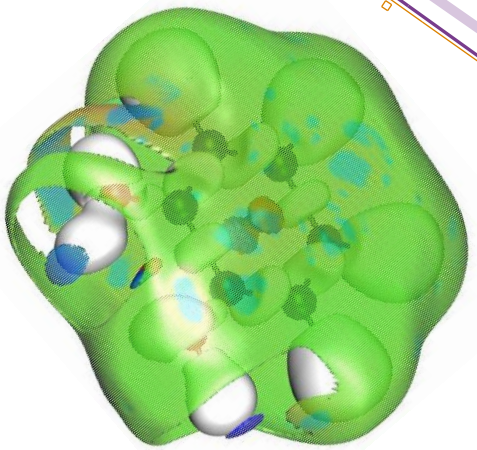
Analysis of non covalent interactions within dynamic systems: the aNCI approach

R. Chaudret

W. Yang presentation (Friday 28th June at 9.30am)



Wu, P.; Chaudret, R.; Hu, X.; Yang, W. *J. Chem. Theo. Comput* **2013**, 9, 2226-2234.

Limits of the NCI approach

NCI analysis of the interactions betwen phenol and water solvent

- Doesn't correspond to the reality
- Strong modifications along the dynamic

- NCI : 1 structure
- Problem : What is the representativity of that structure in solute/solvent systems?

→ **Problem for dynamic systems**

The aNCI analysis

NCI

- 1 structure
- optimization, reaction mechanism…
- Density: ρ
- Reduced density grandient (RDG):

$$s(\rho) = \frac{1}{2(\pi^2)^{\frac{1}{3}}} \frac{|\nabla\rho|}{\rho^{\frac{4}{3}}}$$

- Interaction surfaces

aNCI

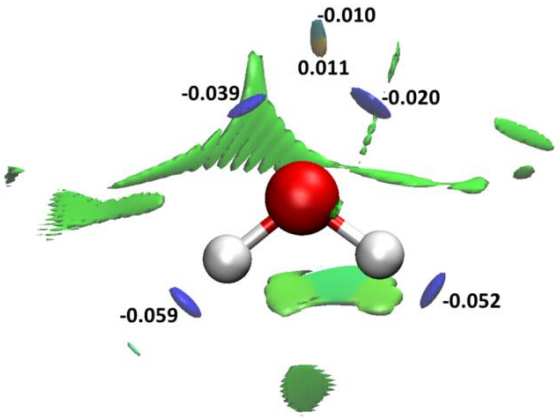
- Ensemble of structures (>100)
- Molecular dynamic…
- Averaged density : $\bar{\rho}$
- Averaged reduced density grandient:

$$\overline{s(\rho)} = \frac{1}{2(\pi^2)^{\frac{1}{3}}} \frac{|\overline{\nabla\rho}|}{\bar{\rho}^{\frac{4}{3}}}$$

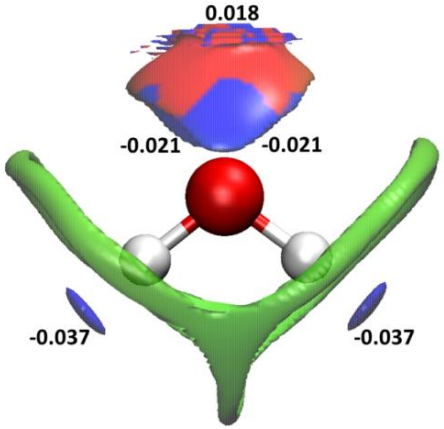
- Interaction surfaces

Comparison NCI and aNCI for solute/solvent systems

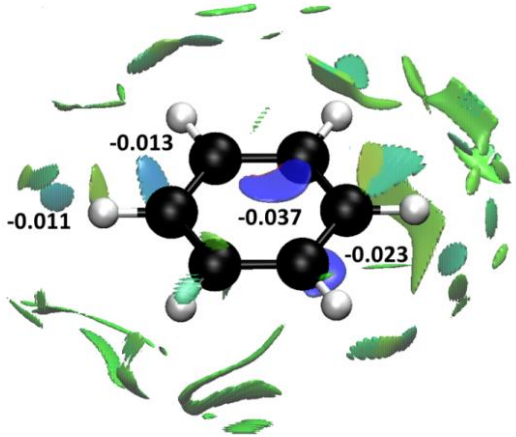
NCI

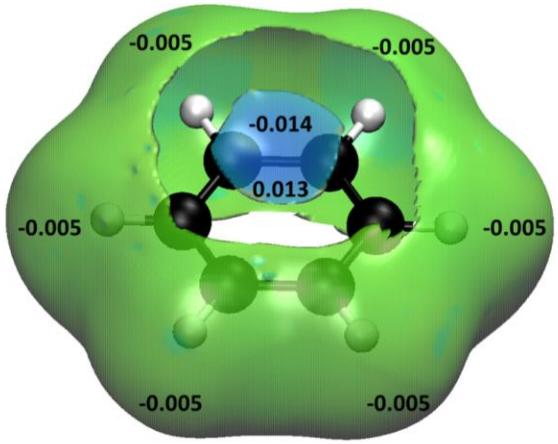


aNCI



- Hidrogen bonds (lone pairs, hydrogens)
- Exculsion area between the 2 lone pairs





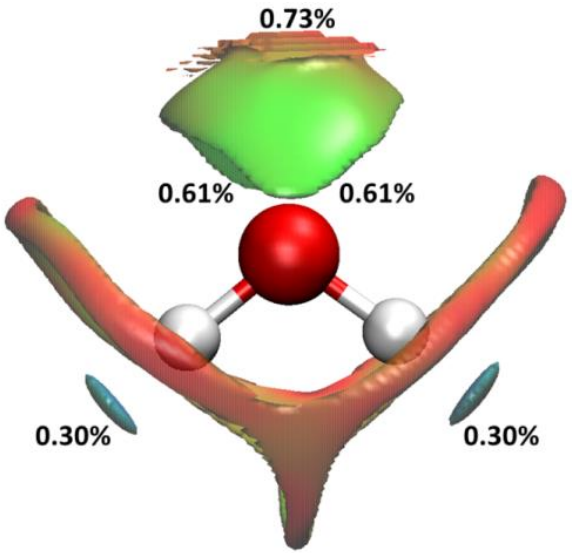
- O-H…π interactions
- vdW interaction in the plane of benzene

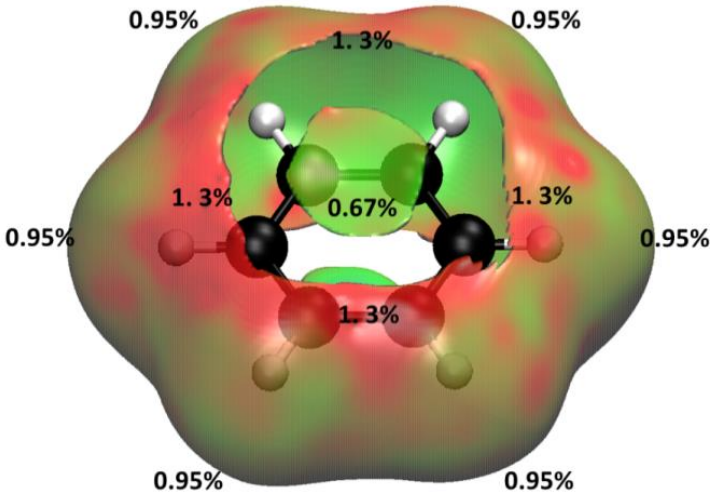
Post aNCI analysis: using other statistical tools

Statistical ensemble of structure → Possility to use statistical tools

Fluctuation index :

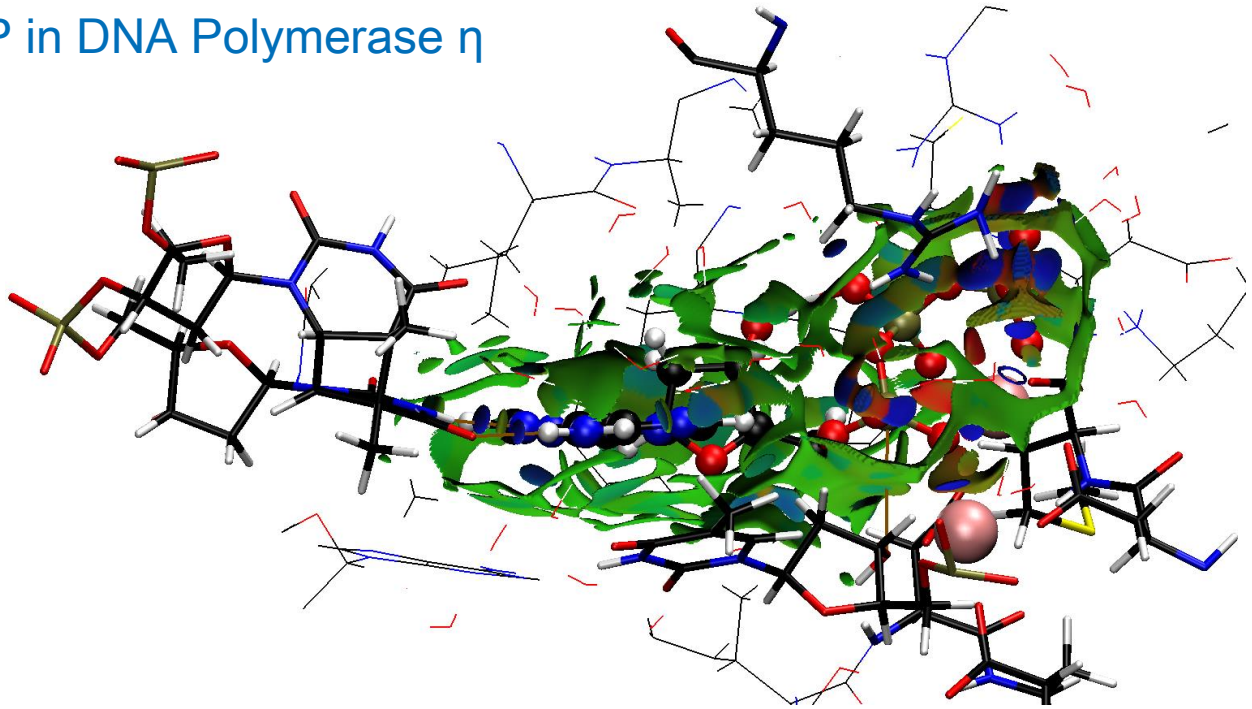
$$f(\mathbf{r}) = std\left(\{\rho_i(r)\}\right) \Big/ mean\left(\{\rho_i(r)\}\right)$$





aNCI analysis within protein/ligand interactions

ATP in DNA Polymerase η



Equivalent to NCI if the interaction is rigid

Different for more flexible interactions (solvent exposed surfaces, vdW…)

Summary

- Access to non covalent interaction within various dynamic systems

  (solute/solvent, protein/ligand…)

- Possibility to use statistical tools to get more indexes (fluctuation index)

Running aNCI simulation

aNCI input is very similar to NCI one but need some preparation steps

1. Get dcd file from MD simulation (can be either classical or QM/MM)

   Standard outputfrom CHARMM or LAMMPS

2. Extract .xyz (coordinate) file from all the different configurations

   - Create structures directory and move dcd and psf files in it.
   - vmd –dispdev none –e get-structures.vmd (you need to change the file if you change the system)
   - Copy pdb2nci.pl in structures and Run pdb2nci.pl :

     ./pdb2nci.pl NAME (for files NAME-*.pdb)

Running aNCI analysis

3. Get solute.xyz file either from pdb or xyz file. This file is used to tell NCI what is the solute to consider.
4. Modify aNCI input (add the desired keywords…)
5. Run aNCI (submit it, it is much longer than NCI, not a 1000 time but still)
   - setenv NCIPLOT_HOME /home/irsrvhome1/R07/chaudrer/programmes/nciplot
   - anci NAME.inp > name.out

Running aNCI: a quick look at aNCI input

```
801  !Number of structures considered
mol.xyz  !solute xyz file name
Frame1.xyz
Frame2.xyz
…
Frame800.xyz
LIGAND 1 5 1  !Compute the interactions between structure #1 (mol.xyz)
                ! and the other structures within 5Å of structure 1
FRAME 800  !Number of frames considered
A-NCI-STD  !Look at std dev index
ACCE_R  12  !Cut all interactions within 12Å of structure 1
ONAME mol  !Output name
```

aNCI output

Same output as in NCI

+

cube and dat for std deviation

Exercice 3

1. For methanol molecule: transfer the dcd file from hydrogene (nci_workshop/aNCI/methanol).
2. Create structures directory and create all the xyz files.
3. Run aNCI analysis for 1, 5, 50, 100, 500, 800 and 1000 frames. What do you see? When do you achieve the convergence?
4. Compare the aNCI and the fluctuation indexes results. What's similar? What's different
5. Perform the aNCI analysis of catechol molecule. Comment the properties of the oxygen lone pairs. How previous calculations help you to understand their nature?