Introduction to Computational Quantum Chemistry

Lesson 8: Population analysis

Importance

Pictures of orbitals are informative, however numerical values are much easier to quantified and compared. For example σ vs π bonding in organic molecules.

What does a population analysis deliver?

- Determination of the distribution of electrons in a molecule
- Creating orbital shape
- Derivation of atomic charges and dipole (multiple) moments

Methods of calculation

- Based on the wave function (Mulliken, NBO)
- Based on the electron density (Atoms in Molecules)
- Fitted to the electrostatic potential (CHELPG, MK)



Mulliken Population Analysis

Mulliken Population Analysis

Advantages

- Most popular method
- Standard in program packages like Gaussian
- Fast and simple method for determination of electron distribution and atomic charged

Disadvantage

 Strong dependance of the results from the level of theory (basis set or kind of calculation)

Example: Li-charge in LiF

Population	basis set	q(Li,RHF)	q(Li,B3LYP)
Mulliken	STO-3G	+0.227	+0.078
	6-31G	+0.743	+0.593
	6-311G(d)	+0.691	+0.558

Natural Bond Orbital Analysis

Natural Bond Orbital Analysis

Based on the theory of Natural Orbitals by Lowdin.

Two parts of the methods

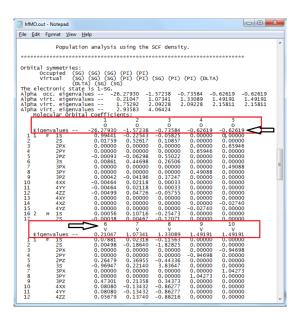
- NPA → Natural population analysis to identify the population numbers
- NBO → Analysis of the bond order based on the electron population obtained by NPA

Advantages

- Smaller dependence on the basis set
- better reproducibility for different molecules
- Orientates itself at the formalism for Lewis formulas

Practical task

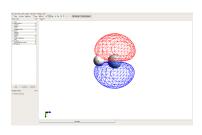
- Draw HF molecule, optimize the geometry and generate G09 input.
- Use pop=(nbo,savenbo) for NBO or Pop=Full for Mulliken
- After Pop command, add a space and type "FormCheck"
- Run the calculation

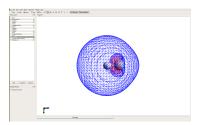


Visualizing the orbitals

- Open the *FChk file in Avogadro
- Click on Extensions → Create Surface
- Select "Molecular Orbital" as surface type
- Choose the MO you want to visualize and calculate

You should be able to see something like these that shows the HOMO and LUMO of HF molecules





Lesson 8: Solvation models

Solvent effects

- The solvent environment influences structure, energies, spectra etc
- Short-range effects
 - Typically concentrated in the first solvation sphere
 - Examples: h-bonds, preferential orientation near an ion
- Long-range effects
 - Polarization

Imlicit vs. Explicit solvation

- Implicit solvation
 - Dielectric continuum
 - No water molecules per se
 - Wavefunction of solute affected by dielectric constant of solvent
 - At 20 °C: Water $\epsilon = 78.4$; benzene: $\epsilon = 2.3 \dots$
- Explicit solvation
 - Solvent molecules included (i.e. with electronic & nuclear structure)
 - Used mainly in MM approaches
 - Microsolvation: only few solvent molecules placed around solute
 - Charge transfer with solvent can occur

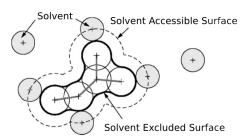
Implicit Models

Basic assumptions

- Solute characterized by QM wavefunction
- Born-Oppenheimer approximation
- Only interactions of electrostatic origin
- Isotropic solvent at equilibrium
- Static model

Cavity

- Solute is placed in a void of surrounding solvent called "cavity"
- Size of the cavity:
 - Computed using vdW radii of atoms (from UFF, for example)
 - Taken from the electronic isodensity level (typically ~0.001 a.u.)
- The walls of cavity determine the interaction interface (Solvent Excluded Surface, SES)
- Size of the solvent molecule determines the Solvent Accessible Surface (SAS)



Visualizing cavity

- Geomview software (in the modules)
- SCRF=(read) in the route section of the job
- Use G03Defaults in SCRF command
- "geomview" in the SCRF specification
- Visualize the "tesserae.off" file

Electrostatic Interactions

- Self-consistent solution of solute-solvent mutual polarizations
- Solute induces polarization at the interface of cavity
- This polarization acts back on the solute changing its wavefunction
- Various solvation models use different schemes for evaluation of solvation effects
- Problems arise when electrostatics do not dominate solvent-solute interactions

Polarizable Continuum Model (PCM)

- Treats the solvent as polarizable dielectric continuum
- Induced surface charged represent solvent polarization
- Implemented in Gaussian, GAMESS

Solvation Model "Density" (SMD)

- Full solute density is used instead of partial charges
- Lower unsigned errors against experimental data than other models

COnductor-like Screening MOdel (COSMO)

- Solute in virtual conductor environment
- Charge q on molecular surface is lower by a factor $f(\epsilon)$:

$$q = f(\epsilon)q^* \tag{1}$$

- where $f(\epsilon) = (\epsilon 1)/(\epsilon + x)$; x being usually set to 0.5 or 0
- Implemented in Turbomole, ADF

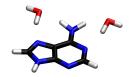
Beyond basic models

- Anisotropic liquids
- Concentrated solutions

Explicit Models

Two models:

- Microsolvation
 - Few solvent molecules (1 to 3) put at chemically reasonable place
 - Water close to exchangeable protons (OH, NH₂...)



- Macrosolvation
 - First (sometimes second) solvent layer around the whole molecule
 - Usually snapshots from MD

Pros & Cons

- +++ Modelling of real interactions with solvent (this can be crucial for exchangeable protons in protic solvents)
- Microsolvation lacks sampling
- Computationally more demanding
- For macrosolvation only single point calculations the geometry is as good as forcefield

Practical task

Reaction

- Model the Cl[−] + CH₃Br → CH₃Cl + Br[−]
- Find the energy barrier for the reaction
- Select any solvent from Gaussian library (be not concerned about solubility of species or chemical relevance)
- Assume S_{n1} and S_{n2} reaction pathways
- Use "SCRF=(solvent=XY)" in the route section of the calculation

Procedure

- Use B3LYP 6-31++g(d,p) method
- Usage of difuse functions when dealing with anions is crucial!
- Use ultrafine integration grid
- Use Frequency calculations to be sure where on PES you are
- For the scan use the distance between C and Cl as RC
- Negative value of step defines two atoms approaching

Module "qmutil"

- Extraction of values from gaussian runs:
 - extract-gopt-ene logfile
 - extract-gopt-xyz logfile
 - extract-gdrv-ene logfile
 - extract-gdrv-xyz logfile
 - extract-xyz-str xyzfile framenumber
 - extract-xyz-numstr xyzfile
- Values ready for plotting in your favorite software

Turbomole

- Prepare job using *define* module (see presentation 6 for help)
- Setup COSMO using cosmoprep module
- Set epsilon to 78.4 and rsolv to 1.93
- Leave all other values at their default
- Define radii of atoms using "r all o" for optimized values
- Optimize all geometries