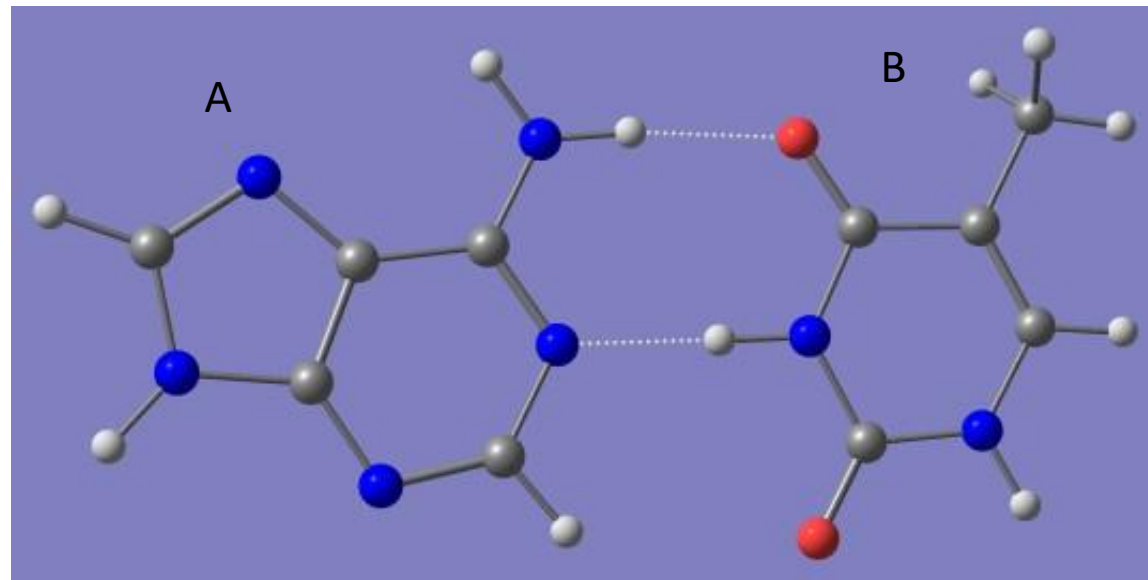
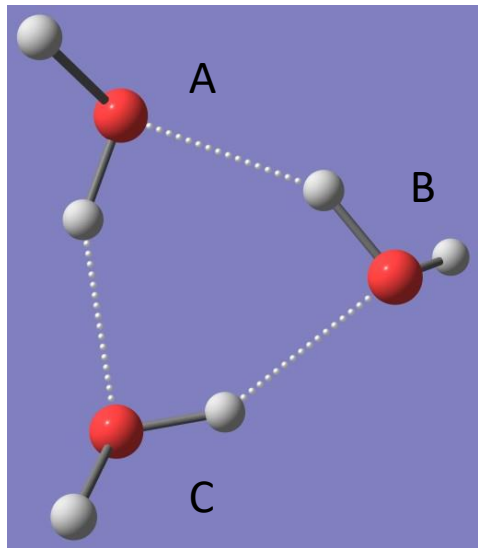


Interaction energies in non-covalent complexes, various decomposition schemes

Prepared by Radek Marek group

Interaction energy



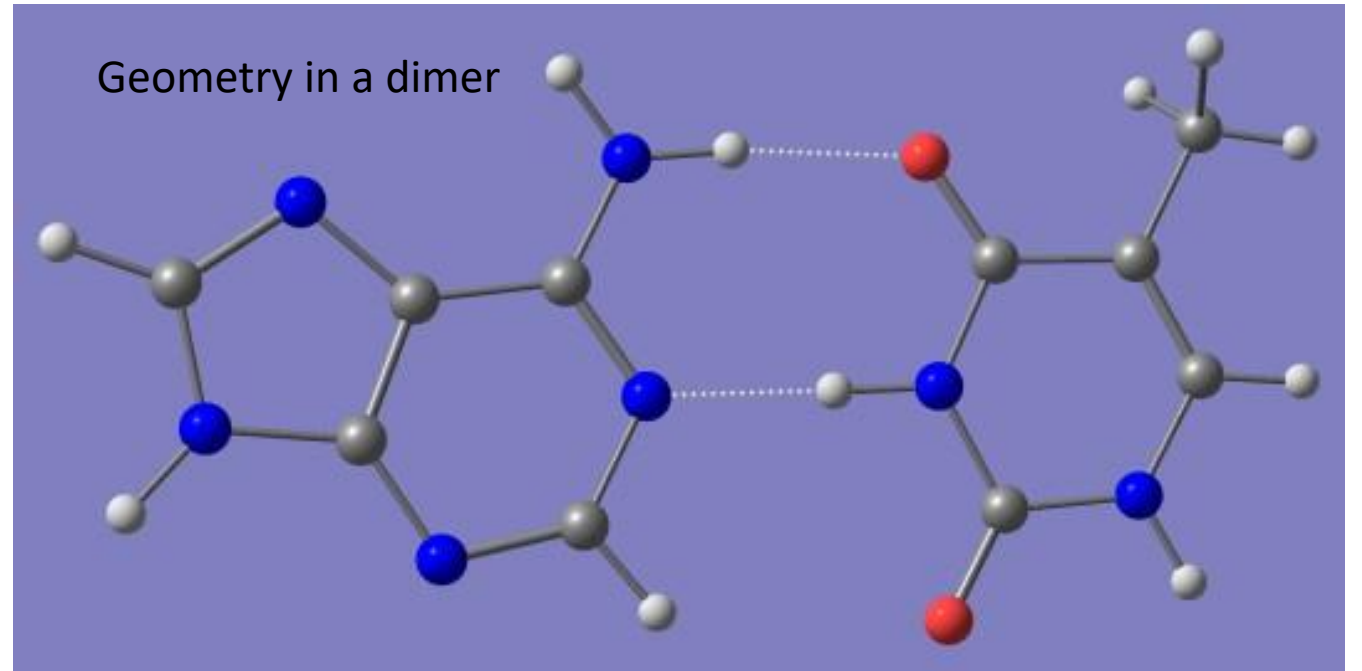
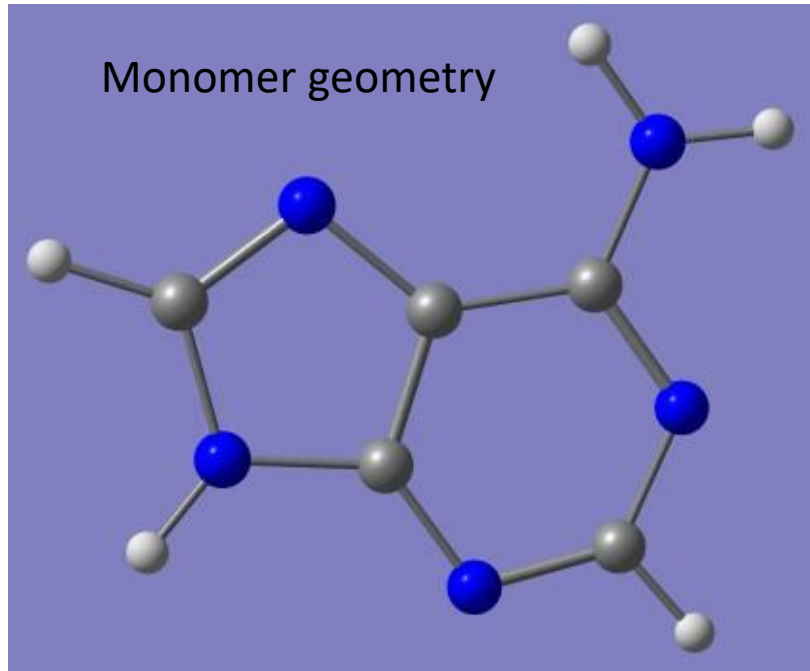
$$\Delta E^{ABC} = E^{ABC} - [E^A + E^B + E^C]$$

$$\Delta E^{AB} = (E^{AB}) - (E^A + E^B).$$

$$\Delta E^{ABC} = \Delta E^{AB} + \Delta E^{AC} + \Delta E^{BC} + \Delta E^3 = E^{AB} - [E^A + E^B] + E^{AC} - [E^A + E^C] + E^{BC} - [E^B + E^C] + \Delta E^3$$

$$\Delta E^3 = E^{ABC} - E^{AB} - E^{AC} - E^{BC} + E^A + E^B + E^C$$

Deformation energy



$$\Delta E^{\text{DEF}} = (E^{\text{A}} - E^{\text{Ai}}) + (E^{\text{B}} - E^{\text{Bi}})$$

Deformation (preparation) energy

$$\Delta E^{\text{T(AB)}} = \Delta E^{\text{AB}} + \Delta E^{\text{DEF}}$$

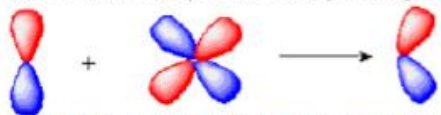
Binding (total) energy

Basis sets

- Set of functions representing atomic orbitals
- Molecular orbital = linear combination of atomic orbitals (MO-LCAO)
- Minimal basis set (one function per orbital)
- Gaussian-type and Slater-type functions
- 6-311++G(d,p)
- LANL2DZ
- aug-cc-pVTZ
- Diffuse and polarization functions



An s orbital is polarized by using a p-type orbital



A p orbital is polarized by mixing in a d-type orbital

Basis Set	Bond Length (Å)
6-31G(d)	0.93497
6-31G(d,p)	0.92099
6-31+G(d,p)	0.94208
6-31++G(d,p)	0.92643
6-311G(d,p)	0.91312
6-311++G(d,p)	0.91720
6-311G(3df,3pd)	0.91369
6-311++G(3df,3pd)	0.91739

bond length of HF

- experimental: 0.917 Å
- calculated at MP4 level

Formaldehyde in 3-21 basis set

atom	primitives	contracted
H1	3s	1s
H2	3s	1s
C	6s,3p	3s,2p
O	6s,3p	3s,2p
Total	36	22

Number of contracted gaussians
in the function describing a
core orbital

Number of contracting gaussians
forming the second valence function

3-21G

Number of contracting gaussians
forming the first valence function

$$\varphi_i = \sum_{\mu=1}^{36} g_{\mu} c_{\mu i} \quad ; i=1,36$$

Pople and Dunning basis sets

3-21G(d,p)		
atom	primitives	contracted
H1	3s,1p	2s,1p
H2	3s,1p	2s,1p
C	6s,3p,1d	3s,2p,1d
O	6s,3p,1d	3s,2p,1d
total	54	40

Dunning

N = D, T, Q, 5, 6

cc-pVNZ

polarized

correlation consistent

$$g(\alpha, \vec{r}) = cx^n y^m z^l e^{-\alpha r^2}$$

Gaussian-type

$$s(\zeta, \vec{r}) = cx^n y^m z^l e^{-\zeta r}$$

Slater-type

Anatomy of the Basis Set

```
C 0
S 6 1.00
    3047.52490      0.183470000E-02
    457.369510     0.140373000E-01
    103.948690     0.688426000E-01
    29.2101550     0.232184400
    9.28666300     0.467941300
    3.16392700     0.362312000
SP 3 1.00
    7.86827240     -0.119332400     0.689991000E-01
    1.88128850     -0.160854200     0.316424000
    0.544249300     1.14345640      0.744308300
SP 1 1.00
    0.168714400     1.000000000     1.000000000
```

<https://www.basissetexchange.org/> - Basis set exchange library

Basis set vs. Accuracy

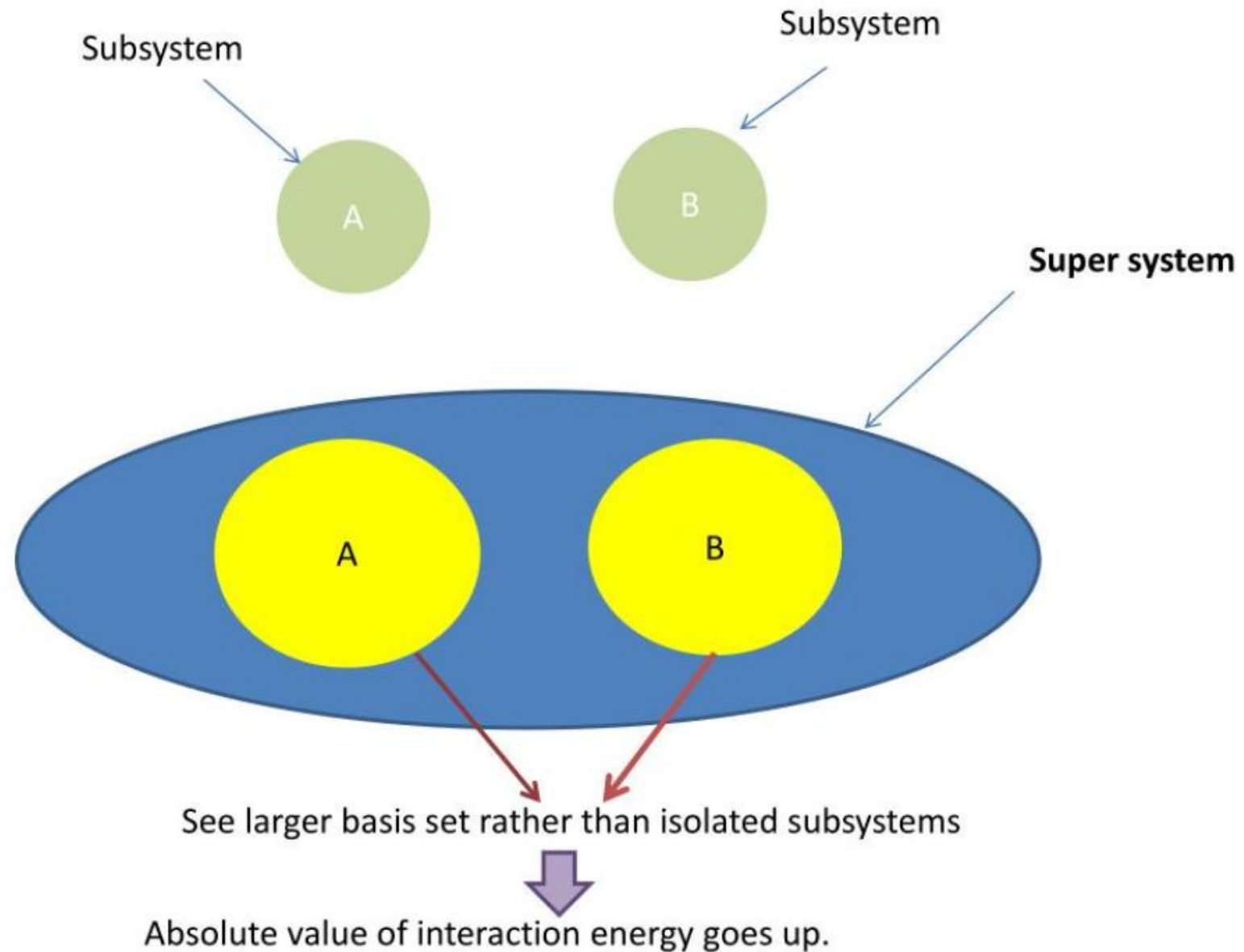
	HF	MP2	QCISD	QCISD(T)	... FCI
6-31G(d)					
6-31G(d,p)					
⋮					
6-311+G(2df,p)					
⋮					
∞					

Increasing electron correlation

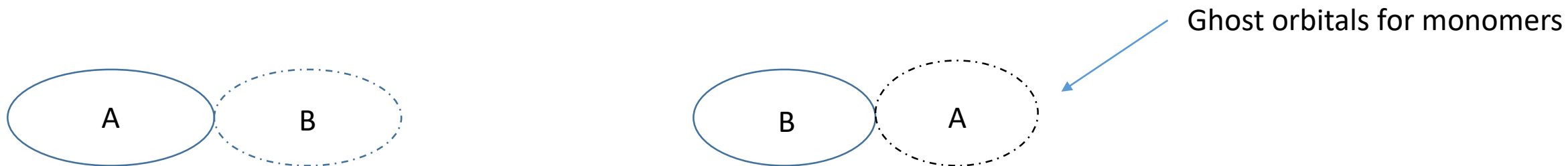
Increasing basis set size

Exact

Basis set superposition error (BSSE)



Counterpoise (CP) method



The uncorrected interaction energy is

$$E_{\text{interaction}}^{\text{AB}} = E_{\text{AB}}^{\text{Opt}} - E_{\text{A}}^{\text{Opt}} - E_{\text{B}}^{\text{Opt}}$$

The counterpoise interaction energy is

$$E_{\text{interaction}}^{\text{AB}} = E_{\text{AB}}^{\text{Opt}} - E_{\text{A}}^{\text{Opt}} - E_{\text{B}}^{\text{Opt}} + \delta_{\text{AB}}^{\text{BSSE}}.$$

The basis set for the subsystems contain the basis function of the whole molecule

Practice1: counterpoise correction in Gaussian

```
/home/yevg_yur/Water_dimer_MP2/w2.com - yevg_yur@fundy.ncbr.muni.cz - Editor - WinS
Encoding Color
%Mem=16384MB
%nprocshared = 7
# rmp2/aug-cc-pVDZ counterpoise=2

Water dimer CP

0,1 0,1 0,1
O(Fragment=1)      -1.62893      -0.04138      0.37137
H(Fragment=1)      -0.69803      -0.09168      0.09337
H(Fragment =1)     -2.06663      -0.73498     -0.13663
O(Fragment =2)      1.21457       0.03172     -0.27623
H(Fragment =2)      1.44927       0.91672     -0.58573
H(Fragment =2)      1.72977      -0.08038      0.53387
```

Water dimer from <http://www.begdb.org/> web page, section “Water clusters – updated”, system name [water-2-Cs](#)

Practice 1: Counterpoise correction in Gaussian: output

```
4 0 -0.000000
      Mulliken charges condensed to fragments:
1      0.000000
2     -0.000000
Electronic spatial extent (au): <R**2>=          93.4042
Charge=          -0.0000 electrons
Dipole moment (field-independent basis, Debye):
  X=      1.2156   Y=      0.0009   Z=      -1.6024   Tot=      2.0113
Quadrupole moment (field-independent basis, Debye-Ang):
  XX=     -3.5624   YY=     -4.2713   ZZ=     -6.8094
  XY=      0.0014   XZ=     -2.9721   YZ=      0.0010
Traceless Quadrupole moment (field-independent basis, Debye-Ang):
  XX=      1.3186   YY=      0.6098   ZZ=     -1.9283
  XY=      0.0014   XZ=     -2.9721   YZ=      0.0010
Octapole moment (field-independent basis, Debye-Ang**2):
  XXX=    -22.8233   YYY=      0.0020   ZZZ=     -1.2167   XYY=     -5.3888
  XXY=      0.0024   XXZ=     -5.7172   XZZ=     -9.6777   YZZ=     -0.0005
  YYZ=     -1.2037   XYZ=      0.0018
Hexadecapole moment (field-independent basis, Debye-Ang**3):
  XXXX=   -79.7064   YYYY=     -6.0810   ZZZZ=     -7.3380   XXXY=      0.0038
  XXXZ=   -10.8619   YYYY=      0.0033   YYYZ=      0.0001   ZZZX=     -1.6532
  ZZZY=      0.0005   XXYY=     -8.8972   XXZZ=   -16.1078   YYZZ=     -2.1568
  XXYZ=      0.0031   YYXZ=     -2.0208   ZZXY=     -0.0010
N-N= 9.106981851130D+00 E-N=-1.987109173839D+02 KE= 7.589137640258D+01
CPIOFr: IOPCl= 0 IRwI=-1 IRwCP= 731 ICalc= 4 LCPTot= 11458 Len1M0= 29304 IndFrg= 157978
CPIOFr: IOPCl= 0 IRwI=-2 IRwCP= 731 ICalc= 0 LCPTot= 11458 Len1M0= 29304 IndFrg= 40762
Counterpoise corrected energy = -152.528876344028
      BSSE energy = 0.001330539401
      sum of fragments = -152.521763258480
      complexation energy = -5.30 kcal/mole (raw)
      complexation energy = -4.46 kcal/mole (corrected)
Unable to Open any file for archive entry.
1\1\GINC-IVAVIK\SP\RMP2-FC\Aug-CC-pVDZ\H402\YEVG_YUR\11-Oct-2023\0\#\#
rmp2/aug-cc-pVDZ counterpoise=2\Water dimer CP\0,1\0,0,-1.62893,-0.0
```

Practice 1: Counterpoise (CP)-corrected interaction energy in Gaussian

- Build any small non-covalent complex of your choice in Avogadro , GaussView or ChemCraft
- Perform geometry optimization and frequency calculation at the RHF/6-311G(d,p) computational level
- Obtain counterpoise-corrected interaction energy and BSSE value for optimized geometry
- Repeat the same procedure using RHF/3-21G computational level. How the geometry, interaction energy and BSSE values are different?
- Visualize the output files in GaussView

Energy decomposition analysis (EDA)

■ **Energy decomposition analysis (EDA)** methods bridge the gap between electronic structure calculations and **conceptual interpretations of molecular interaction energy (i.e. $\Delta E_{\text{int}}(\zeta)$)**.

(NOTE: Theoretically, Morokuma-Kitaura model and ASM can be regarded as a kind of EDA. However, in this presentation, the term of EDA is used only for the decomposition of $\Delta E_{\text{int}}(\zeta)$.)

■ **EDA is the Kohn-Sham molecular orbital (KS-MO) theory-based approach**, enabling to further analyze $\Delta E_{\text{int}}(\zeta)$ as follows:

$$\Delta E_{\text{int}}(\zeta) = \Delta E_{\text{elstat}}(\zeta) + \Delta E_{\text{Pauli}}(\zeta) + \Delta E_{\text{oi}}(\zeta)$$

ΔE_{elstat} : **electrostatic energy** (the Classic Coulomb interaction between the unperturbed charge distributions of the deformed reactants, usually attractive)

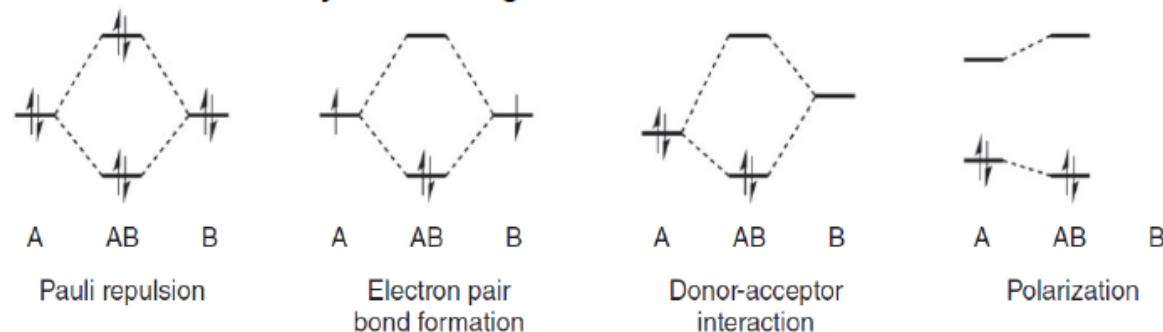
→ further analyzed by Hirshfeld surface analysis, molecular electrostatic potential (MEP) etc.

ΔE_{Pauli} : **Pauli repulsion** (destabilizing interaction between occupied orbitals; i.e. steric repulsion)

ΔE_{oi} : **polarization** (empty-occupied orbital) and **charge transfer** (donor-acceptor interactions including HOMO-LUMO interaction)

→ further decomposed into contributions from each irreducible representations Γ of the point group to which the molecular system belongs.

$$\Delta E_{\text{oi}}(\zeta) = \sum_{\Gamma} E_{\text{oi}}^{\Gamma}$$



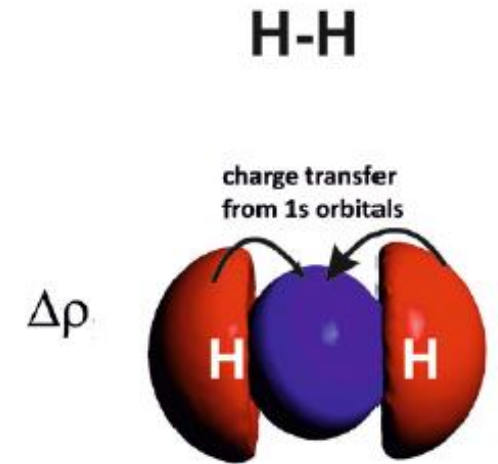
Orbital interaction diagrams for the most commonly appearing interactions.

■ **In EDA, not only equilibrium structures but transition states (TS) and nonstationary points along intrinsic reaction coordinate (IRC) can be analyzed.**

Differential (deformation) density

$\Delta \rho < 0$  charge depletion
 $\Delta \rho > 0$  charge accumulation

$$\Delta \rho(r) = \rho^{mol.}(r) - \sum_{i=1}^{N_{at}} \rho_i^{at.}(r)$$



The positive values the point of density accumulation in the molecule (relative to isolated atoms).

When the molecule is formed from atoms the density flows from the area of negative value towards the area with positive value

The Natural Orbitals for Chemical Valence (NOCV)

NOCV's ($\psi_i = \sum_j C_{ij} \lambda_j$) **diagonalize the deformation density matrix:**

$$\Delta P C_i = v_i C_i \quad ; \quad i = 1, M$$

where $\Delta P = P - P_0$, **density matrix of the combined molecule**,
 P_0 - density matrix of the considered molecular fragments.

NOCV's also decompose the deformation density $\Delta\rho$:


$$\Delta\rho(r) = \sum_{k=1}^M v_k \psi_k^2(r)$$

useful qualitative data
by inspection of the sign
of $\Delta\rho$: negative (outflow),
positive (inflow) of density

NOCV's are in pairs:

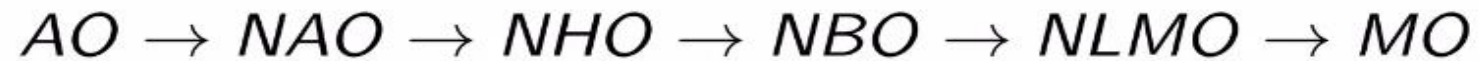
$$\Delta\rho(r) = \sum_{k=1}^{M/2} v_k [-\psi_{-k}^2(r) + \psi_k^2(r)] = \sum_{k=1}^{M/2} \Delta\rho_k(r)$$

Practice 2: NH₃ → BH₃ dative bond in the ammoniaborane

- Build NH₃BH₃ molecule (shown by instructor)
- Symmetrize the system by clicking on 
- Select **Task** → **Geometry Optimization**
- Select **XC functional** → **GGA:BP86**
- Select **Basis set** → **DZP**
- Select **Numerical quality** → **Good**
- Run the calculation with **File** → **Run** (save with the name ammoniaborane)
- After the geometry optimization is completed, Select **Yes** → **New Job**
- Set **Task** → **Single Point**
- Go in the panel bar to **Model** → **Regions**
- Select the atoms of NH₃ (holding Shift), click the + button, rename region to NH₃, the same procedure for BH₃
- Go in the panel bar to **MultiLevel** → **Fragments**
- Check the 'Use fragments' check box
- **Properties** → **ETS-NOCV**
- Select an **Closed-Shell** ETS-NOCV analysis
- EDA results and NOCV channels visualization (shown by instructor)
- **Homework**: optimize NH₃ and BH₃ separately at the same computational level, find the total deformation energy

NBO: Brief Overview

- NBO is a calculated bonding orbital with maximum electron density.
- Hierarchical Atomic/Molecular Orbitals in the NBO analysis:



- NAO: Natural Atomic Orbitals
- NHO: Natural Hybrid Orbitals
- NBO: Natural Bond Orbitals
- NLMO: Natural (Semi-)Localized Molecular Orbitals

Natural Atomic Orbitals

- "Natural" atomic orbitals are the optimal (maximum occupancy), effective AOs in the molecular environment, derived by:
 - diagonalizing the *localized block* of the full density matrix of a given molecule,
 - which is associated with basis functions on that atom
- Thus they meet simultaneous requirements of **orthonormality** and **maximum occupancy**.
- For isolated atoms: NAOs coincide with NOs.
- For a polyatomic molecule: the NAOs mostly retain one-centre character (in contrast to NOs that become delocalized over all nuclear centers).

Natural population analysis (NPA)

```
Enter /users/chem/Software/Gaussian/G09D/g09/l607.exe
*****Gaussian NBO Version 3.1*****
  NATURAL ATOMIC ORBITAL AND
  NATURAL BOND ORBITAL ANALYSIS
*****Gaussian NBO Version 3.1*****

  /RESON / : Allow strongly delocalized NBO set
  /BNDIDX / : Print bond indices based on the NAO density matrix

Analyzing the SCF density

Job title: Calculation from 1.zmat

Storage needed:   210228 in NPA,   279750 in NBO ( 536870096 available)

NATURAL POPULATIONS:  Natural atomic orbital occupancies

  NAO  Atom  No  lang  Type(AO)  Occupancy  Energy
-----
   1   C    1  S    Cor( 1S)   1.99925   -10.03093
   2   C    1  S    Val( 2S)   0.97335    -0.19649
   3   C    1  S    Ryd( 3S)   0.00107    1.79215
   4   C    1  S    Ryd( 4S)   0.00011    2.92070
   5   C    1  px   Val( 2p)   1.04920   -0.05131
   6   C    1  px   Ryd( 3p)   0.00316    1.26268
   7   C    1  px   Ryd( 4p)   0.00029    3.21844
   8   C    1  py   Val( 2p)   1.16301   -0.05401
   9   C    1  py   Ryd( 3p)   0.00583    1.30046
  10   C    1  py   Ryd( 4p)   0.00005    3.05652
  11   C    1  pz   Val( 2p)   0.99764   -0.10850
  12   C    1  pz   Ryd( 3p)   0.00110    0.62283
  13   C    1  pz   Ryd( 4p)   0.00010    2.06595
  14   C    1  dxy  Ryd( 3d)   0.00150    2.38711
```

NPA

```
WARNING: Population inversion found on atom C 1
Population inversion found on atom C 2
Population inversion found on atom C 3
Population inversion found on atom C 4
Population inversion found on atom C 5
Population inversion found on atom C 6
Population inversion found on atom H 8
Population inversion found on atom H 9
Population inversion found on atom H 11
Population inversion found on atom H 12
```

Summary of Natural Population Analysis:

Natural Population						
Atom	No	Natural Charge	Core	Valence	Rydberg	Total
C	1	-0.20116	1.99925	4.18319	0.01872	6.20116
C	2	-0.20116	1.99925	4.18319	0.01872	6.20116
C	3	-0.20116	1.99925	4.18319	0.01872	6.20116
C	4	-0.20116	1.99925	4.18319	0.01872	6.20116
C	5	-0.20116	1.99925	4.18319	0.01872	6.20116
C	6	-0.20116	1.99925	4.18319	0.01872	6.20116
H	7	0.20116	0.00000	0.79679	0.00205	0.79884
H	8	0.20116	0.00000	0.79679	0.00205	0.79884
H	9	0.20116	0.00000	0.79679	0.00205	0.79884
H	10	0.20116	0.00000	0.79679	0.00205	0.79884
H	11	0.20116	0.00000	0.79679	0.00205	0.79884
H	12	0.20116	0.00000	0.79679	0.00205	0.79884
* Total *		0.00000	11.99551	29.87986	0.12463	42.00000

Natural bond orbitals

(Occupancy)	Bond orbital/	Coefficients/	Hybrids
1. (1.98219)	BD (1) C	1 - C	2
(50.00%)	0.7071* C	1 s(36.00%)p 1.77(63.89%)d 0.00(0.09%)	
		f 0.00(0.02%)	
		0.0000 0.6000 -0.0089 0.0023 0.7060	
		-0.0304 -0.0031 -0.3731 -0.0172 0.0023	
		0.0000 0.0000 0.0000 -0.0189 -0.0128	
		0.0000 0.0000 0.0000 0.0000 0.0009	
		0.0076 -0.0148 -0.0077 0.0000 -0.0082	
		0.0043 0.0000 0.0000 0.0025 -0.0089	
(50.00%)	0.7071* C	2 s(36.00%)p 1.77(63.89%)d 0.00(0.09%)	
		f 0.00(0.02%)	
		0.0000 0.6000 -0.0089 0.0023 -0.6762	
		0.0003 0.0035 0.4249 -0.0349 -0.0016	
		0.0000 0.0000 0.0000 -0.0102 -0.0130	
		0.0000 0.0000 0.0000 0.0000 0.0159	
		0.0073 -0.0148 -0.0077 0.0000 0.0079	
		-0.0050 0.0000 0.0000 0.0025 0.0089	
2. (1.66388)	BD (2) C	1 - C	2
(50.00%)	0.7071* C	1 s(0.00%)p 1.00(99.95%)d 0.00(0.02%)	
		f 0.00(0.03%)	
		0.0000 0.0000 0.0000 0.0000 0.0000	
		0.0000 0.0000 0.0000 0.0000 0.0000	
		0.9997 0.0102 0.0088 0.0000 0.0000	
		0.0021 0.0069 -0.0096 -0.0091 0.0000	
		0.0000 0.0000 0.0000 -0.0159 0.0000	
		0.0000 -0.0001 0.0006 0.0000 0.0000	
(50.00%)	0.7071* C	2 s(0.00%)p 1.00(99.95%)d 0.00(0.02%)	
		f 0.00(0.03%)	
		0.0000 0.0000 0.0000 0.0000 0.0000	
		0.0000 0.0000 0.0000 0.0000 0.0000	
		0.9997 0.0102 0.0088 0.0000 0.0000	

Natural Bond Orbitals

(Occupancy) Bond orbital/ Coefficients/ Hybrids

```

-----
1. (1.98219) BD ( 1) C 1 - C 2
   ( 50.00%)  0.7071* C 1 s( 36.00%)p 1.77( 63.89%)d 0.00( 0.09%)
                                     f 0.00( 0.02%)
                                     0.0000  0.6000 -0.0089  0.0023  0.7060
                                     -0.0304 -0.0031 -0.3731 -0.0172  0.0023
                                     0.0000  0.0000  0.0000 -0.0189 -0.0128
                                     0.0000  0.0000  0.0000  0.0000  0.0009
                                     0.0076 -0.0148 -0.0077  0.0000 -0.0082
                                     0.0043  0.0000  0.0000  0.0025 -0.0089
   ( 50.00%)  0.7071* C 2 s( 36.00%)p 1.77( 63.89%)d 0.00( 0.09%)
                                     f 0.00( 0.02%)
                                     0.0000  0.6000 -0.0089  0.0023 -0.6762
                                     0.0003  0.0035  0.4249 -0.0349 -0.0016
                                     0.0000  0.0000  0.0000 -0.0102 -0.0130
                                     0.0000  0.0000  0.0000  0.0000  0.0159
                                     0.0073 -0.0148 -0.0077  0.0000  0.0079
                                     -0.0050  0.0000  0.0000  0.0025  0.0089

2. (1.66388) BD ( 2) C 1 - C 2
   ( 50.00%)  0.7071* C 1 s(  0.00%)p 1.00( 99.95%)d 0.00( 0.02%)
                                     f 0.00( 0.03%)
                                     0.0000  0.0000  0.0000  0.0000  0.0000
                                     0.0000  0.0000  0.0000  0.0000  0.0000
                                     0.9997  0.0102  0.0000  0.0000  0.0000
                                     0.0021  0.0069 -0.0096 -0.0091  0.0000
                                     0.0000  0.0000  0.0000 -0.0159  0.0000
                                     0.0000 -0.0001  0.0006  0.0000  0.0000
   ( 50.00%)  0.7071* C 2 s(  0.00%)p 1.00( 99.95%)d 0.00( 0.02%)
                                     f 0.00( 0.03%)
                                     0.0000  0.0000  0.0000  0.0000  0.0000
                                     0.0000  0.0000  0.0000  0.0000  0.0000
                                     0.9997  0.0102  0.0000  0.0000  0.0000

```

2nd Order Perturbation Analysis of the Fock Matrix

Second Order Perturbation Theory Analysis of Fock Matrix in NBO Basis

Threshold for printing: 0.50 kcal/mol

Donor NBO (i)	Acceptor NBO (j)	E(2) kcal/mol	E(j)-E(i) a.u.	F(i,j) a.u.
within unit 1				
1. BD (1) C 1 - C 2	/ 72. RY*(1) C 3	0.99	2.29	0.043
1. BD (1) C 1 - C 2	/ 73. RY*(2) C 3	1.28	3.52	0.060
1. BD (1) C 1 - C 2	/147. RY*(1) C 6	0.99	2.29	0.043
1. BD (1) C 1 - C 2	/148. RY*(2) C 6	1.28	3.52	0.060
1. BD (1) C 1 - C 2	/252. BD*(1) C 1 - C 6	1.87	1.25	0.043
1. BD (1) C 1 - C 2	/253. BD*(1) C 1 - H 7	0.81	1.12	0.027
1. BD (1) C 1 - C 2	/254. BD*(1) C 2 - C 3	1.87	1.25	0.043
1. BD (1) C 1 - C 2	/255. BD*(1) C 2 - H 8	0.81	1.12	0.027
1. BD (1) C 1 - C 2	/258. BD*(1) C 3 - H 9	2.71	1.12	0.049
1. BD (1) C 1 - C 2	/264. BD*(1) C 6 - H 12	2.71	1.12	0.049
2. BD (2) C 1 - C 2	/ 75. RY*(4) C 3	1.26	0.79	0.031
2. BD (2) C 1 - C 2	/150. RY*(4) C 6	1.26	0.79	0.031
2. BD (2) C 1 - C 2	/257. BD*(2) C 3 - C 4	20.61	0.28	0.068
2. BD (2) C 1 - C 2	/262. BD*(2) C 5 - C 6	20.61	0.28	0.068
3. BD (1) C 1 - C 6	/ 47. RY*(1) C 2	0.99	2.29	0.043
3. BD (1) C 1 - C 6	/ 48. RY*(2) C 2	1.28	3.52	0.060
3. BD (1) C 1 - C 6	/122. RY*(1) C 5	0.99	2.29	0.043
3. BD (1) C 1 - C 6	/123. RY*(2) C 5	1.28	3.52	0.060
3. BD (1) C 1 - C 6	/250. BD*(1) C 1 - C 2	1.87	1.25	0.043
3. BD (1) C 1 - C 6	/253. BD*(1) C 1 - H 7	0.81	1.12	0.027
3. BD (1) C 1 - C 6	/255. BD*(1) C 2 - H 8	2.71	1.12	0.049
3. BD (1) C 1 - C 6	/261. BD*(1) C 5 - C 6	1.87	1.25	0.043
3. BD (1) C 1 - C 6	/263. BD*(1) C 5 - H 11	2.71	1.12	0.049
3. BD (1) C 1 - C 6	/264. BD*(1) C 6 - H 12	0.81	1.12	0.027
4. BD (1) C 1 - H 7	/ 28. RY*(7) C 1	0.53	2.22	0.031

Practice 3: NBO analysis

- Go to <http://www.begdb.org/>
- Download geometry of a non-covalent complex, e.g. A-T base pair in S22 - benchmark non-covalent complexes
- Perform NBO analysis, B3LYP/6-311++G(d,p) computational level, add `Pop=NBO output=wfn external="/software/ncbr/softrepo/ncbr/nbo"` to Gaussian root section
- Analyze natural charges of atoms involved in non-covalent interactions, NBOs and characteristic donor-acceptor interactions
- **Homework:** try natural energy decomposition analysis for this complex