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# Electronic Supplementary Information (ESI) for MD-GAN with multi-particle input: the machine learning of long-time molecular behavior from short-time MD data

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# Section 1. Effects of introducing latent variables and distribution stabiliza tion mechanisms

MD-GAN succeeds in reducing the exposure bias by introducing latent variables and distri-14 bution stabilization mechanisms. In general, most real-world data can be considered as lying 15 along a low-dimensional manifold in a high-dimensional space [1, 2, 3]. Based on this idea, 16 the evolution of the extracted trajectory of the subsystem is also represented as the evolution of 17 dense latent variables, embedded in a low-dimensional space. Supplementary Fig. 1 shows the 18 effects of these latent variables. The left figure is a conceptual figure of time evolution of a raw 19 trajectory in high-dimensional space wherein no latent variables are introduced, while the right 20 figure shows a conceptual figure of time evolution in low-dimensional space wherein latent vari-21 ables are introduced. Each sphere represents M steps of trajectory information. In the figure on 22 the left, the gray sphere is  $Y_{k*M:(k+1)*M-1}$ , and the red and yellow spheres represent examples 23 of points that might be taken as  $Y_{(k+1)*M:(k+2)*M-1}$  after the next time evolution. In the figure 24 on the right, the gray sphere is  $z_i$ , and the red sphere and yellow sphere represent examples of 25 points that may be taken as  $z_{i+1}$  next. For visualization purposes, the figure on the left is drawn 26 in three dimensions, but the actual dimension is 3M for single-particle input. The reason for 27 the 3M dimension is that  $Y_{k*M:(k+1)*M-1}$  is the information in xyz coordinates for M steps. 28 Similarly, for the figure on the right, the latent variable may be more than two-dimensional(4 29 dimensions for single-particle input). The blue region represents the support where variables  $z_i$ 30 and  $Y_{k*M:(k+1)*M-1}$  can exist respectively, and it is called the manifold. When the gray sphere 31 has information of the current M steps, it can take various states via stochastic transition, during 32 the next time evolution. In this evolution, although the red sphere is on the manifold, the yellow 33 sphere is off it. Assuming that a yellow sphere is input to MD-GAN in the estimation phase, 34 the input is an unknown input in the training phase, and this may result in exposure bias. In the 35 time evolution of a high-dimensional and sparse space, as shown in the left figure, it is likely to 36

deviate from the manifold, while in a low-dimensional and dense potential space, as shown in the right figure, it is less likely to deviate from the manifold. Therefore, the introduction of latent variables is expected to make it harder to deviate from the manifold through time evolution and contribute to the reduction of exposure bias.

The initial latent variable  $z_0$  is sampled from the  $n_z$ -dimensional uniform distribution  $U(S^{n_z})$ . 41  $G_z$  generates further  $z_i$  using the previous  $z_{i-1}$  and a random value. We then apply  $G_z$  to  $z_0$  and 42 repeatedly generate  $z_1$ ,  $z_2$ , and so forth. After  $z_0$  is time evolved by  $G_z$ , there is no guarantee 43 that the distribution of  $z_1$  will be as uniform as that of  $z_0$ . If they are different, the trajectories 44 generated by  $G_Y$  from  $z_0$  and  $z_1$  will not satisfy the third assumption of MD-GAN. If the trajec-45 tories generated from  $z_0$  and  $z_1$  are used for training, then  $z_1$  is input to  $G_z$  in estimation phase, 46 and this implies an unknown input and leads to the occurrence of exposure bias. Therefore,  $G_z$ 47 is applied repeatedly until the distribution of latent variables becomes stationary. After seven 48 or more time evolutions, the latent variables obtain a stationary distribution and trajectories are 49 generated from these latent variables. Thus, the mechanism that evolves in time until a station-50 ary distribution is obtained is the distribution stabilization mechanism, which contributes to the 51 reduction of exposure bias. 52

#### 53 Section 2. Detailed architecture of MD-GAN

<sup>54</sup> Supplementary Fig. 2 shows the overall architecture of MD-GAN, and the architectures of  $G_Y$ , <sup>55</sup>  $G_z$ , and  $D_G$  are shown in Supplementary Fig. 2A, B, and C, respectively. Supplementary Fig. <sup>56</sup> 2 describes the parameters used for the single-particle input. For the three-particle input, the <sup>57</sup> number of channels for convolution was increased from three to nine, and the shape of  $y_k$  was <sup>58</sup> set to  $64 \times 9$ . The optimizer was Adam[4], and the batch size was 64. The architecture of MD-<sup>59</sup> GAN in a previous study[5] was based on U-Net. However, for ease of use, we changed the <sup>60</sup> architecture to consist mainly of affine layers. There was no significant change in the execution results owing to architectural changes. In addition, the previous study used two discriminators:  $D_G$  and a discriminator that calculates the Wasserstein distance of two latent variables before and after the time evolution. In this study, we did not use the discriminator between the two latent variables.

#### 65 Section 3. How to calculate *err*

 $_{66}$  In this paper, err, the evaluation index, is defined as

$$err := \int_{s_1}^{s_2} f(t) ds / \int_{s_1}^{s_2} ds$$
 (1)

In the MSD prediction,  $s = \log_{10} t$ ,  $s_1$  corresponds to the time when n = 1/2 diffusion ends, transition to n = 1 diffusion begins, and  $s_2$  corresponds to the time when the transition ends and the normal diffusion to n = 1 begins. When calculating *err*, appropriate discretization should be performed depending on the number of step skips. Transforming Eq. 1 into an expression with respect to *t*:

$$\int_{s_1}^{s_2} f(t)ds / \int_{s_1}^{s_2} ds = \int_{t_1}^{t_2} f(t) \frac{1}{t} dt / \int_{t_1}^{t_2} \frac{1}{t} dt$$
(2)

<sup>72</sup> Let  $t_k = k\Delta t$  be the width of the time increment to be discretized, where  $\Delta t$  is the tick width <sup>73</sup> after applying step skip, and is thus the product of the number of step skips and the output tick <sup>74</sup> width of the MD data. k is the number of steps after applying step skip. Discretizing Eq. 2, we <sup>75</sup> get

$$\sum_{k \in transition \, area} f(k\Delta t) \frac{1}{k\Delta t} \Delta t / \sum_{k \in transition \, area} \frac{1}{k\Delta t} \Delta t \tag{3}$$

$$=\sum_{k\in transition\ area}f(k\Delta t)\frac{1}{k}/\sum_{k\in transition\ area}\frac{1}{k}$$
(4)

From the above equation, the value of err in the MSD prediction can be obtained. In the prediction of the end-to-end vectors, considering s = t, we get

$$\sum_{k \in area in which C(t) is greater than 0.1} f(k\Delta t)\Delta t/(t_2 - t_1)$$
(5)

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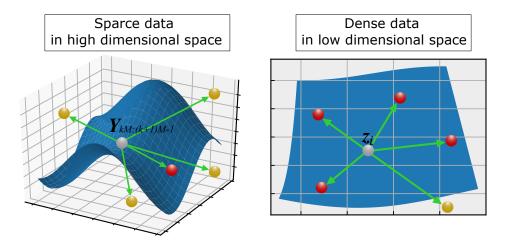


Fig. S 1. Schematic view of time evolution in a low-dimensional space. The gray, red, and yellow spheres contain the trajectory information for M steps of the extracted subsystem. The blue region is the manifold where the information of M steps can be found.

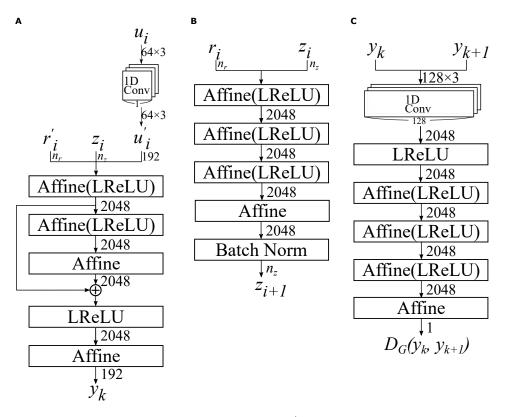


Fig. S 2. Detailed architecture of MD-GAN.  $r_i$ ,  $r'_i$  are random numbers sampled from the uniform distribution,  $u_i$  are random numbers sampled from the normal distribution,  $z_i$  is a latent variable,  $n_r$  is the dimension of the random number,  $n_z$  is the dimension of the latent variable, and  $y_k$  is the trajectory for 64 steps. The numbers next to the arrows represent the shape of the output (batch size is omitted). (A) Architecture of  $G_Y$  In one-dimensional convolution, the kernel size is 1, the stride is 1, and the number of input and output channels are both 3. (B) Architecture of  $G_z$  (C) Architecture of  $D_G$  In one-dimensional convolution, the kernel size is 128, the stride is 128, the number of input channels is 3, and the number of output channels is 2048.