

Generative models for molecules in equilibrium

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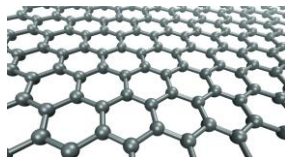
Berlin



Microsoft

Why generative modeling for molecules?

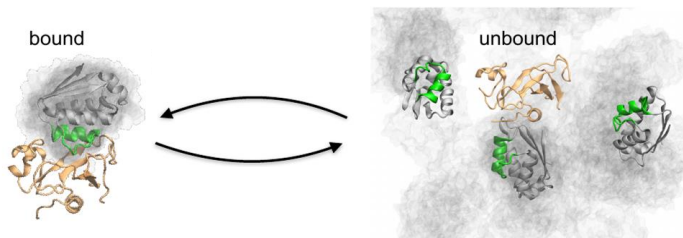
find candidates for drugs and materials (inverse design)



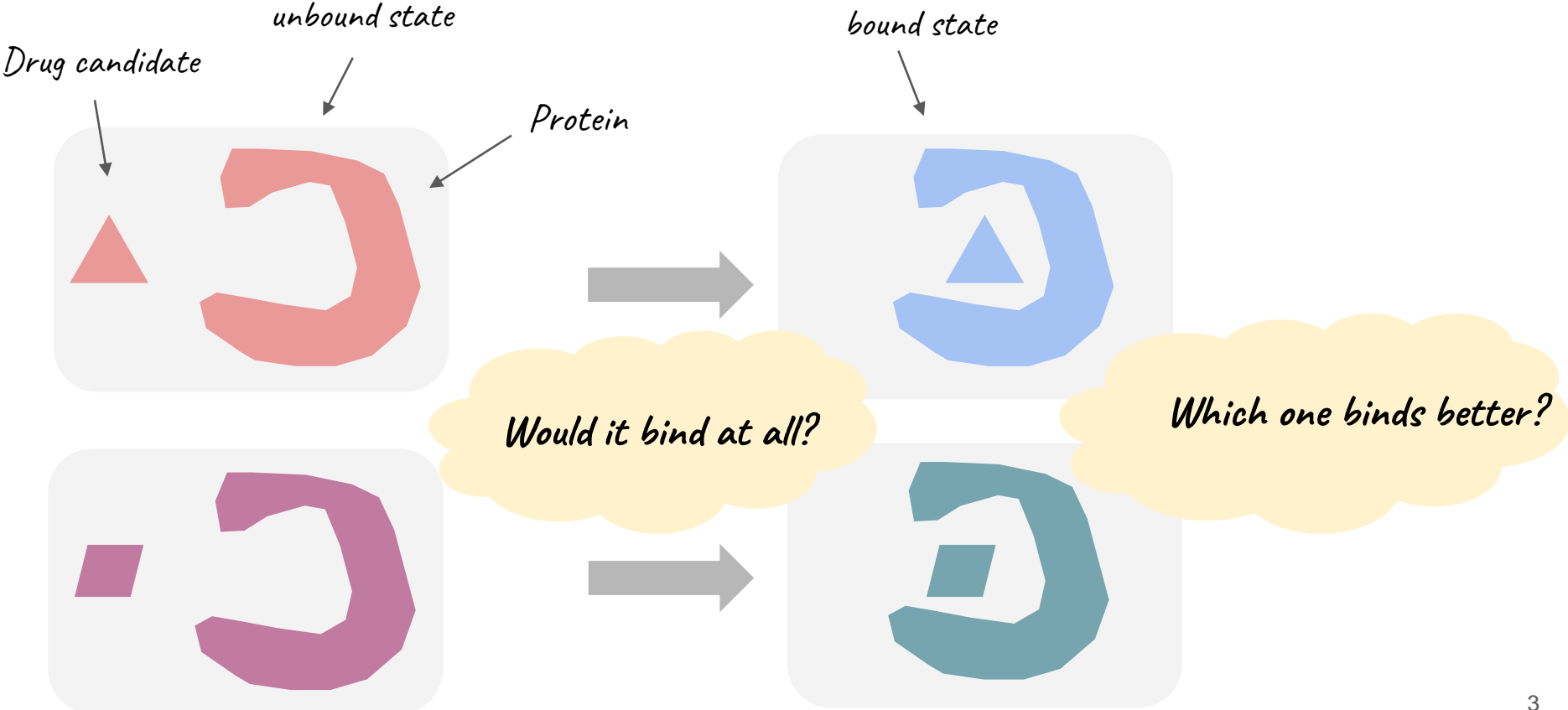
advance science



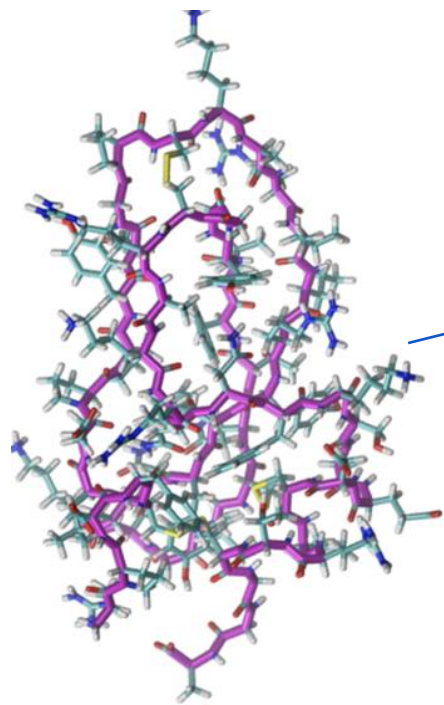
understand molecular origin of diseases



Some Motivation: binding affinity prediction



Molecules are not static...

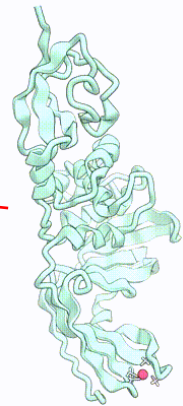


Potential energy

$$u(x)$$

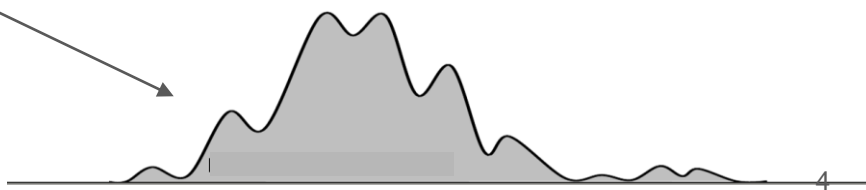
structure = "single event"

state = "whole ensemble"

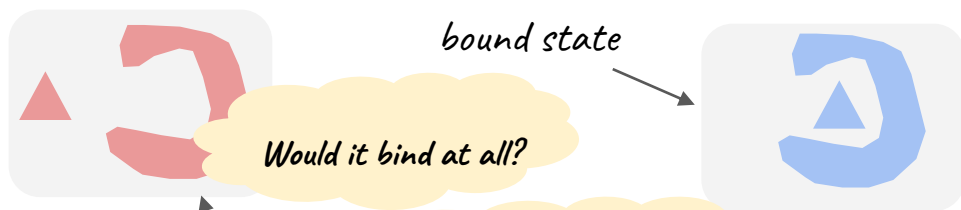


Boltzmann density

$$\mu(x) = \frac{\exp(-u(x)/kT)}{Z}$$



unbound state



Boltzmann density

$$\mu(\mathbf{x}) = \frac{\exp(-u(\mathbf{x})/kT)}{Z}$$

"likelihood of a state"

Partition function

$$Z_A = P(A) = \int_{A \subset \mathbb{R}^d} \mu(\mathbf{x})$$

"log likelihood ratio"

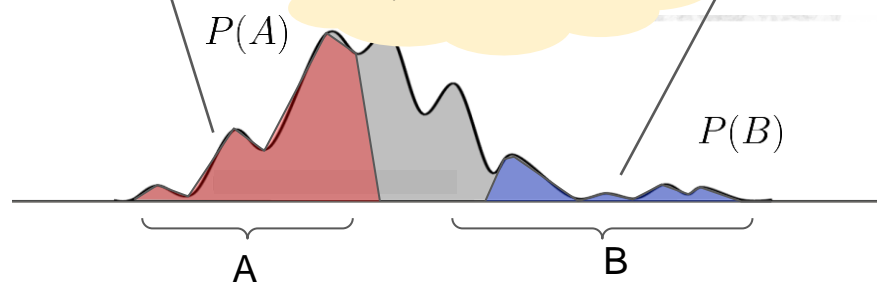
Free energy difference

$$\Delta F_{A \rightarrow B} = F_A - F_B$$

bound state

Would it bind at all?

Which one binds better?



"neg. log likelihood. of state"

Free energy

$$F_A = -kT \log Z_A$$

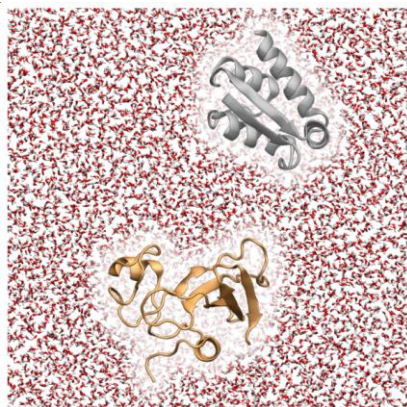
Computing FED requires sampling...

$$\mathbf{x} \sim \exp(-u(\mathbf{x}))/Z \leftarrow \therefore$$

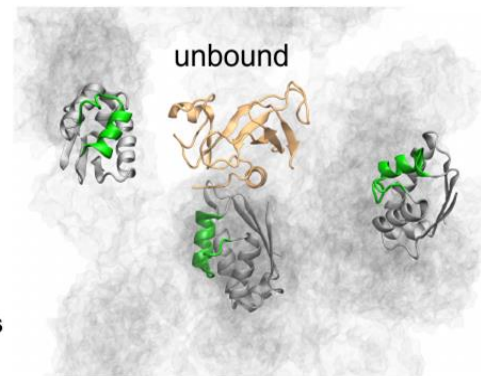
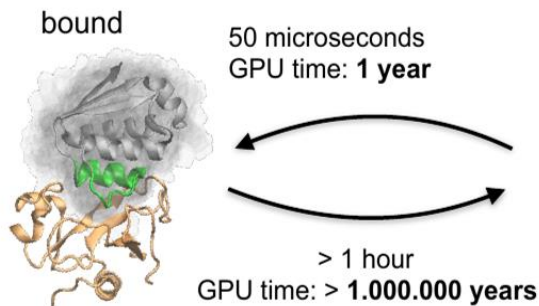
Answers requires sampling...

$$\mathbf{x} \sim \exp(-u(\mathbf{x}))/Z$$

↙ :-)



easy to make mistakes...



Numerical precision: step size 1-4 fs

Relevant biological scales: 1 ms → hours...

Classic workhorse:
Molecular / Langevin dynamics simulations

$$\mathbf{x} \leftarrow \mathbf{x} - \nabla_{\mathbf{x}} u(\mathbf{x}) dt + \sqrt{2dt} \eta, \quad \eta \sim \mathcal{N}(0, I)$$

Computing FED requires sampling...

Classic workhorse: Molecular / Langevin dynamics simulations

2ms of molecular dynamics

= ~1 Ph.D.

= ~ 500 GJ

3 ×  =



Nu
Source: Frank Noé

Relevant biological scales: 1 ms → hours...

Boltzmann Generators



Frank Noé



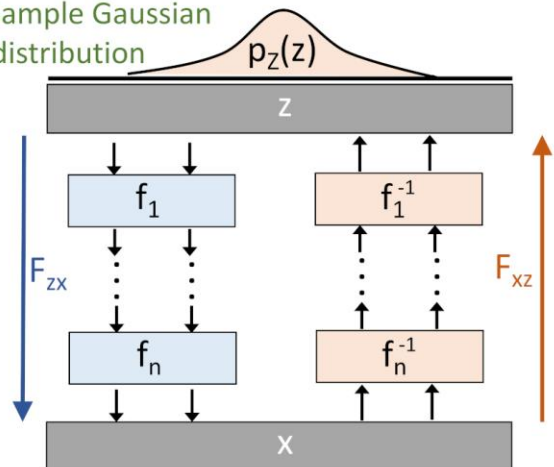
Simon Olsson



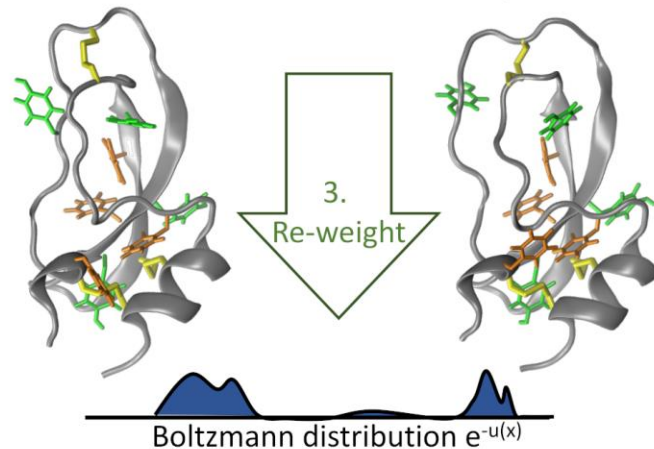
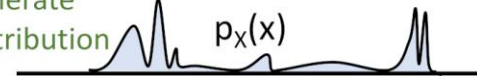
Hao Wu

1. Sample noise from base distribution
2. Transform via a trainable diffeomorphism (Normalizing Flow)
3. Reweigh against the target

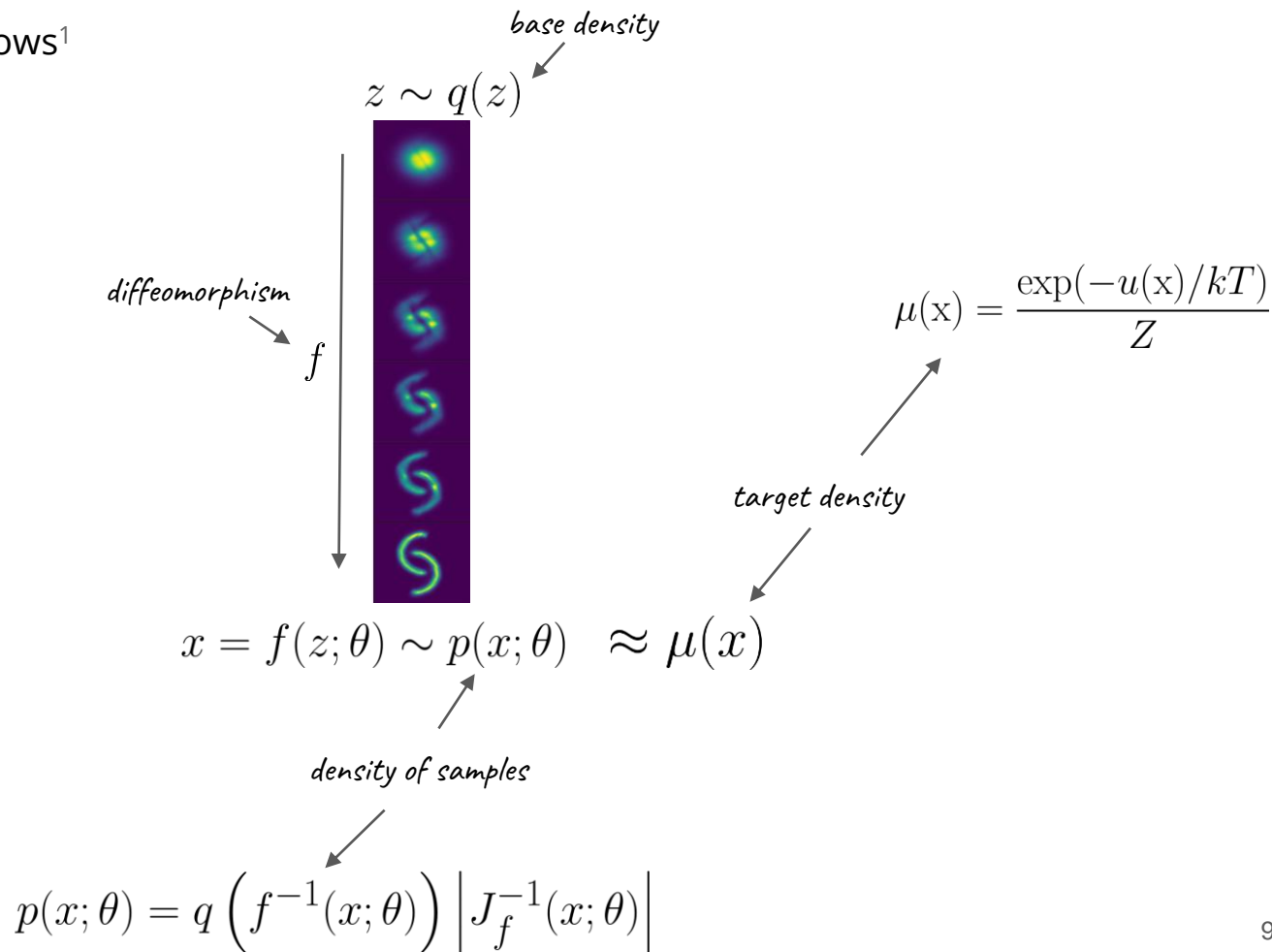
1. Sample Gaussian distribution



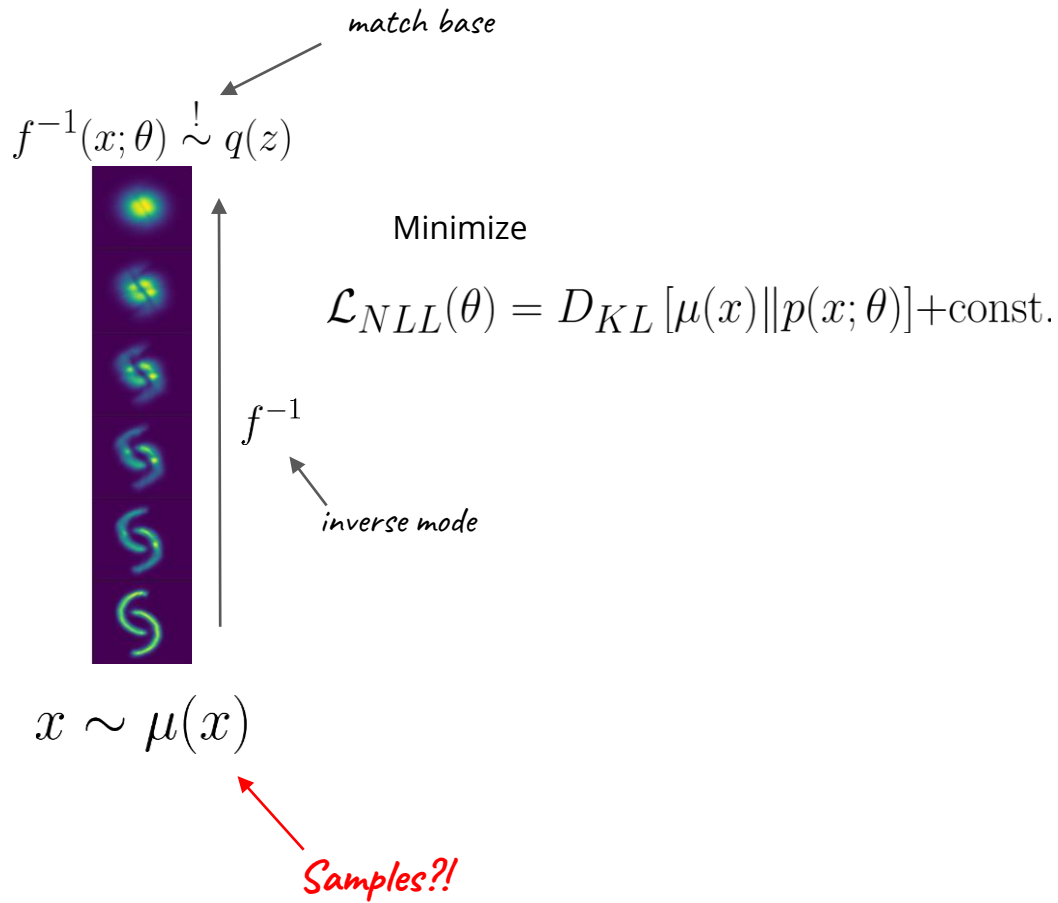
2. Generate distribution



Quick Recap: Normalizing Flows¹



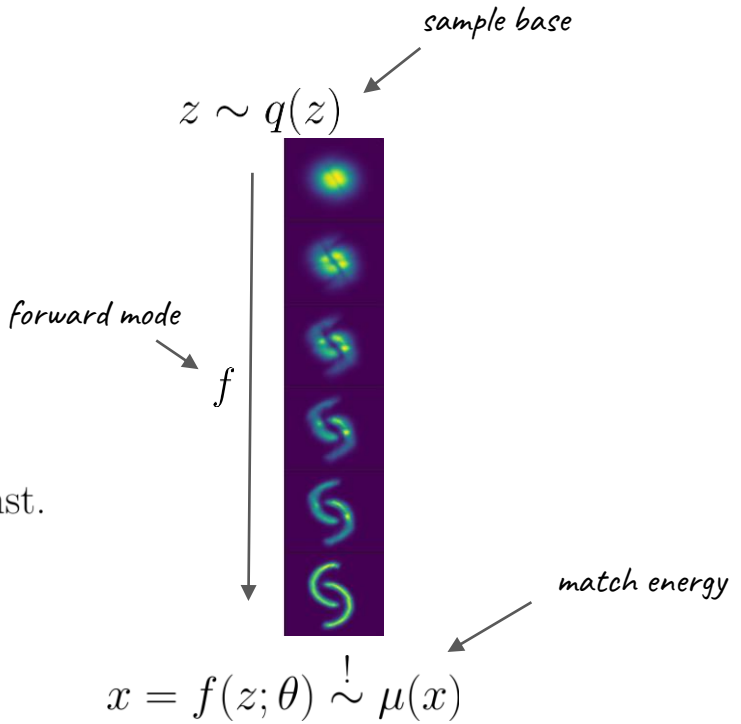
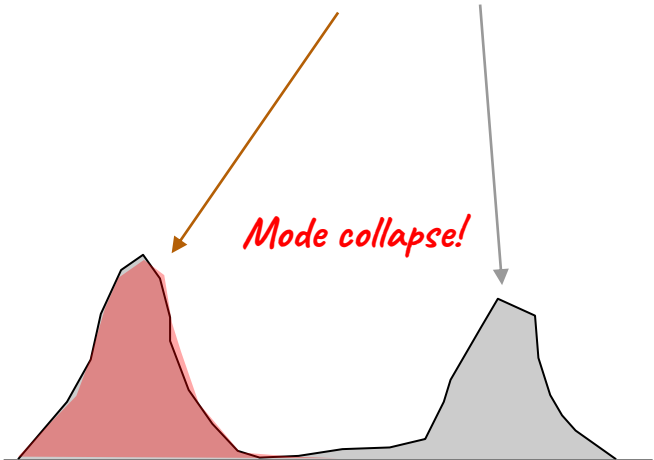
Training mode I: negative log-likelihood



Training mode II: reverse KL

Minimize

$$\mathcal{L}_{KL}(\theta) = D_{KL}[p(x; \theta) || \mu(x)] + \text{const.}$$



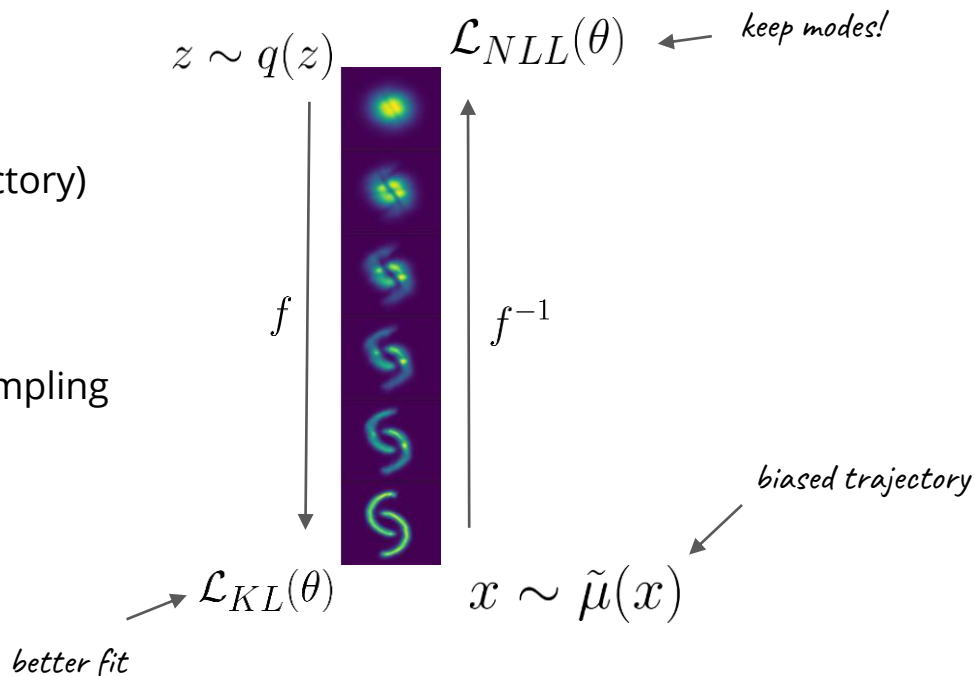
Our setup

1. NLL on biased samples
(e.g. non-converged MD trajectory)

2. combine with KL training

3. correct with importance sampling

$$\mathbb{E}_{\mu}[O(x)] = \mathbb{E}_{x \sim p} \left[\frac{\mu(x)}{p(x)} O(x) \right]$$

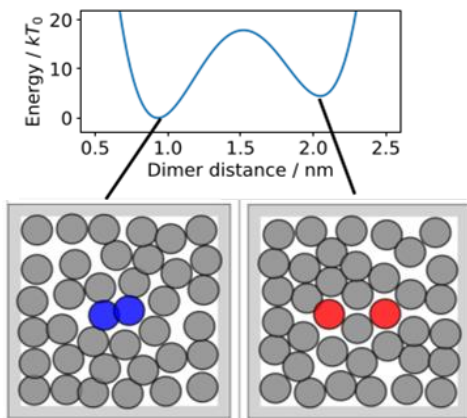


Joint loss:

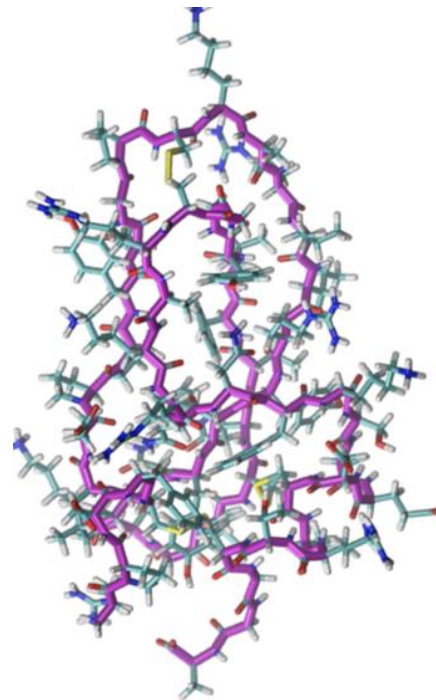
$$\mathcal{L}(\theta) = \alpha \cdot \mathcal{L}_{KL}(\theta) + \beta \cdot \mathcal{L}_{NLL}(\theta)$$

convex combination

Test systems



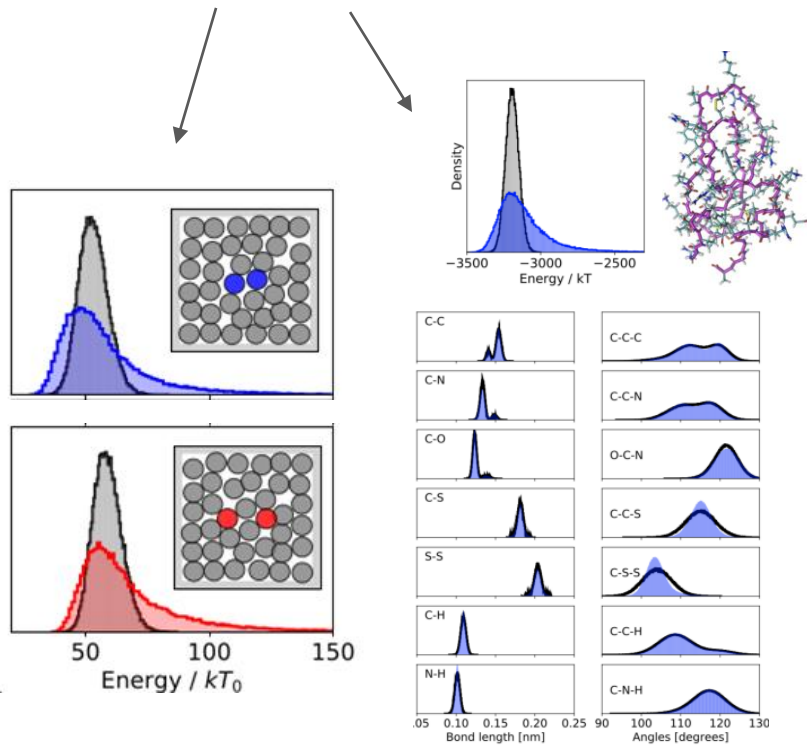
dimer in particle box



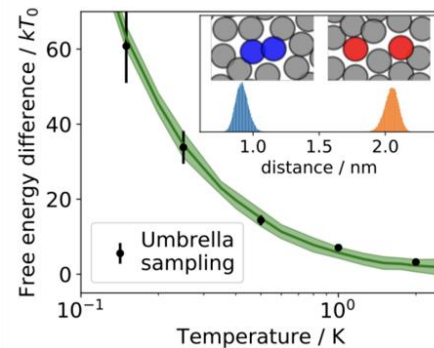
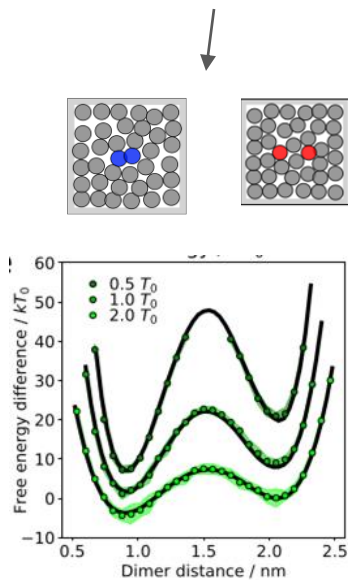
protein (BPTI) in implicit solvent

Results

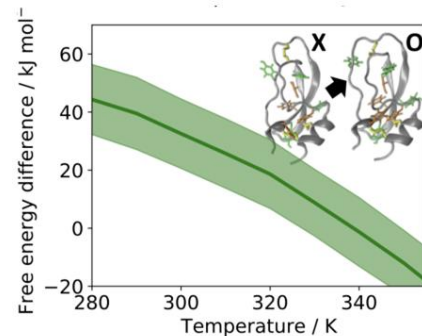
energies + marginals match

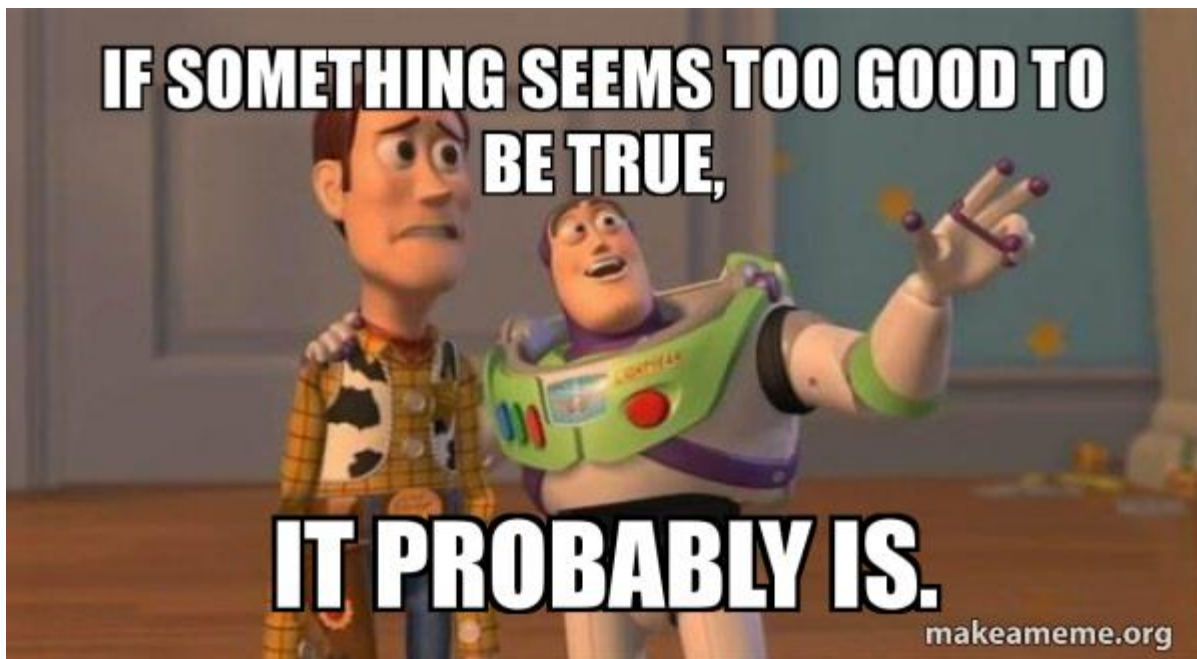


reweighing works



estimate free energy diff.



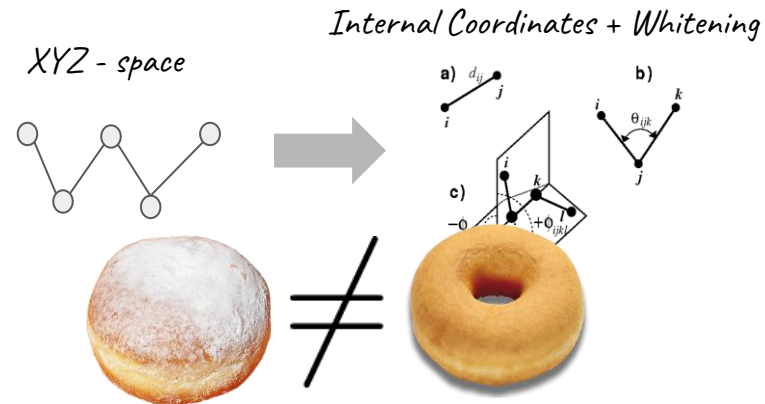


*Actual picture of the method
at this state...*

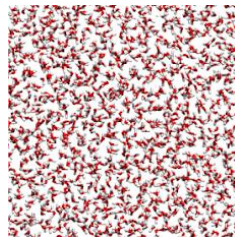
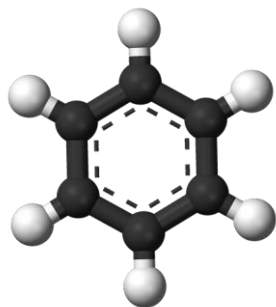


Topology / representation?

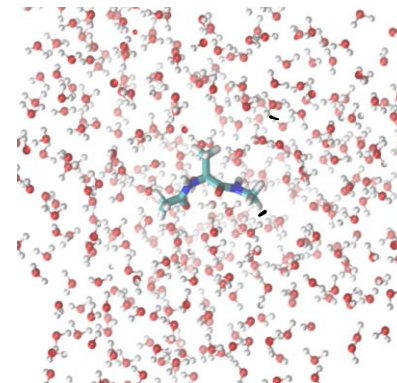
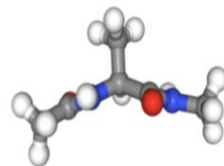
What are the problems?



Symmetries?



Bulk systems?

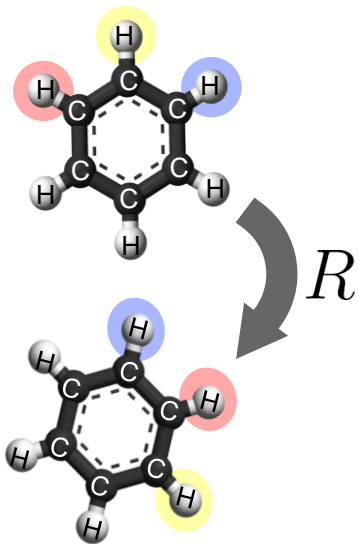


Equivariant Flows



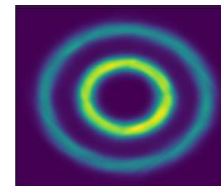
TL/DR: normalizing flows with group symmetries

Symmetries

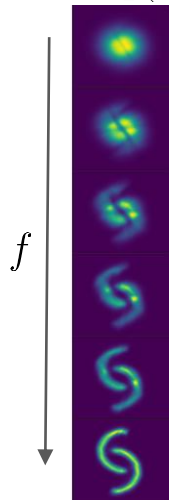


Invariant energy / density

$$\forall R \in \rho(G): u(Rx) = u(x)$$



$$z \sim q(z)$$



Arbitrary flow maps

$$p(Rx; \theta) \neq p(x; \theta) \leftarrow \text{Bad for reweighing!}$$

Handles data inefficiently!

$$x = f(z; \theta) \sim p(x; \theta)$$

Equivariant Flows

Constraint on group representations

$$\mu(\rho(g)x) = \mu(x)$$



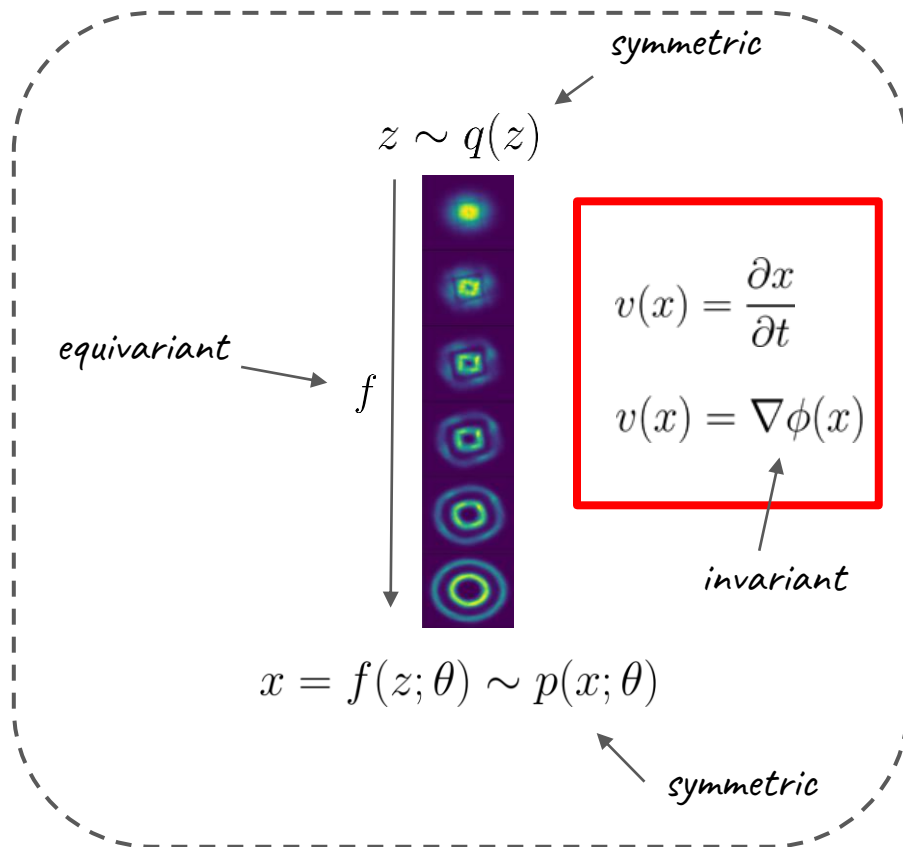
$$|\det \rho(g)| = 1.$$

Important for molecules:

$$G \leq O(n)$$

permutations

rotations



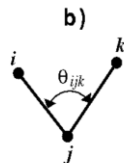
Smooth Flows



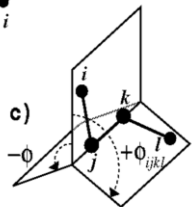
TL/DR: fix broken topology with smooth transforms on hypertorus!

Constrained manifold of internal coordinates

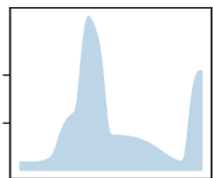
Bond Lengths $d_{ij} \in (0, \infty)$



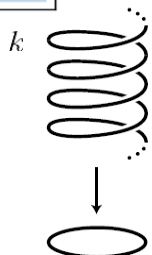
Angles $\theta_{ijk} \in [0, \pi]$



Torsions $\phi_{ijkl} \in S^1$



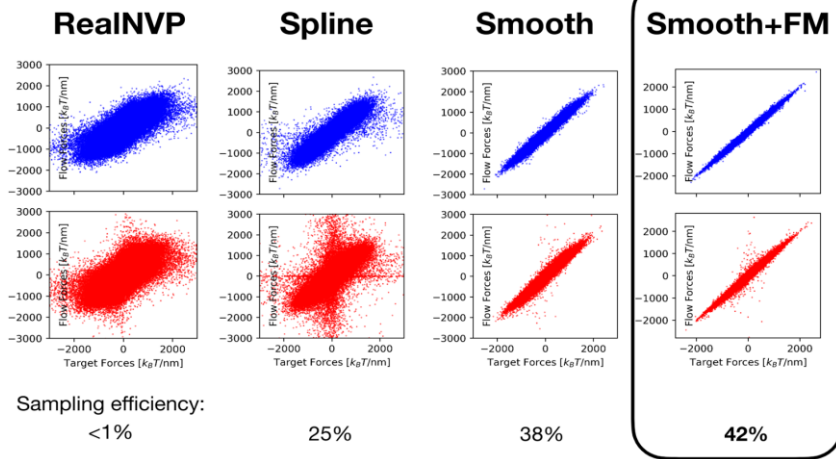
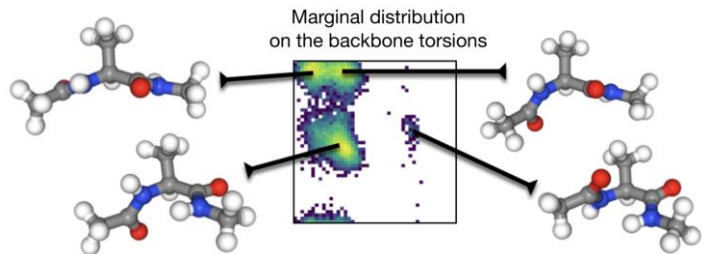
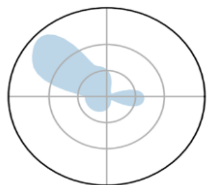
$p(x)$



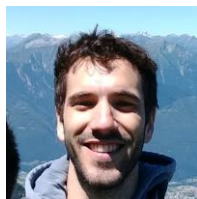
compact support

= finite sum!

$$\tilde{p}(x) = \sum_{k \in \mathbb{Z}} p(x + k)$$



Rigid body flows for molecular crystals



Michele
Invernizzi



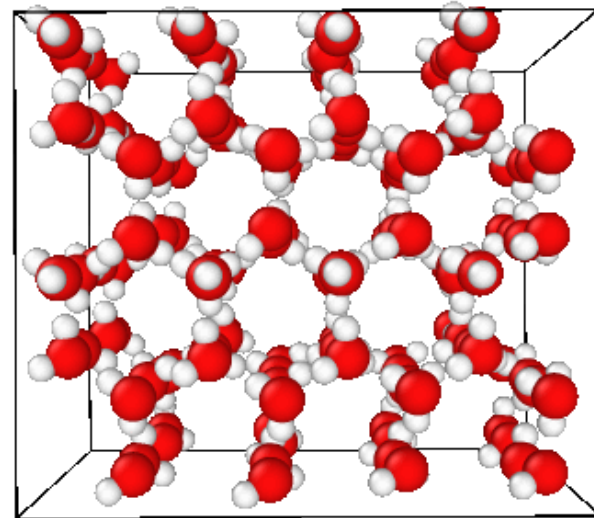
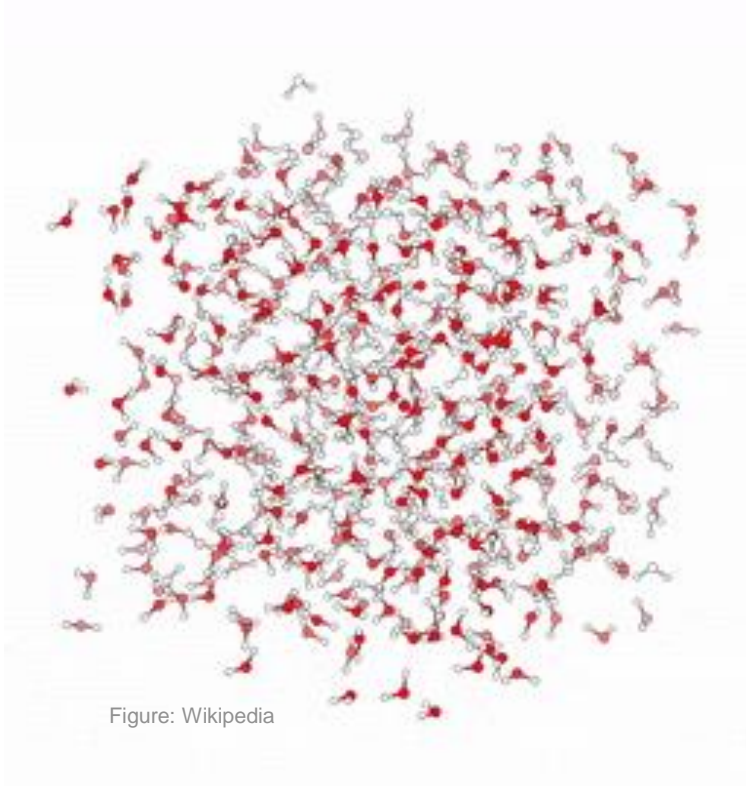
Pim de
Haan

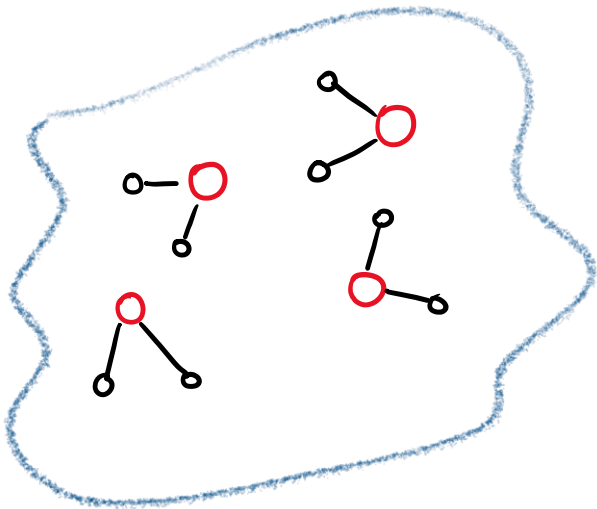


Frank Noé

TL/DR: smooth and equivariant flows on $SE(3)$

Motivation: solvent systems and crystals

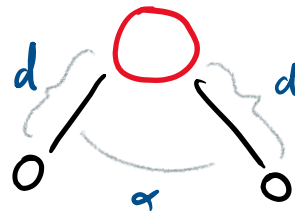




$x \in \mathbb{R}^{n \cdot a \cdot 3}$
 for water $a=3$

Usually fixed:

1x angle
 2x bond length



Degrees of freedom:

position $r \in \mathbb{R}^{3n}$

rotation $R \in \underline{\underline{SO(3)}}^n$

} $6 < 9$ dof!

Support manifold:

$$M = \left\{ x \in \mathbb{R}^{n \cdot a \cdot 3} \mid \mu(x) \neq 0 \right\} = \left[\mathbb{R}^3 \times SO(3) \right]^n \neq \mathbb{R}^{n \cdot a \cdot 3}$$

Charting

Cut manifold open into charts and apply flow to chart

- Easy to implement
- Fast
- Non-smooth solutions!

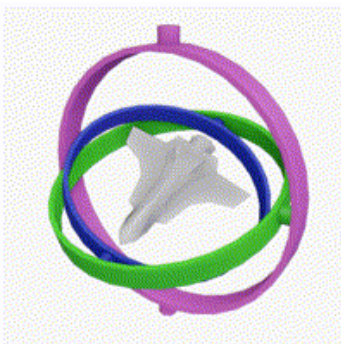
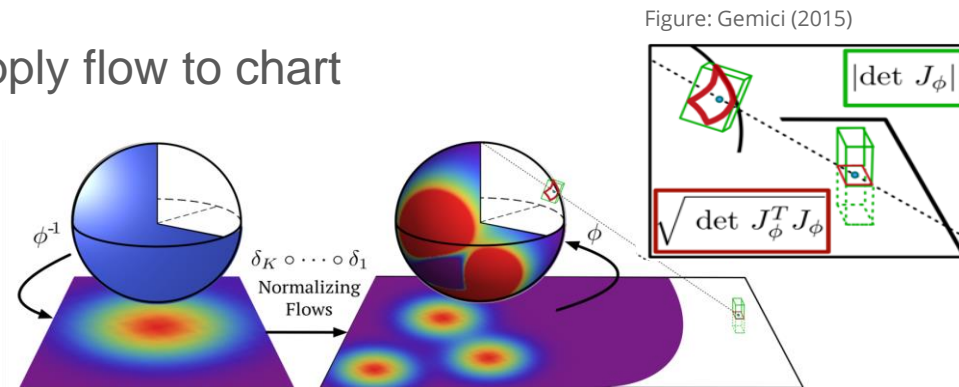
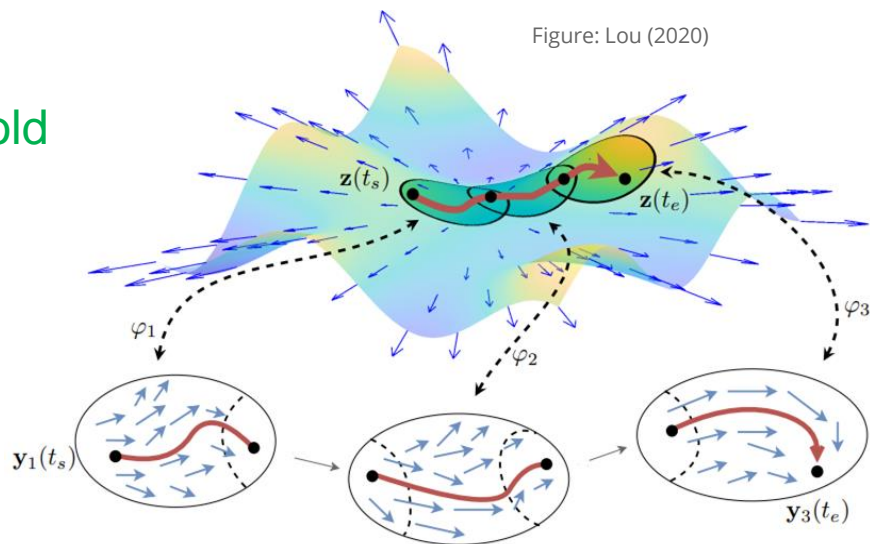


Figure: Wikipedia

Continuous flows on manifolds

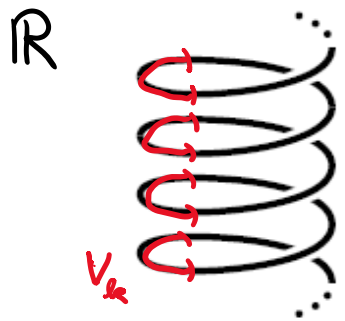
Integrate NN dynamics on manifold

- Works on every Riemannian manifold
- Smooth
- Difficult to train
 - Likelihood easy with flow-matching...
 - Rev. KL: adjoint method
- Slow integration
- Not scalable to high dimensions

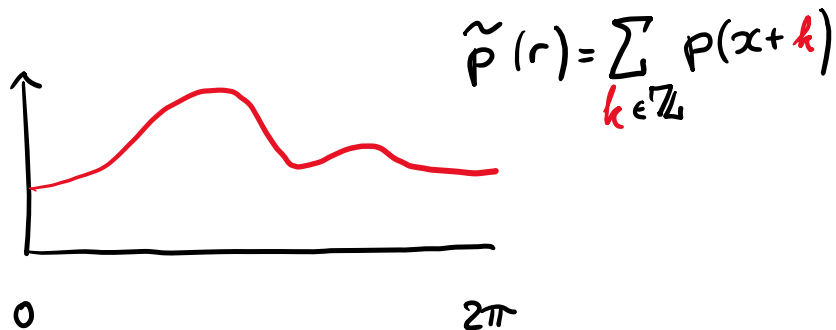
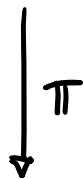
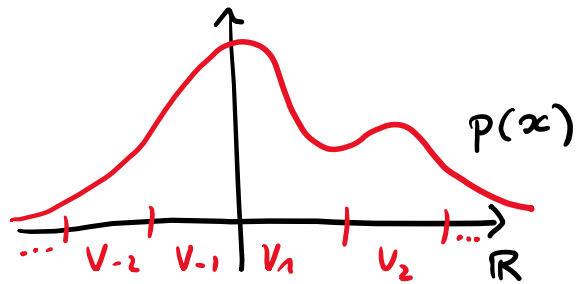
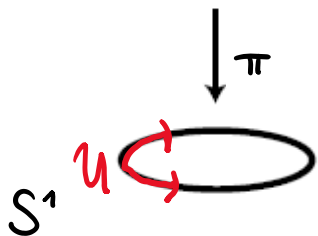


Covering flows

$$\pi: \mathbb{R} \rightarrow S^1, x \mapsto \exp(i \cdot x)$$



$$\pi^{-1}(u) \cong u \times \mathbb{Z}$$



Quaternions:

$$q = \underbrace{a \cdot 1}_{\text{scalar}} + \underbrace{b \cdot i + c \cdot j + d \cdot k}_{\text{vector} = \text{vec}(q)} \in \mathbb{R}^4$$

$$\text{Rule: } i \cdot j \cdot k = -1$$

conjugate:

$$q^* = a - b \cdot i - c \cdot j - d \cdot k$$

action on \mathbb{R}^3 :

$$p = (x, y, z) \in \mathbb{R}^3 \longrightarrow \hat{p} = (0, x, y, z) \in \mathbb{R}^4$$
$$q \curvearrowright p = \text{vec}(q^* \cdot \hat{p} \cdot q)$$

For $q \in S^3 = \{q \in \mathbb{R}^4 \mid \|q\| = 1\}$: ① $q \curvearrowright p$ is 3D rotation!

② $-q$ and q give same rotation

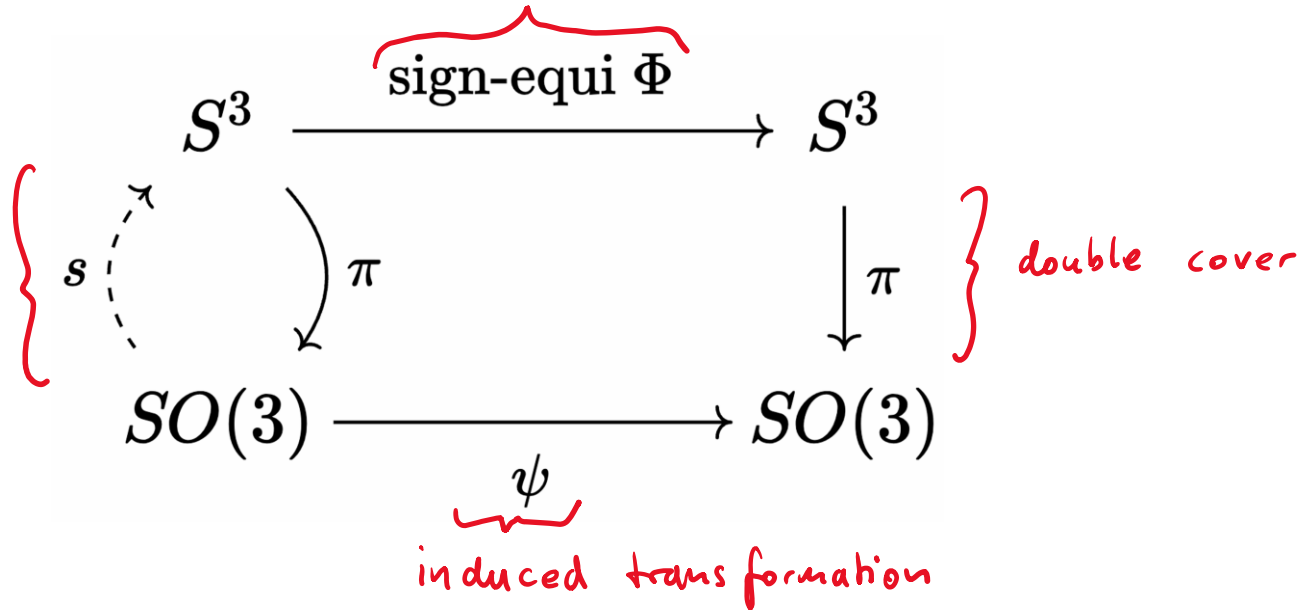
\Rightarrow surjective map $\pi: S^3 \rightarrow SO(3)$ \Rightarrow " $S^3 \rightarrow SO(3)$ double cover"

Main Result:

$$\Phi(-\varphi) = -\Phi[\varphi]$$

Section:

$$\pi \circ s = 1$$



Result:

For any [even stock.] s :
① ψ is a flow
② vol. change $\psi = \text{vol. change } \Phi$!

\Rightarrow no sum over preimages!

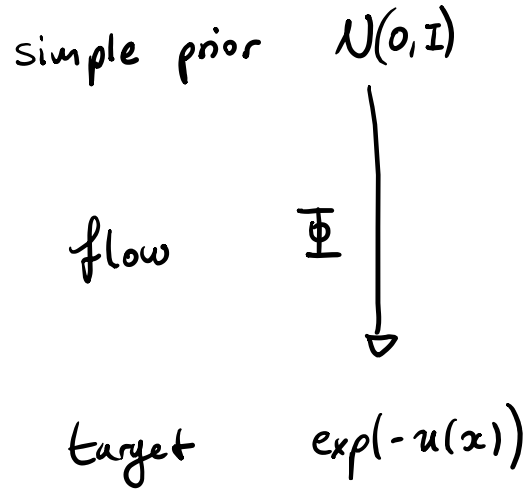
Return of the gradient flows

Strictly convex $\phi: \mathbb{R}^4 \rightarrow \mathbb{R}$

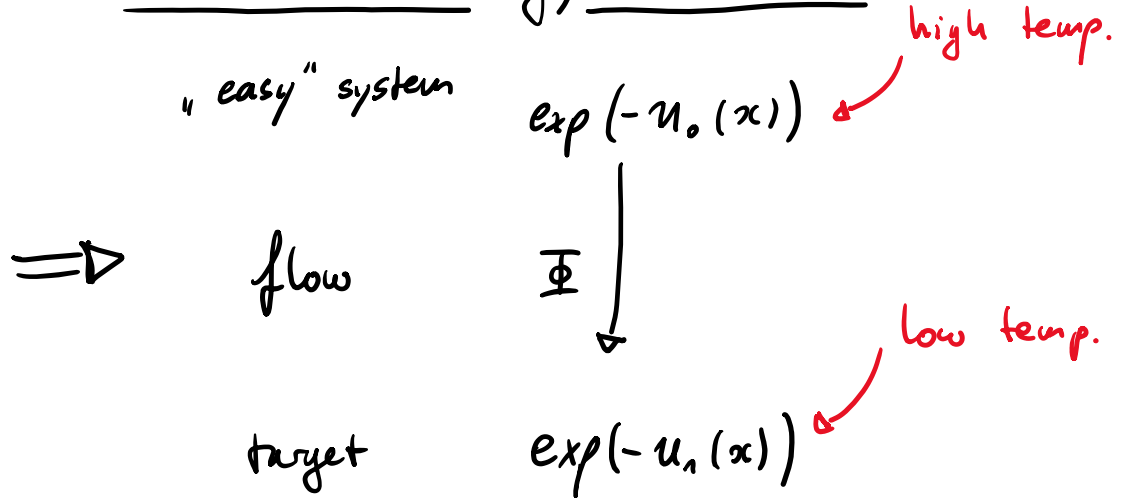
$$\Phi_{CG}(\mathbf{x}) = \frac{\nabla_{\mathbf{x}}\phi(\mathbf{x})}{\|\nabla_{\mathbf{x}}\phi(\mathbf{x})\|}$$

Result: ϕ sign-invariant $\Rightarrow \Phi_{CG}$ satisfies constraints!

Boltzmann Generators:

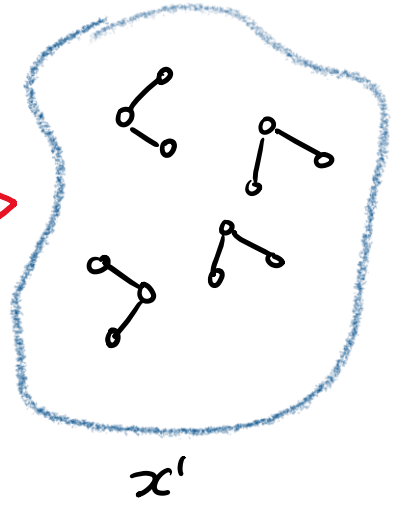
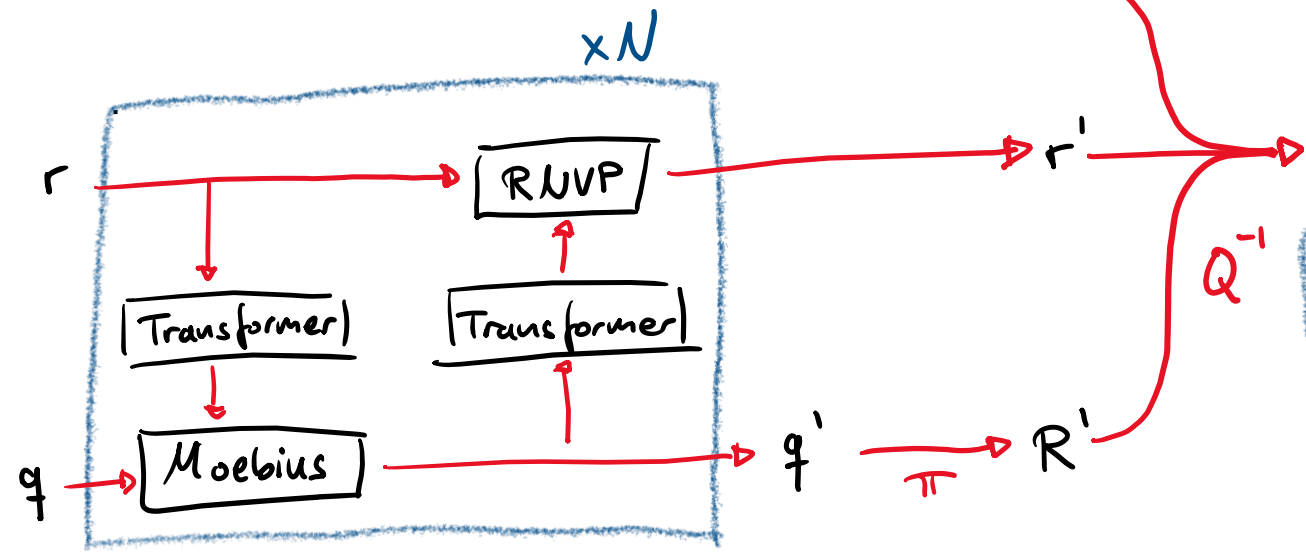
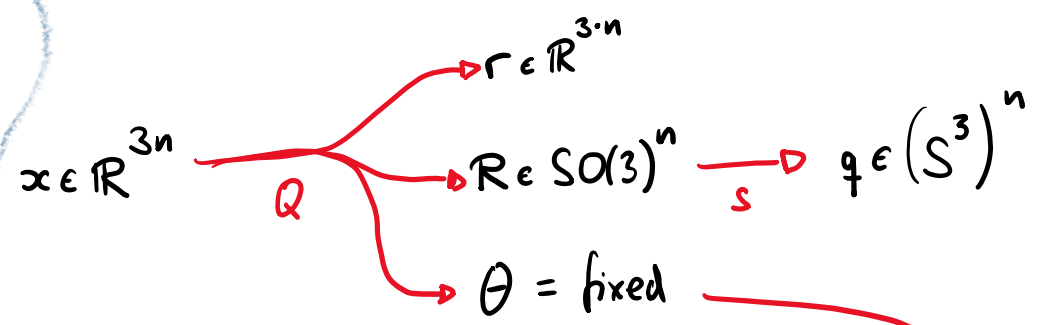
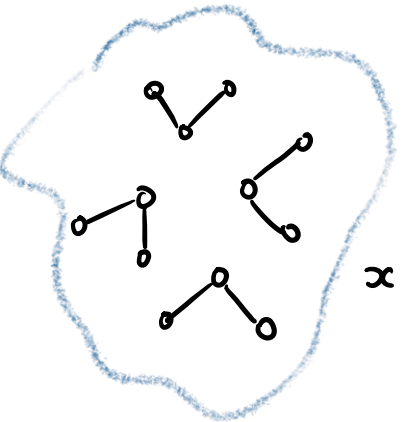


Learned Free Energy Perturbation

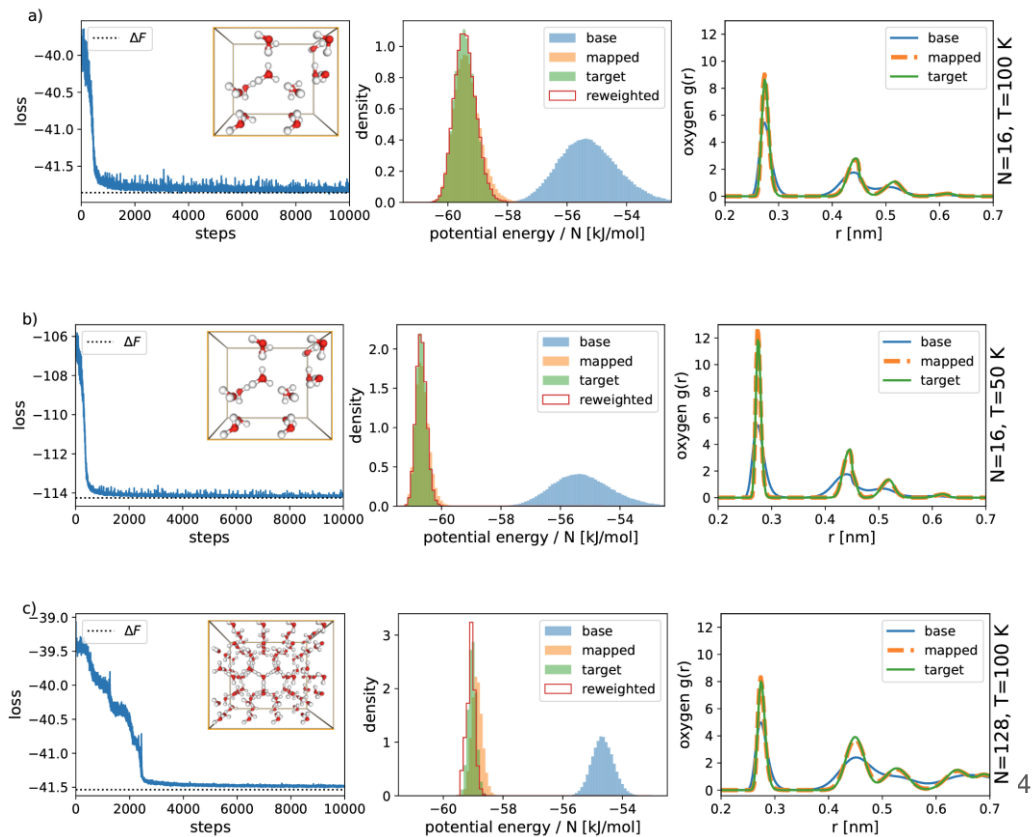
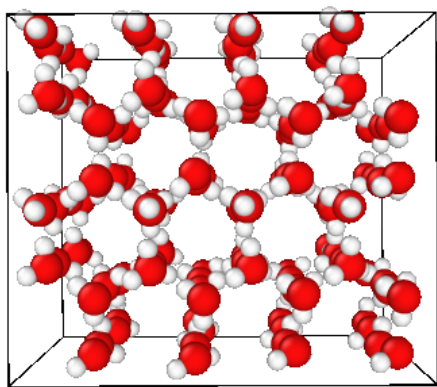


$$\Delta F [u_0; u_1] \leq \text{KL} [P_{\text{flow}} \parallel P_{\text{target}}]$$

Full Picture

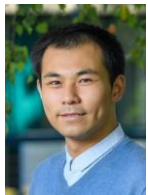


Results: Ice in different thermodynamic states



TARGET	MBAR	LFEP
N=16, T=100 K	-41.857 ± 0.007	-41.859 ± 0.002
N=16, T=50 K	-114.251 ± 0.007	-114.252 ± 0.005
N=128, T=100 K	-41.535 ± 0.002	-41.534 ± 0.003

Thanks!



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