

Orca

An Introduction and Running Basic Jobs









What is Orca?

The program ORCA is a modern electronic structure program package written by Prof. F. Neese, with contributions from Ute Becker, Dmytro Bykov, Dmitry Ganyushin, Andreas Hansen, Robert Izsak, Dimitrios G. Liakos, Christian Kollmar, Simone Kossmann, Dimitrios A. Pantazis, Taras Petrenko, Christoph Reimann, Christoph Riplinger, Michael Roemelt, Barbara Sandhöfer, Igor Schapiro, Kantharuban Sivalingam, Frank Wennmohs, Boris Wezisla and contributions from our collaborators: Mihály Kállay, Stefan Grimme, Edward Valeev. The binaries of ORCA are available free of charge for academic users for a variety of platforms.

ORCA is a flexible, efficient and easy-to-use general purpose tool for quantum chemistry with specific emphasis on spectroscopic properties of open-shell molecules. It features a wide variety of standard quantum chemical methods ranging from semiempirical methods to DFT to single- and multireference correlated ab initio methods. It can also treat environmental and relativistic effects.

Due to the user-friendly style, ORCA is considered to be a helpful tool not only for computational chemists, but also for chemists, physicists and biologists that are interested in developing the full information content of their experimental data with help of calculations.



The Basics

	Basic Computational Models	Basic Computations	Basic Analysis
Molecule - 3D Coords Charge Multiplicity	Density Functional Theory (DFT) Hartree-Fock (HF) + Basis Set	Energy Gradient Hessian	MO Energies MO Isosurfaces Partial Charges Bond Orders Vibrational Frequencies Checking Optimized Geometry IR Spectra
	You Must Provide!!!		



Your First Task When You Have a Problem You Can't Answer





The Input File





The Basics

Molecule

- 3D Coords

- You need to have a "good" set of coords for the program to work
- My suggestions to obtain a decent guess:
 - Use WebMO (as discussed in the WebMO tutorial), and import coordinates from the WebMO guess
 - 2. PyMOL can do organics
 - 3. Chem3D (if you have a PC)
 - 4. Avogadro
 - 5. OpenBabel
 - 6. wxMacMolPlt
 - 7. ChemCraft
 - 8. Mercury

<u>Charge</u>

You MUST know this beforehand

Multiplicity (2S+1)

Is your molecule magnetic? No? 2S+1=1

Is it an open-shell singlet? More complicated...

Transition Metal? High/Intermediate/Low Spin?



DFT – Recommendations for GS energies





DFT – Recommendations Optimization Basis Sets

POPLE [6-31G(d), 6-311+G(2d,p), etc...]

I don't recommend the Pople Basis sets for use with Orca

- No Auxiliary Basis Sets Available
- No "automatic" effective core potentials (ECP).
- Limited scope of periodic table (PT)

KARLSRUHE/AHLRICHS [def2-SVP, def2-TZVP, def2-QZVP, etc...]

My basis set of choice in most cases.

- Built-in "automatic" Auxiliary Basis Set (DEF2/J)
- Automatically loads ECP
- Systematic (SVP-TZVP-QZVP-QZVPP)
- Covers most of the PT
- Well-known to work well with DFT

CORRELATION CONSISTENT [cc-pVDZ, cc-pVTZ, etc...]

- I don't recommend for DFT optimizations.
- This basis set is tailor-made for post-HF methods like MP2, so I definitely recommend this BS for these types of theories.

JENSEN [pcseg-0, pcseg-1, etc...]

- Better than POPLE, but I still don't recommend for use with ORCA for "normal" calculations.
- Useful for some properties, however!



DFT – Recommendations for Optimizations

PBEh-3C, r²SCAN-3C: Built-In Basis Set

Inorganic: def2-TZVP PBE0, B3LYP, TPSSh, M06-2X, ωB97X-D3 Organics: def2-SV(P)

PWPB95, DSD-PBEP86 - Wouldn't optimize with these

> Inorganic: def2-TZVP TPSS, r²SCAN Organics: def2-SV(P)

Inorganic: def2-TZVP BLYP, PBE, PW91 Organics: def2-SV(P)

Default convergence and DFT grid usually OK



DFT – Recommendations for SP

PBEh-3C, r²SCAN-3C: Built-In Basis Set

Inorganic: As Big As Possible PBE0, B3LYP, TPSSh, M06-2X, ωB97X-D3 Organics: def2-TZVP

PWPB95, DSD-PBEP86 DEF2-TZVP

BLYP, PBE, PW91 Woudn't Use for SP Inorganic: As Big As Possible TPSS, r²SCAN Organics: def2-TZVP

I Would Use TightSCF and consider DEFGRID3



By default, ORCA uses the RIJCOSX Approximation For Coulomb integrals, normally we have:

 $J_{\mu\nu\sigma\tau} = P_{\mu\nu}P_{\sigma\tau}\langle\mu(1)\nu(1)\big|r_{12}^{-1}\big|\sigma(2)\tau(2)\rangle$

In the RIJ approximation, we make the following approximate substitution:

 $P_{\sigma\tau}\sigma\tau \approx \sum_k P_k \zeta_k$

This turns a 4-center integral into a 3-center integral (which is faster to evaluate)

Requires an Auxiliary Basis Set (As mentioned previously)



Under the hood: the RIJCOSX Approximation

By default, ORCA uses the RIJCOSX Approximation For Exchange integrals, normally we have:

 $K_{\mu\nu\sigma\tau} = P_{\mu\nu}P_{\sigma\tau} \left\langle \mu(1)\nu(1) \left| r_{12}^{-1} \right| \sigma(2)\tau(2) \right\rangle$

In the COSX approximation, we make the following approximate substitution:

$$\langle \mu(1)\sigma(1) | r_{12}^{-1} | \nu(2)\tau(2) \rangle \approx \sum_g X_{\mu g} X_{\sigma g} A_g^{\nu \tau}$$

where with g being grid-points

$$A_g^{\nu\tau} = \int \frac{\nu(r)\tau(r)}{|r-r_g|} dr$$
 and $X_{\mu g} = \sqrt{w_g}\mu(r_g)$

We thus reduce the 4-center exchange integral to a two-center integral applied over a numerical grid.



Integration Grids: the "Other" Basis Set

By default, ORCA uses the so-called DEFGRID2 which sets a numerical integration grid for both the xc-kernel as well as the COSX grid.

It might sometimes be necessary to improve the grid by moving to DEFGRID3:

- 1. This can sometimes happen when very tight accuracy is needed for an energy calculation.
- 2. Weaker grids can be susceptible to numerical problems for optimizations with shallow PESs.

If DEFGRID3 is still not good enough, you can turn off RIJCOSX by using the keyword NORI



Our First Job: A Single Point Run

Let's do a single-point energy calculation with the r²SCAN-3C model on cisplatin.

- 1. First we'll build the molecule
- 2. Next we'll create the input file.
- 3. Finally, we'll create the runscript and submit the job.



We'll use a combination of WebMO and OpenBabel

- 1. Use the symmetry fragments in WebMO to get a square planar structure and make the necessary modifications.
- 2. Go to the WebMO submission dialog to get the Cartesian coordinates, and Copy the coords
- 3. Use OpenBabel to clean the geometry with the UFF force field.



GNU nano 2.9.8

! R2SCAN-3C TightSCF %pal nprocs 8 end %maxcore 4500 *xyzFile 0 1 cleaned.xyz

cisplatin.inp



	GNU	nano	2.9.8	orcarun.sh
	5 -N 5 -P 5 -q 5 -pe 5 -M 5 -M 5 -l	CisPl webmo chem1 e omp eas jmcne h_rt=	atin 8 eel1@bu.edu 24:00:00	
# # e>	Tell and cport	l the libra t PATH t LD_L	OS where to aries =/project/w _IBRARY_PATH	o find necessary parallelization exectuables webmo/openmpi/416/bin:\$PATH H=/project/webmo/openmpi/416/lib:\$LD_LIBRARY_PATH
# # e>	Reme it a cport	ember at the t ACTI	your currer e end VE=`pwd`	it location so we can copy files back into



- qsub *runscript_name*
- qstat –u *your_username*
- qacct -d *num_days* -o *your_username* -j

Our Second Job: A Geometry Optimization + Hessian

We'll use the same level of theory and use Chemdraw+OpenBabel to build a alkynylcyclobutanol recently listed in JOC.

https://pubs.acs.org/doi/10.1021/acs.joc.4c00505





GNU nano 2.9.8

opt.inp

! R2SCAN-3C OPT FREQ
%pal nprocs 8 end
%maxcore 4500
*xyzFile 0 1 cleaned.xyz



Optimizations in Orca

	Opt	TightOpt	VeryTightOpt
TolE	5e-6	1e-6	2e-7
TolRMSG	1e-4	3e-5	8e-6
TolMAXG	3e-4	1e-4	3e-5
TolRMSD	2e-3	6e-4	1e-4
TolMAXD	4e-3	1e-3	2e-4

An important keyword to remember if you're having convergence problems and you notice the energy is "oscillating".

Use the TRUST option in the %geom end block. Maybe set to -0.1 and then keep going down until the oscillations stop



Checking for Imaginary Frequencies

grep imag output_file

OPT: Total number of imaginary perturbations ... 0

TIGHTOPT:

Total number of imaginary perturbations ... 0 6: -1.50 cm**-1 ***imaginary mode***

VERYTIGHTOPT: Total number of imaginary perturbations ... 0



Solving Imaginary Frequencies

```
for i in `seq 5 5 20`; do
mkdir P${i}
mkdir M${i}
head -n4 tightopt.inp > P${i}/tightopt.inp
head -n4 tightopt.inp > M${i}/tightopt.inp
d=`echo ``${i}/100" | bc -l`
na=`head -n1 tightopt.xyz`
sed -i ``s/xyzFile/xyz/g" P${i}/tightopt.inp
sed -i ``s/xyzFile/xyz/g'' M${i}/tightopt.inp
sed -i ``s/cleaned.xyz/\ /g" P${i}/tightopt.inp
sed -i ``s/cleaned.xyz/\ /g" M${i}/tightopt.inp
/projectnb/webmo/jmcneel1/bin/displace.py tightopt.hess 6 ${d} | tail -n${na} >> P${i}/tightopt.inp
/projectnb/webmo/jmcneel1/bin/displace.py tightopt.hess 6 - \{d\} | tail -n \{na\} >> M \{i\}/tightopt.inp
echo "*" >> P${i}/tightopt.inp
echo "*" >> M${i}/tightopt.inp
cp orcarun.sh P${i}/
sed -i "s/verytightopt/tightopt/g" P${i}/orcarun.sh
cp P${i}/orcarun.sh M${i}/orcarun.sh
done
```



```
for i in `seq 5 5 20`; do
cd P${i}
qsub orcarun.sh
cd ../M${i}
qsub orcarun.sh
cd ../
done
```







The Electronic Energy

grep FINAL *output_file* | tail -n1

The Gibbs Free Energy

grep Gibbs *output_file* | tail –n2 | head –n1 grep FREEENERGYG *property_file*

Absolute energies are fairly useless, YOU SHOULD ONLY BE PAYING ATTENTION TO RELATIVE ENERGIES



HOMO/LUMO Gaps

grep -A 200 ORBITAL\ EN *output_file*

			0 1 0 2 0
43	2.0000	-0.244693	-6.6584
44	2.0000	-0.241850	-6.5811
45	2.0000	-0.207847	-5.6558
46	0.0000	-0.056409	-1.5350
47	0.0000	-0.036385	-0.9901
48	0.0000	0.003727	0.1014
49	0.0000	0.053546	1.4571

/projectnb/webmo/orca/6_0_0/orca_plot gbw_file -i





Population Analysis

grep -n MULL output_file less +# output_file

			* MULLIKEN POPULATION ANALYSIS *

JLLI	[KE	N	ATOMIC CHARGES
0	0	:	-0.412190
1	С	:	0.317008
2	С	:	-0.403077
3	С	:	-0.299046
4	С	:	-0.405100
5	С	:	0.124029
6	С	:	0.208068
7	С	:	-0.302237
8	С	:	-0.188703
9	С	:	-0.165368
10	С	:	-0.137786
11	С	:	-0.167285
10	C		0 102004