

SE(3) Diffusion Model with Applications to Protein Backbone Generation

by Yim, Trippe, De Bortoli, Mathieu, et. al

M2 MVA, Algorithms for Protein Science

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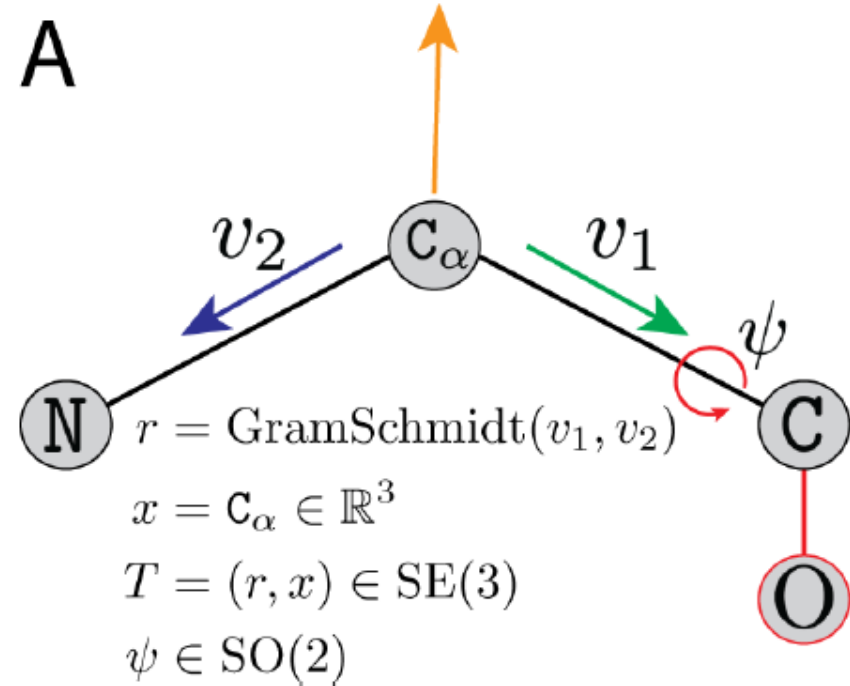
Representation of the protein backbone

A frame $X \in \mathbb{R}^3$ is positioned via a rigid transformation,

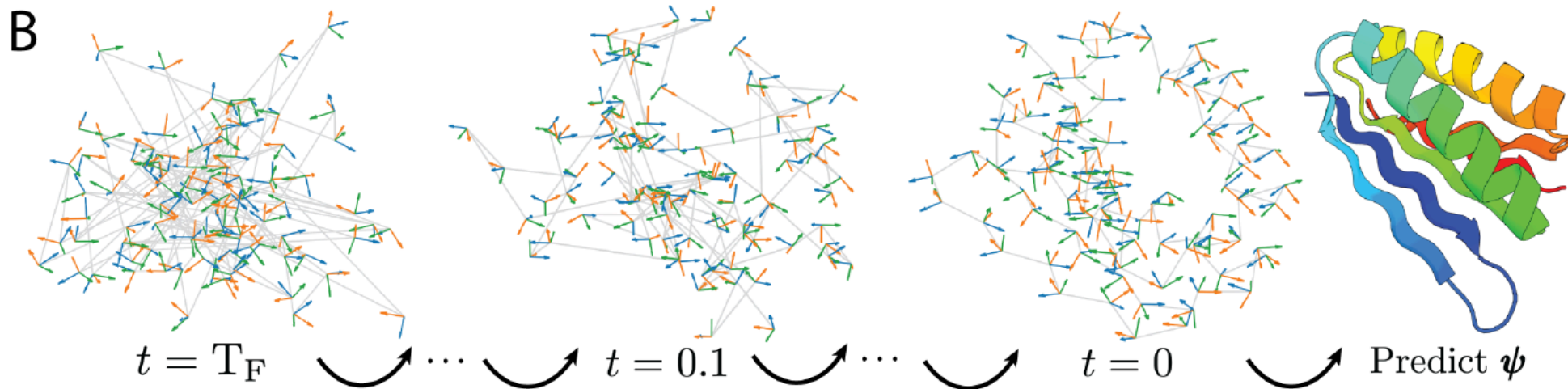
$$T \cdot X = RX + x$$

with,

$$\begin{cases} T = (R, x) \in \text{SE}(3) \\ R \in \text{SO}(3) \\ x \in \mathbb{R}^3 \end{cases}$$



Goal: diffusion on $SE(3)^N$



Reminder on diffusion processes

Transform initial distribution p_I into data distribution p_T

Denosing equations:

Forward equations: $\dot{X}_t = b_t(X_t) + dB_t, X_0 \sim p_T$

Fokker-Planck: $\dot{p}_t = \nabla^* p_t b_t + \Delta p_t$

Backward equations: $\dot{X}_t = -b_t(X_t) + \underbrace{\nabla_X \log p(X_t)}_{\text{score}} + dB_t, X_0 \sim p_I$

Score approximation: $\nabla_X \log p(X_t) = \mathbb{E}_{X_0 | X_t} [\nabla_{X_t} \log p(X_t | X_0)]$

The group SE(3)

As a group $SE(3) = SO(3) \ltimes \mathbb{R}^3$

$$\Rightarrow (R, x) \cdot (R', x') = (RR', Rx' + x)$$

As a manifold $SE(3) = SO(3) \times \mathbb{R}^3$

$$\Rightarrow \langle (R, x) \mid (R', x') \rangle_{SE(3)} = \langle R \mid R' \rangle_{SO(3)} + \langle x \mid x' \rangle_{\mathbb{R}^3}$$

The group $SO(3)$

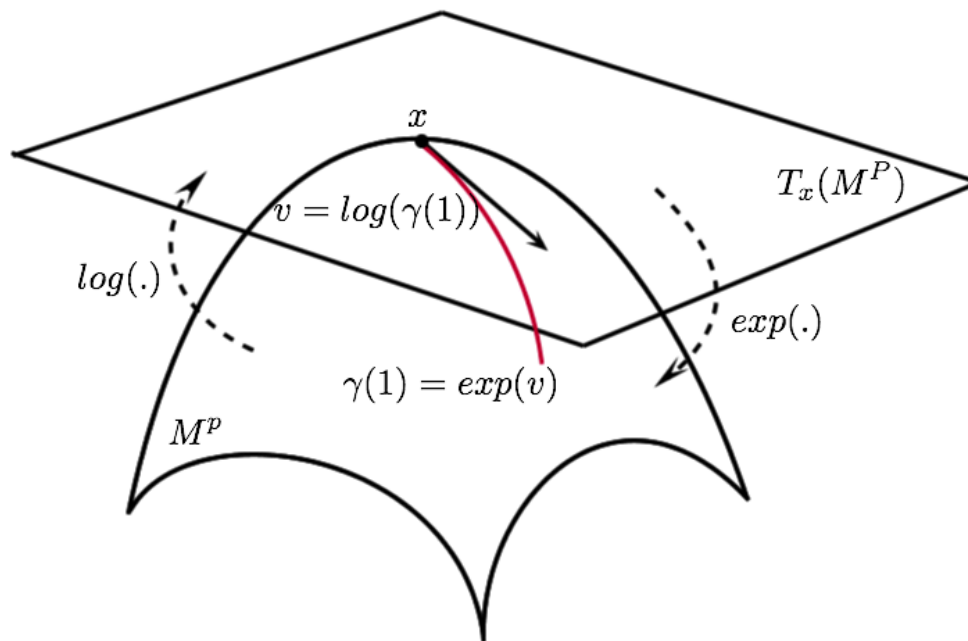
The Lie algebra $\mathfrak{so}(3)$ is the tangent space at identity.

Basis of $\mathfrak{so}(3)$:

$$\begin{array}{c} \underbrace{\hspace{1.5cm}}_{Y_1} \quad \underbrace{\hspace{1.5cm}}_{Y_2} \quad \underbrace{\hspace{1.5cm}}_{Y_3} \\ \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & -1 \\ 0 & 1 & 0 \end{pmatrix} \quad \begin{pmatrix} 0 & 0 & 1 \\ 0 & 0 & 0 \\ -1 & 0 & 0 \end{pmatrix} \quad \begin{pmatrix} 0 & -1 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \end{array}$$

Exponential map $\exp : \mathfrak{so}(3) \rightarrow SO(3)$:

$$\exp(R) = \sum_{k \geq 0} \frac{R^k}{k!}$$



Brownian motion on $SO(3)$

Separation of metrics \Rightarrow brownian motion splits:

$$B^{\text{SE}(3)} = (B^{\text{SO}(3)}, B^{\mathbb{R}^3})$$

Sample $z_1, z_2, z_3 \sim \mathcal{N}(0, \Delta t)$

Brownian motion increment: $R_{t+\Delta t} = R_t \exp(\sum_i z_i Y_i)$

\Rightarrow Associated Fokker-Planck equation ?

Parametrization of SO(3)

Axis-angle parametrization: $R = \exp(\theta K)$ with

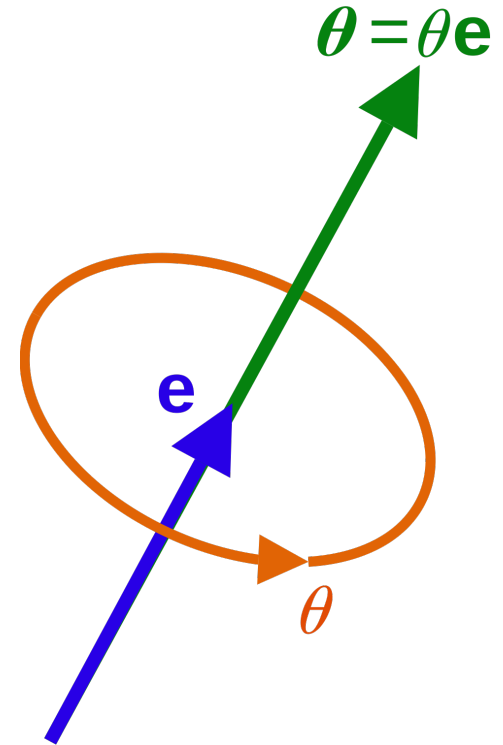
$$\begin{cases} \theta \in [0, 2\pi] \\ K = \sum_i e_i Y_i \\ e = (e_1, e_2, e_3) \in \mathbb{S}^2 \end{cases}$$

Rodrigues formula:

$$\exp(\theta K) = \text{Id} + \sin(\theta)K + (1 - \cos(\theta))K^2$$

Inverse:

$$\begin{cases} \theta(R) = \cos^{-1}\left(\frac{\text{Tr}(R)-1}{2}\right) \\ K(R) = \frac{(R_{32}-R_{23})Y_1 + (R_{13}-R_{31})Y_2 + (R_{21}-R_{12})Y_3}{2 \sin(\theta)} \end{cases}$$



Representations and characters of $SO(3)$

l -dimensional representation $\rho : SO(3) \rightarrow GL(V)$ with $\dim(V) = l$, respecting

$$\begin{cases} \rho(RR') = \rho(R)\rho(R') \\ \rho(e) = \text{Id} \end{cases}$$

l -dimensional character $\chi_l : SO(3) \rightarrow \mathbb{R}$ associated with ρ :

$$\chi_l(R) = \text{Tr}(\rho(R)) = \frac{\sin\left(\left(l + \frac{1}{2}\right)\theta(R)\right)}{\sin\left(\frac{1}{2}\theta(R)\right)}$$

Peter-Weyl theorem: $(\chi_l)_l$ is orthonormal basis of $L^2(SO(3))$

$$\Rightarrow f = \sum_l d_l \chi_l$$

The Laplace-Beltrami operator

For $f \in C^\infty(\text{SO}(3), \mathbb{R})$:

$$\Delta_{\text{SO}(3)} f(R) = \sum_i \partial_t^2 f(R \exp(tY_i))$$

Its eigenfunctions are the characters:

$$\begin{cases} \Delta_{\text{SO}(3)} \chi_l = \lambda_l \chi_l \\ \lambda_l = -l(l+1) \end{cases}$$

On $\text{SE}(3)$, the operator splits:

$$\Delta_{\text{SE}(3)} = \Delta_{\text{SO}(3)} + \Delta_{\mathbb{R}^3}$$

Heat equation on $SO(3)$

$$\begin{aligned}
 \dot{p}_t &= \frac{1}{2} \Delta_{SO(3)} p_t \Leftrightarrow \sum_l d'_l(t) \chi_l = \frac{1}{2} \sum_l d_l(t) \Delta_{SO(3)} \chi_l \\
 &\Leftrightarrow \sum_l d'_l(t) \chi_l = -\frac{1}{2} \sum_l d_l(t) l(l+1) \chi_l \\
 &\Leftrightarrow d'_l(t) = -\frac{1}{2} l(l+1) d_l(t) \\
 &\Leftrightarrow d_l(t) = d_l(0) e^{-\frac{1}{2} l(l+1)t}
 \end{aligned}$$

Fokker-Planck in $SO(3)$: $p(R_t | R_0) = \sum_l (2l+1) e^{-\frac{1}{2} l(l+1)t} \chi_l(R_0^T R_t)$

Score function on $SO(3)$

The gradient splits:

$$\nabla_{R,x} f(R, x) = (\nabla_R f(R, x), \nabla_x f(R, x))$$

Translation gradient is given by:

$$\nabla_{x_t} \log p(x_t | x_0) = \frac{e^{-\frac{1}{2}t} x_0 - x_t}{1 - e^{-t}}$$

For rotations: $\nabla_R \theta(R) = \frac{R \log(R)}{\theta(R)}$ so that:

$$\nabla_{R_t} \log p(R_t | R_0) = \frac{\nabla_{\theta} p(R_t | R_0)}{p(R_t | R_0)} \frac{R_0^T R_t \log(R_0^T R_t)}{\theta(R_0^T R_t)}$$

Diffusion equations on SE(3)

$$\text{Forward diffusion: } \begin{cases} \dot{x}_t = -\frac{1}{2}x_t + dB_t^{\mathbb{R}^3} \\ \dot{R}_t = dB_t^{\text{SO}(3)} \\ (R_0, x_0) \sim p_T \end{cases}$$

$$\text{Backward diffusion: } \begin{cases} \dot{x}_t = \frac{1}{2}x_t + \nabla_{x_t} \log p(x_t | x_0) + dB_t^{\mathbb{R}^3} \\ \dot{R}_t = \nabla_{R_t} \log p(R_t | x_0) + dB_t^{\text{SO}(3)} \\ (R_0, x_0) \sim p_I \end{cases}$$

Rotation-invariant diffusion

Work on $\text{SE}(3)_0^N = \left\{ (R, x) \in \text{SE}(3)^N \text{ such that } \frac{1}{N} \sum_i x_i = 0 \right\}$

\Rightarrow Centered equations for translations:

$$\text{Forward centered: } \dot{x}_t = -\frac{1}{2}Px_t + PdB_t^{\mathbb{R}^3} \xrightarrow{t \rightarrow \infty} P_{\#}(\mathcal{N}(0, 1)^{\otimes N} \otimes \mathcal{U}(\text{SO}(3))^{\otimes N})$$

$$\text{Backward centered: } \dot{x}_t = \frac{1}{2}Px_t + \nabla_{x_t} \log p(x_t | x_0) + PdB_t^{\mathbb{R}^3}$$

Theorem: if p_I is $\text{SO}(3)$ -invariant and drift and diffusion coefficients are $\text{SO}(3)$ -equivariant, the backward equations remain $\text{SO}(3)$ -invariant and the score remains $\text{SO}(3)$ -equivariant.

The score network

The FramePred algorithm predicts a denoised frame:

$$\hat{T}_0^t = f_t^\theta(T_t)$$

and optimized to minimize the DSM loss:

$$\mathbb{E} \left[\lambda_t \left\| s_t^\theta(T_t) - \nabla_{T_t} \log p(T_t | T_0) \right\|^2 \right]$$

$$\text{with } s_t^\theta(T_t) = \nabla_{T_t} \log p(T_t | \hat{T}_0^t)$$

f_t^θ also outputs ψ angles for oxygen atoms.

Practice: FramePred

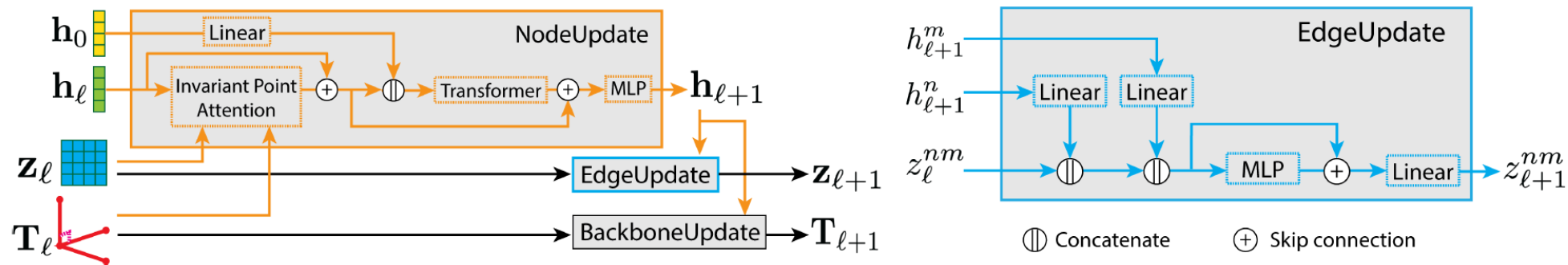


Figure 1: Backbone transformer. h_i : node embedding, z_i : edge embedding. IPA is SE(3)-invariant.

Practice: auxiliary losses

To avoid steric clashes or chain breaks at the end of training:

$$\mathcal{L}_{\text{bb}} = \frac{1}{4N} \sum_{a,n} \|a_n - \hat{a}_n\|^2$$
$$\mathcal{L}_{\text{2D}} = \frac{1}{Z} \sum_{\substack{n,m \\ a,b \\ d_{ab}^{\text{nm}} < 0.6}} \|d_{ab}^{\text{nm}} - \hat{d}_{ab}^{\text{nm}}\|^2$$

⇒ Allows to train the positioning of oxygen atoms.

Results: designability

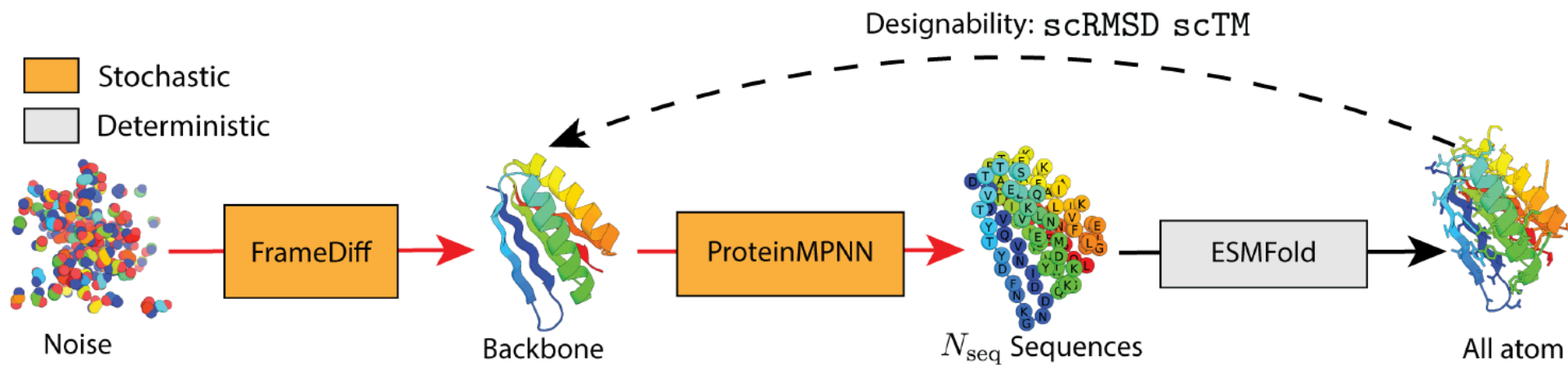


Figure 2: Protocol for computing designability of a generated backbone.

Results: plots

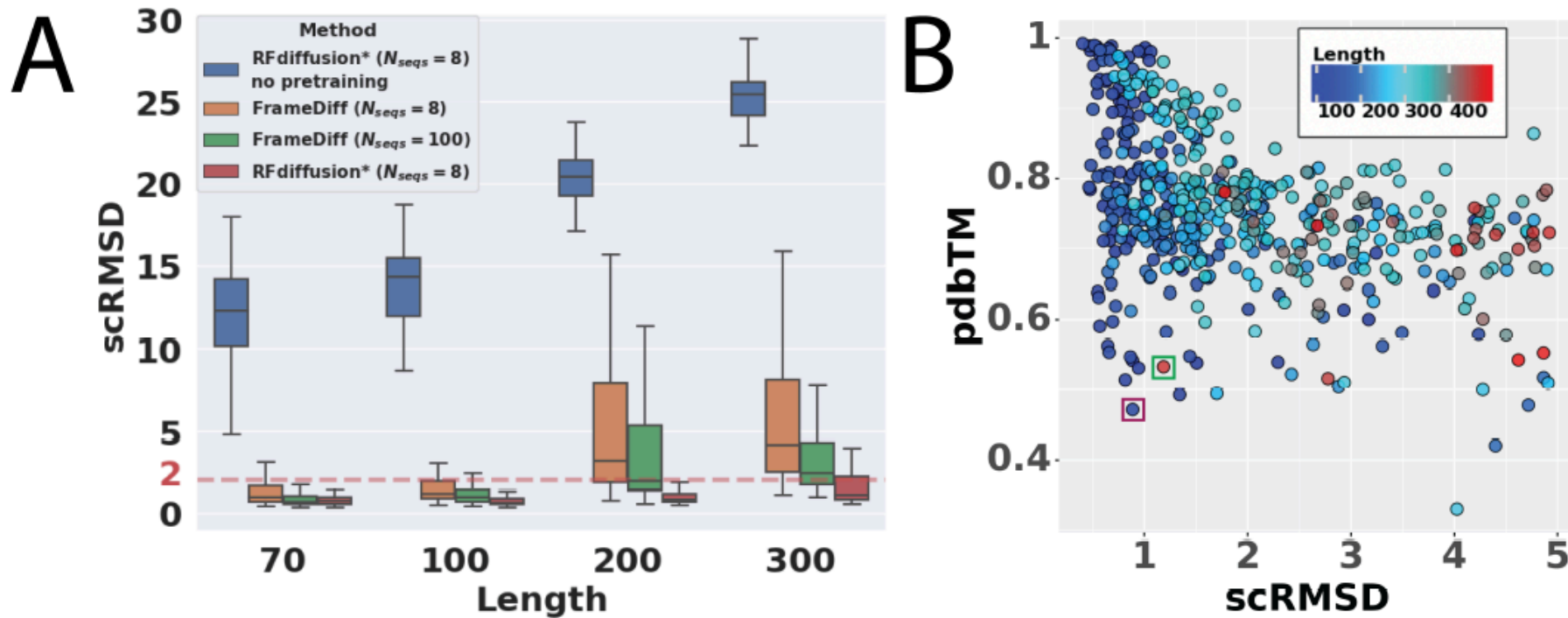


Figure 3: (A) Designability (scRMSD) against length of the generated backbone for different models. (B) Novelty (pdbTM) against designability (scRMSD) for FrameDiff.

Experiments (1/2): Noise

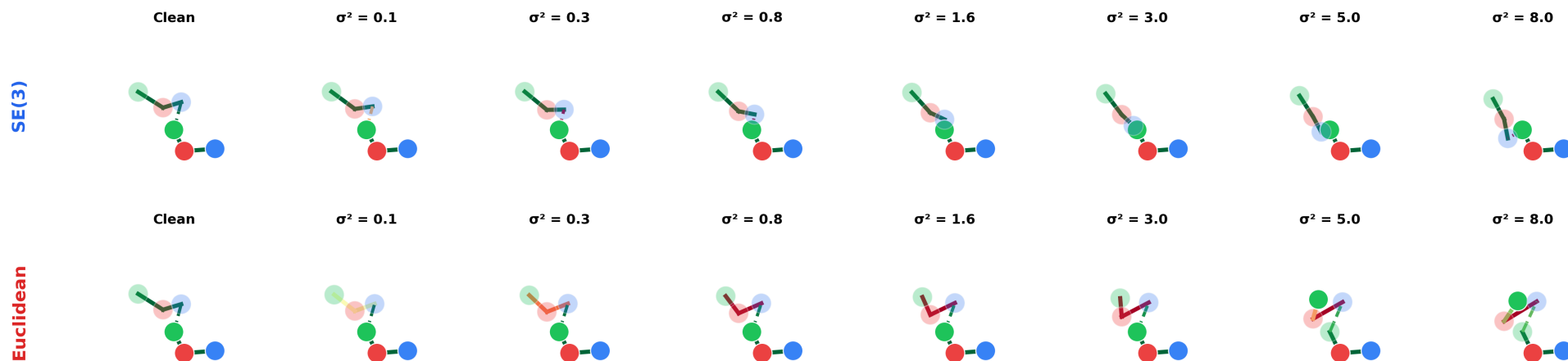


Figure 4: Noise propagation in both $SO(3)$ and \mathbb{R}^3 . Blue: N , red: C_α , green: C , red bond: broken bond.

Experiments (2/2): Interpolation

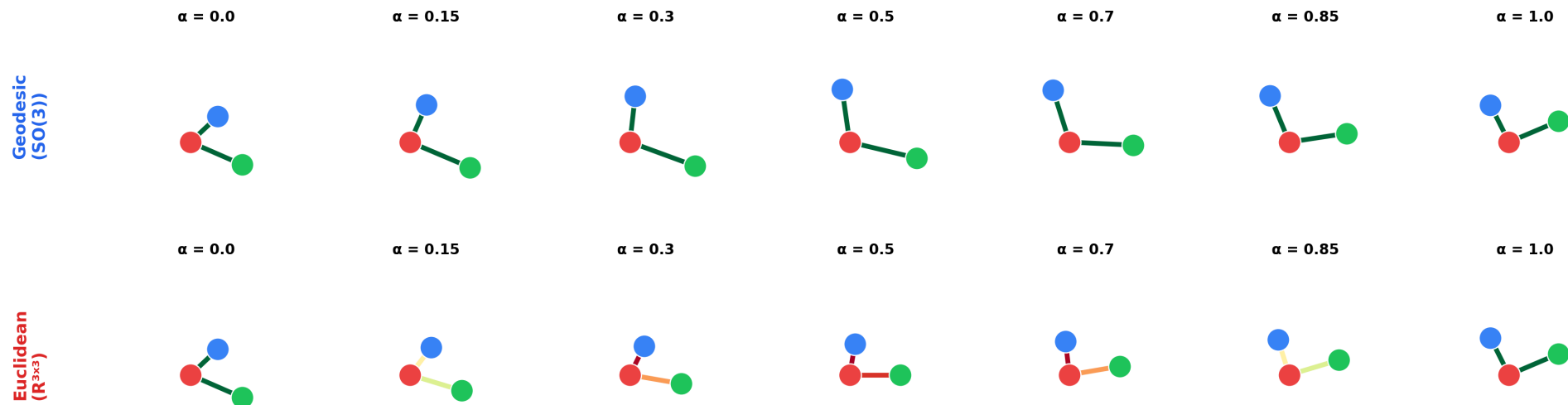


Figure 5: Interpolation in $SO(3)$ and \mathbb{R}^3 . Blue: N , red: C_α , green: C , peptide bond: - -, red bond: broken bond.

Conclusion & future work

From diffusion to flow matching

- FrameFlow [1] → **ReQFlow** [2]
- OriginFlow [3]
- EffieDes [4] / MAProt [5]

Conclusion

- Rigorous framework
- Samples can generalize beyond the PDB
- ReQFlow → AlphaFold → Lab

Bibliography

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