Development of an Applications for a Simulater of Intermolecular Potentials. III.[1] Development of SIMP/II and SIMP/D and Their Application

Tatsuya TAKAGI,*[a] Sanshiro MATSUO,[b] Akito TANAKA,[b] Yoko MOTOI,[b] Mika TANI,[b] Hideaki FUJIWARA,[b] and Yoshio SASAKI[b]

Genome Information Research Center, Osaka University,[a] 3–1 Yamadaoka, Suita, Osaka 565, Japan and Faculty of Pharmaceutical Sciences, Osaka University,[b] 1–6 Yamadaoka, Suita, Osaka 565, Japan.

Received September 6, 1993; accepted December 26, 1993

SIMP/II, a revised version of SIMP which is a simulater of intermolecular potentials based on modified neglect of diatomic overlap (MNDO) approximation, has been developed. SIMP/D, which can approximately estimate dispersion energies using the second order sum-of-state perturbation method based on neglect of diatomic differential overlap (NDDO) approximation, has also been developed. The SIMP/II and SIMP/D systems were used to calculate the stacking energies between the two bases in nucleic acids. The results were in fair agreement with the *ab initio* calculations, thus confirming the utility benefits of the new versions.

Keywords molecular interaction; semiempirical molecular orbital method; dispersion energy; perturbation method; stacking energy; SIMP

The authors have developed the SIMP[1a)] (Simulater of Intermolecular Potentials) system for estimating intermolecular interaction energies between relatively large molecules such as natural products. SIMP, hereafter referred to as SIMP/I to avoid confusion, showed satisfactory results with regard to the neutral molecular systems. SIMP/I has also been used to estimate the solvent effects on the conformation of bioactive molecules.[1b)]

Two minor defects were found in the system, however. (1) SIMP/I has a tendency to underestimate the relatively strong intermolecular interactions in a system such as one composed of neutral molecules and an ionic molecule. (2) Dispersion energies are not taken into account in the SIMP/I system, and hence very weak intermolecular interaction energies are underestimated when calculated by this version.

Here, the authors reparameterized SIMP/I so as to reproduce the systems containing ionic molecules more correctly, and developed the SIMP/D method using the second order sum-of-state perturbation method for estimating dispersion energies. The revised systems were applied to the stacking energy calculations between the bases in nucleic acids.

Computation

The QCPE (Quantum Chemistry Program Exchange) program[2)] was greatly improved[3)] and modified to include the corrections itemized below and the program NICER[4)] was used as a diagonalization routine. SIMP/D programs were written by the authors. *Ab initio* MO calculations were performed using the GAUSSIAN88[5)] program. Pople's 4-31G basis set[6)] is adopted throughout.

All the computations were performed on an NEC ACOS 1000 plus SX-2N system at the Computation Center Osaka University and a HITAC M680H plus S820 system at the Computation Center, Institute for Molecular Science.

Theoretical

General Concept Three methods are now available to estimate intermolecular interactions: (1) *ab initio* MO method, (2) revised semiempirical molecular orbital method, and (3) empirical force field method. In the *ab initio* method, it is frequently necessary in the computation of dispersion interactions to use approximations more accurate than the SCF level. Therefore, it is not easy to treat such large molecular systems as bioactive molecules. complete neglect of differential overlap (CNDO)/2H,[7)] modified intermediate neglect of differential overlap (MINDO)/3H,[7)] modified neglect of diatomic overlap (MNDO)/H,[8)] and the SIMP method are included in method (2); the former three were developed to treat only hydrogen bonding systems but the SIMP method was intended for use in treating any kind of molecular interaction. Although its accuracy is inferior to the *ab initio* MO method, SIMP system can treat larger systems. Although method (3) can treat very large molecular systems, two drawbacks prevent the authors from selecting this technique. Firstly, we cannot obtain the variations of electronic distributions induced by the molecular interactions. Secondly, the number of parameters to be treated abruptly increase when various kinds of atoms are included in the molecular systems, because atomic-pair parameters are needed for all pairs in the molecules.

The authors developed the SIMP/I[1a)] system which belongs to the above-mentioned method (2) but dispenses with atomic-pair parameters such as are contained in the MINDO/3 approximation. The purpose of the system is to utilize semiquantitative estimations for intermolecular interactions of large systems and to provide, to a certain extent, components of intermolecular interaction energies. Computations of subtle differences between similar molecular systems should be performed by the *ab initio* MO method.

SIMP/D, which is based on the second order sum-of-state perturbation method,[9)] was developed with the same concept as the other SIMP systems.

SIMP/II Formulation of SIMP/II is similar to that of SIMP/I. The core-core repulsion functions in SIMP/II are as follows:

$$E_{ij}^{\rm core}({\rm SIMP/II}) = E_{ij}^{\rm core}({\rm MNDO}) - (A_i + A_j)[\exp\{-B_i(R_{ij}+\alpha)\} + \exp\{-B_j(R_{ij}+\alpha)\}] \quad (1)$$

for atomic pairs of N–H and O–H,

$$E_{i{\rm H}}^{\rm core}({\rm SIMP/II}) = E_{i{\rm H}}^{\rm core}({\rm MNDO}) - (A_i + A_{\rm H})[(R_{i{\rm H}}+\alpha) \times \exp\{-B_i(R_{i{\rm H}}+\alpha)\} + \exp\{-B_{\rm H}(R_{i{\rm H}}+\alpha)\}] \quad (2)$$

where A_i, B_i, and α are the intermolecular parameters, $E_{ij}^{\rm core}$, $E_{i{\rm H}}^{\rm core}$, R_{ij}, and $R_{i{\rm H}}$ are the core-core repulsion energy terms and the interatomic distances between atoms i and j (or i and hydrogen atom, H), respectively. A's and B's vary depending on the atomic species, but A_i plus A_j is set to zero when i and j belong to a same molecule.

In MNDO approximations,[10] two center repulsion integrals are expanded in terms of multipole-multipole interactions $[M_{lm}^{\rm A}, M_{km}^{\rm B}]$. The formula for the integrals is expanded as follows:

$$\langle {\rm rs} | {\rm tu} \rangle = \sum_l \sum_k \sum_{m=-l_{\min}}^{l_{\min}} e^2/2^{l+k} \sum_{i=1}^{2^l} \sum_{j=1}^{2^k} [R_{ij}^2 + (\rho_l^{\rm A} + \rho_k^{\rm B})^2]^{-1/2} \quad (3)$$

where R_{ij} is the distance between the point charges i and j in the interacting configurations at atoms A and B. For example, $\langle {\rm ss} | {\rm sp_z} \rangle$ is given by:

$$\begin{aligned}\langle {\rm ss} | {\rm sp_z} \rangle &= [q^{\rm A}, \mu_{\rm z}^{\rm B}] \\ &= -(e^2/2)\{(R_{\rm AB} - D_1^{\rm B})^2 + (\rho_0^{\rm A} + \rho_1^{\rm B})^2\}^{-1/2} \\ &\quad + (e^2/2)\{(R_{\rm AB} - D_1^{\rm B})^2 + (\rho_0^{\rm A} + \rho_1^{\rm B})^2\}^{-1/2} \quad (4)\end{aligned}$$

where D_k is the charge separation in the dipole and quadrupole configurations.[10] Because D_k in MNDO approximations is determined so as to reproduce well the molecular constants of each isolated molecule, the values of D_k are too small in the interacting systems which include large interatomic distances as mentioned in the previous study.[1a] The charge separations in SIMP/II are expressed as:

$$D_k({\rm SIMP/II}) = f_k \cdot D_k({\rm MNDO}) \quad (k = 1 \text{ or } 2) \quad (5)$$

where f_k is the intermolecular parameter and becomes nontrivial (see Table I) when atoms i and j belong to different molecules, but is set equal to 1.0 when they belong to a same molecule. Equation 5 is applied only to the case of linear quadrupole, $Q_{\alpha\alpha}$[10] and between hydrogen and heavy atoms when $k=2$.

A's, B's and f_k's are determined to minimize the function below:

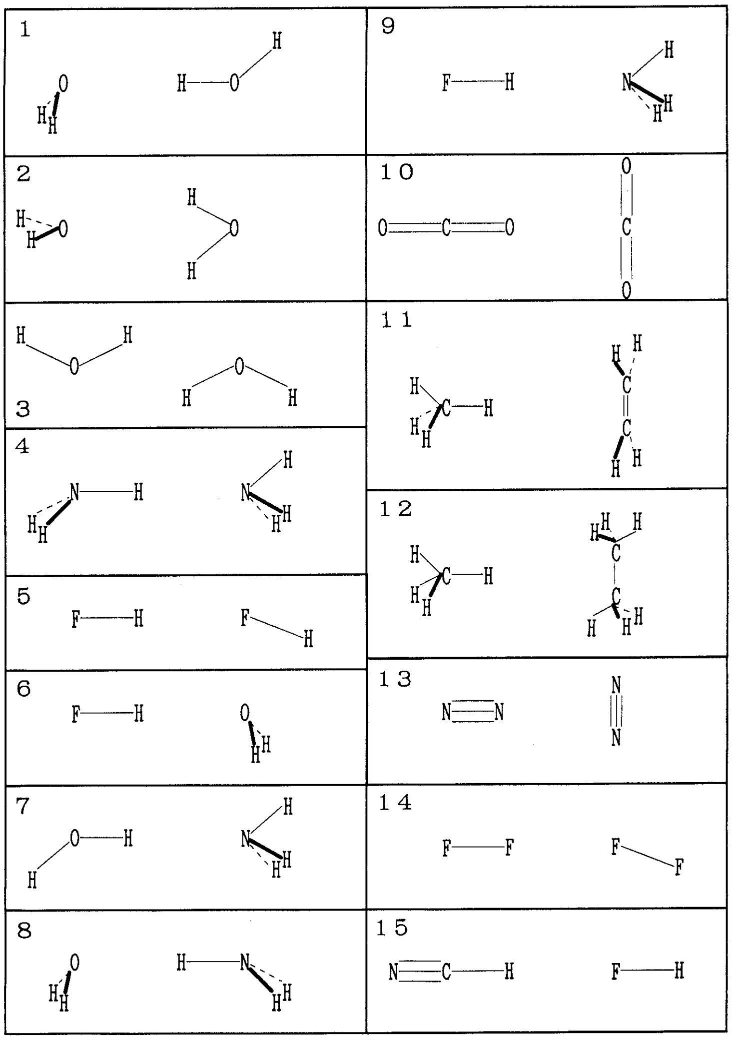


Fig. 1. Intermolecular Configurations of the Standard Molecular Systems Adopted for the SIMP/II Parameterization

$$F=\sum[W_p\{\Delta E_{\mathrm{SCF,p}}(\mathrm{SIMP/II})-\Delta E_{\mathrm{SCF,p}}(4\text{-}31\mathrm{G})\} + 100W_p\{Re_p(\mathrm{SIMP/II})-Re_p(4\text{-}31\mathrm{G})\}] \tag{6}$$

where W_p is the weight coefficient, and $\Delta E_{\mathrm{SCF,p}}$ and Re_p are the intermolecular interaction energies and the most stable intermolecular distances, respectively, which are calculated using the SIMP/II or the ab initio MO method with 4-31G basis set. α is set equal to 1.20 A in all cases. Inherently, semiempirical MO methods such as MNDO MO are thought to be based on a minimal basis set besides the effective core potential approximation. Hence, for references to the SIMP method, the *ab initio* MO method using a minimal basis set is most desirable. In the present study, a split valence basis set, 4-31G, was selected which gave satisfactory calculations as shown below.[11)]

Table I lists the reparameterized values of the SIMP/II intermolecular parameters for elements of H, N, O, and F with those for elements C which are unchanged from the values of the SIMP/I parameters. Tables II and III list the interaction energies and the most stable intermolecular distances, respectively, for the 15 systems used in the reparameterization which are the same systems as in the SIMP/I parameterization.[1a)] The results by *ab initio* (4-31G) MO method are also presented in Tables II and III. The regression analyses according to a relation $y=ax$ resulted in:

$$\Delta E_{\mathrm{SCF}}(\mathrm{SIMP/II})=0.845\,\Delta E_{\mathrm{SCF}}(4\text{-}31\mathrm{G}) \tag{7}$$

$n=15,\quad R=0.938,\quad s=6.20\,\mathrm{kJ/mol}$

$$Re(\mathrm{SIMP/II})=1.00\,Re(4\text{-}31\mathrm{G}) \tag{8}$$

$n=15,\quad R=0.904,\quad s=0.32\,\mathrm{A}$

Compared with the regression equations for the SIMP/I[1a)] ($R=0.822$), the equations for the *Re* values were much improved.

Table I. Optimized SIMP/II Parameters

	A	B	f_1	f_2
H	2.9055	1.6552	—	—
C	0.00211	2.8058	1.0	1.0
N	36.3248	2.4708	1.7813	2.2296
O	59.2903	2.5649	1.0334	1.1562
F	54.6521	2.2198	1.4591	2.3265

Table II. Comparison of Intermolecular Interaction Energies[a)] Calculated by Various Procedures

No.[b)]	SIMP/II	SIMP/I	*Ab initio* (4-31G)
1	−28.2	−24.2	−32.6
2	−33.5	−30.4	−27.0
3	−26.1	−21.6	−25.5
4	−23.5	−19.6	−17.2
5	−33.1	−22.2	−31.8
6	−37.5	−31.0	−56.1
7	−28.6	−27.9	−37.7
8	−25.9	−17.2	−17.2
9	−53.5	−45.7	−68.2
10	−1.6	−1.8	−7.8
11	−0.7	−0.9	−2.7
12	−2.4	−3.4	−0.2
13	−2.8	−0.4	−1.1
14	−0.8	−0.3	−0.7
15	−31.4	−28.4	−36.2

a) Values in kJ/mol. *b)* See Fig. 1.

Table III. Comparison of the Most Stable Intermolecular Distances[a)] Calculated by Various Procedures

No.[b)]	SIMP/II	SIMP/I	*Ab initio* (4-31G)
1	2.82	3.05	2.88
2	2.67	2.80	2.90
3	2.95	3.08	2.85
4	3.05	3.15	3.30
5	2.70	2.86	2.71
6	2.64	2.98	2.62
7	2.95	3.06	2.93
8	2.97	3.20	3.22
9	2.79	2.99	2.68
10	4.93	4.95	4.10
11	4.61	4.50	4.40
12	4.43	4.27	5.00
13	3.37	3.61	3.60
14	3.08	3.35	2.70
15	3.02	3.16	2.99

a) Values in A. *b)* See Fig. 1.

SIMP/D Dispersion energy is the most difficult to compute theoretically among the different types of intermolecular interaction energies. These days, the second order sum-of-state perturbation method and the Möller-Pleset perturbation method are often applied to calculate dispersion energies for small super-molecular systems. Nevertheless, it is not easy to calculate them for large super-molecular systems.

Here, the authors applied the second order sum-of-state perturbation method within MNDO approximations to calculate the dispersion interaction energies. The dispersion interaction energy between the two molecules, A and B, is expressed within the Hartree-Fock approximations as follows[9)]:

$$\begin{aligned} E_{\mathrm{disp}} &= \sum_{i}^{\mathrm{occ}}\sum_{k}^{\mathrm{vac}}\sum_{\mu}^{\mathrm{occ}}\sum_{\nu}^{\mathrm{vac}} \frac{|\langle A_0B_0|H'|A_{i\to k}B_{\mu\to\nu}\rangle|^2}{E_{i_A\to k_A,\mu_B\to\nu_B}-E^0} \\ &= 4\sum_{i}^{\mathrm{occ}}\sum_{k}^{\mathrm{vac}}\sum_{\mu}^{\mathrm{occ}}\sum_{\nu}^{\mathrm{vac}} \frac{|\langle i_Ak_A|\mu_B\nu_B\rangle|^2}{E^A_{i\to k}+E^B_{\mu\to\nu}-E^A_0-E^B_0} \end{aligned} \tag{9}$$

where A_0B_0 is the Hartree product of the Hartree-Fock wave functions for the ground states of molecules A and B, $A_{i\to k}B_{\mu\to\nu}$ is the Hartree product of the wave functions for the singly excited states of A and B, H' is the molecular interaction part of the Hamiltonian, $\langle i_Ak_A|\mu_B\nu_B\rangle$ is a two-electron integral over the Hartree-Fock MO's of isolated molecules, and E^A_0 and $E^B_{\mu\to\nu}$ are the unperturbed energies of isolated molecules in the ground and singly excited states. In the MNDO approximation, a two electron integral, $\langle i_Ak_A|\mu_B\nu_B\rangle$, can be expressed as follows:

$$\langle i_Ak_A|\mu_{B\nu B}\rangle=\sum_p\sum_q\sum_r\sum_s C_{pi}C_{qi}C_{rk}C_{sl}\langle pq|rs\rangle \tag{10}$$

where $\langle pq|rs\rangle$ is a two electron integral using atomic orbital functions.

The results calculated by Eqs. 9 and 10 using *ab initio* and MNDO approximations are given in Table IV. It is clear that the results using MNDO approximations

Table IV. Dispersion Energies[a)] at Equilibrium Intermolecular Distances Calculated by Second Order Sum-of-State Perturbation Method Using the Two Approximations

System[b)]	MNDO	*Ab initio* (4-31G)
$H_2O\cdots H_2O$	−0.276	−1.792
$NH_3\cdots NH_3$	−0.291	−1.776
$NH_3\cdots H_2O$	−0.219	−1.190
$H_2O\cdots NH_3$	−0.381	−2.524
$CH_4\cdots H_2O$	−0.085	−0.472
$CH_4\cdots H_2O$	−0.126	−0.766
$CH_4\cdots NH_3$	−0.162	−1.000
$CH_4\cdots C_2H_6$	−0.141	−0.889

a) Values in kJ/mol. *b)* See Fig. 2.

Table V. Distance Dependencies of the Dispersion Energies Calculated by Second Order Sum-of-State Perturbation Method Using MNDO and *ab Initio* MO Approximations

R/A[a)]	ΔE_{disp}/kJ mol^{-1}		Ratio[b)]
	MNDO	*Ab initio* (4-31G)	
2.0	−1.321	−16.670	12.619
3.0	−0.219	−1.386	6.329
4.0	−0.041	−0.202	4.927
5.0	−0.010	−0.045	4.500
6.0	−0.003	−0.013	4.333

a) See Fig. 2. *b)* ΔE_{disp} (4-31G)/ΔE_{disp} (MNDO).

underestimate the dispersion energies compared with the *ab initio* approximations: the regression analysis results are as follows:

$$E_{\text{disp}}(ab\ initio)=6.73\,E_{\text{disp}}(\text{MNDO})+0.11 \qquad (11)$$

$$n=8,\quad R=0.99$$

Despite the underestimation, Eq. 11 shows good linearity between the dispersion energies calculated by the two approximations; this suggests that the dispersion energies calculated by the MNDO approximations can be corrected to give exact values. In this study, accuracy of our method to calculate dispersion energies is limited within the range of second order sum-of-state perturbation approximation because of the cost performance and simplicity. The 4-31G basis set was selected using the same concept as the SIMP/II. More accurate calculation should be obtained with the *ab initio* MO method with a larger basis set including electron correlation.

Table V shows the dependence of the ratio, $E_{\text{disp}}(ab\ initio)/E_{\text{disp}}(\text{MNDO})$, on the intermolecular distances. It indicates that a simple correction such as Eq. 11 is not adequate for various molecular configurations, and that dependency on intermolecular distance is required to correct the dispersion energies.

Therefore, the authors attempted to correct the dispersion energies with MNDO approximations by increasing the values of two electron integrals, $\langle pq\,|\,rs\rangle$, as follows:

$$\langle p_Aq_A\,|\,r_Bs_B\rangle_{\text{SIMP/D}}=\langle p_Aq_A\,|\,r_Bs_B\rangle_{\text{MNDO}}\times(M_AM_B)\cdot\exp\{-(N_A+N_B)R_{AB}\} \qquad (12)$$

where A and B (A≠B) indicate the atoms belonging to different molecules, M and N are the SIMP/D parameters which are dependent on the atomic species, and R_{AB} is the interatomic distance between the atoms A and B. The parameters, M and N, are determined in order to reproduce the intermolecular dispersion energies for the eight systems with five intermolecular distances as follows:

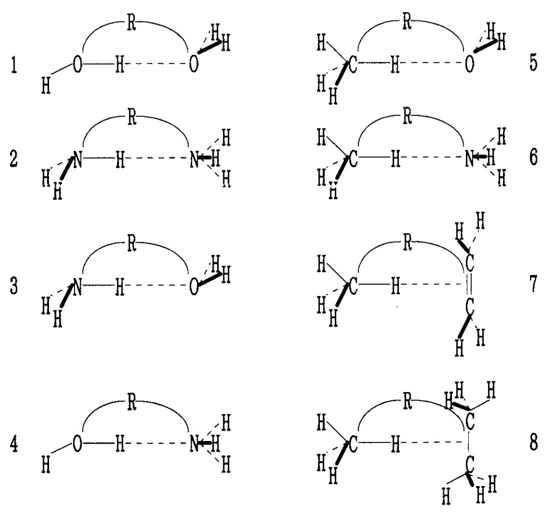


Fig. 2. Intermolecular Configurations of the Standard Molecular Systems Adopted for the SIMP/D Parameterization

Table VI. Optimized SIMP/D Parameters

Atom	M	N
H	1.6026	0.28893
C	1.7930	0.22613
N	1.5323	0.24329
O	1.5271	0.23411

$$F=\sum_{i=1}^{8}\sum_{j=1}^{5}\left|\frac{E_{\text{disp},i,j}(ab\ initio)-E_{\text{disp},i,j}(\text{SIMP/D})}{\{E_{\text{disp},i,j}(ab\ initio)\}^{1/2}}\right| \qquad (13)$$

The eight systems used for the parameterization are shown in Fig. 2.

The optimized parameters are shown in Table VI and the obtained dispersion energies calculated using Eq. 9 with optimized parameters are shown in Table VII with those using the *ab initio* MO method. The regression analysis result was follows:

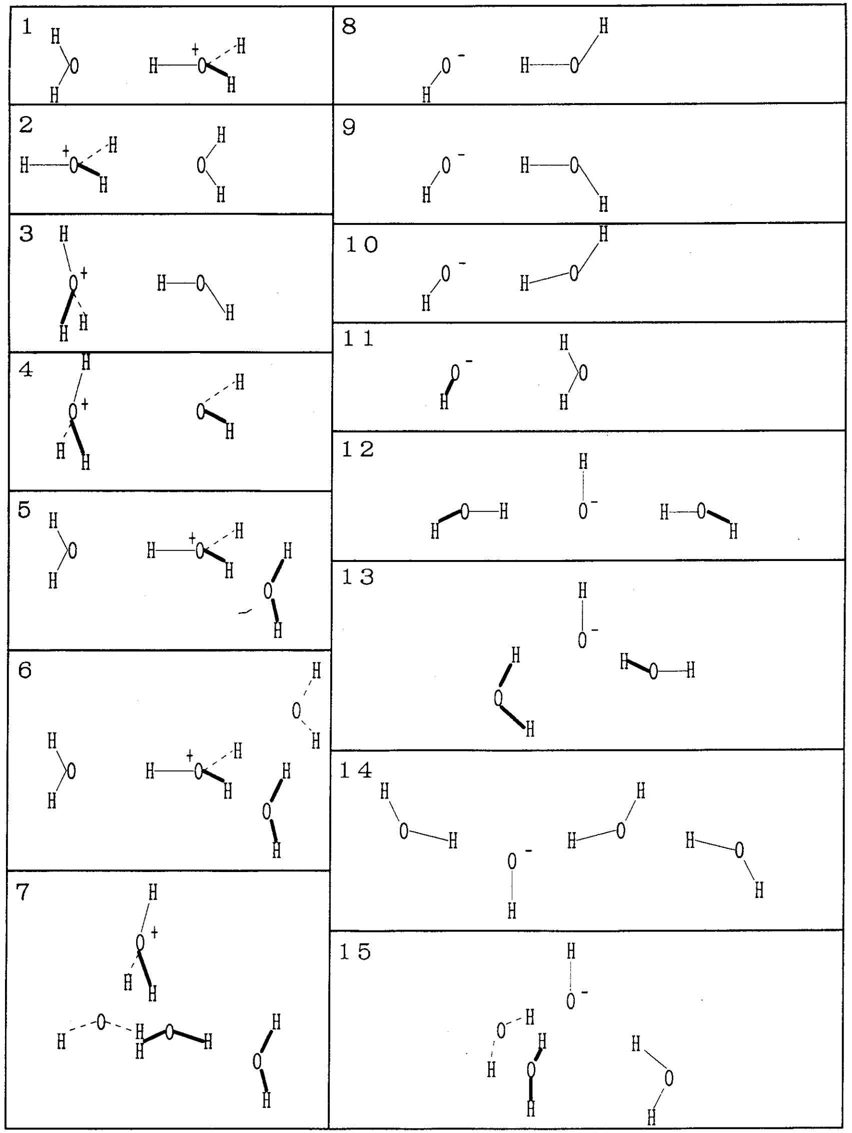
$$E_{\text{disp}}(\text{SIMP/D})=0.969\,E_{\text{disp}}(\text{4-31G}) \qquad (14)$$

$$n=40,\quad R=0.999$$

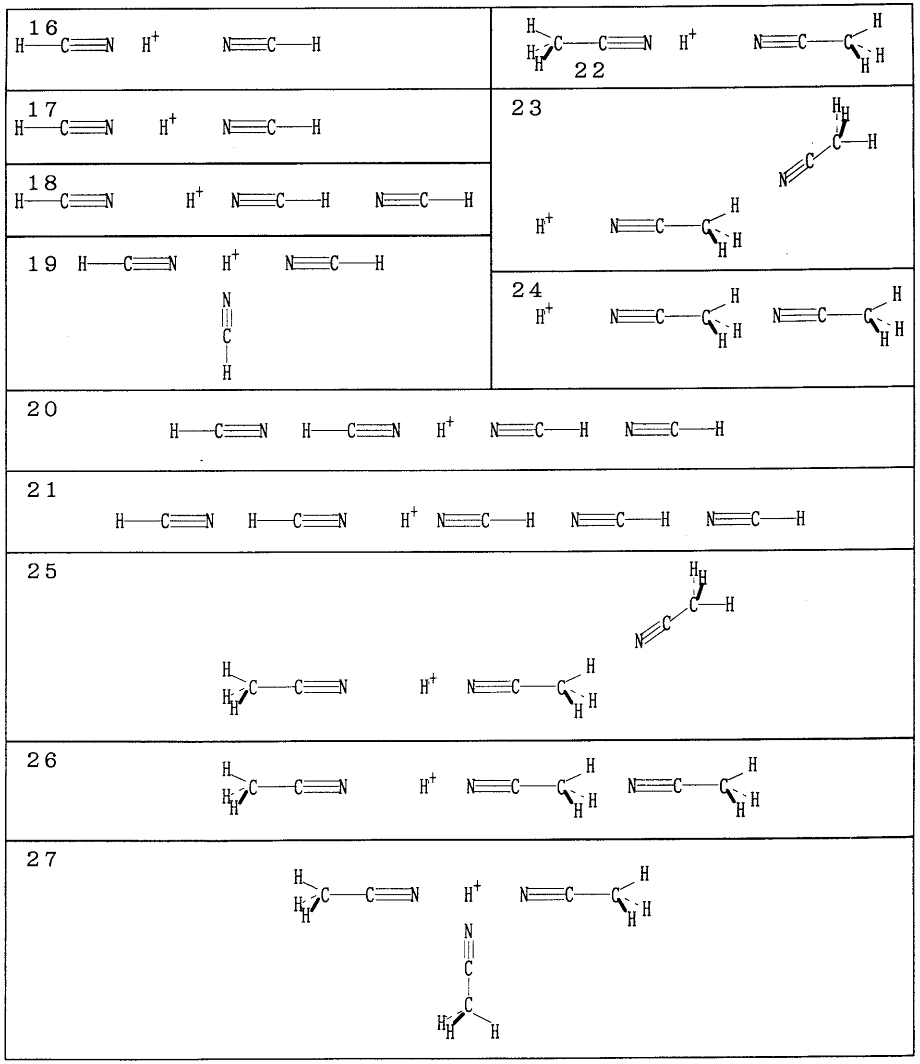
These results indicate that the SIMP/D system is appropriate for the estimation of dispersion energies.

Application and Discussion

SIMP/II Since SIMP/II is thought to be superior to SIMP/I in case of relatively strong intermolecular interactions, the authors applied it to ion-molecule interactions such as those in the $H_3O^+ + H_2O$ system. The 27 ion-molecule systems, which were studied by Hirao *et al.*[12)] and Newton and Ehrenson[13)] using the *ab initio* MO method (4-31G basis set), were selected to test the SIMP/II performance. The structures of the selected systems are



(a)



(b)

Fig. 3a. Intermolecular Configurations of the Ion-Molecule Systems Used for the Application of SIMP/II

Fig. 3b. Intermolecular Configurations of the Ion-Molecule Systems Used for the Application of SIMP/II

Table VII. Dispersion Energies Calculated by the SIMP/D and *ab Initio* (4-31G Basis Set) Methods

System[a]	R/A	ΔE_{disp}/kJ mol^{-1}		System[a]	R/A	ΔE_{disp}/kJ mol^{-1}	
		SIMP/D	4-31G			SIMP/D	4-31G
1	2.0	−16.667	−16.670	5	3.0	−3.015	−3.055
	3.0	−1.445	−1.386		4.0	−0.472	−0.472
	4.0	−0.178	−0.202		5.0	−0.113	−0.105
	5.0	−0.030	−0.045		6.0	−0.034	−0.032
	6.0	−0.007	−0.013		7.0	−0.012	−0.012
2	2.0	−33.571	−35.830	6	3.0	−5.022	−4.715
	3.0	−3.515	−3.118		4.0	−0.792	−0.789
	4.0	−0.477	−0.519		5.0	−0.179	−0.182
	5.0	−0.086	−0.121		6.0	−0.051	−0.056
	6.0	−0.019	−0.038		7.0	−0.019	−0.021
3	3.0	−2.041	−2.004	7	4.0	−13.753	−13.775
	4.0	−0.266	−0.304		5.0	−2.270	−2.428
	5.0	−0.049	−0.068		6.0	−0.534	−0.533
	6.0	−0.011	−0.021		7.0	−0.162	−0.157
	7.0	−0.003	−0.008		8.0	−0.056	−0.058
4	2.0	−25.135	−25.130	8	5.0	−5.442	−5.065
	3.0	−2.556	−2.196		6.0	−1.273	−1.228
	4.0	−0.331	−0.357		7.0	−0.348	−0.359
	5.0	−0.056	−0.083		8.0	−0.111	−0.129
	6.0	−0.012	−0.026		9.0	−0.039	−0.053

a) See Fig. 2.

shown in Fig. 3. The resulting intermolecular interaction energies are shown in Table VIII. The regression analysis result was follows:

$$\Delta E_{SCF}(\mathrm{SIMP/II}) = 0.879\,\Delta E_{SCF}(ab\ initio) \qquad (15)$$

$$n=27, \quad R=0.994$$

Considering the characteristics of the split valence basis set, that is, the overestimation of electrostatic interaction energies, the regression coefficient, 0.879, is thought to be reasonable for such a regression analysis.

SIMP/II+SIMP/D The estimation of stacking energies between bases in nucleic acids is thought to be one of the most efficient cases in which to apply the SIMP/II and SIMP/D systems since the dispersion energy plays an important role in the intermolecular interaction energies. Aida and Nagata[14] earlier reported the stacking energies for all combinations of bases included in A and B DNA using the *ab initio* MO method with 4-31G basis set. They calculated the stacking energies not only using the SCF method but also the second order sum-of-state perturbation method in order to obtain the dispersion interaction parts. They obtained good correlation between their computational results in the conformations of A DNA and the experimental results. The authors selected the conformation of B DNA since Aida's results for the cytosine-cytosine stacking energies in the conformation of B DNA showed positive interaction energies and it was considered that whether or not this unstabilization could be reproduced should be a good test for the SIMP/II and SIMP/D methods.

The structures of monomer bases were optimized by AM1 method, and other details (for example, the distances between two bases) of these computations followed the literature.[14] The resulting intermolecular interaction energies are shown in Table IX. The obtained values are

Table VIII. Ion-Molecule Interaction Energies Calculated by the SIMP/II and *ab Initio* (4-31G Basis Set) MO Methods

System[a]	ΔE/kJ mol^{-1}		System[a]	ΔE/kJ mol^{-1}	
	SIMP/II	4-31G		SIMP/II	4-31G
1	−36.7	−43.6[b]	15	−97.1	−109.9[b]
2	−23.3	−28.3[b]	16	−25.7	−28.8[c]
3	−25.4	−18.4[b]	17	−25.7	−28.3[c]
4	−66.2	−74.8[b]	18	−44.6	−47.6[c]
5	−90.1	−100.9[b]	19	−35.3	−37.5[c]
6	−83.1	−96.2[b]	20	−57.5	−62.1[c]
7	−104.4	−118.6[b]	21	−68.4	−73.5[c]
8	−35.2	−40.6[b]	22	−24.1	−30.6[c]
9	−34.2	−39.0[b]	23	−14.5	−15.1[c]
10	−35.2	−40.7[b]	24	−14.0	−13.7[c]
11	−20.4	−29.9[b]	25	−34.8	−42.5[c]
12	−59.6	−70.8[b]	26	−34.8	−41.6[c]
13	−76.5	−90.9[b]	27	−33.0	−38.9[c]
14	−84.2	−93.9[b]			

a) See Fig. 3. *b*) Taken from ref. 12. *c*) Taken from ref. 11.

Table IX. Stacking Energies Calculated by the SIMP/D+SIMP/II System and *ab Initio* (4-31G Basis Set) MO Method

	ΔE/kJ mol^{-1}				
	SIMP/II+ SIMP/D	4-31G[a]		SIMP/II+ SIMP/D	4-31G[a]
TT[b]	−10.84	−10.84	CA	−21.89	−13.69
TC	−10.23	−9.58	CG	−23.61	−24.23
CC	3.87	2.43	TA	−14.23	−16.87
CT	−11.43	−15.70	TG	−12.47	−15.32
AA	−16.03	−19.50	AT	−12.89	−14.77
AG	−17.29	−20.68	AC	−13.35	−14.19
GG	−5.69	−4.02	GT	−10.80	−11.38
GA	−17.66	−26.08	GC	−27.29	−30.97

a) Taken from ref. 13. *b*) For example, TC indicates T3′-5′C.

thought to be sufficiently close to Aida's results, supporting the method developed by the authors. Also, our systems, SIMP/II and SIMP/D, have potential for wider practical applicability to larger super-molecular systems in future.

Conclusion

1) SIMP parameters are reparameterized in order to reproduce more precisely the intermolecular interaction energies as well as the most stable intermolecular distances.

2) SIMP/II can reproduce relatively strong intermolecular interactions such as ion-molecule interactions which are not used for the reparameterization.

3) SIMP/D was developed, based on the second order sum-of-state perturbation method and MNDO approximations.

4) The SIMP/II plus SIMP/D systems can provide sufficiently accurate stacking energies between the bases included in B DNA.

Acknowledgement The authors wish to thank the Institute for Molecular Science for allotting them CPU time on the HITAC M680H plus S820/80 computer system. This investigation was supported as one of the Special Projects for Program Development at the Computation Center Osaka University using the NEC ACOS 1000 plus SX-2N computer system.

References and Notes

1) *a*) T. Takagi, A. Tanaka, S. Maeda, S. Matsuo, H. Fujiwara, Y. Sasaki, *Bull. Chem. Soc. Jpn.*, **59**, 1317 (1986); *b*) T. Takagi, A. Tanaka, M. Tani, H. Maezaki, H. Fujiwara, Y. Sasaki, *Bull. Chem. Soc. Jpn.*, **61**, 329 (1988).
2) W. Thiel, *QCPE*, #353 (1978).
3) Y. Sasaki, T. Takagi, A. Tanaka, R. Tokura, *Bull. Computation Center Osaka Univ.*, **14**(4), 103 (1985).
4) Y. Beppu, I. Ninomiya, *QCPE*, #409 (1981).
5) M. J. Frisch, M. Head-Gordon, H. B. Schlegel, K. Raghavachari, J. S. Binkley, C. Gonzalez, D. J. Dferees, O. J. Fox, R. A. Whiteside, R. Seeger, C. F. Melius, J. Baker, R. Martin, L. R. Kahan J. J. P. Stewart, E. M. Fluder, S. Topiol, J. A. Pople, GAUSSIAN88, the library program of the Computer Center of the Institute for Molecular Science.
6) R. Ditchfield, W. Hehre, J. A. Pople, *J. Chem. Phys.*, **54**, 724 (1971).
7) S. N. Mohammad, A. J. Hopfinger, *Int. J. Quant. Chem.*, **22**, 1189 (1982).
8) K. Ya. Burstein, A. N. Isaev, *Theor. Chim. Acta*, **64**, 397 (1984).
9) A. Lathan, G. R. Pack, K. Morokuma, *J. Am. Chem. Soc.*, **97**, 6624 (1975).
10) M. J. S. Dewear, W. Thiel, *J. Am. Chem. Soc.*, **99**, 4899 (1977).
11) A minimal basis set such as STO-3G is widely accepted to give only poor results in calculating intermolecular interactions. A larger basis set such as 6-31G** was examined for the parameterization of new SIMP for several systems, but only a poor result was obtained in reproducing the ion-neutral molecule interactions.
12) K. Hirao, S. Yamabe, M. Sano, *J. Phys. Chem.*, **86**, 2626 (1982); S. Yamabe, K. Hirao, *J. Am. Chem. Soc.*, **103**, 2176 (1981).
13) M. D. Newton, S. Ehrenson, *J. Am. Chem. Soc.*, **93**, 4971 (1971).
14) M. Aida, C. Nagata, *Int. J. Quant. Chem.*, **29**, 1253 (1986).