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# A method for population and bonding analyses in calculations with extended basis sets

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Summary. A method for population and bonding analyses in the calculations with extended basis sets is proposed. The definition and evaluation method of the atomic orbitals in molecular environments (AOIMs) are described. It is shown that the AOIMs can be divided into two subsets, the strongly occupied minimal compact subset  $\{AOIM\}_B$  and the very weakly occupied "Rydberg" subset  $\{AOIM\}_R$ , according to the orbital population obtained from Mulliken analysis with AOIMs as basis sets. The viewpoint of "molecular orbitals consisting of minimal atomic orbital sets" can be optimally realized in terms of  $\{AOIM\}_B$ . The Mulliken population based on AOIMs is reasonable and fairly stable to changes of basis sets; therefore they can be used to measure objectively the contribution of individual atomic orbitals to bonding.

Key words: Population analysis – Bond order – AOIM – Basis set

# **1** Introduction

It is well known that the population and bonding analysis method proposed by Mulliken [1] can transform the complicated quantum chemical calculation results into a simplified physical picture familiar to chemists. Thus it is very popular among chemists. It is based on the "LCAO-MO" formulation, that is, the molecular orbitals are expressed as the linear combination of the minimal orbital set of the constituent atoms. Thus Mulliken analysis method can give clear and reasonable pictures only under the "balanced" minimal basis sets [1]. However, in order to obtain accurate results extended basis sets have to be used in quantum chemical calculations, which results in some difficulties in the population and bonding analyses. Using extended basis sets the Mulliken analysis cannot give results with unequivocal physical meaning, because in that case a basis function does not correspond to an atomic orbital. Furthermore, the results are rather sensitive to

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changes in the basis sets. It may give in some cases even unreasonable results. Several approaches have been proposed to remove the defects of Mulliken analysis method [2-9]. However, none of them have completely succeeded due to their own weaknesses.

In this paper, it will be shown that in the calculations with extended basis sets, if the atomic orbitals in molecular environments (AOIMs) are taken as the basis sets of population and bonding analyses the defects of Mulliken analysis method can be overcome to a certain extent, while keeping the advantage of simplicity and being easy to use. Therefore an approach is provided to obtain a clear and simplified physical picture from the results calculated with extended basis sets.

### 2 Method and principle

It has been recognized for a long time that the orbitals of an atom in free states and in molecular environments may be different [10–14]. The changes of atomic orbitals in molecular environments have to be taken into account for explanation of many chemical phenomena [15–17]. Therefore it seems more reasonable to adopt the atomic orbitals in molecular environments as basis sets in the LCAO-MO formulation. In a free atom the electrons move in a potential field with spherical symmetry. In molecular environments the potential which the electrons experience is non-spherical. Its spherical component with respect to an atom is also different from the potential of that atom in free states. Both the atomic feature and the effect of molecular environments should be taken into account. It has been proposed [18] to define the atomic orbitals in molecular environments as the wave functions of an electron moving in an effective potential which is the spherical average of the molecular potential with the center at the related atomic nucleus. In other words, the AOIMs,  $\{\phi_i^A(r)\}$ , are the eigenfunctions of the following equation:

$$\left[-\frac{1}{2}\nabla^{2} + V_{00}^{A}(r)\right]\phi_{i}^{A}(r) = E_{i}^{A}\phi_{i}^{A}(r), \qquad (1)$$

where the effective potential  $V_{00}^{A}(r)$  is the spherical average of the molecular potential field with the center at the nucleus of atom A. When the spherical coordinate  $(r, \theta, \varphi)$  with origin at nucleus A is adopted, then

$$V_{00}^{A}(\mathbf{r}) = (1/4\pi) \int V(\mathbf{r}) \sin \theta \, \mathrm{d}\theta \, \mathrm{d}\varphi, \qquad (2)$$

where  $V(\mathbf{r})$  is the molecular potential field.  $E_i^A$  is the corresponding eigenvalue. Let

$$\phi_i^{\mathbf{A}}(\mathbf{r}) = (1/r) P_{nl}^{\mathbf{A}}(r) Y_{lm}(\theta, \varphi), \tag{3}$$

where n, l, m are the principal, angular and magnetic quantum numbers. Substituting Eq. (3) into Eq. (1), the radial Schroedinger equation for atom A can be obtained:

$$\left[-\frac{1}{2}\frac{\mathrm{d}^2}{\mathrm{d}r^2} + l(l+1)/2r^2 + V^{\mathrm{A}}_{00}(r)\right]P^{\mathrm{A}}_{nl}(r) = E^{\mathrm{A}}_i P^{\mathrm{A}}_{nl}(r). \tag{4}$$

Expanding  $P_{nl}(r)$  with the basis set  $\{\chi_k^A(r)\}$  centered on nucleus A

$$P_{nl}^{A}(r) = \sum_{k} C_{ki} \chi_{k}^{A}(r)$$
<sup>(5)</sup>

and substituting it into Eq. (4), the matrix equation (6) can be obtained:

$$\boldsymbol{F}_{l}^{\mathrm{A}}\boldsymbol{C}_{l}^{\mathrm{A}} = \boldsymbol{S}_{l}^{\mathrm{A}}\boldsymbol{C}_{l}^{\mathrm{A}}\boldsymbol{E}_{l}^{\mathrm{A}}, \tag{6}$$

where the matrix elements of  $F_l^A$  are

$$(F_{l}^{A})_{kj} = \left\langle \chi_{k}^{A}(r) \left| \left[ -\frac{1}{2} \frac{\mathrm{d}^{2}}{\mathrm{d}r^{2}} + l(l+1)/2r^{2} + V_{00}^{A}(r) \right] \right| \chi_{j}^{A}(r) \right\rangle$$
(7)

and the overlap matrix elements  $(S_i^A)_{ki}$  are

$$(\mathbf{S}_{l}^{\mathbf{A}})_{kj} = \langle \chi_{k}^{\mathbf{A}}(r) | \chi_{j}^{\mathbf{A}}(r) \rangle.$$
(8)

 $C_i^A$  is the combination coefficient matrix and  $E_i^A$  is the eigenvalue matrix. Solving Eq. (6) and substituting the obtained  $P_{nl}^A(r)$  into Eq. (3), the orbitals of atom A in the molecular environment can be obtained.

For computational convenience,  $\{\chi_k^A(r)\}\$  can be taken as the same as the radial functions of the basis sets used in the related molecular calculation, though this is by no means necessary. Denote the basis set used in the molecular calculation as  $\{\chi_{nlm}^A, X = A, B, C, ...\}\$  and the subset of the functions centered on atom A as  $\{\chi_{nlm}^A\}\$ . Suppose that  $F_{lm}^A$  and  $S_{lm}^A$  are the Fock and overlap matrix blocks, respectively, corresponding to the basis functions with quantum numbers l,m and belonging to atom A, it is easy to prove that [18]

$$\sum_{m} (F_{lm}^{A})/(2l+1) = F_{l}^{A},$$
(9)

$$\sum_{m} (S_{lm}^{A})/(2l+1) = S_{l}^{A}.$$
(10)

So after the molecular calculation finishes, the matrices  $F_i^A$  and  $S_i^A$  can be evaluated by use of Eqs. (9) and (10), and then Eq. (6) is solved to obtain  $C_i^A$  and the AOIMs. When the basis set is complete for the molecular calculation and the subset is complete too for the atomic calculations, the obtained AOIMs will be exact and unique. The result of Mulliken analysis using the exact AOIMs as basis set should be unique, because the first-order density matrix with AOIMs as basis is uniquely determined. Even though  $\{\chi_{nlm}^{\chi}(r)\}$  is not a complete basis set, so long as it is a balanced one, the obtained AOIMs would be the optimal approximate solution for the given basis set, because they are obtained from variational calculations. Then the arbitrariness of the Mulliken analysis results would be decreased to a certain extent. It has been found [19] that the molecular calculations using the extended basis sets of  $3\zeta$  plus polarization functions can give sufficiently accurate results. Therefore the approximate AOIMs should be good enough when the used basis sets are extended to  $3\xi$  or higher quality.

By use of the matrix of transformation from basis functions to AOIMs, the overlap and density matrices can be transformed into those using the AOIMs  $\{\phi_{nlm}^X(r)\}$  as basis set. Then the population and bonding analyses can be carried out in the ordinary way.

# 3 Results and discussion

The aforementioned method can be applied to any calculations based on orbital approximation, e.g. ab initio Hartree–Fock method or density functional theory (DFT) method. In recent years, the calculation practice has shown [20, 21] that the

DFT method based on Kohn-Sham equation usually gives more satisfactory results than the Hartree-Fock method does. In this work, a series of small molecules were calculated with different quality basis sets by the approximate density functional theory (LDA) method. The Kohn-Sham equation was solved, then the population and bonding analyses were carried out. The program for DFT calculations and that for population and bonding analyses with AOIMs as basis sets were developed in author's laboratory [22]. The reliability of the used DFT program has been confirmed by checking its outputs with those from the famous ADF program [23]. The minimal basis sets are numerical ones obtained by the approximate density functional theory calculations for free atoms. The double zeta basis sets were taken from Ref. [24]. The three and multiple zeta basis sets were taken from Ref. [25].

As an example, some calculation results for hydrogen fluoride are presented. The three  $\zeta$  plus polarization function basis set was used. After the convergent result of the molecular calculation for hydrogen fluoride was obtained, the angular averaged Fock matrix  $F_i^A$  and overlap matrix  $S_i^A$  for the subshell l of atom A were calculated by means of Eqs. (9) and (10). Then Eq. (6) was solved to get the eigenvector matrix  $C_i^A$  of AOIMs for the subshell l of atom A. In Table 1a presented are the Fock matrix  $F_0^F$  and the overlap matrix  $S_0^F$  for the s type orbitals of fluorine atoms in HF molecules. The AOIM vector matrix  $C_0^F$  for s type orbitals of fluorine atoms in HF molecules is presented in Table 2a. Similarly, the matrices  $F_1^F$  and  $S_1^F$ as well as  $C_1^F$  for p type orbitals of fluorine atoms in HF molecules are presented in Tables 1b and 2b, respectively. In Tables 1c and 2c, the corresponding data of  $F_0^{\rm H}$ ,  $S_0^{\rm H}$  and  $C_0^{\rm H}$  for hydrogen atoms in HF molecules are presented, respectively. Because single  $\zeta$  bases were used for the polarization functions, the corresponding AOIMs are just the same as the bases. Therefore the matrix of transformation from bases to AOIMs could be constructed, with which the molecular density matrix and overlap matrix were transformed into those with AOIMs as the basis set. The transformed matrices were used to carry out the population and bonding analyses based on AOIMs. The results are presented in the following sections.

#### 3.1. Population analysis

According to the definition [1], the electron population in the *nl* subshell of atom A is

$$q_{nl}^{\mathrm{A}} = \sum_{i \in (\mathrm{A}nl)} \sum_{j}^{\mathrm{all}} P_{ij} S_{ij}, \qquad (11)$$

where  $P_{ij}$  and  $S_{ij}$  are the density and overlap matrix elements, respectively. For the minimal basis sets the basis functions are just the approximate AOIMs. For the extended basis sets, the population on the basis functions cannot be correlated to the electronic occupancy on subshells, because there is no simple correspondence between the basis functions and the atomic orbitals. When the population analysis is based on AOIMs, the results can be identified with the electronic configurations of atoms in molecular environments.

In Table 3 listed are the results of Mulliken population analysis based on AOIMs for some molecules calculated using different quality of basis sets. It can be seen from Table 3 that no matter which type of basis sets was used in the molecular calculations, the AOIMs can be divided into two clear-cut subsets. One subset

	Overlap mai	trix (upper tria	ngular matrix)			
	1.0000	0.9841	0.9964	0.0000	0.3357	0.1589
- 24.074		1.0000	0.9655	0.0763	0.2406	0.1053
- 23.692	- 22.452		1.0000	- 0.0352	0.3762	0.1818
- 23.987	- 24.053	- 23.668		1.0000	- 0.9191	- 0.9479
0.0018	- 0.0714	0.0356	-1.0434		1.0000	0.8682
- 8.0846	- 8,1416	- 7.9588	0.9434	- 3.4278		1.0000
- 3.8257	- 3.6379	- 3.8687	1.0114	- 2.3175	-1.4228	

Table 1a. The angular-averaged Fock and overlap matrix blocks for s orbitals of F atoms in HF molecules

Fock matrix (lower triangular matrix)

Table 1b. The angular-averaged Fock and overlap matrix blocks for p orbitals of F atoms in HF molecules

	Overlap matrix (	upper triangular ma	trix)	
	1.00000	0.83734	0.96422	
- 0.35592		1.00000	0.66709	
-0.23488	0.76120		1.00000	
- 0.37198	-0.71016	- 0.14501		

Fock matrix (lower triangular matrix)

Table 1c. The angular-averaged Fock and overlap matrix blocks for s orbitals of F atoms in HF molecules

	- · ·		
	1.00000	0.91016	0.98483
- 0.08417		1.00000	0.96471
- 0.15624	0.01610		1.00000
- 0.12870	-0.12033	-0.14217	

is strongly occupied, denoted as  $\{AOIM\}_B$ . It corresponds to the sum set of the occupied subshells of free atoms in ground states, in general, being a minimal compact set. The occupancy on  $\{AOIM\}_B$  describes the basic electronic configurations of an atom. Thus it is fundamental and indispensable for essentially correct description of the electron distribution on individual atomic orbitals. The population on the orbitals of the other subset is very small in general, called "Rydberg set" according to Ref. [7], and denoted by  $\{AOIM\}_R$ . The electron population on "Rydberg" set is unessential for describing the charge distribution of a molecule. It reflects the fact that the LCAO-MO formulation based on minimal basis sets

1s	2 <i>s</i>	3s	4 <i>s</i>	5s	6 <i>s</i>
1.0027	0,3448	- 22.211	45.014	- 128.93	487.22
-0.0009	- 0.1283	8.2373	- 16.576	46.949	- 159.70
-0.0008	- 0.0941	1.5196	4.8850	107.97	- 345.55
- 0.0039	- 1.3933	42.317	- 117.05	- 88.253	50.814
-0.0024	- 0.3182	29.704	- 75.465	- 55.192	31.548
-0.0018	-0.1136	16.477	- 51.819	- 39.824	23.002

Table 2a. The s type AOIMs of F atoms in HF molecules

Table 2b. The p type AOIMs of F atoms in HF molecules

2 <i>p</i>	3 <i>p</i>	4 <i>p</i>	
$ \begin{array}{r} 1.4803 \\ - 0.2183 \\ - 0.3096 \end{array} $	18.052 - 6.9496 - 12.727	9.6451 2.2298 8.0430	

Table 2c. The s type AOIMs of H atoms in HF molecules

1s	2 <i>s</i>	35	
- 1.4777	7.5082	- 9.0325	
-0.7720	1.4083	- 7.6339	
3.1920	- 8.6572	16.177	

cannot accurately describe the charge distribution in a molecule. The fact that two subsets,  $\{AOIM\}_B$  and  $\{AOIM\}_R$ , can be clearly distinguished and the population on the subset  $\{AOIM\}_R$  is very small, shows that the LCAO-MO picture can be optimally realized by taking AOIMs as basis sets. In other words, by use of  $\{AOIM\}_B$ , the charge distribution of a molecule can be described as accurately as possible within the limitation of minimal basis sets being used. For obtaining the simplified physical pictures of the charge distribution as accurately as possible, one can consider the population on subset  $\{AOIM\}_B$  only, while neglecting the subset  $\{AOIM\}_R$  completely. The above consideration may be helpful to explain the fact that in the DV-X $\alpha$ -SCC method, although the molecular charge is approximately decomposed into the superposition of the spherical atomic charges by Mulliken population analysis method, which seems a very rough approximation, the obtained results approach to those from much more accurate treatment.

Two points should be noted. The first is that in some cases, some orbitals, e.g. the Li 2p orbitals in LiF and the S 3d orbitals in SF, possess significant population, although these orbitals are unoccupied in the related free atoms in ground states. These phenomena are usually ascribed to the change of atomic orbitals when the atoms transform to molecular environments from free states. It is well known that the chemical properties of some elements, such as Li, Be, P, S, some transition metals, lanthanides, etc., cannot be completely elucidated if only their occupied valent orbitals of free atoms in ground states are considered [15–17, 26]. This type of orbitals should be put in the subset {AOIM}<sub>B</sub> instead of {AOIM}<sub>R</sub>.

point is that small negative population appears on some orbitals in the subset  ${AOIM}_R$ , which is obviously unreasonable. This is correlated with the inherent flaw of the Mulliken analysis method [2]. Fortunately, the drawback is not so serious here. First, the negative population on the orbitals in  $\{AOIM\}_{R}$  is very small, less than 0.01 electrons as usual, thus it can be neglected for obtaining a simplified physical picture of the electron distribution on individual atomic orbitals through population analysis. Second, as has been mentioned above, the population on  $\{AOIM\}_{R}$  represents the deviation of the LCAO-MO formulation based on minimal basis sets under the optimal situation, its values may be positive or negative. If one wants to remove this unreasonable point, there are two approaches. The first approach is to perform a symmetrical orthogonalization of AOIMs before the population analysis, which has been used in the natural population analysis by Reed et al. [7]. This approach has the defect that the population in fact is not localized on individual atoms in view of its space distribution. Furthermore, the orthogonalized atomic orbitals cannot be conveniently used to the bonding analysis in terms of overlap charges. The other approach is to assign the small population on an orbital in subset  $\{AOIM\}_{R}$  to the highest valence orbital with the same symmetry. This approach corresponds to construction of a valent orbital consisting of the AOIM in the highest valence shell and the orbitals in  $\{AOIM\}_{R}$ . But it seems usually unnecessary.

As an intermediate step of constructing the natural atomic orbitals (NAO), Reed et al. [7] obtained the pre-NAO through diagonalization of one center angular symmetry blocks of the density matrix and indicated that the PNAOs could be divided into two sets on the basis of occupancy, the "minimal" set corresponding to all atomic subshells of non-zero occupancy in the ground state of free atoms, and the "Rydberg" set consisting of the remainder orbitals. For comparison, the Mulliken population analysis based on PNAOs for N<sub>2</sub> molecules has been carried out and the result is listed in the row of  $N_2$  in Table 3 (the data in the parentheses). It is obvious that, according to the orbital population, the PNAOs cannot be clearly divided into the two subsets, the strongly occupied minimal subset and the very weakly occupied "Rydberg" subset. Through the "occupancy-weighted symmetric orthogonalization" procedure, Reed et al. [7] got the natural atomic orbitals, then reached the aim to clearly divide the basis set into two subsets. Their procedure not only made the calculation more complicated, but also introduced additional arbitrariness. Thus it is not so simple and objective as the AOIM method proposed in this paper. It can be seen from Table 3 that the population based on AOIMs is fairly stable to changes of the basis sets used in the molecular calculations. Of course, there must be some variation of the population, because when the basis sets used in the molecular calculations are not large enough, not only the AOIMs are approximate, but also the result of the molecular calculation is approximate. Maybe because both the MOs and AOIMs are obtained through the variational procedure, the population based on AOIMs can be comparatively more stable.

#### 3.2. Bonding potential

Wiberg defined the orbital bonding potential as [27]

$$b_i = 2(PS)_{ii} - (PS)_{ii}^2$$
  
= 2q<sub>i</sub> - q<sub>i</sub><sup>2</sup>, (12)

Table 3. Popi	ulation analysis	based on AOI	Ms: The distr	ibution of elect	trons on individ	lual atomic sı	ıbshells			
Molecules	Basis sets	ls	2s	3 <i>s</i>	4 <i>s</i>	2p	$_{3p}$	4p	5p	3d
N2	MIN	2.001	1.756			3.243				
		(2.001)	(1.756)			(3.243)				
	DZ	1.999	1.872	0.027	0.000	3.099	0.004			
		(1.817)	(1.711)	(0.251)	(0.154)	(2.645)	(0.457)			
	DZP	2.000	1.772	0.030	0.000	3.123	0.011			0.065
		(1.701)	(1.621)	(0.328)	(0.152)	(2.651)	(0.481)			(0.065)
	TZ	1.999	1.860	0.047	- 0.003	3.070	0.043	- 0.015		
		(1.674)	(1.000)	(0.985)	(0.240)	(666))	(1.074)	(0.024)		
	TZP	2.000	1.749	0.044	- 0.003	3.112	0.040	- 0.008		0.066
		(1.700)	(1.173)	(0.720)	(0.195)	(2.459)	(0.667)	(0:020)		(0.066)
	MZ	1.999	1.836	0.057	- 0.003	3.041	0.079	- 0.009	0.000	
		(1.380)	(1.318)	(0.703)	(0.449)	(2.026)	(0.584)	(0.275)	(0.225)	
co	O NIM	2.000	1.865			4.461				
	C	2.001	1.676			1.994				
	DZ 0	1.999	1.920	-0.016	0.000	4.340	- 0.009			
	C	2.001	1.802	0.080	0.001	1.824	0.058			
	TZ 0	2.000	1.894	- 0.019	0.000	4.361	- 0.002	-0.003		
	C	2.000	1.829	0.088	0.000	1.821	0.025	0.005		
	MZ 0	2.000	1.896	- 0.028	0.000	4.202	0.031	- 0.004	0.000	
	C	2.000	1.941	0.074	0.001	1.811	0.057	0.021	-0.012	
HF	MIN F	2.000	1.971			5.554				
	Η	0.476								
	DZP F	2.000	1.996	-0.006		5.501	- 0.005			0.022
	Η	0.440	0.014			0.039				
	TZP F	2.000	1.970	- 0.005	0.000	5.553	-0.003	- 0.003		0.022
	Н	0.404	0.015	0.003		0.042				

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LiF	MIN	Ц	2.000	1.994			5.730				
		Li	2.000	0.227							
	DZ	ц	2.000	2.003	-0.002	0.000	5.808	-0.001			
		Ľ	2.001	0.192	-0.002	0.000					
	DZP	ĹĿ,	2.000	1.948	0.000		5.774	0.008			0.006
		Li	1.996	0.024	-0.002	0.001	0.228				0.019
	TZP	Ц	2.000	1.958	-0.001	0.000	5.718	0.006	-0.001		0.005
		Li	1.997	0.035	0.006	-0.001	0.242	0.011			0.025
	MZP	ţL,	2.000	1.914	0.000	0.000	5.785	0.007	0.000	0.000	0.005
		Li	1.999	0.035	0.007	0.004	0.222	0.010			0.019
SF	MIN	Ц	2.000	1.979			5.249				
		s	2.000	2.000	1.958		6.000	3.814			
	DZ2P	ы	2.000	1.949	-0.028		5.440	-0.020			0.038
		s	2.000	2.000	1.962		6.000	3.385	0.022		0.255
	<b>TZ2P</b>	ц	2.000	1.971	-0.014	0.000	5.331	0.000	-0.002		0.041
		S	2.000	2.000	1.945	0.002	6.000	3.398	0.056	-0.010	0.290
CCI₄	MIN	c	2.000	1.332			3.003				
		ច	2.000	2.000	1.950		6.000	4.967			
	DZP	с	2.000	1.181	0.068		2.793	0.045			0.070
		Ū	2.000	2.000	1.946	- 0.009	6.000	4.977	- 0.006		0.051
	TZP	U	2.000	1.094	0.097	0.000	2.883	0.051	- 0.060		0.070
		ច	2.000	2.000	1.941	-0.006	6.000	4.938	0.054	-0.012	0.052
Note: MIN, I polarization fi based on prer	DZ, TZ, M unctions au	IZ, deno re added	te minimal, c to the basis itals	louble zeta, ti sets. In the ro	riple zeta and ow of N <sub>2</sub> mole	multiple zeta b cules the data i	asis sets, respe in the parenthe	sctively; **P or * eses are the popu	**2P is used to ulation obtained	indicate that l from Mullik	one or two en analysis
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Table 4. The	Wiberg orb	ital bonding potent	tials based on A	OIMs for som	ne molecules					
Molecules	Basis sets	1s	2s	38	4s	2p	3 <i>p</i>	4p	Бp	3d
H2	MIN	1.000								
	DZ DZP	1.000	0.002 0.003			0.014				
	TZP	1.000	0.013	- 0,004		0.014				
$ m N_2$	MIN	- 0.001	0.428			2.941				
I	DZ	0.003	0.240	0.053	0.000	2.994	0.010			
	DZP	- 0.001	0.405	0.059	0.000	2.978	0.020			0.067
	ΤZ	0.001	0.261	0.092	0.006	2.998	0.084	-0.032		
	TZP	0.000	0.440	0.086	-0.007	2.980	0.075	- 0.013		0.131
	MZ	0.001	0.302	0.111	- 0.006	2.999	0.149	- 0.018	0.001	
CO	MIN	O - 0.001	0.246			2.278				
		C – 0.001	0.543			2.591				
	DZ	O 0.003	0.153	- 0.033	0.000	2.400	-0.016			
		C – 0.003	0.357	0.155	0.001	2.530	0.109			
	ΤZ	O 0.000	0.201	- 0.038	0.000	2.380	- 0.002	- 0.006		
		C 0.000	0.313	0.169	0.000	2.510	0.051	0.011		
	TZP	0000	0.286	-0.025	0.000	2.301	- 0.005	- 0.002		0.097
		C 0.000	0.452	0.143	0.000	2.456	0.047	0.015		0.101
	MZ	O 0.000	0.197	-0.057	0.001	2.501	0.060	- 0.008	0.000	
		C 0.000	0.443	0.115	0.002	2.517	0.111	0.044	0.000	
HF	MIN	F 0.000	0.058			0.694				
		H 0.725								
	DZP	F 0.000	0.008	-0.012	0.000	0.782	- 0.010			0.044
		H 0.687	0.029			0.078				
	TZP	F 0.000	0.058	- 0.010	0.000	0.722	- 0.004	- 0.004		0.044
		H 0.645	0:030	0.007		0.082				

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DZP MZP MIN SP FF TZP TZP FF FF FF FF FF FF FF FF TZP MIN NZ2P FF FF FF CC DZP MIN SP FF FF CC CC CC CC CC CC CC CC CC CC CC	0.000         0.102         0.001         0.000         0.436         0.000         0.012         0.001         0.003         0.012         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.013         0.011         0.001         0.011 <th< th=""><th>0.009 0.014 0.002 -0.00/ 0.425 0.019 0.000 0.000 0.037 0.000 0.000 0.083 0.000 2.770 0.000 0.042 0.001 0.000 2.946 0.040 0.481 0.000 0.099 -0.056 1.001 -0.039</th><th><math display="block">\begin{array}{cccccccccccccccccccccccccccccccccccc</math></th><th><math display="block">\begin{array}{cccccccccccccccccccccccccccccccccccc</math></th><th><math display="block">\begin{array}{cccccccccccccccccccccccccccccccccccc</math></th></th<>	0.009 0.014 0.002 -0.00/ 0.425 0.019 0.000 0.000 0.037 0.000 0.000 0.083 0.000 2.770 0.000 0.042 0.001 0.000 2.946 0.040 0.481 0.000 0.099 -0.056 1.001 -0.039	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
DZP F MZP F Li MIN S DZ2P S TZP S TZP S MIN O DZP H DZP H H TZP 0 DZP 0 DZP C DZP C DZP C CI CI CI	0.000 0.102 0.00 0.047 0.007 - 0.00 0.000 0.165 0.00	0.009 0.014 0.000 0.000 0.000 0.08 0.000 0.042 0.07 0.000 0.000 0.07 0.000 0.059 - 0.05	0.000 0.000 0.000 0.10 0.000 0.086 - 0.03 0.000 0.000 0.000 0.10 0.000 0.000 - 0.01 0.000 0.000 - 0.01	0.000 0.165 0.823 0.542 - 0.00 0.001 0.542 - 0.00 0.799 0.083 - 0.02 0.762 0.109 - 0.00	0.000         0.987         0.987           0.000         0.000         0.000           0.000         0.967         0.13           0.000         0.967         0.13           0.000         0.000         0.10           0.000         0.000         0.111           0.000         0.000         0.018           0.000         0.000         0.018
	DZP F Li MZP F	MIN S MIN S DZ2P S F	TZP S F TZ2P S MZ2P S F	MIN O H H O DZD H H TZP H	MIN C DZP C TZP C C C

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where  $q_i$  is the Mulliken population on orbital *i*. It is obvious that when the electron population on orbital i is zero or two,  $b_i = 0$ , which means that orbital *i* contributes nothing to bonding. This is in accordance with the general concept of chemists. Thus  $b_i$  can be used to measure the bonding potential of orbital *i*. It should be noted that  $q_i = (PS)_{ii} = \sum_{j}^{\text{all}} P_{ij}S_{ij}$ , includes the overlap charges between orbital *i* and all other orbitals and correlates to Mulliken bond orders. Usually, when the extended basis sets are used in the calculations, a basis function cannot represent an atomic orbital. Furthermore, the basis functions centered at one atom are not necessarily orthogonalized to each other. Therefore  $b_i$  will involve the unphysical "bond orders" within an atom. Thus it cannot be used to measure the bonding potential of basis function *i*. When AOIMs are taken as basis sets, there is no such problem. The bonding potentials calculated based on AOIMs for some molecules under different basis sets are listed in Table 4. It can be seen from the data in Table 4 that in general the Wiberg orbital bonding potential calculated based on AOIMs is fairly stable with respect to changes of the basis sets used in the molecular calculations. The results are reasonable. For example, the bonding potential for the core orbitals and for the orbitals in Rydberg subset is very small, while the bonding potential of the main valence orbitals is in general large. It is weaker for 2s than that of 2p orbitals, and so on. The Li 2p orbitals in LiF and S 3d orbitals in SF possess comparatively larger bonding potential, showing that they significantly participate in bonding, which is consistent with the experiments.

#### 3.3. Bonding extent between atoms: the bond orders

The Bonding extent between atoms in a molecule is a topic discussed very often among chemists. Mulliken proposed in 1955 [1] to measure it by the overlap charge, that is, the Mulliken bond order  $M_{AB}$ :

$$M_{AB} = \sum_{i \in A} \sum_{j \in B} 2P_{ij}S_{ij}.$$
 (13)

Mulliken bond order has been distributed widely among chemists. Its flaw is that the values of the bond order are considerably different from those conventional to the chemists. For example, for the typical single, double and triple bonds the Mulliken bond order values often differ considerably from 1, 2 and 3, respectively. Furthermore, the values are not quite stable to changes of the basis sets. Wiberg [27] defined the bond order between atoms A and B,  $W_{AB}$ , as

$$W_{AB} = \sum_{i \in A} \sum_{j \in B} (P_{ij})^2.$$
(14)

This definition, however, can only be adopted for orthogonalized basis sets. Mayer [28] extended it to non-orthogonalized basis sets and defined the bond order  $B_{AB}$  as

$$B_{AB} = \sum_{i \in A} \sum_{j \in B} 2[(P^{\alpha}S)_{ij}(P^{\alpha}S)_{ji} + (P^{\beta}S)_{ij}(P^{\beta}S)_{ji}],$$
(15)

where  $P^{\alpha}$  and  $P^{\beta}$  are the density matrices of  $\alpha$  and  $\beta$  electrons, respectively. For the typical chemical bonds the values of Mayer bond order are very close to those conventional to chemists. For example, the Mayer bond order between N-N atoms in N<sub>2</sub> molecules is  $B_{AB} = 3.0$ . Furthermore,  $B_{AB}$  is rather insensitive to changes of the basis sets.

Molecules	Basis sets	Mulliken b	ond orders	Mayer bond orders	
		AO	{AOIM} <sub>B</sub>	AO	{AOIM} <sub>B</sub>
H <sub>2</sub>	MIN	0.884	0.884	1.000	1.000
	DZ	0.814	0.844	1.000	1.000
	DZP	0.832	0.888	1.000	1.000
	TZP	0.832	0.890	1.000	1.000
	$SD^{a}$	0.015	0.011	0.000	0.000
$N_2$	MIN	1.073	1.073	3.000	3.000
-	DZ	0.681	0.936	2.750	2.780
	DZP	1.237	1.216	2.896	2.820
	ΤZ	0.789	0.972	2.744	2.732
	TZP	1.382	1.316	2.934	2.816
	MZ	1.004	1.146	2.857	2,766
	SD	0.108	0.059	0.042	0.039
0	MIN	0.888	0.888	2.411	2.411
	DZ	0.603	0.728	2.307	2.270
	TZ	0.598	0.808	2.276	2.259
	TZP	0.894	0.900	2.293	2.215
	MZ	0.370	0.656	2.293	2.159
	MZP	0.275	0.804	2.144	2.139
	SD	0.081	0.038	0.038	0.034
HF	MIN	0 352	0 352	0.725	0.725
Hr	DZP	0.332	0.352	0.725	0.720
	<u>т</u> 7Р	0.422	0.426	0.741	0.700
	SD	0.039	0.023	0.006	0.016
iF	MIN	0.040	0.040	0.476	0.476
	DZ	0.029	0.038	0.342	0.345
	DZP	0.342	0.260	0.542	0.523
	DEI	0.542	0.200	0.527	(0.430) <sup>b</sup>
	TZP	0.400	0.276	0.598	0.594
					(0.455)
	MZP	0.372	0.270	0.545	0.544
					(0.418)
	SD	0.017	0.005	0.021	0.021
F	MIN	0.574	0.574	1.139	1.139
SF	DZ2P	0.431	0.608	0.946	0.970
					(0.160) <sup>b</sup>
	TZP	0.117	0.490	1.126	1.149
					(0.186)
	TZ2P	0.183	0.490	1.090	1.115
					(0.181)
	MZ2P	0.520	0.454	0.937	1.026
					(0.172)
	SD	0.091	0.029	0.044	0.035
I <sub>2</sub> O	MIN	0.509	0.509	0.798	0.798
O-H)	DZP	0.914	0.914	1,181	1.153
	TZP	0.796	0.810	1.075	1.037
	SD	0.120	0.121	0.114	0.105

Table 5. The Mulliken and Mayer bond orders under different basis sets

Molecules	Basis sets	Mulliken bond orders		Mayer bo	ond orders
		AO	{AOIM} <sub>B</sub>	AO	{AOIM} <sub>B</sub>
CCl <sub>4</sub>	MIN	0.396	0.396	0.972	0.972
(C–Cl)	DZP	0.479	0.524	0.995	0.978
	TZ	0.360	0.442	0.975	0.954
	TZP	0.560	0.526	1.030	0.991
	SD	0.045	0.038	0.013	0.008
	TSD°	0.069	0.040	0.035	0.032

Table 5. (Continued)

<sup>a</sup> Standard deviation

<sup>b</sup> The contribution of Li 2p or S 3d orbitals to the Mayer bond orders

" Weighted standard deviation averaged over all molecules

In Table 5 are listed the Mulliken bond orders and Mayer bond orders, and those calculated based only on subset  $\{AOIM\}_{B}$ . Different basis sets have been used and the standard deviation to the changes of the basis sets are listed.

It can be seen from Table 5 that the Mulliken bond orders calculated based on AOIMs are more stable with respect to the changes of basis sets than the conventional ones. In comparison to Mulliken bond orders, the Mayer bond orders are, in consistency with the previous conclusion [28], more stable to the changes of basis sets. The Mayer bond orders calculated based on  $\{AOIM\}_B$  are more stable with respect to the changes of basis sets than the conventional ones. The Mayer bond orders calculated based on  $\{AOIM\}_B$  are more stable with respect to the changes of basis sets than the conventional ones. The Mayer bond order can be decomposed into the contributions of individual subshells of atoms, which are also stable to the changes of basis sets. The contribution of a subshell to Mayer bond orders calculated based on  $\{AOIM\}_B$  can be used to objectively measure their contribution to bonding. For example, the contribution of Li 2p orbitals in LiF to Mayer bond orders is over 75%, showing that they are the main bonding orbitals. In SF the contribution of S 3d orbitals to Mayer bond orders is up to 17%, thus it cannot be neglected.

#### 4. Concluding remarks

In this paper, it is proposed to perform the population and bonding analyses based on the AOIMs when the extended basis sets are used. The AOIMs are defined as the solution of the Schroedinger equation of an electron moving in the potential field which is the spherical average of the molecular potential field with the center at one atomic nucleus. The method to construct the AOIMs from the Fock matrix of molecular calculations is presented. The results of the practical calculations for a series of molecules show that AOIMs can be clearly divided into two subsets. According to the Mulliken population on individual orbitals, the strongly occupied minimal compact subset  $\{AOIM\}_B$  and the very weakly occupied "Rydberg" subset  $\{AOIM\}_R$  can be distinguished. The formulation of "the molecular orbitals consisting of minimal atomic orbital sets" can be optimally realized in terms of  $\{AOIM\}_B$ . Through addition of very weakly occupied subset  $\{AOIM\}_R$  to construct the extended basis sets the molecular electronic structure can be described accurately. In terms of AOIMs the results of population analyses and the

calculated Wiberg orbital bonding potentials are fairly stable to the changes of basis sets. The results of the bonding analysis based on AOIMs are reasonable and quite stable to the changes of basis sets. Mayer bond orders are more stable than Mulliken bond orders. The Mayer bond orders based on  $\{AOIM\}_B$  are even more stable. Thus it can be used to objectively measure the contribution of individual atomic orbitals to bonding.

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