

# **Supporting information**

## **Subnano Pt Particles from First Principles Stochastic Surface Walking Global Search**

**Guang-Feng Wei<sup>†,‡</sup> and Zhi-Pan Liu<sup>\*,‡</sup>**

<sup>†</sup>Shanghai Key Laboratory of Chemical Assessment and Sustainability, Department of Chemistry, Tongji University, Shanghai 200092, China

<sup>‡</sup> Collaborative Innovation Center of Chemistry for Energy Material, Shanghai Key Laboratory of Molecular Catalysis and Innovative Materials, Key Laboratory of Computational Physical Science (Ministry of Education), Department of Chemistry, , Fudan University, Shanghai 200433, China \*email: zpliu@fudan.edu.cn

## SSW Method

The SSW algorithm<sup>1,2</sup> features with an automated climbing mechanism to manipulate one minimum to a high energy configuration along one random direction, which is inherited from the bias-potential driven constrained-Broyden-dimer (BP-CBD) method for TS location developed in the group<sup>3</sup>. The method has been successfully utilized for predicting the structure of finite clusters with complex PES, such as C<sub>100</sub> fullerene, and the detail of the algorithm can be found in our previous papers<sup>1,2</sup>. Here we briefly outline the central idea of the SSW method and an illustration of the SSW method is shown in Figure S1.

In one particular SSW step, labeled as  $i$ , a modified PES  $V_{m\text{-to-}H}$ , as shown in Eq. S1, is utilized for moving from the current minimum,  $\mathbf{R}_i^m$  to a high energy configuration  $\mathbf{R}_i^H$ , in which a series of bias Gaussian potential  $v_n$  ( $n$  is the index of the bias potential,  $n=1,2\cdots H$ ) is added one by one consecutively along the direction  $\mathbf{N}_i^n$ .

$$V_{m\text{-to-}H} = V_{real} + \sum_{n=1}^H v_n = V_{real} + \sum_{n=1}^H w_n \times \exp \left[ -\left( (\mathbf{R}^t - \mathbf{R}_t^{n-1}) \cdot \mathbf{N}_i^n \right)^2 / (2 \times ds^2) \right] \quad (S1)$$

$$\mathbf{F}_{tot} = \mathbf{F}_{real} + \sum_n w_n \cdot \exp \left[ -\frac{(\mathbf{R}^t - \mathbf{R}_t^{n-1}) \cdot \mathbf{N}_i^n}{2 \times ds^2} \right] \cdot \frac{(\mathbf{R}^t - \mathbf{R}_t^{n-1}) \cdot \mathbf{N}_i^n}{ds^2} \cdot \mathbf{N}_i^n \quad (S2)$$

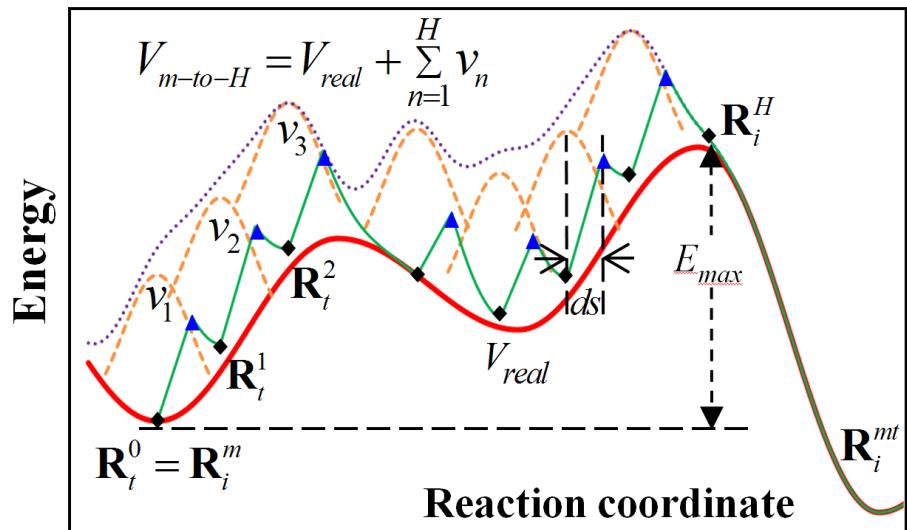
where  $\mathbf{R}$  is the coordination vector of the structure and  $V_{real}$  represents the unmodified PES;  $\mathbf{R}_t^n$  are the  $n^{th}$  local minima along the movement trajectory on the modified PES that is created after adding  $n$  Gaussian functions (see Figure S1). The PES at  $\mathbf{R}_t^n$  is thus defined by  $V_{m\text{-to-}n} = V_{real} + \sum_{k=1}^n v_k$ . The Gaussian function is controlled by its height  $w$  and its width  $ds$ , and is always added along one particular walking direction as defined by  $\mathbf{N}^n$ .

$\mathbf{N}^n$  should desirably be one eigenstate of Hessian matrix (normal mode) with low eigenvalues. Since the computation of Hessian is expensive, SSW method optimizes  $\mathbf{N}^n$  iteratively from the initial random direction  $\mathbf{N}^0$  using the biased CBD rotation method<sup>1,3</sup>, which is utilized practically to fast locate one soft eigenvector of Hessian matrix. It should be noticed that as inherited from CBD rotation<sup>4</sup>, the biased CBD rotation does not compute the whole Hessian matrix but aims to find one vector close to a soft eigenvector of Hessian using the numerical approach. Owing to the extra bias added in the CBD rotation<sup>5,6</sup>, the biased CBD rotation distinguishes from other existing eigenvector updating schemes as utilized in

single-ended TS searching method like dimer<sup>7</sup>, CBD<sup>4</sup>, hybrid eigenvector-following<sup>8</sup> and GAD<sup>9,10</sup>, the rotation does not necessarily converges to the softest eigenvector or even any eigenvector of Hessian exactly, but to a vector that mimics the initial random direction  $\mathbf{N}^0$  and at the meantime is close to a soft eigenvector of Hessian. In short, the biased CBD method is able to follow up one particular moving direction to escape the basin region, which is not always the softest mode direction (e.g. frustrated translational/rotational modes). More details on the random mode generation and optimization can be found in our previous works.<sup>1,3</sup>

Overall, the movement from  $\mathbf{R}_i^m$  to  $\mathbf{R}_i^H$  (see Figure S1) is a repeated procedure containing (i) the update of the direction  $\mathbf{N}_i^n$  at  $\mathbf{R}_i^{n-1}$ ; (ii) the adding of a new Gaussian function  $v_n$  and the displacement of  $\mathbf{R}_i^{n-1}$  along the direction  $\mathbf{N}_i^n$  by a magnitude of  $ds$  ( $\mathbf{R}_i^{n-1} + \mathbf{N}_i^n \cdot ds$ ); and (iii) the local relaxation to  $\mathbf{R}_i^n$  on the modified PES (the energy minimization is constrained by the added potentials). The force for the local optimization on the modified PES can be evaluated according to Eq. S2. After reaching the high energy structure  $\mathbf{R}_i^H$ , we remove all the added bias potentials and relax fully until a new minimum is found.

It might be noticed that the purpose of adding bias potential in SSW method is quite different from the MD-based metadynamics<sup>6</sup> method. In SSW method, the bias potential is for driving the structure across the TS and will be removed before the full energy minimization. In metadynamics, the bias potentials are kept during the simulation to gradually fill the basins. Special reaction coordinate, i.e. collective variables, needs to be designed in order to fill only those related basins and drive the simulation to the target state. In contrast, the bias potential in SSW method is imposed simply using the Cartesian coordinate, the direction of which is obtained from the biased CBD rotation. There is no need for guessing the reaction coordinate.



**Figure S1.** The illustration of the SSW method. The real PES is described by the red curve showing separated minima. one SSW step from one minimum to another, where the bias Gaussian potentials are imposed only on the atom degrees of freedom<sup>1,2</sup>. The green curve represents the subsequent atom relaxation.

#### References:

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**Table S1** The comparison of the bond number (BN) and average bond length (BL) of the GM and SLM

Atom Number (N)	Bond Number of GM (BN <sub>a</sub> )	Bond Number of SLM (BN <sub>b</sub> )	ΔBN*	ΔBL** (Å)
12	25	25	0	0.002
13	29	33	-4	-0.030
14	36	36	0	-0.011
15	39	38	1	-0.014
16	39	37	2	0.000
17	37	35	2	0.019
18	39	37	2	0.017
19	42	40	2	0.015
20	48	47	1	-0.003
21	59	62	-3	-0.021
22	65	65	0	-0.011
23	72	72	0	0.004
24	75	57	18	0.067
25	57	50	7	0.052
26	55	81	-26	-0.125
27	54	54	0	-0.010
28	58	88	-30	-0.128
29	90	63	27	0.104
30	96	98	-2	-0.007
31	104	102	2	0.009
32	103	103	0	-0.004
33	111	108	3	0.000
34	108	110	-2	-0.004
35	110	110	0	-0.002
36	111	111	0	-0.002
37	121	128	-7	-0.017
38	125	120	5	0.014
39	132	139	-7	-0.027
40	152	148	4	0.008
41	141	138	3	0.006
42	160	160	0	0.001
43	164	150	14	0.038
44	168	146	22	0.055
45	153	166	-13	-0.041
46	157	159	-2	-0.012

\*: ΔBN( = BN<sub>a</sub> – BN<sub>b</sub>) is the difference of the bond number (BN) between the GM and SLM.

\*\*: ΔBL is the difference of the average Pt-Pt bond length (BL) between the GM and SLM.

The trends of  $\Delta BN$  is same as the average coordination number shown in Fig. 4. And the  $\Delta BL$  of most  $Pt_N$  is very small ( $< 0.05 \text{ \AA}$ ). As listed in Table 1, for only 3 clusters ( $Pt_{26}$ ,  $Pt_{28}$  and  $Pt_{29}$ ), the absolute values of  $\Delta BL$  are larger than  $0.10 \text{ \AA}$ . The large difference is due to the presence of the simple cubic packing local structure, which has much smaller BN and shorter BL.

### **The XYZ coordinates for the GM of $Pt_N$ clusters**

12

Pt	11.338200	10.252740	9.994580
Pt	10.088000	9.626160	14.222640
Pt	10.823480	8.584800	12.045220
Pt	7.798440	9.969820	13.070600
Pt	6.621280	10.506740	10.820900
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Pt	8.483860	12.254160	10.328040
Pt	9.218420	7.497460	8.989800
Pt	8.421420	8.383860	11.240240
Pt	11.583180	7.730220	9.780140

Pt	8.90361	8.34517	11.05539
Pt	11.10054	8.61645	9.43356
Pt	13.10709	9.77233	10.47145
Pt	9.48723	13.08749	10.33148
Pt	8.07504	10.55390	10.16763
Pt	9.20232	9.26654	13.40187
Pt	8.84429	11.58825	12.32561
Pt	8.04796	9.72503	7.79018
Pt	11.79435	11.96928	10.11230
Pt	8.94522	7.49197	8.65416
Pt	8.07464	12.34459	8.21797
Pt	10.18615	10.80453	8.57285
Pt	10.91147	10.26066	11.74278

Pt	12.92784	12.60233	10.16370
Pt	12.12270	7.77398	11.32302
Pt	10.98864	8.64396	9.21236
Pt	12.55388	10.22499	10.92003
Pt	7.98434	13.47713	10.50049
Pt	9.66425	8.23101	11.64359
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