
Transition Path Sampling with Boltzmann Generator-based MCMC Moves

Anonymous Author(s)

Affiliation

Address

email

Abstract

1 Sampling all possible transition paths between two 3D states of a molecular system
2 has various applications ranging from catalyst design to drug discovery. Current
3 approaches to sample transition paths use Markov chain Monte Carlo and
4 rely on time-intensive molecular dynamics simulations to find new paths. Our
5 approach operates in the latent space of a normalizing flow that maps from the
6 molecule’s Boltzmann distribution to a Gaussian, where we propose new paths
7 without requiring molecular simulations. Using alanine dipeptide, we explore
8 Metropolis-Hastings acceptance criteria in the latent space for exact sampling and
9 investigate different latent proposal mechanisms.

10 1 Introduction

11 Sampling the trajectories in which a molecular system changes from
12 one 3D configuration to another—a task known as transition path
13 sampling (TPS)—has many applications, such as designing cata-
14 lysts [Crehuet and Field, 2007], materials [Selli et al., 2016], or drug
15 discovery [Kirmizialtin et al., 2012, 2015]. In fact, the transition path
16 ensemble is the ideal description of a chemical reaction’s mecha-
17 nism. We explore how this problem can be solved using a Boltzmann
18 generator (a normalizing flow trained to sample a molecule’s Boltz-
19 mann distribution) [Noé et al., 2019] and its latent space to obtain
20 or approximate the ensemble.

21 In the TPS problem, we are given a single molecular system and
22 two 3D conformations of interest for it: states A and B, as seen in
23 Figure 1. These could be the structure of reactants before a reaction
24 and the structure of the product molecule after the reaction. With
25 this, we aim to sample the transition paths between them with the
26 likelihood at which they occur. To describe a transition path, we use
27 a sequence of time-equidistant 3D atom configurations (i.e., frames)
28 that starts in state A and ends in state B.

29 Existing approaches for this problem [Dellago et al., 1998b,a, Bol-
30 huis et al., 2002] use Markov chain Monte Carlo (MCMC) sampling
31 to iteratively sample a new path given the current one. New paths
32 are commonly proposed using shooting moves that require molecular dynamics simulation. Given a
33 path, the proposal is generated by first randomly selecting a frame of the path and sampling a random
34 velocity from a Gaussian. The selected frame with the new velocity is then simulated forward and
35 backward in time. If the backward simulation reaches state A and the forward simulation ends in
36 state B, this trajectory constitutes a new non-zero probability transition path, which is accepted or

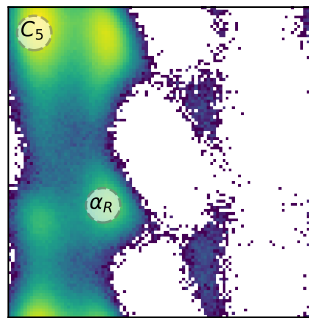


Figure 1: Distribution of alanine dipeptide’s 3D configurations visualized via a histogram of its main dihedral angles ϕ, ψ . Two metastable states are highlighted, between which we aim to sample the ensemble of all possible transition paths.

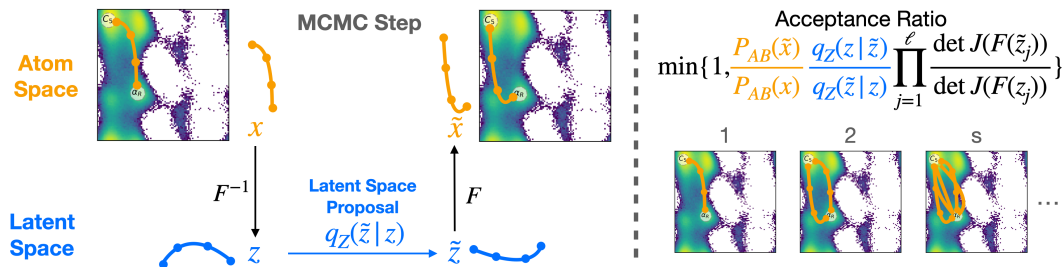


Figure 2: **MCMC proposals for latent space transition paths.** We move a transition path x into latent space using a Boltzmann generator $F(\cdot)$. With this path z and our latent space proposal kernel $q_Z(\tilde{z}|z)$ we propose \tilde{z} and bring it back to configuration/atom space to obtain the transition path proposal \tilde{x} . The likelihood of all steps can be computed, and we use them in a Metropolis-Hastings acceptance criterion to sample the transition path ensemble with MCMC.

37 rejected based on its probability and a Metropolis-Hastings [Metropolis et al., 1953, Hastings, 1970]
 38 acceptance criterion. All paths that do not transition between A and B will be rejected. Repeating this
 39 is guaranteed to eventually produce the exact transition path ensemble, but convergence is slow since
 40 many proposals will not fulfill the constraints, paths are correlated, and finding transitions requires
 41 expensive simulation.

42 In this work, we explore how the TPS problem can be addressed when having access to a trained
 43 Boltzmann generator, which solves the easier problem of sampling the molecular systems distribution
 44 of 3D conformers. Given this, we generate MCMC proposals by first moving every frame in a path
 45 into our latent space. We modify each frame of this path by adding independent Gaussian noise such
 46 that the overall likelihood can easily be evaluated. Then, we use the Boltzmann generator to bring the
 47 whole path back to configuration space, compute the probability of the path, and use it to accept or
 48 reject the proposed path. This procedure is depicted in Figure 2.

49 Our contributions are investigating this novel method for transition path sampling and highlighting
 50 its challenges. To that end, we describe the difficulty of calculating likelihoods for paths that were
 51 not generated with molecular dynamics and the obstacles for calculating path probabilities in parallel.
 52 Additionally, we provide insights into what configuration space paths are produced from simple paths
 53 in the latent space of a Boltzmann generator.

54 2 Background and Related Work

55 **Boltzmann generators.** Given a molecule, the probability of each 3D configuration is proportional
 56 to the exponential of its negative energy, i.e., they follow a Boltzmann distribution. Noé et al. [2019]
 57 train a normalizing flow [Tabak and Vanden-Eijnden, 2010, Tabak and Turner, 2013] to sample
 58 a molecule’s Boltzmann distribution, known as Boltzmann generator. While recent innovations
 59 [Midgley et al., 2023b,a] improved their training efficiency, training them for larger systems remains
 60 an open problem and a limitation of our Boltzmann generator-based approach.

61 **Deep learning for transition path sampling.** The TPS problem, with the goal to sample the whole
 62 transition path ensemble, is more challenging than finding a single low-energy transition path: A
 63 problem that also has been explored with deep learning (DL) approaches [Liu et al., 2022, Holdijk
 64 et al., 2023]. For the harder TPS problem, DL methods require MCMC with shooting moves as
 65 proposed by Dellago et al. [1998b,a]. For instance, Falkner et al. [2023] replace the shooting point
 66 selection with DL and sample them with a Boltzmann generator. Similarly, Jung et al. [2023] increase
 67 the acceptance rate of shooting moves by selecting the frames to shoot from with a learned function.
 68 These approaches still require sequential MD simulation. In this work, we explore a novel molecular
 69 dynamics-free MCMC paradigm using DL.

70 3 Method

71 We assume access to a Boltzmann generator for the molecule of interest and two of its states, A
 72 and B, between which we wish to sample the transition path ensemble. In the following, we lay out
 73 the overall MCMC framework over latent space paths (see § 3.1). This requires two components:

74 Calculating the path probability (see § 3.2), and a proposal kernel for a path in latent space for which
75 we lay out several options (see § 3.3).

76 3.1 MCMC Framework for Latent Paths

77 Let \mathbf{x} be our current path with frames $\mathbf{x}_i \in \mathbb{R}^{n \times 3}$ and $i \in \{1, \dots, l\}$, where n is the number of atoms
78 of our molecule and l the number of frames which we keep constant (the spacing of the frames
79 can change with changing path lengths). For our MCMC procedure, we further need a proposal
80 kernel $q(\tilde{\mathbf{x}} | \mathbf{x})$ that produces a new path proposal $\tilde{\mathbf{x}}$ from our current path \mathbf{x} ¹. If we can additionally
81 compute the probability of a path p_{AB} , we can sample the transition path ensemble with the MCMC
82 algorithm using Metropolis-Hastings acceptance criterion

$$\alpha = \min \left\{ 1, \frac{p_{AB}(\tilde{\mathbf{x}})}{p_{AB}(\mathbf{x})} \cdot \frac{q(\mathbf{x} | \tilde{\mathbf{x}})}{q(\tilde{\mathbf{x}} | \mathbf{x})} \right\}. \quad (1)$$

83 In our work, the proposal consists of first using a Boltzmann generator F trained on the molecule
84 to move the path \mathbf{x} into latent space to obtain the latent path $\mathbf{z} = \{F^{-1}(\mathbf{x}_1), \dots, F^{-1}(\mathbf{x}_l)\}$.
85 Subsequently, we make a proposal in latent space to obtain a new latent path $\tilde{\mathbf{z}}$ using the latent
86 proposal kernel $q_z(\tilde{\mathbf{z}} | \mathbf{z})$ which we design in § 3.3. Lastly, the latent path is projected back to
87 configuration space using the Boltzmann generator $\mathbf{x} = \{F(\tilde{\mathbf{z}}_1), \dots, F(\tilde{\mathbf{z}}_l)\}$.

88 The proposal kernel thus takes the form $q(\tilde{\mathbf{x}} | \mathbf{x}) = p(\mathbf{z} | \mathbf{x})q_z(\tilde{\mathbf{z}} | \mathbf{z})p(\tilde{\mathbf{x}} | \tilde{\mathbf{z}})$, where $p(\mathbf{z} | \mathbf{x})$ accounts
89 for the change of density when using our Boltzmann generator to move the path \mathbf{x} into latent space
90 and $p(\tilde{\mathbf{x}} | \tilde{\mathbf{z}})$ arises from moving the new latent path back to configuration space. Since the Boltzmann
91 generator processes all the frames independently, the change of density factors can be written as
92 the product of the individual frames $p(\mathbf{z} | \mathbf{x}) = \prod_{i=1}^l p(\mathbf{z}_i | \mathbf{x}_i)$. With this in mind, the ratio of the
93 forward path proposal $q(\tilde{\mathbf{x}} | \mathbf{x})$ and the backward proposal $q(\mathbf{x} | \tilde{\mathbf{x}})$, as it is required in the acceptance
94 criterion in Equation 1, takes the form

$$\frac{q(\mathbf{x} | \tilde{\mathbf{x}})}{q(\tilde{\mathbf{x}} | \mathbf{x})} = \frac{q_z(\mathbf{z} | \tilde{\mathbf{z}})}{q_z(\tilde{\mathbf{z}} | \mathbf{z})} \cdot \prod_{i=1}^l \frac{p(\tilde{\mathbf{z}}_i | \tilde{\mathbf{x}}_i)p(\mathbf{x}_i | \mathbf{z}_i)}{p(\mathbf{z}_i | \mathbf{x}_i)p(\tilde{\mathbf{x}}_i | \tilde{\mathbf{z}}_i)}. \quad (2)$$

95 Each term in the product can be simplified as follows, where we write \mathbf{x}, \mathbf{z} for an individual frame
96 $\mathbf{x}_i, \mathbf{z}_i$ and use the change of variables formula $p(\mathbf{x}) = p(\mathbf{z}) \cdot (\det J(F(\mathbf{z})))^{-1}$ in the third equality

$$\frac{p(\tilde{\mathbf{z}} | \tilde{\mathbf{x}})p(\mathbf{x} | \mathbf{z})}{p(\mathbf{z} | \mathbf{x})p(\tilde{\mathbf{x}} | \tilde{\mathbf{z}})} = \frac{\frac{p(\tilde{\mathbf{x}}, \tilde{\mathbf{z}})}{p(\tilde{\mathbf{x}})} \frac{p(\mathbf{x}, \mathbf{z})}{p(\mathbf{z})}}{\frac{p(\mathbf{x}, \mathbf{z})}{p(\mathbf{x})} \frac{p(\tilde{\mathbf{x}}, \tilde{\mathbf{z}})}{p(\tilde{\mathbf{z}})}} = \frac{p(\mathbf{x})p(\tilde{\mathbf{z}})}{p(\tilde{\mathbf{x}})p(\mathbf{z})} = \frac{p(\mathbf{z})(\det J(F(\mathbf{z})))^{-1}p(\tilde{\mathbf{z}})}{p(\tilde{\mathbf{z}})(\det J(F(\tilde{\mathbf{z}})))^{-1}p(\mathbf{z})} = \frac{\det J(F(\tilde{\mathbf{z}}))}{\det J(F(\mathbf{z}))}. \quad (3)$$

97 Thus, the ratio of proposals we need to calculate is

$$\frac{q(\mathbf{x} | \tilde{\mathbf{x}})}{q(\tilde{\mathbf{x}} | \mathbf{x})} = \frac{q_z(\mathbf{z} | \tilde{\mathbf{z}})}{q_z(\tilde{\mathbf{z}} | \mathbf{z})} \cdot \prod_{j=1}^l \frac{\det J(F(\tilde{\mathbf{z}}_j))}{\det J(F(\mathbf{z}_j^{(i-1)}))}, \quad (4)$$

98 which we can readily use to calculate the acceptance ratio for the MCMC algorithm as laid out in
99 Algorithm 1. The remaining challenges are the ability to compute the path probability p_{AB} and a
100 concrete latent space proposal kernel $q_z(\tilde{\mathbf{z}} | \mathbf{z})$, which we will tackle next.

101 3.2 Calculating the Path Probability

102 A path’s probability is defined with respect to a molecular dynamics model. Here, we assume
103 Langevin dynamics² under which the transition from frame \mathbf{x}_i to the next frame \mathbf{x}_{i+1} can be
104 calculated as

$$\begin{aligned} \mathbf{x}_{i+1} &= \mathbf{x}_i + \Delta t \mathbf{v}_{i+1} \\ \mathbf{v}_{i+1} &= \alpha \mathbf{v}_i + (1 - \alpha) \nabla U(\mathbf{x}_i) + \sqrt{k_B T (1 - \alpha^2)} \mathbf{W}, \end{aligned} \quad (5)$$

¹An initial path can be obtained from, for example, a high-temperature MD simulation or by linearly interpolating in the Boltzmann generator’s latent space.

²For the sake of brevity, we omit the constant atom masses and the friction coefficient.

105 given the velocity \mathbf{v}_i , and the molecule’s energy function $U : \mathbb{R}^{d \times 3} \mapsto \mathbb{R}$. $\alpha = \exp(-\Delta t)$ for a
 106 time step size Δt^3 and $\mathbf{W} \sim \mathcal{N}(0, \mathbb{1})$ corresponds to random motion that is scaled proportional
 107 to the Boltzmann constant k_B and temperature T . Notice that in Langevin dynamics, the only
 108 randomness when obtaining \mathbf{x}_{i+1} from \mathbf{x}_i given the velocity \mathbf{v}_i stems from the Gaussian variable
 109 $\sqrt{k_B T(1 - \alpha^2)}\mathbf{W}$. Thus, the probability density $p(\mathbf{x}_{i+1}, \mathbf{v}_{i+1} | \mathbf{x}_i, \mathbf{v}_i)$ of moving from \mathbf{x}_i to \mathbf{x}_{i+1}
 110 is that of a Gaussian with mean $\mu = \mathbf{x}_i + \Delta t(\alpha \mathbf{v}_i + (1 - \alpha)\nabla U(\mathbf{x}_i))$ and standard deviation
 111 $\sigma = k_B T(1 - \alpha^2)$.

112 Given this probability $p(\mathbf{x}_{i+1}, \mathbf{v}_{i+1} | \mathbf{x}_i, \mathbf{v}_i)$ of moving between individual frames with the auxiliary
 113 velocity variable, the probability of a whole path in configuration space is

$$p_{AB}(\mathbf{x}) = p(\mathbf{x}_1) \cdot \prod_{i=1}^{l-1} p(\mathbf{x}_{i+1}, \mathbf{v}_{i+1} | \mathbf{x}_i, \mathbf{v}_i), \quad (6)$$

114 where $p(\mathbf{x}_i)$ follows the molecule’s Boltzmann distribution, meaning that $p(\mathbf{x}_i) \propto$
 115 $\exp(-U(\mathbf{x}_i)/k_B T)$ with an unknown proportionality constant. However, this constant is unneces-
 116 sary since it will cancel out with the same constant of the reverse path density p_{BA} in the acceptance
 117 ratio in Equation 1.

118 Thus, the last missing link to computing $p_{AB}(\mathbf{x})$ is the initial velocity \mathbf{v}_1 . Since our path definition
 119 does not include an initial velocity (because we do not have a Boltzmann generator that operates over
 120 both velocities and positions), we opt to marginalize over all possible velocities and approximate the
 121 following expectation as our final path probability

$$p_{AB}(\mathbf{x}) = \mathbb{E}_{\mathbf{v}_1 \sim \mathcal{N}(\mathbf{0}, \text{diag}(k_B T))} \left[p(\mathbf{x}_1) \cdot \prod_{i=1}^{l-1} p(\mathbf{x}_{i+1}, \mathbf{v}_{i+1} | \mathbf{x}_i, \mathbf{v}_i) \right]. \quad (7)$$

122 All subsequent velocities $\{\mathbf{v}_i\}_{i \in \{2, \dots, l\}}$ can then be inferred by solving the previous step, allowing us
 123 to compute $p(\mathbf{x}_{i+1}, \mathbf{v}_{i+1} | \mathbf{x}_i, \mathbf{v}_i)$ sequentially.

124 **Desirable properties.** In designing our MCMC procedure, we set out to avoid the time-consuming
 125 sequential molecular dynamics simulation. While the path probability can be computed easily for
 126 paths generated by MD [Jung et al., 2017], calculating the path probability $p_{AB}(\mathbf{x})$ still requires
 127 sequential computation in our approach. However, this amounts to sequentially performing l vector
 128 additions, which is very cheap and can be done in parallel for all different initial velocities when ap-
 129 proximating the expectation. The expensive, time-consuming computations stem from the evaluation
 130 of the energy function $U(\mathbf{x}_i)$ for each frame. In our procedure, this can be done in parallel, while in
 131 molecular dynamics, it has to be performed sequentially.

132 3.3 Latent Space Path Proposal Kernel

133 As for the concrete latent space path proposal kernel $q_Z(\tilde{\mathbf{z}} | \mathbf{z})$, we propose three different options:
 134 1) Gaussian noise added to each frame. 2) A Gaussian Process (GP) with the current path as its mean.
 135 3) A GP that is adaptively fit to the history of all sampled transition paths and only weakly depends
 136 on the current path. All these proposals are symmetric and will not contribute to our acceptance ratio
 137 with $q_Z(\tilde{\mathbf{z}} | \mathbf{z})/q_Z(\mathbf{z} | \tilde{\mathbf{z}}) = 1$.

138 **Gaussian proposal.** From a latent path \mathbf{z} , we propose a new path $\tilde{\mathbf{z}} = \{\mathbf{z}_1 + \epsilon_1, \dots, \mathbf{z}_l + \epsilon_l\}$ where
 139 $\epsilon_1, \dots, \epsilon_l \sim \mathcal{N}(\mathbf{0}, \Sigma)$. While this independent noise for each frame makes it unlikely that all frames
 140 move coherently and produce high-probability paths, this operation can be performed efficiently and
 141 allows for fast exploration of the latent space.

142 **Conditional Gaussian process path proposals.** We employ a GP $f(t) \sim \mathcal{GP}(m(t), k(t, t'))$, where
 143 $f : \mathbb{R} \mapsto \mathbb{R}^{3n-6}$ maps the time $t \in [1, l]$ along the path to a Gaussian from which a frame at time t is
 144 sampled⁴. We fit the GP mean $m(\cdot)$ and kernel function $k(\cdot, \cdot)$, which is not to be confused with the
 145 proposal kernel, to a set of s latent paths $\{\mathbf{z}^i\}_{i \in \{1, \dots, s\}}$, where the index of each frame is used as the

³Similar to classical fixed length transition path sampling, the timestep size Δt is not trivial to choose. We discuss this further in Appendix B.

⁴The latent space dimensionality is \mathbb{R}^{3n-6} for n atoms since the Boltzmann generator operates on internal coordinates that are invariant to the 6 degrees of freedom from rigid translations and rotations.

146 time t . In the following, we first detail the set of latent paths before explaining how the GP is used to
147 propose a new path.

148 Our set of latent paths $\{z^i\}_{i \in \{1, \dots, s\}}$ to fit the GP is either the history of all previously sampled paths or
149 we obtain it via linear interpolation in latent space. Specifically, to obtain an interpolation, we sample
150 a start x_1 and an end frame x_l from states A and B, move them to latent space to generate $z_1, z_l =$
151 $F^{-1}(x_1), F^{-1}(x_l)$, and produce the latent path as the linear interpolation $z_i = \frac{i}{l}z_1 + (1 - \frac{i}{l})z_l$
152 for $i \in \{1, \dots, l\}$. After moving it back to configuration space with the Boltzmann generator, this
153 constitutes a coarse path. This produces a fixed proposal kernel, where the quality depends on the
154 paths it was trained on.

155 When using the history of all previously sampled paths as $\{z^i\}_{i \in \{1, \dots, s\}}$, the proposal kernel \mathcal{GP}_s
156 changes over the course of MCMC steps s , leading to an adaptive MCMC algorithm. For this to be
157 correct, the proposal kernel has to converge and satisfy vanishing adaptation [Andrieu and Thoms,
158 2008] where, as the Markov chain progresses, the influence of its most recent states on the proposal
159 kernel has to diminish. Intuitively, this is the case for our adaptive kernel since the influence of the
160 most recent path on the fitted mean and covariance kernel vanishes as the size of the history (the
161 Markov chain) increases.

162 We re-fit this adaptive GP proposal to the history of latent paths $\{z^i\}_{i \in \{1, \dots, s\}}$ at each step s when
163 a new path has been accepted. To efficiently do so, we start optimization from the parameters
164 of the previous GP proposal kernel that are optimal for $\{z^i\}_{i \in \{1, \dots, s-1\}}$. The new optimization’s
165 convergence is typically fast since the minimum under the new set of latent paths at step s is likely
166 close to that at step $s - 1$, with the difference diminishing as the length of the Markov chain increases.

167 Given the fitted GP, a new latent path \tilde{z} is proposed conditioned on the current one z by sampling
168 \mathcal{GP}_s at times $t = 1, \dots, l$ (which correspond to the frame numbers of the paths) after setting the
169 means of \mathcal{GP}_s at those times to the frames of z , meaning that $m(t) = z_t$ for $t \in \{1, \dots, l\}$. This
170 amounts to sampling \mathcal{GP}_s unconditionally at $t = 1, \dots, l$, subtracting the means $m(t)$, and adding
171 the frames z_t at each time.

172 **Unconditional Gaussian process path proposals.** Here, we use the adaptive Gaussian process \mathcal{GP}_s
173 and propose new paths \tilde{z} unconditionally, meaning that each proposal is a sample of \mathcal{GP}_s and the
174 only influence of z is through its presence in the set of paths $\{z^i\}_{i \in \{1, \dots, s\}}$ that \mathcal{GP}_s was fit on. This
175 means that with a progressively increasing number of accepted paths, the influence of the current
176 path will diminish. This would fit a Gaussian process that could be used to sample transition paths
177 without any latent space, which is an interesting aspect on its own.

178 Further, since we will rely on the mean of the Gaussian process, we can also estimate it between the
179 frames. This allows us to introduce more variance by evaluating the Gaussian process not at the fixed
180 points $1, \dots, l$, but to uniformly draw l sorted samples from $\mathcal{U}_{[0.5, l+0.5]}$. With this, the individual
181 frames of the path can shift more easily towards and from each other.

182 4 Experiments

183 **Latent space analysis.** When moving configurations from the meta-stable states C_5 and α_R of
184 alanine dipeptide (ALDP) into the latent space, we can linearly interpolate between them and map
185 them back with the trained Boltzmann generator. For this, we train a Boltzmann generator by
186 minimizing the forward KL-divergence loss (compare Appendix A.3). Figure 3 shows that linear
187 paths in latent space produce non-linear paths in configuration space. While linearly interpolating
188 atom positions of a molecule produces unrealistic paths, this naive latent space approach recovers
189 two different modes of transitions between the meta-stable states.

190 **Ground truth ensemble.** We simulated 10 nanoseconds with a timestep of 1 femtosecond at 300K
191 with the openMM MD engine [Eastman et al., 2017]. From this data, we can determine for each
192 conformation whether it belongs to a meta-stable state, allowing us to find paths by looking for
193 sequences that start in A and transition to B (or vice versa). This approach finds variable-length
194 transition paths. We rely on the two-way shooting scheme implemented by OPS [Swenson et al.,
195 2018a,b] with the same MD setup to sample a fixed-length transition path ensemble. Transitions that
196 only rarely occur (Figure 4 bottom) are particularly difficult to produce with classical MD, already
197 for the small molecule alanine dipeptide.

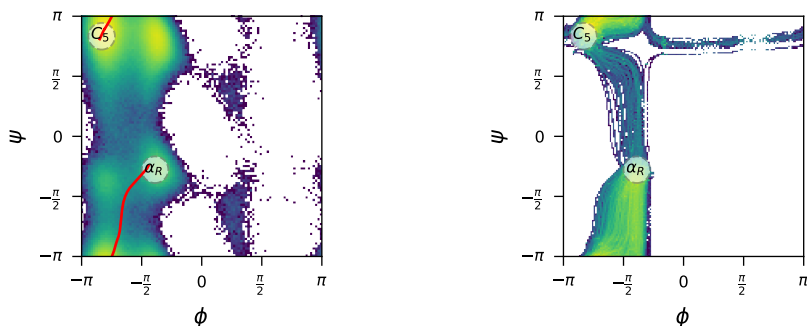


Figure 3: **Linear latent space interpolation.** *Left:* A histogram of the two main dihedral angles ϕ, ψ as they occur in the MD simulation. The meta-stable states C_5 and α_R , and a linear interpolation in latent space (red line) are shown. *Right:* The resulting density of transition paths when linearly interpolating between those states in latent space.

198 **Results.** Figure 4 shows for all methods a histogram of the sampled transition paths between the
 199 states $C_5 \leftrightarrow \alpha_R$ and $\alpha_R \leftrightarrow C_7$, respectively. *Unconditional GP Uni* refers to the adaptive GP
 200 proposal with uniform timepoint sampling while *Unconditional GP* always samples the index of the
 201 frame as timepoint. *Conditional GP* uses the adaptive proposal.

202 The main finding is that due to the low acceptance rate of our MCMC steps, we are only able to
 203 produce a low amount of paths or a set of paths with low diversity. When increasing the variance,
 204 paths will be more diverse but are also less likely to be accepted. To overcome this, proposals that
 205 produce more physically likely paths are required.

206 Some proposal strategies, such as the Gaussian proposal, are computationally efficient, while fitting
 207 a high-dimensional Gaussian process is time-consuming. With an increasing number of paths, the
 208 proposals are more likely to be stuck in a local minimum. For the more computationally expensive
 209 proposals, this makes it challenging to produce the high number of transitions needed to overcome
 210 this threshold.

211 While training a fixed Gaussian process on simple paths in latent space is computationally favorable,
 212 the results do not indicate that it can capture the transition paths. Since the iterative Gaussian
 213 processes do not seem to fit the distribution either, our choice of kernel or formulation might be
 214 inappropriate. In general, we have seen in our experiments that the selection for a kernel of the
 215 Gaussian process (compare Appendix A.2) poses a difficult problem for this task because it must
 216 capture an adequate amount of noise without overfitting to the previous paths.

217 Overall, the results qualitatively show that the simplest proposal kernel, one that simply adds Gaussian
 218 noise in latent space, appears to be the most efficient and effective choice. Further, conditioning the
 219 Gaussian process on the current path appears to slightly increase the variance and leads to a more
 220 diverse set of paths.

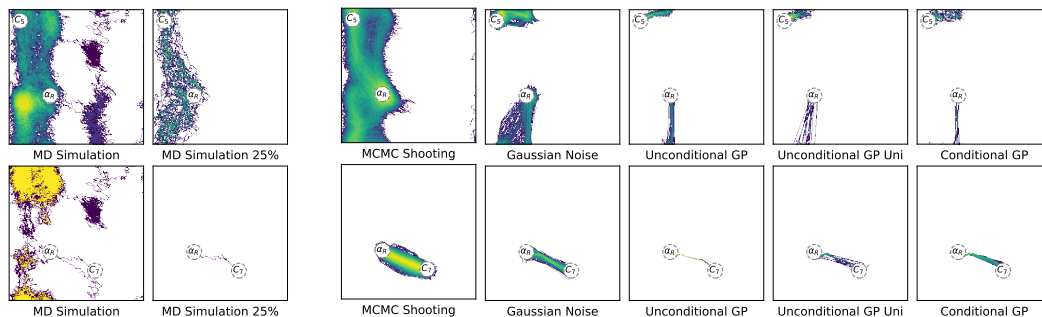


Figure 4: **Comparison of sampling methods.** Each row shows the transitions between two different metastable states. *Left:* "Ground truth" path ensemble from MD simulation of all paths (sub-left) and the 25% of paths with the highest probability (sub-right). *Right:* Shooting move MCMC ensemble and the ensembles of our different latent space proposal kernels. Note that it is unclear what a meaningful ground truth ensemble is.

221 5 Discussion and Conclusion

222 **Limitations** Our approach relies on a trained Boltzmann generator, of which high-quality ones for
223 larger molecular systems do not exist yet. Furthermore, the latent space path proposal kernels we
224 devise have too low acceptance rates to be useful. This limits them to a low-variance, slowing down
225 mode-mixing. Better latent space proposals would be necessary. Lastly, an avenue toward a practical
226 solution could be adaptively fine-tuning the Boltzmann generator to make simple paths in latent space
227 correspond to physical paths that obey Langevin dynamics in configuration space.

228 **Conclusion** In this paper, we presented a novel way to propose transition paths in the latent space of a
229 Boltzmann generator. Throughout this work, we have introduced multiple latent space path proposal
230 kernels that perform (learned) operations. This enables a transition path sampling MCMC procedure
231 without the need for molecular dynamics simulation. We believe that learned transition path sampling
232 methods and, in general, simulation-free MCMC approaches are interesting research questions to
233 explore and might lead to faster sampling methods.

234 References

- 235 Christophe Andrieu and Johannes Thoms. A tutorial on adaptive mcmc. *Statistics and Computing*,
236 18(4):343–373, Dec 2008.
- 237 Peter G. Bolhuis, David Chandler, Christoph Dellago, and Phillip L. Geissler. Transition path
238 sampling: Throwing ropes over rough mountain passes, in the dark. *Annual Review of Physical
239 Chemistry*, 53(1):291–318, October 2002.
- 240 Ramon Crehuet and Martin J. Field. A transition path sampling study of the reaction catalyzed by the
241 enzyme chorismate mutase. *The Journal of Physical Chemistry B*, 111(20):5708–5718, May 2007.
- 242 Christoph Dellago, Peter G. Bolhuis, and David Chandler. Efficient transition path sampling:
243 Application to lennard-jones cluster rearrangements. *The Journal of Chemical Physics*, 108(22):
244 9236–9245, June 1998a.
- 245 Christoph Dellago, Peter G. Bolhuis, Félix S. Csajka, and David Chandler. Transition path sampling
246 and the calculation of rate constants. *The Journal of Chemical Physics*, 108(5):1964–1977, 02
247 1998b.
- 248 Laurent Dinh, Jascha Sohl-Dickstein, and Samy Bengio. Density estimation using real NVP. In
249 *International Conference on Learning Representations*, 2017.
- 250 Conor Durkan, Artur Bekasov, Iain Murray, and George Papamakarios. Neural spline flows. In
251 H. Wallach, H. Larochelle, A. Beygelzimer, F. d'Alché-Buc, E. Fox, and R. Garnett, editors,
252 *Advances in Neural Information Processing Systems*, volume 32. Curran Associates, Inc., 2019.
- 253 Peter Eastman, Jason Swails, John D. Chodera, Robert T. McGibbon, Yutong Zhao, Kyle A.
254 Beauchamp, Lee-Ping Wang, Andrew C. Simmonett, Matthew P. Harrigan, Chaya D. Stern,
255 Rafal P. Wiewiora, Bernard R. Brooks, and Vijay S. Pande. OpenMM 7: Rapid development
256 of high performance algorithms for molecular dynamics. *PLOS Computational Biology*, 13(7):
257 e1005659, July 2017.
- 258 Sebastian Falkner, Alessandro Coretti, Salvatore Romano, Phillip Geissler, and Christoph Dellago.
259 Conditioning normalizing flows for rare event sampling, 2023.
- 260 W. K. Hastings. Monte carlo sampling methods using markov chains and their applications.
261 *Biometrika*, 57(1):97–109, April 1970.
- 262 Lars Holdijk, Yuanqi Du, Ferry Hooft, Priyank Jaini, Bernd Ensing, and Max Welling. Stochastic
263 optimal control for collective variable free sampling of molecular transition paths, 2023.
- 264 Hendrik Jung, Kei ichi Okazaki, and Gerhard Hummer. Transition path sampling of rare events by
265 shooting from the top. *The Journal of Chemical Physics*, 147(15), August 2017.
- 266 Hendrik Jung, Roberto Covino, A. Arjun, Christian Leitold, Christoph Dellago, Peter G. Bolhuis,
267 and Gerhard Hummer. Machine-guided path sampling to discover mechanisms of molecular
268 self-organization. *Nature Computational Science*, 3(4):334–345, April 2023.

- 269 Serdal Kirmizialtin, Virginia Nguyen, Kenneth A. Johnson, and Ron Elber. How conformational
270 dynamics of DNA polymerase select correct substrates: Experiments and simulations. *Structure*,
271 20(4):618–627, April 2012.
- 272 Serdal Kirmizialtin, Kenneth A. Johnson, and Ron Elber. Enzyme selectivity of HIV reverse
273 transcriptase: Conformations, ligands, and free energy partition. *The Journal of Physical Chemistry*
274 *B*, 119(35):11513–11526, August 2015.
- 275 Tianyi Liu, Weihao Gao, Zhirui Wang, and Chong Wang. Pathflow: A normalizing flow generator that
276 finds transition paths. In James Cussens and Kun Zhang, editors, *Proceedings of the Thirty-Eighth*
277 *Conference on Uncertainty in Artificial Intelligence*, volume 180 of *Proceedings of Machine*
278 *Learning Research*, pages 1232–1242. PMLR, 01–05 Aug 2022.
- 279 Nicholas Metropolis, Arianna W. Rosenbluth, Marshall N. Rosenbluth, Augusta H. Teller, and Edward
280 Teller. Equation of state calculations by fast computing machines. *The Journal of Chemical Physics*,
281 21(6):1087–1092, June 1953.
- 282 Laurence I. Midgley, Vincent Stimper, Javier Antorán, Emile Mathieu, Bernhard Schölkopf, and
283 José Miguel Hernández-Lobato. Se(3) equivariant augmented coupling flows, 2023a.
- 284 Laurence Illing Midgley, Vincent Stimper, Gregor N. C. Simm, Bernhard Schölkopf, and José Miguel
285 Hernández-Lobato. Flow annealed importance sampling bootstrap. In *International Conference*
286 *on Learning Representations*, 2023b.
- 287 Frank Noé, Simon Olsson, Jonas Köhler, and Hao Wu. Boltzmann generators: Sampling equilibrium
288 states of many-body systems with deep learning. *Science*, 365(6457), September 2019.
- 289 Danilo Jimenez Rezende, George Papamakarios, Sebastien Racaniere, Michael Albergo, Gurtej Kan-
290 war, Phiala Shanahan, and Kyle Cranmer. Normalizing flows on tori and spheres. In *International*
291 *Conference on Machine Learning*, pages 8083–8092. PMLR, 2020.
- 292 Daniele Selli, Salah Eddine Boulfefel, Philipp Schapotschnikow, Davide Donadio, and Stefano Leoni.
293 Hierarchical thermoelectrics: crystal grain boundaries as scalable phonon scatterers. *Nanoscale*, 8
294 (6):3729–3738, 2016.
- 295 David W. H. Swenson, Jan-Hendrik Prinz, Frank Noe, John D. Chodera, and Peter G. Bolhuis.
296 OpenPathSampling: A python framework for path sampling simulations. 1. basics. *Journal of*
297 *Chemical Theory and Computation*, 15(2):813–836, October 2018a.
- 298 David W. H. Swenson, Jan-Hendrik Prinz, Frank Noe, John D. Chodera, and Peter G. Bolhuis.
299 OpenPathSampling: A python framework for path sampling simulations. 2. building and customiz-
300 ing path ensembles and sample schemes. *Journal of Chemical Theory and Computation*, 15(2):
301 837–856, October 2018b.
- 302 E. G. Tabak and Cristina V. Turner. A family of nonparametric density estimation algorithms.
303 *Communications on Pure and Applied Mathematics*, 66(2):145–164, 2013.
- 304 Esteban G. Tabak and Eric Vanden-Eijnden. Density estimation by dual ascent of the log-likelihood.
305 *Communications in Mathematical Sciences*, 8(1):217–233, 2010.

306 **A Method Details**

307 **A.1 Latent Path MCMC Algorithm**

308 Our latent space path sampling approach builds on the Metropolis-Hastings method but relies on a modified acceptance criteria and an adapted proposal kernel.

Algorithm 1: Fixed-length latent space transition path sampling.

Input: Initial path $\mathbf{x}^{(0)}$ with l frames, a trained Boltzmann generator consisting of the map F and its inverse F^{-1} , the number of steps to run N , and a latent proposal kernel K with proposal probability $q_Z(\cdot | \cdot)$.

Output: MCMC samples following target distribution $\{\mathbf{x}^{(1)}, \dots, \mathbf{x}^{(N)}\}$.

1 Calculate latent space representation of initial path $\mathbf{z}^{(0)} = \{F^{-1}(\mathbf{x}_1^{(0)}), \dots, F^{-1}(\mathbf{x}_l^{(0)})\}$.

2 **for** $i \leftarrow 1 \dots N$ **do**

3 **repeat**

4 Propose new path in latent space $\tilde{\mathbf{z}} = K(\mathbf{z}^{(i-1)})$.

5 Compute the proposed path in configuration space $\tilde{\mathbf{x}} = \{F(\tilde{\mathbf{z}}_1), \dots, F(\tilde{\mathbf{z}}_l)\}$.

6 Compute acceptance probability

$$\alpha = \min \left\{ 1, \frac{p_{AB}(\tilde{\mathbf{x}})}{p_{AB}(\mathbf{x}^{(i-1)})} \cdot \frac{q_Z(\mathbf{z}^{(i-1)} | \tilde{\mathbf{z}})}{q_Z(\tilde{\mathbf{z}} | \mathbf{z}^{(i-1)})} \cdot \prod_{j=1}^l \frac{\det J(F(\tilde{\mathbf{z}}_j))}{\det J(F(\mathbf{z}_j^{(i-1)}))} \right\}.$$

7 Draw a uniformly distributed random number $u \sim \mathcal{U}_{[0,1]}$.

8 **until** proposed path $\tilde{\mathbf{x}}$ is reactive **and** $u \leq \alpha$;

9 Accept proposed path $\mathbf{z}^{(i)} = \tilde{\mathbf{z}}, \mathbf{x}^{(i)} = \tilde{\mathbf{x}}$.

10 **end**

309

310 **A.2 Gaussian Process Kernel**

311 A Gaussian process fits the parameters of a kernel k . As for the concrete choice of kernel, we have
 312 decided to use an RBF-Kernel with an additional White kernel that can capture variance in the
 313 individual points. It can be formulated as

$$k(x, x') = c \cdot \exp\left(-\frac{\|x - x'\|_2^2}{2l^2}\right) + n \cdot \mathbb{1}_{x \neq x'}, \quad (8)$$

314 with learnable parameters l, c, n .

315 **A.3 Boltzmann Generator Training**

316 We trained a Boltzmann generator F on the molecule ALDP, consisting of multiple neural spline
 317 layers [Durkan et al., 2019] with a randomly masked coupling architecture between them. The
 318 coupling layers allow us to use arbitrarily complex neural networks, that do not have to be invertible
 319 while still allowing the overall function to be invertible [Dinh et al., 2017]. In this architecture, the
 320 neural network learns to predict 8 knots and the parameters of a quadratic rational spline function.
 321 Overall, we use 12 of these neural spline coupling layers each using a residual block with two layers
 322 with 256 hidden units. The performance of the trained Boltzmann generator is illustrated in Figure 5.

323 To train the normalizing flow, we use the samples from the long-running MD simulation of ALDP
 324 and maximize the likelihood of the frames in latent space is. The goal of the loss is that the samples
 325 in latent space are distributed according to the base distribution. This is achieved by minimizing the
 326 forward KL divergence

$$\mathcal{L}_{KL}(\theta) \propto -\mathbb{E}_{x \sim X} [\log(p_u(F_\theta^{-1}(x))) - \log(\det J(F_\theta^{-1}(x)))] . \quad (9)$$

327 J represents the Jacobian and p_u is the distribution of our latent space. F represents the invertible
 328 function of the Boltzmann generator that maps between the ground truth data distribution X and is
 329 parameterized by θ .

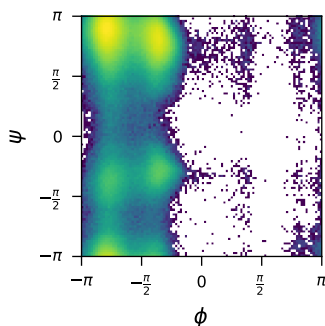


Figure 5: **Histogram of states sampled by Boltzmann generator.** This histogram shows the main dihedral angles of 1 million ALDP conformations sampled from the base distribution and then transported with the normalizing flow.

330 To represent the molecule, we rely on an internal coordinate representation for our flow, which
 331 describes the molecule’s state by the dihedral angles and bond lengths [Rezende et al., 2020] as this
 332 has shown good performance [Noé et al., 2019, Midgley et al., 2023b]. Since some of these variables
 333 are periodic, we use a mixture between a Gaussian and a uniform distribution as the base distribution.
 334 This mixture is only used for training; at inference, we change this to a standard normal distributed
 335 space by using the cumulative and inverse cumulative function to map uniform values from and to a
 336 normal distribution.

337 A.4 Further Latent Space Investigation

338 To ensure that the learned latent space is meaningful and can separate between different meta-stable
 339 states, we have reduced samples of the states C_5 and α_R to two dimensions, as seen in Figure 6.
 340 Already a PCA, a non-linear dimensionality reduction, is capable the separating the states by a single
 341 dimension. This motivates that a linear interpolation between configurations in latent space can
 produce feasible transition paths.

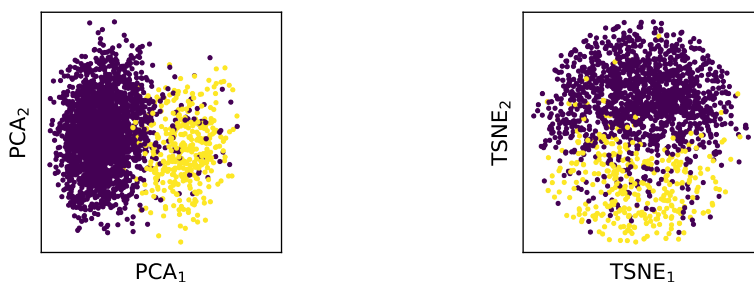


Figure 6: **Separability of meta-stable States in latent space.** Transforming molecule conformations following the states C_5 and α_R into the latent space, and plotting them in 2D with PCA and TSNE. The colors indicate the different conformations.

342

343 **B Determining the Timestep for TPS**

344 Finding out the transition time between two states is necessary to be able to determine a suitable
345 timestep Δt and the number of frames. While this task can be challenging for large systems, this is
346 not a task we set out to solve. To determine meaningful values, we have estimated the density of the
347 transition times as they occur in a long-running MD simulation, as can be seen in Figure 7. With
348 this, we have decided to sample transition paths with a duration of $1.6ps$. Similar studies can be
349 performed to determine the transition times with high probability for transitions between α_R and C_7 ,
where we decided to use a time of $320fs$.

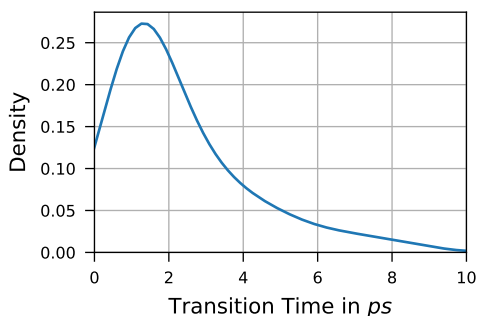


Figure 7: **Duration of ALDP transitions.** This is the approximated density that shows the duration of the transition between the states C_5 and α_R and their respective densities.

350