

# ABC of DFT: Hands-on session 2

Molecules: structure optimization,  
visualization of orbitals, charge & spin densities

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**Wo?** KIT Campus Nord, Flachbau Physik, Geb. 30.22, Computerpool, Raum FE-6

- Structure optimization, visualization of molecular orbitals and charge densities
  - Examples: [benzene](#), [pyridine](#)
  
- Open shell systems, Jan-Teller distortions
  - Example: [cobaltocene](#)

# Preparing for the hands-on session 2 ...

- Log into **intact** cluster (have a look at a separate sheet of paper with instructions)

- Switch to a working directory:

```
cd ~/ABC_of_DFT/hands-on-sessions/
```

- Copy a script `session2` from **dft20** account:

```
cp ~/../dft20/ABC_of_DFT/session2 .
```

- Type from a command line:

```
./session2
```

- Examples (with this tutorial) will be imported to a directory

```
~/ABC_of_DFT/hands-on-sessions/session2
```

# Example 1 – Benzene: structure visualization

- Go to a directory with example 1 (benzene):

```
cd ~/ABC_of_DFT/hands-on-
```

```
sessions/session.2/example.1.benzene
```

- Create you own directory where you are going to run a calculation:

```
cp -r structure.benzene my.benzene
```

```
cd my.benzene
```

- Your directory contains a file `coord` with atomic positions:

```
cat coord
```

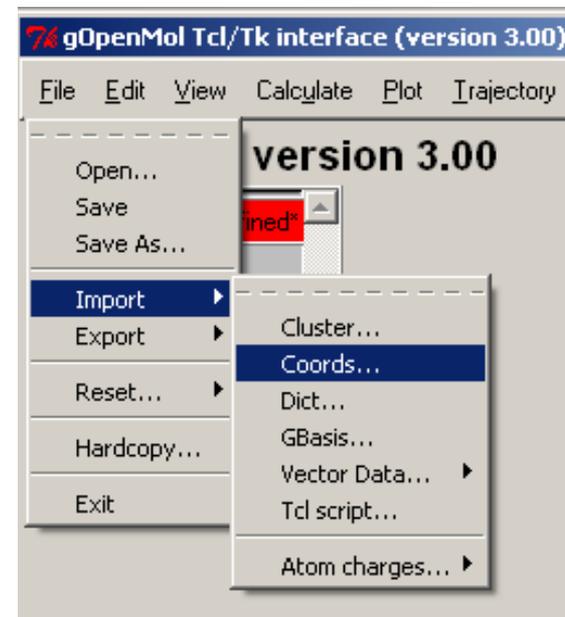
```
$coord
```

```
  2.27353301545502    -1.31262489848446    0.00000000000000    c
  2.27353301545502     1.31262489848446    0.00000000000000    c
  0.00000000000000     2.62524979696891    0.00000000000000    c
 -2.27353301545502     1.31262489848446    0.00000000000000    c
 -2.27353301545502    -1.31262489848446    0.00000000000000    c
  0.00000000000000    -2.62524979696891    0.00000000000000    c
  4.03777188872899    -2.33120868688398    0.00000000000000    h
  4.03777188872899     2.33120868688398    0.00000000000000    h
  0.00000000000000     4.66241737376797    0.00000000000000    h
 -4.03777188872899     2.33120868688398    0.00000000000000    h
 -4.03777188872899    -2.33120868688398    0.00000000000000    h
  0.00000000000000    -4.66241737376797    0.00000000000000    h
```

```
$end
```

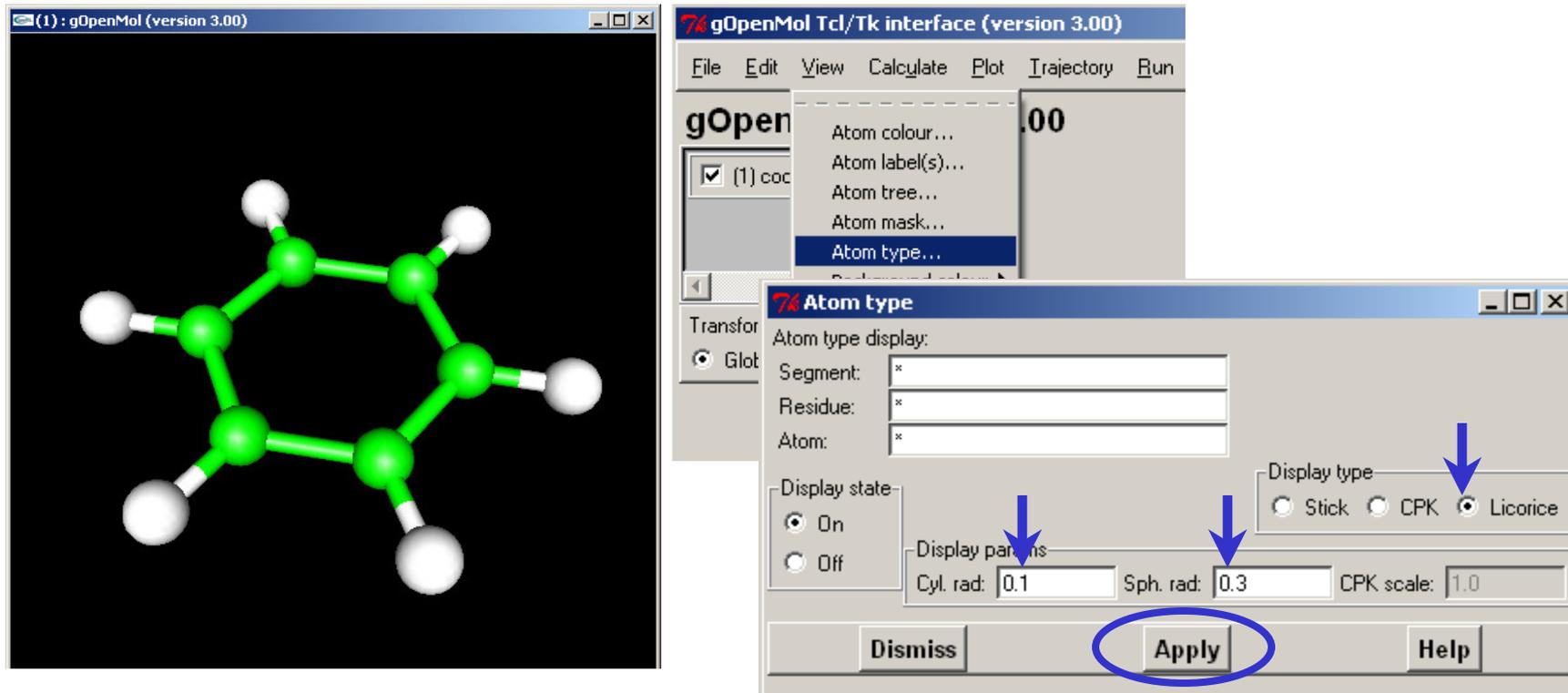
# Example 1 – Benzene: structure visualization

- Convert file `coord` to the `.xyz` format:  
`t2x coord > coord.xyz`
- Start a visualization program gOpenMol:  
`rungOpenMol &`
- Load in coordinates by using a menu of gOpenMol:  
`File -> Import -> Coords...`
- You will get a sub-menu where you can select coordinates from. Load the `coord.xyz` file from your directory and click on the `<Apply>` button.



# Example 1 – Benzene: structure visualization

- You can tune the way your structure is viewed by selecting **View -> Atom type...** and by choosing in the upcoming window **Licorice** with parameters **Cyl.rad = 0.1; Sph.rad = 0.3** followed by the **<Apply>** button.



The image shows two windows from the gOpenMol software. The left window, titled '(1) : gOpenMol (version 3.00)', displays a 3D ball-and-stick model of a benzene molecule with green carbon atoms and white hydrogen atoms. The right window, titled 'gOpenMol Tcl/Tk interface (version 3.00)', shows the main menu with 'View -> Atom type...' selected. Below it, the 'Atom type' dialog box is open. In this dialog, the 'Display type' section has 'Licorice' selected. The 'Display parameters' section shows 'Cyl. rad.' set to 0.1 and 'Sph. rad.' set to 0.3. The 'Apply' button at the bottom of the dialog is circled in blue, and blue arrows point to the 'Licorice' radio button, the 'Cyl. rad.' and 'Sph. rad.' input fields, and the 'Apply' button.

# Example 1 – Benzene: creating an input (step 1)

- Call an interactive module **define** from the directory `my.benzene`:

**define**

...

```
DATA WILL BE WRITTEN TO THE NEW FILE control
IF YOU WANT TO READ DEFAULT-DATA FROM ANOTHER control-TYPE FILE,
THEN ENTER ITS LOCATION/NAME OR OTHERWISE HIT >return<.
```

- Hit **<Enter>** for the name of input file

- INPUT TITLE OR  
ENTER & TO REPEAT DEFINITION OF DEFAULT INPUT FILE

Type e.g. **benzene** for the title, followed by **<Enter>**

- You will get the „molecular geometry“ menu

```
SPECIFICATION OF MOLECULAR GEOMETRY ( #ATOMS=0      SYMMETRY=c1  )
YOU MAY USE ONE OF THE FOLLOWING COMMAND
sy <group> <eps> : DEFINE MOLECULAR SYMMETRY (default for eps=3d-1)
desy <eps>      : DETERMINE MOLECULAR SYMMETRY AND ADJUST
                  COORDINATES (default for eps=1d-6)
susy           : ADJUST COORDINATES FOR SUBGROUPS
ai            : ADD ATOMIC COORDINATES INTERACTIVELY
a <file>      : ADD ATOMIC COORDINATES FROM FILE <file>
....
```

Type **a coord <Enter>** to append your structure

# Example 1 – Benzene: creating an input (step 2)

- You will see that 12 atoms have been added:

```
CARTESIAN COORDINATES FOR 12 ATOMS HAVE SUCCESSFULLY
BEEN ADDED.
. . . .
SPECIFICATION OF MOLECULAR GEOMETRY ( #ATOMS=12 SYMMETRY=c1 )
YOU MAY USE ONE OF THE FOLLOWING COMMAND
sy <group> <eps> : DEFINE MOLECULAR SYMMETRY (default for eps=3d-1)
desy <eps>      : DETERMINE MOLECULAR SYMMETRY AND ADJUST
                  COORDINATES (default for eps=1d-6)
susy           : ADJUST COORDINATES FOR SUBGROUPS
. . . .
```

- Switch on the symmetry detection by entering

**desy <Enter>**

... symmetry detection will print out Schönflies symbol, group generators and the main menu with correct symmetry  $D_{6h}$

```
SPECIFICATION OF MOLECULAR GEOMETRY ( #ATOMS=12 SYMMETRY=d6h )
YOU MAY USE ONE OF THE FOLLOWING COMMANDS :
. . .
```

# Example 1 – Benzene: creating an input (step 3)

- Next step is to provide internal coordinates (bonds, angles, etc...) required for a geometry optimization; type

**ired <Enter>**

```
JUST FOUND ISOLATED RING OF SIZE 6 :
  1   2   3   4   5   6
GEOSPY: NBDIM:           2  NDEGR:           2
  Lowest Eigenvalue of BmBt is:           0.3819660113
GEOSPY: ATTENTION!
  natural internals not linearly independent?
  Decoupling with "globtry"=  0.9999999999000000
  Lowest Eigenvalue of projected BBt           0.3819660113 No:           2
  Quotient of Eigenvalues           1.0000000000
OCCUPATION OF BLOCKS:    2    0    0    0    0

SPECIFICATION OF MOLECULAR GEOMETRY ( #ATOMS=12    SYMMETRY=d6h )
YOU MAY USE ONE OF THE FOLLOWING COMMANDS :
....
```

- We are done with the molecular geometry menu; to proceed, type  
**\* <Enter>**

# Example 1 – Benzene: creating an input (step 4)

- Next is the „atomic attributes“ menu:

```
ATOMIC ATTRIBUTE DEFINITION MENU ( #atoms=12    #bas=12    #ecp=0    )  
  
b      : ASSIGN ATOMIC BASIS SETS  
bb     : b RESTRICTED TO BASIS SET LIBRARY  
bl     : LIST ATOMIC BASIS SETS ASSIGNED  
.....
```

- You may check that a default basis set def-SV(P) is assigned:

```
bl <Enter>
```

```
-----  
INDEX | BASIS SET NICKNAME  
-----
```

```
  1  | c def-SV(P)  
  2  | h def-SV(P)  
-----
```

- You may switch to other basis (e.g. def-TZVP, of triple- $\zeta$  quality):

```
b all def-TZVP <Enter>
```

- To proceed for the next menu, type

```
* <Enter>
```

# Example 1 – Benzene: creating an input (step 5)

- The next menu is the one where **define** determines initial molecular orbitals with, e.g., an extended Hückel guess.

OCCUPATION NUMBER & MOLECULAR ORBITAL DEFINITION MENU

CHOOSE COMMAND

```
infsao      : OUTPUT SAO INFORMATION
eht         : PROVIDE MOS && OCCUPATION NUMBERS FROM EXTENDED HUECKEL GUESS
use <file>  : SUPPLY MO INFORMATION USING DATA FROM <file>
man         : MANUAL SPECIFICATION OF OCCUPATION NUMBERS
hcore       : HAMILTON CORE GUESS FOR MOS
&           : MOVE BACK TO THE ATOMIC ATTRIBUTES MENU
THE COMMANDS use OR eht OR * OR q(uit) TERMINATE THIS MENU !!!
FOR EXPLANATIONS APPEND A QUESTION MARK (?) TO ANY COMMAND
```

To choose the Hückel guess, type

**eht** <Enter>

- You will be asked a lot questions: accept all defaults

# Example 1 – Benzene: creating an input (step 6)

- There are **two important** questions during that procedure:

```
ENTER THE MOLECULAR CHARGE (DEFAULT=0)
```

If you have a charged system, you have to tell that **define** at this point. For now, we accept a neutral molecule by hitting **<Enter>**

- The second question is about occupation numbers

```
AUTOMATIC OCCUPATION NUMBER ASSIGNMENT ESTABLISHED !
```

```
FOUND CLOSED SHELL SYSTEM !
```

```
HOMO/LUMO-SEPARATION : 0.167139
```

ORBITAL (SHELL)	SYMMETRY TYPE	ENERGY	DEFAULT OCCUPATION
11	3e1u	-0.51863	4
12	1b1u	-0.50821	2
13	1e1g	-0.48203	4
14	3e2g	-0.43095	4
15	1e2u	-0.26381	0
16	1b1g	-0.08611	0
17	4e1u	0.39013	0

```
DO YOU ACCEPT THIS OCCUPATION ? DEFAULT=y
```

For our case, the restricted single occupation is OK, press **<Enter>**

# Example 1 – Benzene: creating an input (step 7)

- We will get the last “general menu”:

```
GENERAL MENU : SELECT YOUR TOPIC
scf      : SELECT NON-DEFAULT SCF PARAMETER
mp2/cc2 : OPTIONS AND DATA GROUPS FOR MP2, CC2, ETC.
ex       : EXCITED STATE AND RESPONSE OPTIONS
prop     : SELECT TOOLS FOR SCF-ORBITAL ANALYSIS
drv      : SELECT NON-DEFAULT INPUT PARAMETER FOR EVALUATION
          OF ANALYTICAL ENERGY DERIVATIVES
          (GRADIENTS, FORCE CONSTANTS)
rex      : SELECT OPTIONS FOR GEOMETRY UPDATES USING RELAX
stp      : SELECT NON-DEFAULT STRUCTURE OPTIMIZATION PARAMETER
e        : DEFINE EXTERNAL ELECTROSTATIC FIELD
dft      : DFT Parameters
...

```

- Choose DFT, by entering `dft` **<Enter>** , and then `on` **<Enter>**

```
STATUS OF DFT_OPTIONS:
DFT is used
  functional b-p
  ....
Just <ENTER>, q or '*' terminate this menu.

```

Type `q` **<Enter>** to quit and go back to the general menu

# Example 1 – Benzene: creating an input (step 8)

- General menu allows further options to control over the calculation

```
GENERAL MENU : SELECT YOUR TOPIC
```

```
.....
```

```
ri      : RI Parameters  
rijk   : RI-JK-HF Parameters  
trunc  : USE TRUNCATED AUXBASIS DURING ITERATIONS  
marij  : MULTIPOLE ACCELERATED RI-J  
dis    : DISPLAY MOLECULAR GEOMETRY  
list   : LIST OF CONTROL FILE  
&      : GO BACK TO OCCUPATION/ORBITAL ASSIGNMENT MENU  
* or q : END OF DEFINE SESSION
```

- Calculations for larger molecules can be substantially accelerated if one employs a so-called resolution of the identity (RI) approximation for the evaluation of Coulomb energy integral, where the charge density is expanded over the auxiliary basis set.

## Example 1 – Benzene: creating an input (step 9)

- To activate RI approximation, type `ri <Enter>`, followed by `on <Enter>` in the upcoming sub-menu.

- After done so, you will find

```
STATUS OF RI-OPTIONS:
```

```
RI IS USED
```

```
Memory for RI:           200 Mb
```

```
Filename for auxbasis: auxbasis
```

```
....
```

```
Use <ENTER>, q, end, or '*' to leave this menu
```

- Type `q <Enter>` to go back to the general menu, followed by `q <Enter>` to finish `define` session.

# Example 1 – Benzene: creating an input (remarks)

- After **define** session is finished, you'll find following files in your directory: **control**, **basis**, **auxbasis**, **mos**.
- File **control** contains all settings to control over your calculation.
- Files **basis** & **auxbasis** contain information about basis functions (contracted Gaussian type orbitals) and auxiliary basis set to be used for wave functions (molecular orbitals = MOs) and charge density expansions, respectively.
- File **mos** contains MO energies and expansion coefficients of MOs over the basis functions.
- Files **control** and **mos** will be updated during the calculation.

# Example 1 – Benzene: running calculation

- To run a DFT calculation, call from the current directory  
`ridft > ridft.out &`
- After a minute, scroll up the output file: you'll find the energy diminishes within the self-consistent cycle, and is converged after 9 iterations:

ITERATION	ENERGY	1e-ENERGY	2e-ENERGY	NORM[dD (SAO) ]	TOL
.....					
4	-232.06592645088	-715.02052527	278.59415462	0.000D+00	0.327D-09
.....					
5	-232.07193048496	-715.42066923	278.98829454	0.000D+00	0.327D-09
.....					
6	-232.07269666729	-715.66752979	279.23438892	0.000D+00	0.327D-09
.....					
7	-232.07272816194	-715.63626449	279.20309213	0.000D+00	0.327D-09
.....					
8	-232.07273547481	-715.68122603	279.24804636	0.000D+00	0.327D-09
<b>ENERGY CONVERGED !</b>					
.....					
9	-232.07253692230	-715.67741588	279.24443476	0.000D+00	0.327D-09
.....					
convergence criteria satisfied after 9 iterations					

**Reason for a slightly different value:  
a denser grid for a numerical integration is used !**

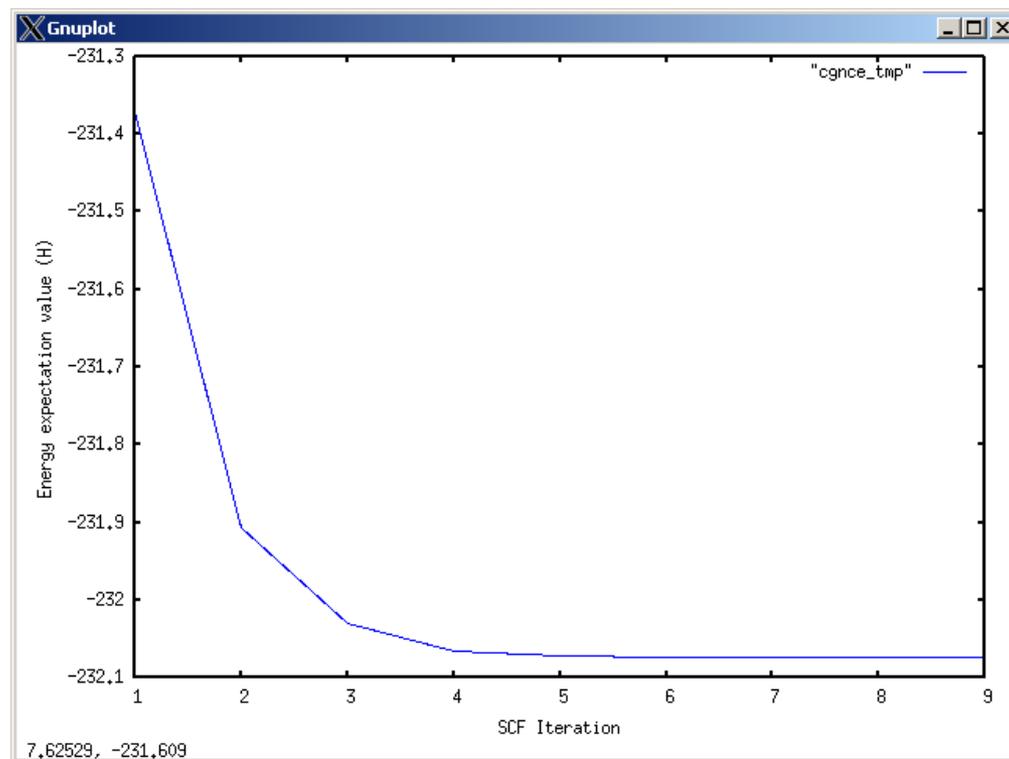
# Example 1 – Benzene: checking convergence

- To check convergence of the energy, you can use script `cgnce`, which exports output info to `gnuplot`. Type `cngce ridft.out`

The window on the right will show up (press `<Enter>` to quit)

- The converged ground state energy (in Hartree units) is appended to file `energy` (first column):

```
$energy          SCF
  1 -232.0725369223
$end
```



```
SCEFKN          SCFPOT
229.7317088723  -461.8042457946
```

# Example 1 – Benzene: data post-processing

- Data post-processing script `eiger` provides information about orbital energies and occupations. Type `eiger > molecular.levels.dat` and afterwards `cat molecular.levels.dat`

```
benzene : bp-86, def-SV(P)  
Total energy = -232.0725369223 H = -6315.0186312 eV
```

## HOMO-LUMO Separation

```
HOMO: 14. 1 e1g -0.23145578 H = -6.29824 eV  
LUMO: 15. 1 e2u -0.03736717 H = -1.01681 eV  
Gap : +0.19408861 H = +5.28142 eV
```

```
Number of MOs= 64, Electrons= 42.00, Symmetry: d6h
```

Nr.	Orbital	Occupation	Energy
....			
16.	4 a1g		+0.043231 H = +1.176 eV
15.	1 e2u		-0.037367 H = -1.017 eV
14.	1 e1g	4.000	-0.231456 H = -6.298 eV
13.	3 e2g	4.000	-0.304977 H = -8.299 eV
12.	1 a2u	2.000	-0.333260 H = -9.068 eV
11.	3 e1u	4.000	-0.378680 H = -10.304 eV
10.	1 b1u	2.000	-0.401898 H = -10.936 eV

2x degenerate  
LUMO

2x degenerate  
HOMO

# Example 1 – Benzene: structure optimization

- To perform geometry optimization of benzene, make a new directory:

```
cd ~/ABC_of_DFT/hands-on-  
    sessions/session.2/example.1.benzene  
cp -r my.benzene my.benzene.relaxed  
cd my.benzene.relaxed
```

- Call from the current directory `jobex` script:

```
jobex -ri -grad -c 25
```

`-ri` tells the script to use modules with RI implementation;

`-grad` tells to perform a gradient evaluation as the first step;

`-c <number>` accounts for a maximum amount of relaxation steps

- Further information can be obtained via `jobex -h`

# Example 1 – Benzene: structure optimization

- At each step of optimization procedure, information on the energy is appended to the file `energy`; type: `cat energy`

```
$energy          SCF          SCFKIN          SCFPOT
  1 -232.0725369223    229.7317088723    -461.8042457946
  2 -232.0764088838    229.3325106808    -461.4089195645
  3 -232.0765621000    229.3004492613    -461.3770113613
  4 -232.0765632300    229.2972414010    -461.3738046309
  5 -232.0765631460    229.2967217448    -461.3732848908
  6 -232.0765631243    229.2965858552    -461.3731489795

$end
```

- Information on gradient and new coordinates is appended to the file `gradient`; type: `grep cycle gradient`

```
cycle =      1      SCF energy = -232.0725369223    |dE/dxyz| = 0.042942
cycle =      2      SCF energy = -232.0764088838    |dE/dxyz| = 0.016091
cycle =      3      SCF energy = -232.0765621000    |dE/dxyz| = 0.001375
cycle =      4      SCF energy = -232.0765632300    |dE/dxyz| = 0.000194
cycle =      5      SCF energy = -232.0765631460    |dE/dxyz| = 0.000021
```

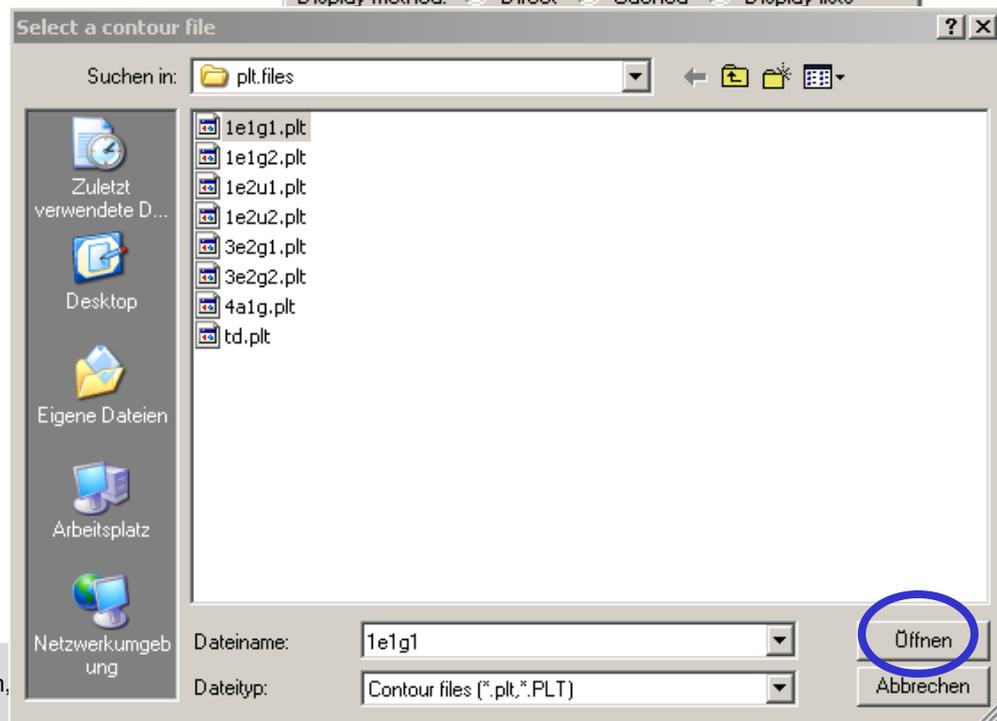
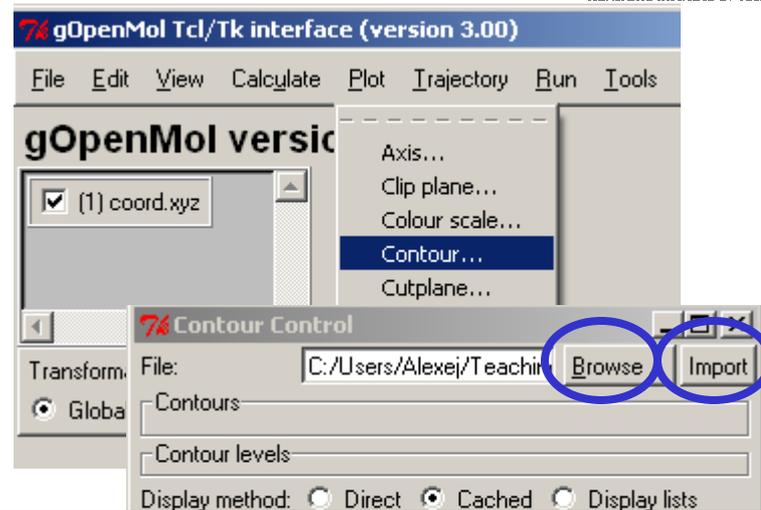
- Question: what are the C-C and C-H bond lengths that you've got?  
How well do these values compare with experimental data?

# Example 1 – Benzene: visualization of orbitals

- Go to your directory with the calculation for benzene, e.g.  
`cd ~/ABC_of_DFT/hands-on-sessions/session.2/example.1.benzene/my.benzene.relaxed`
- Call `eiger` script to get info about orbital energies
- You'll see HOMO is orbital #14, LUMO is #15, etc ...
- To plot frontier orbitals, add to `control` file a line (before `$end`)  
`$pointval mo 13-16`  
and call: `ridft -proper`
- You'll see four `*.plt` files on output. Each file name is associated with one orbital
- To plot a charge density, a line `$pointval dens` is required in `control` file

# Example 1 – Benzene: visualization of orbitals

- **\*.plt** files can be visualized with gOpenMol.
- Call it from a command line:  
**rungOpenMol coord.xyz &**
- Go to the menu:  
**Plot -> Contour...**
- You will get the window where you can load in the **\*.plt** files: first click on **Browse**, load the file, then press **Import**

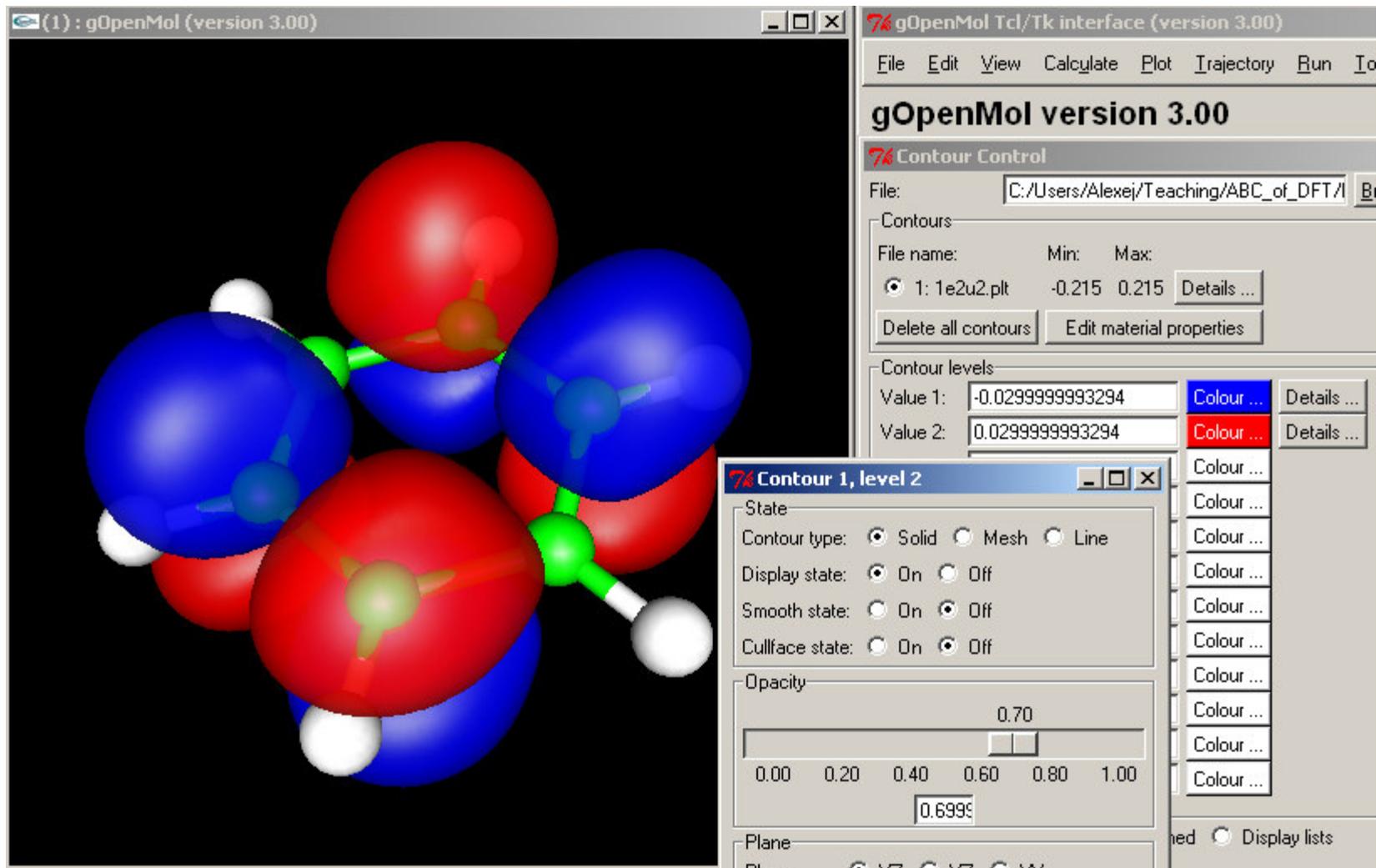


# Example 1 – Benzene: visualization of orbitals

- The Contour Control Window will expand, writing out the minimum and maximum value of the wave function amplitude (or density) that has been read in.
- For each of the 10 fields, called Value 1 till Value 10, you can now enter a value that will define the iso-surface of the wave function's amplitude (or density iso-surface, if charge density is plotted).
- With **Colour...** and **Details...** you can change the color and the opacity of each contour.
- Do not forget to click on the **Apply** button.

# Example 1 – Benzene: visualization of orbitals

- Example shows one of the antibonding ( $\pi^*$ -like) LUMOs of benzene

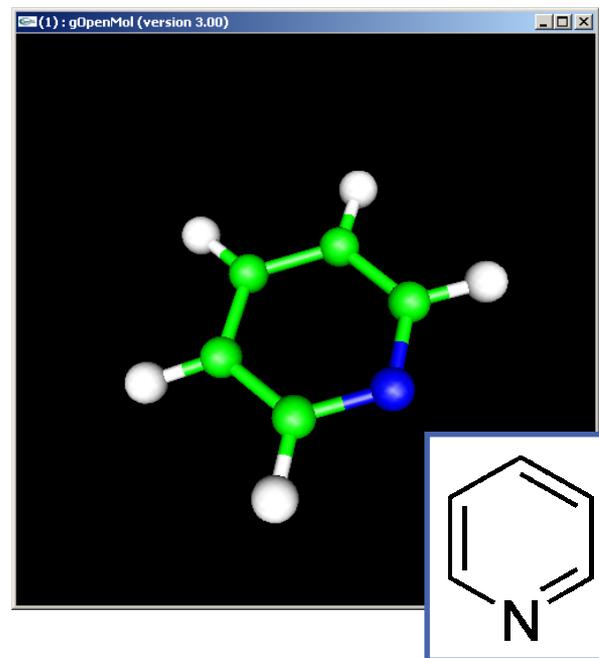


# Example 1 – Benzene: visualization of orbitals

- Exercise: plot two degenerate HOMOs of benzene. Convince yourself that these two orbitals form an aromatic  $\pi$ -electron system, delocalized over the entire ring.
- Useful remark: your pictures can be exported to graphics files. For that, use the menu of gOpenMol  
**File -> Hardcopy ...**  
where an upcoming window allows to choose among graphics formats.

## Example 2 – Pyridine (exercise)

- Consider a pyridine molecule,  $C_5H_5N$ , which is structurally related to benzene, with one CH group replaced by N atom. Look at [~/ABC\\_of\\_DFT/hands-on-sessions/session.2/example.2.pyridine/structure.pyridine](#)
- Visualize atomic structure of the molecule.
- Compute electronic structure of pyridine, assuming a default  $C_{2v}$  symmetry.
- Perform atomic structure relaxation.

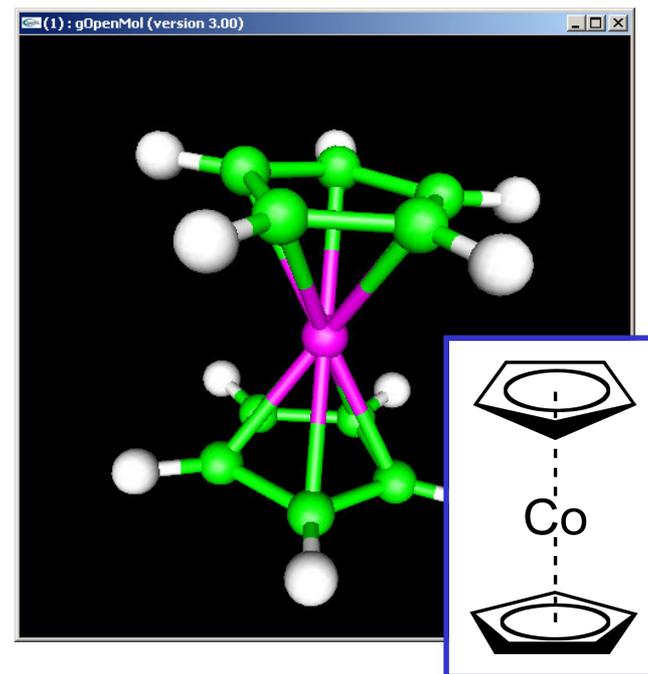


## Example 2 – Pyridine (exercise)

- Visualize frontier molecular orbitals of pyridine (few occupied and few unoccupied ones).
- Questions:
  1. N atom has a single “lone pair” pointing outwards the ring. One of the  $\sigma$ -type molecular orbitals resembles this lone pair. Which orbital is that?
  2. Due to a structural similarity, the some frontier molecular orbitals of pyridine resemble double degenerate HOMO ( $\pi$ ) and LUMO ( $\pi^*$ ) of benzene. Can you show, which are these orbitals? Why degeneracy is lifted in case of pyridine?

## Example 3 – Cobaltocene (open shell: step 1)

- Structure of  $\text{Co}(\text{C}_5\text{H}_5)_2$  can be found at  
[~/ABC\\_of\\_DFT/hands-on-sessions/session.2/example.3.open-shell.cobaltocene.d5d/structure.cobaltocene](#)
- When creating an input with `define`, impose a high  $D_{5d}$  symmetry (`desy 0.3`)
- Due to orbital energies degeneracy, automatic occupation of Hückel's orbitals will fail.
- Help `define` by choosing an open shell occupation for a charge neutral complex with **7 unpaired spins as a starting guess (please, look at the next slide ... )**



## Example 3 – Cobaltocene (open shell: step 2)

- After you've specified a zero charge on the complex, you'll get ...

```
NUMBER OF ELECTRONS IN YOUR MOLECULE IS    97
```

```
YOU HAVE TO ASSIGN OCCUPATION NUMBERS MANUALLY
```

```
>> UHF << : ALPHA AND BETA SHELLS (a,b)
```

```
>> RHF << : CLOSED AND OPEN SHELLS (c,o)
```

```
OCCUPATION NUMBER ASSIGNMENT MENU ( #e=97 #c=0 #o=0)
```

```
s      : CHOOSE UHF SINGLET OCCUPATION
```

```
t      : CHOOSE UHF TRIPLET OCCUPATION
```

```
u <int> : CHOOSE UHF WITH <int> UNPAIRED ELECTRONS
```

```
...
```

```
ENTER COMMAND
```

Type **u 7 <Enter>**

(1, 3, or 5 unpaired spins will not be accepted)

- Proceed further with **define**, setting up DFT, RI, MARI-J options

## Example 3 – Cobaltocene (open shell: step 3)

- After `define` session is finished, you'll find two files, `alpha` and `beta`, accounting for MOs with  $\alpha$  ("up") and  $\beta$  ("down") spins
- Open shell systems (and, also, large systems) require electronic temperature smearing of occupation numbers within first steps of self-consistent cycle to encourage convergence.
- That is done with help of `mkfermi` script, which modifies your `control` file by adding (among others) the following line:  

```
$fermi tmstrt=300 tmend=10 tmfac=0.8 hlcrct=0.5 stop=1.0E-3
```

The initial temperature **300 K** is reduced at each cycle by the factor **0.8** until it reaches the value **10 K**
- To run calculation, type  

```
mkfermi  
ridft | tee cobaltocene.out
```

## Example 3 – Cobaltocene (open shell: step 4)

- After single-point energy calculation is finished, scroll up the output file. You'll find the DFT ground state with **one unpaired spin**:

```
ITERATION ENERGY          1e-ENERGY          2e-ENERGY          NORM[dD(SAO)] TOL
   60 -1769.6462134688 -4216.3089987 1552.3456264 0.000D+00 0.170D-09
      Exc = -117.556943916      Coul = 1669.90257029
      Ntotal = 96.999988223      Nspin = 1.0000005307
      Na = 48.999994377          Nb = 47.999993846
      current damping = 9.900
```

...

**Number of unpaired spins**

End of SCF iterations

convergence criteria satisfied after 60 iterations

- Proceed further with geometry optimization: set electronic temperature to 10 K by modifying (**red**) one line in **control** file to  
`$fermi tmstrt=10 tmend=10 tmfac=1.0 hlcrt=0.5 stop=1.0E-3`

Perform structure relaxation:

```
nohup jobex -ri -grad -c 50 > jobex.out &
```

# Example 3 – Cobaltocene (open shell: step 5)

- Get information about orbital energies (`eiger` script)

```
cobaltocene d5d
```

```
Total energy = -1769.6597050510 H = -48154.9180980 eV
```

```
HOMO-LUMO Separation
```

```
HOMO: 63. a 5 e2g -0.09829840 H = -2.67484 eV
```

```
LUMO: 64. b 5 e2g -0.06691752 H = -1.82092 eV
```

```
Gap : +0.03138089 H = +0.85392 eV
```

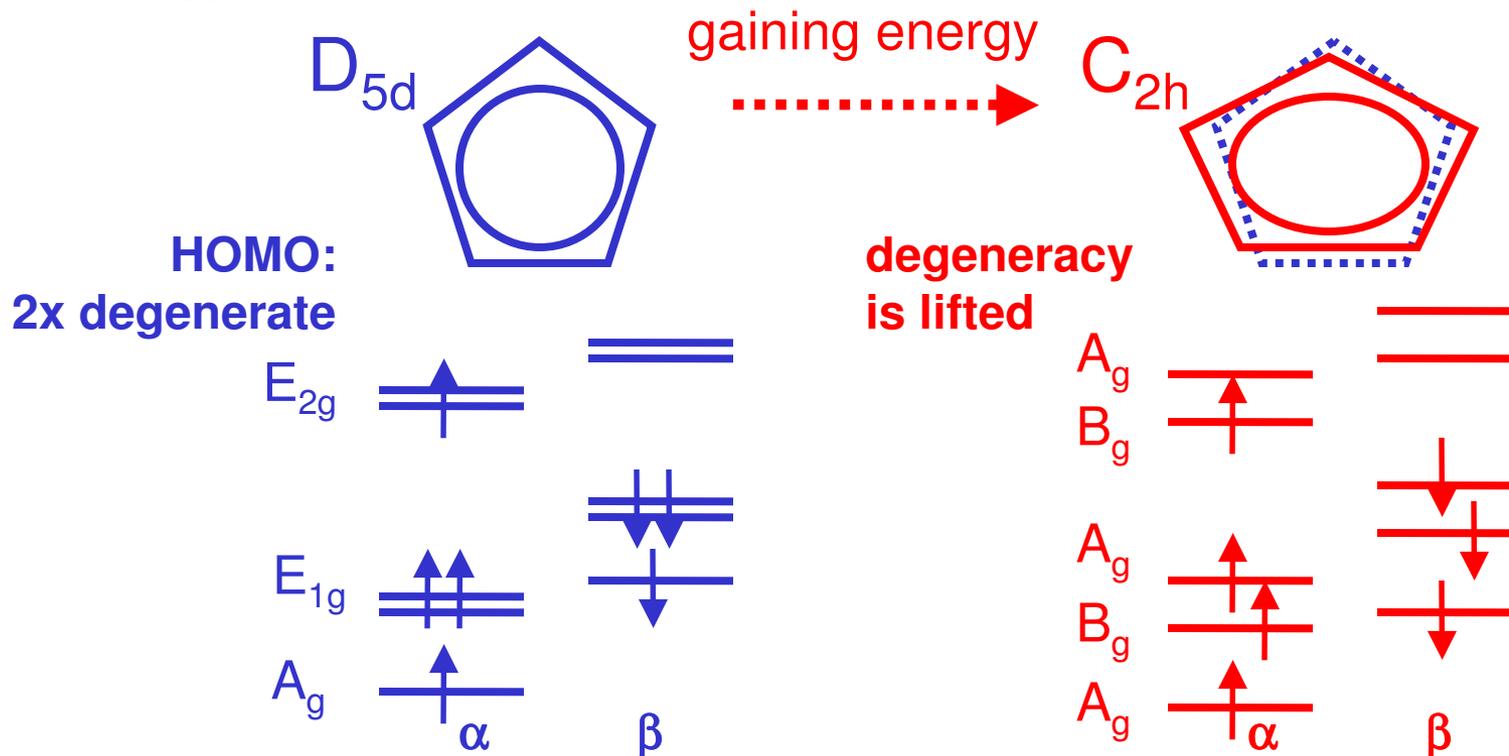
```
Number of MOs= 226, Electrons= 97.00, Symmetry: d5d
```

Nr.	Orbital	Occupation	Energy
...			
65. a	4 e2u		+0.021386 H = +0.582 eV
64. b	5 e2g		-0.066918 H = -1.821 eV
63. a	5 e2g	1.000	-0.098298 H = -2.675 eV
62. b	4 e1g	2.000	-0.162209 H = -4.414 eV
61. b	8 a1g	1.000	-0.174730 H = -4.755 eV
60. a	4 e1g	2.000	-0.179628 H = -4.888 eV
59. a	8 a1g	1.000	-0.187986 H = -5.115 eV

**HOMO : double degenerate  $\alpha$  level ( $E_{2g}$  symmetry) is occupied by one electron**

# Example 4 – Cobaltocene (Jahn-Teller effect)

- In nature, orbital energy degeneracy is lifted due to Jahn-Teller distortions: a non-linear molecule with a degenerate electronic ground state will undergo a geometrical distortion, which removes that degeneracy, because the distortion lowers the overall energy of the complex.



## Example 4 – Cobaltocene (Jahn-Teller effect)

- **Exercise: illustrate Jahn-Teller effect with your calculation**
- Take a structure of  $\text{Co}(\text{C}_5\text{H}_5)_2$  at  
`~/ABC_of_DFT/hands-on-sessions/session.2/example.4.open-shell.cobaltocene.c2h/structure.cobaltocene`
- Within `define` session, choose  $\text{C}_{2h}$  symmetry.
- For a charge neutral complex, approve **an open shell occupation with one unpaired spin**.
- Perform a DFT calculation, and a subsequent structural relaxation: **do not forget about the Fermi smearing (mkfermi script) !**

## Example 4 – Cobaltocene (Jahn-Teller effect)

- Estimate energy difference for structures with  $D_{5d}$  and  $C_{2h}$  symmetry.

**Answer: GS DFT energy for the  $C_{2h}$  structure is lower by  $\sim 0.11$  eV**  
(value is given for the def-SV(P) basis, “b-p” BP86 functional)

- Compare KS spectrum of complexes with different symmetries. You’ll find, the “HOMO doublet” splits to HOMO (occupied) and LUMO (unoccupied) levels. What is the splitting?

**Answer:  $\sim 0.4$  eV** (def-SV(P) basis, “b-p” BP86 functional)

- Hint: you can compare output of your calculations for the two cases with those at

$D_{5d}$ : `.../session.2/example.3.open-shell.cobaltocene.d5d/output.cobaltocene/output.jobex`

$C_{2h}$ : `.../session.2/example.4.open-shell.cobaltocene.c2h/output.cobaltocene/output.jobex`

# Example 4 – Cobaltocene: charge & spin densities

- **Exercise:** Plot charge and spin densities of cobaltocene: show that unpaired spin is localized mainly on Co atom. That may look like ...

