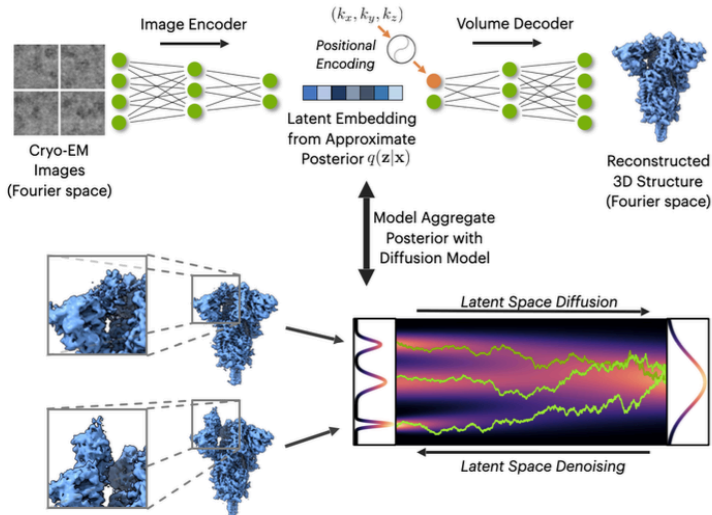
- ▶ Train a denoiser

$D_{\theta}(x; \sigma)(\nabla_{\mathbf{x}} \log p(\mathbf{x}; \sigma) \approx s_{\theta} = (D_{\theta}(\mathbf{x}; \sigma) - \mathbf{x}) / \sigma^2)$ with:

$$\arg \min_{\theta} \mathbb{E}_{\mathbf{x} \sim p_{\text{data}}(\mathbf{x}), \sigma \sim p(\sigma), \mathbf{n} \sim \mathcal{N}(\mathbf{0}, \sigma^2)} \left[\lambda(\sigma) \|D_{\theta}(\mathbf{x} + \mathbf{n}, \sigma) - \mathbf{x}\|_2^2 \right]$$

Model Outview

- First train a cryoDRGN model, then freeze the parameters and train the diffusion model in latent space



Result

Dataset	D	N	Å/pix.	$ z $	Architecture	Epochs
<i>Linear1d</i>	128	50k	6	8	256×3	25
<i>Circular1d</i>	128	100k	6	8	256×3	25
<i>Ribosome</i> (EMPIAR-10076)[42]	256	87,328	1.6375	10	1024×3	50
<i>Covid</i> (Walls et al. [25])	256	276,549	1.640625	8	1024×3	25

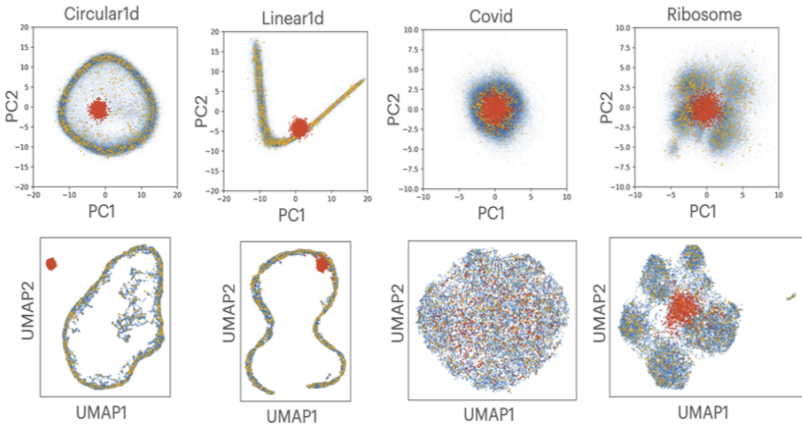
Diffusion Model

- ▶ Network Architecture: ResNet Architecture with 16 hidden layers, using 128 hidden dimensions per layer
- ▶ Training Algorithm: adam
- ▶ Batch size: 1024
- ▶ Sampling: use an adaptive step-size Runge-Kutta solver for the Probability Flow ODE
- ▶ Regularize Sampling:

$$d\mathbf{x} = \underbrace{-\dot{\sigma}(t)\sigma(t)\nabla_{\mathbf{x}} \log p(\mathbf{x}; \sigma(t))dt}_{\text{Probability Flow ODE; see Eq. (2)}} \\ - \underbrace{\beta(t)\sigma^2(t)\nabla_{\mathbf{x}} \log p(\mathbf{x}; \sigma(t))dt + \sqrt{2\beta(t)\sigma(t)}d\omega_t}_{\text{Langevin diffusion component}},$$

Diffusion Prior

- ▶ Diffusion model prior can model the latent distribution of data



- Latent embeddings
- VAE prior samples
- Diffusion prior samples

Dataset	Latent Diffusion Model Prior	Standard Gaussian VAE Prior
<i>circular1d</i>	0.015	0.82
<i>linear1d</i>	0.015	0.86
<i>covid</i>	0.005	0.19
<i>ribosome</i>	0.015	0.58

Diffusion Prior

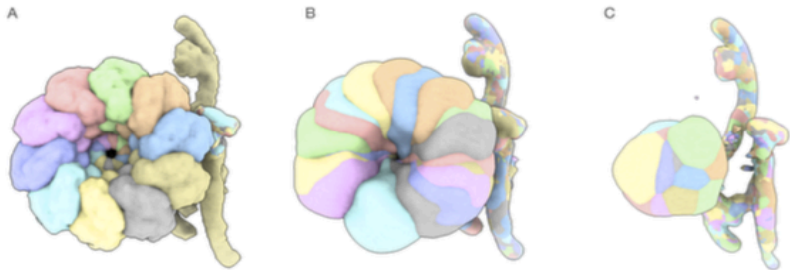
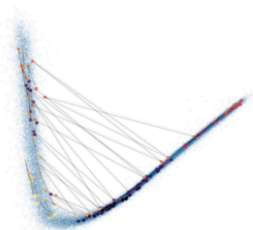


Figure 3: *circular1d* volumes viewed as isosurface contour. **A:** Ground truth volumes. **B:** 20 volumes sampled from diffusion model prior. **C:** 20 volumes sampled from standard Gaussian VAE prior.

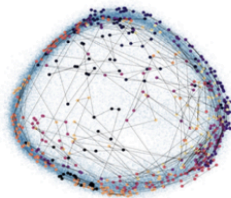
Diffusion Prior

- Run Langevin Dynamics in the latent space

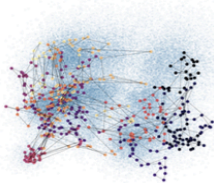
$$\hat{\mathbf{z}}_{n+1} = \hat{\mathbf{z}}_n - \frac{\hat{\mathbf{z}}_n}{2} \Delta t + \sqrt{\Delta t} \mathcal{N}(\mathbf{0}, \mathbf{I})$$



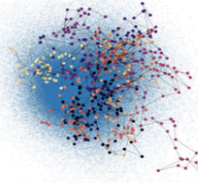
(a) Linear1d



(b) Circular1d



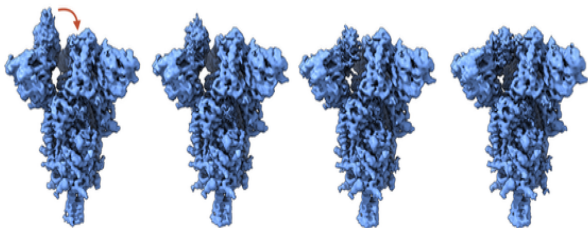
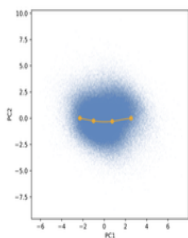
(c) Ribosome



(d) Covid

Diffusion Inteporlation

- ▶ Given z_A and z_B in the latent space, encode $\hat{z}_{AB}(y) = (1 - y)\hat{z}_A + y\hat{z}_B$, then decode $\hat{z}_{AB}(y)$ back to $z_{AB}(y)$
- ▶ Use the Probability FLOW ODE to sample



Diffusion Inteporlation

- ▶ Diffusion model has learnt a sharp transition in its Probability Flow ODE

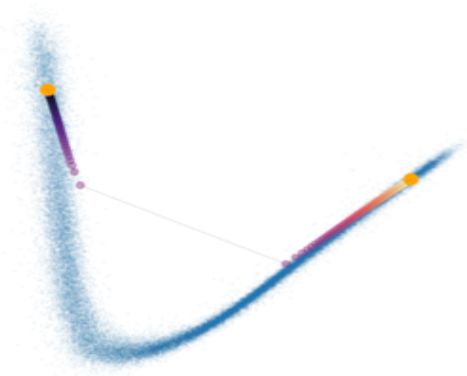


Figure 4: Conformational state interpolation with the diffusion model prior for *linear1d*; Also see Fig. 8.

Diffusion Inteporlation

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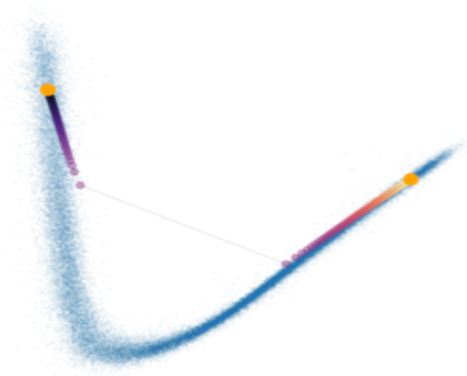


Figure 4: Conformational state interpolation with the diffusion model prior for *linear1d*; Also see Fig. 8.

Future work

- ▶ Conditional Generative Modeling
 - Build on classifier and classifier-free guidance technique
- ▶ Coupling with Atomic Models
 - Combined with future version of CryoDRGN
- ▶ Molecular Simulation
- ▶ End-to-end Training and Hierarchical Models
 - End-to-end training of cryoDRGN together with the latent diffusion model
 - Learn one diffusion model to capture the main data clusters and another to capture the intra-cluster variation



Thank you!