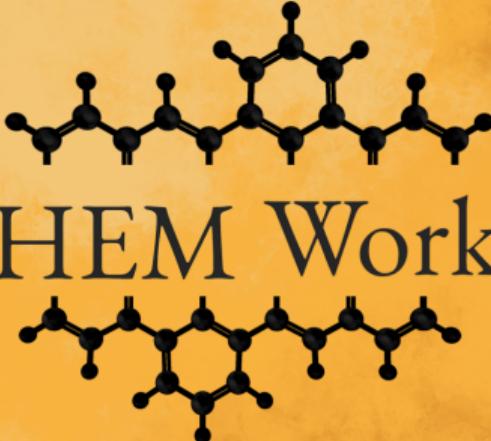


# Q-CHEM Workshop



Thursday 10 July 2025  
Kiama





# The 12<sup>th</sup> Virtual Winter School on Computational Chemistry

**26-30<sup>th</sup> January 2026**



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R. Havenith



C. Trujillo



G. Worth



D. Ghosh



J. Joseph



E. Heid



J. Walkimar de M.  
Carneiro

& more!



Q-Chem is a fully-featured *ab initio* quantum chemistry software package for simulating electronic structure, properties and spectra of molecular systems.

- ▶ Over 30 years of development.
- ▶ State-of-the-art methods for ground and excited states.
- ▶ Extensive library of over 200 density functionals.
- ▶ Specialized methods such as NEO, NAO and EDA.
- ▶ Open teamware development model currently includes over 100 developers.



# IQmol

IQMOL is an open-source molecular editor and visualization package which runs under Windows, Mac OS X and Linux.

- ▶ Wide range of chemical file formats supported
- ▶ Free-form molecular builder:
  - ▶ Structure optimization using MM
  - ▶ Symmetrization of structures
  - ▶ Built-in library of molecules
- ▶ Analysis features:
  - ▶ Animations: reaction pathways and vibrational frequencies
  - ▶ Surface plots: MOs and (spin) densities
  - ▶ Surface properties: ESP and cube data



# Q-CHEM +IQMOL



IQMOL is a standalone program, but has been optimized to work best in a Q-CHEM work flow:

- ▶ Building structures
- ▶ Generating Q-CHEM input
- ▶ Submitting Q-CHEM calculations
- ▶ Visualizing results

This is due to several Q-CHEM specific features:

- ▶ Comprehensive Q-CHEM input file generator
- ▶ Embedded Q-CHEM keyword documentation
- ▶ Submission of Q-CHEM jobs to local and cloud servers including PBS, SGE and Web-based



# Resources

Binary packages for IQMOL can be freely downloaded from:

[www.iqmol.org/downloads.html](http://www.iqmol.org/downloads.html)

The Q-CHEM manual is available online via:

[manual.q-chem.com](http://manual.q-chem.com)

Video resources are available on Q-CHEM's YouTube page:

-  IQMOL introduction
-  Advanced IQMOL usage
-  Checkout Q-CHEM's entire webinar series



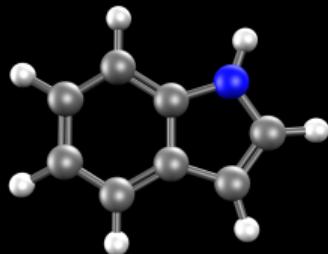
# Demonstration



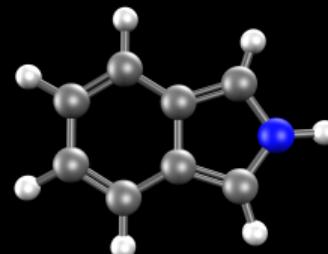
2-Fluoroethanol



# Exercise — Indole



Indole



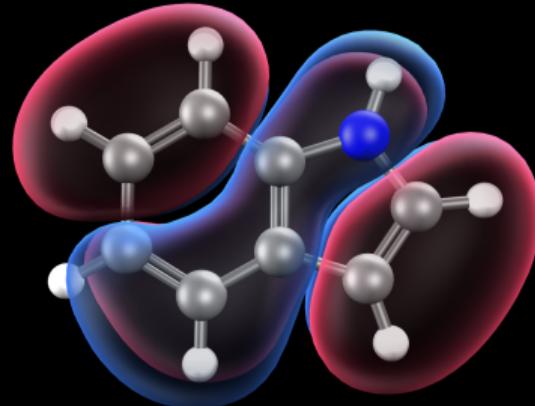
iso-Indole

1. Build structures for indole and iso-indole. Cleanup your strutures using molecular mechanics and symmetrize.
2. Run HF/STO-3G energy calculations to obtain the MOs.
3. Plot the HOMO of each molecule and predict which isomer is the more stable (hint: consider the nodal structure).
4. Optimize each structure using HF/6-31G and determine the energy difference. Was your prediction correct?

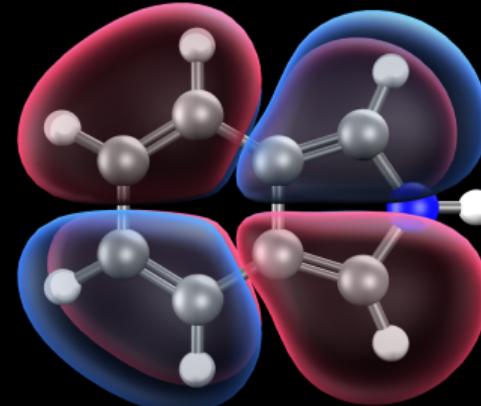


# Results — Indole

Indole has fewer nodes and is more stable.



Indole  
-361.337412 E<sub>h</sub>



iso-Indole  
-361.315424 E<sub>h</sub>

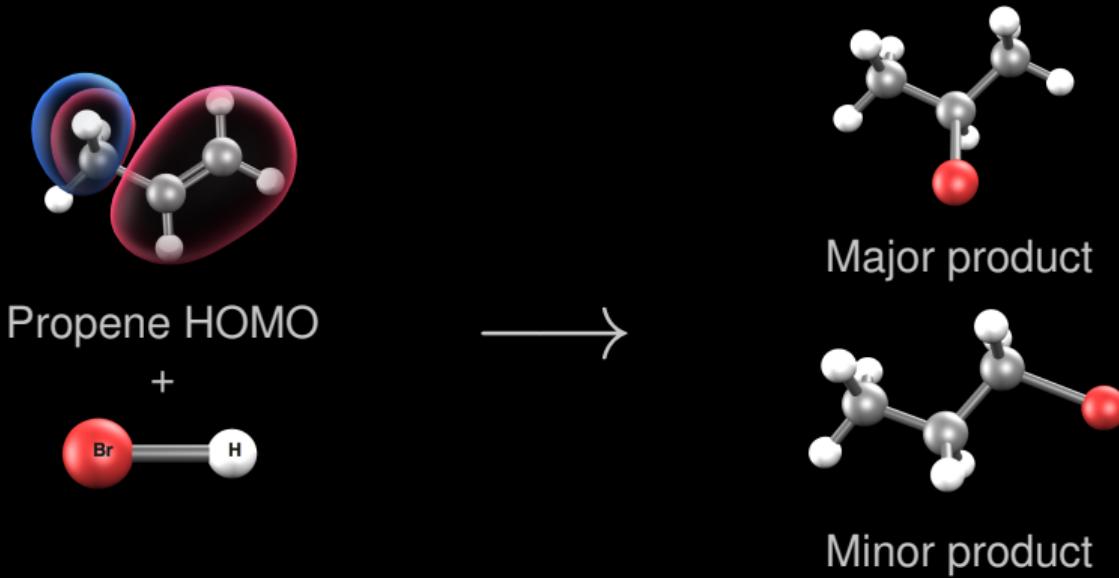
$$\Delta E = 58 \text{ kJ/mol} @ \text{HF/6-31G}$$



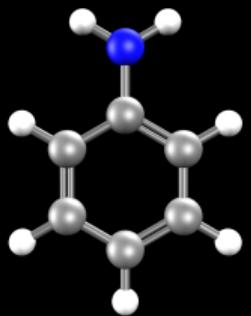
# Electrophilic Attack

In 1952 Kenichi Fukui published his Frontier Molecular Orbital (FMO) theory which provides a qualitative approximation for determining reactivity.

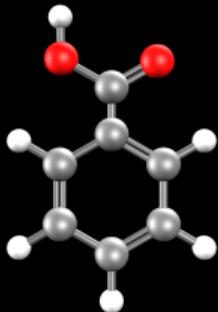
Electrophilic attack is favoured where the HOMO density is largest.



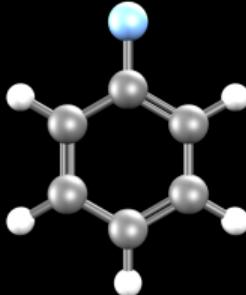
# Exercise — Electrophilic Attack



Aniline



Benzoic Acid



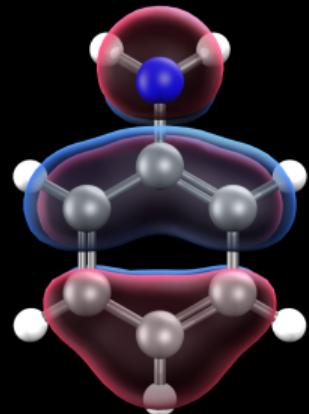
Fluorobenzene

1. Build structures for all three systems.
2. Run HF/6-31G energy calculations.
3. For each molecule, plot the HOMO and predict whether the  $\text{NO}_2^+$  electrophile is ortho, meta or para directing.
  - ▶ Hint: increase the surface isovalue to make it clearer where the density is larger.



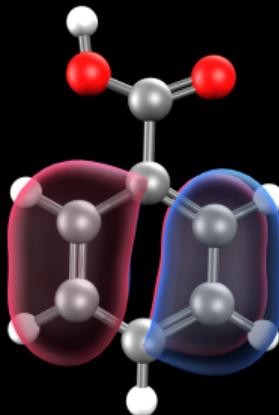
# Results— Electrophilic Attack

Using an isovalue of 0.05



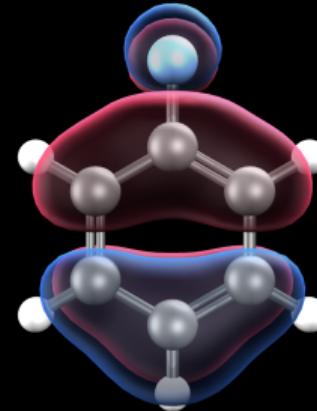
Aniline

- Ortho ✓
- Meta ✗
- Para ✓



Benzoic Acid

- Ortho ✓
- Meta ✓
- Para ✗



Fluorobenzene

- Ortho ✓
- Meta ✗
- Para ✓

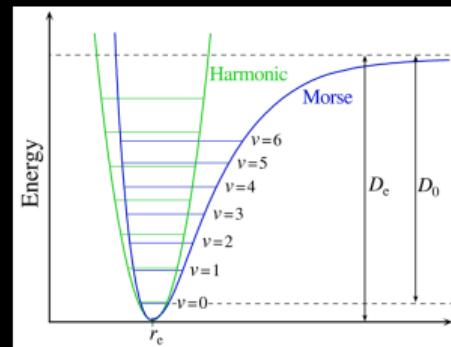
Steric hindrance also plays a role.



# Vibrational Frequencies

Vibrational frequencies can be computed within the harmonic approximation.

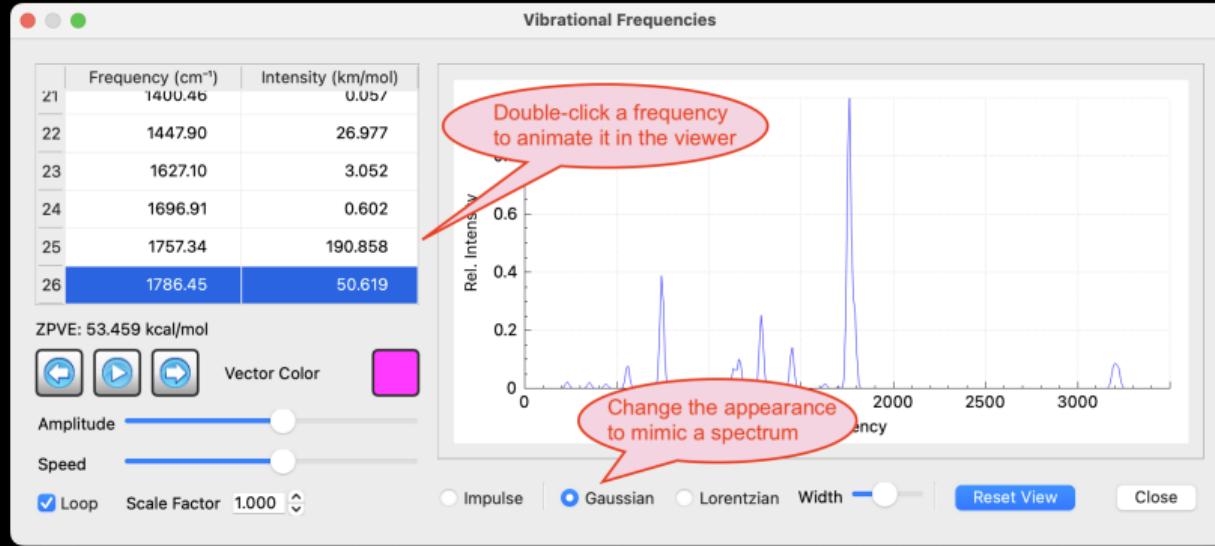
$$\hat{V}_{\text{eff}}(\mathbf{R}) = V(\mathbf{R}_0) + V'(\mathbf{R}_0)(\mathbf{R} - \mathbf{R}_0) + V''(\mathbf{R}_0)(\mathbf{R} - \mathbf{R}_0)^2 + \dots$$



Meaningful frequencies must be computed at an energy minimum obtained at the same level of theory.

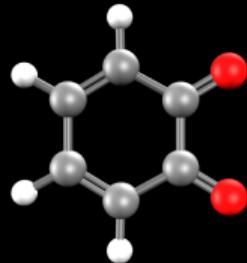


# Frequencies Display

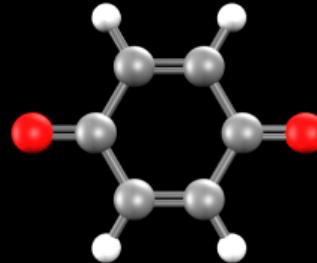


# Exercise — Frequencies

Benzoquinone exists in two isomeric forms:



*o*-Benzoquinone



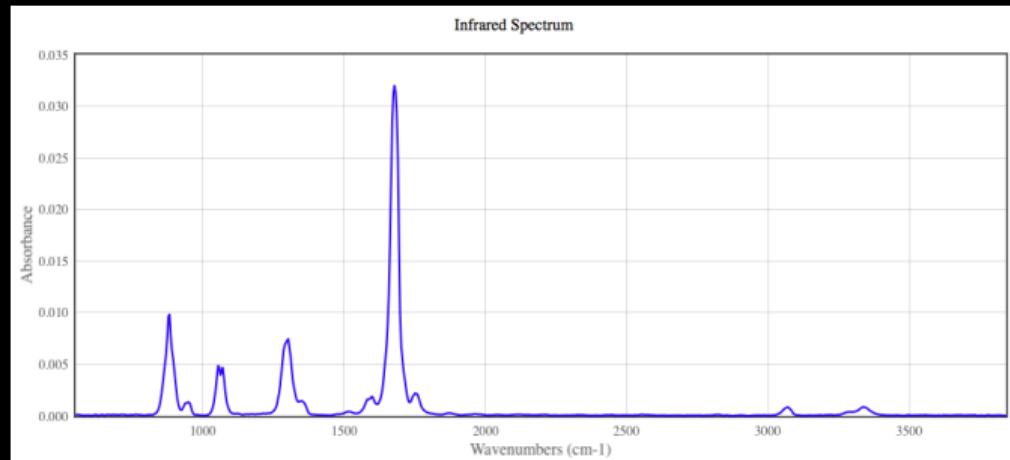
*p*-Benzoquinone

1. Optimize both structures at the B3LYP/6-31G\* level.
2. Compute the harmonic frequencies at the same level.
3. Identify the most intense band for each isomer.
4. Characterize the mode that gives the key difference between the isomers.



# Exercise — Frequencies

The following IR spectrum of benzoquinone was obtained from the NIST website:

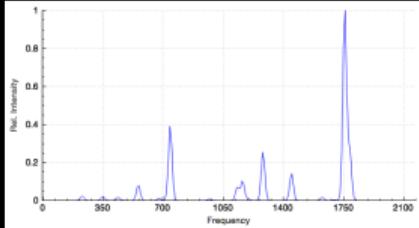


To which isomer does this spectrum correspond?

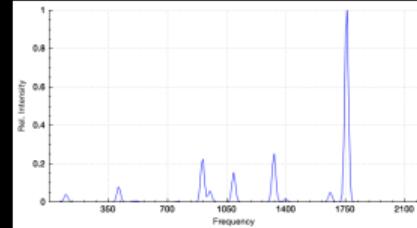


# Results — Frequencies

- ▶ The most intense bands both occur at  $1757\text{ cm}^{-1}$  and correspond to the symmetric (o-benzoquinone) and asymmetric (p-benzoquinone) C=O stretches.
- ▶ The out-of-plane wag of o-benzoquinone ( $742\text{ cm}^{-1}$ ) is intense. The corresponding mode in p-benzoquinone is IR silent.
- ▶ The NIST spectrum is that of p-benzoquinone.



o-Benzoquinone



p-Benzoquinone



# Excited State Methods

Q-CHEM has a wide range of excited state methods including:

- ▶ Single-electron methods (CIS)
- ▶ Time-Dependent Density Functional Theory (TD-DFT)
- ▶ The Maximum Overlap Method (MOM)
- ▶ Correlated wave function methods (EOM-CC)

Furthermore, a range of calculation types are possible:

- ▶ Vertical excitation energies
- ▶ Geometries of excited states
- ▶ Vibrational frequencies of excited states
- ▶ Attachment/detachment densities
- ▶ Properties such as transition dipoles moments



# TD-DFT

- ▶ TD-DFT computes the poles in the response of the ground state energy to a time-varying applied electric field.
- ▶ These poles correspond to excitation energies.
- ▶ Its computation cost is roughly that of CIS,  $\mathcal{O}(N^2)$ , but has the advantage of including correlation.
- ▶ TD-DFT performs well for low-lying valence transitions, but less well for Rydberg and charge-transfer states.
- ▶ Q-CHEM also includes Spin-Flip DFT which is based on a high-spin reference and is able to model di-radicals and systems with stretched bonds.



# TD-DFT Setup

iQmol

Setup Advanced

Method is TD-DFT

Calculate Geometry Charge 0

Method TD-DFT Multiplicity 1

Basis 6-31+G\* ECP None

Exchange B3LYP Correlation None

SCF Control

Determines the number of states to compute

Wavefunction Analysis

CIS/TD-DFT

Number of Roots 5 Singlets RPA Spin Flip

State To Optimize 1 Selects the target state for optimization jobs

Triplets XCIS SF-XCIS

NTO Pairs 0

Analyze Relaxed Density Amplitudes

State Mulliken Charges Excited State Moments Transition Moments

Optimization

Generated Input File:

```
Molecule
1 0
C -0.0000000 0.0000000 0.4138876
O 0.0000000 -1.0000000 -0.8113366
H -0.0000000 0.0000000 1.0000000
H -0.0000000 -1.0119404 1.0231762
Basis
BASIS = 6-31+G*
CIE_M_RHO = 1
CIE_STATE_DERIVATIVE = 1
EXCHANGE = B3LYP
GET = 1
JOB_TYPE = Optimization
SCF_CONVERGENCE = 6
End
```

Server Q-Chem Submit

Reset Disable Controls Cancel



# Excited States Display



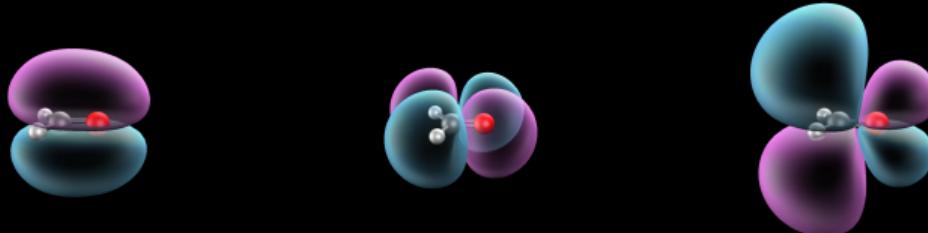
# Exercise — Formaldehyde



1. Build the formaldehyde molecule (ensure  $C_{2v}$  symmetry!)
2. Optimize your structure using B3LYP/6-31+G\*.
3. Compute the 10 lowest triplet and singlet states using TD-DFT/B3LYP.
4. Identify the  $n \rightarrow \pi'$  transition and optimize its geometry.
  - ▶ Set CIS\_STATE\_DERIVATIVE = X where X corresponds to the  $n \rightarrow \pi'$  transition
5. Observe the change in the C-O bond length and compute the adiabatic excitation energy.
6. If you have time, perform the same analysis for the  $\pi \rightarrow \pi'$  state.



# Results — Formaldehyde



HOMO-1 ( $\alpha 7$ )  
 $\pi_b$  ( $b_2$ )

HOMO ( $\alpha 8$ )  
 $n$  ( $b_1$ )

LUMO ( $\alpha 9$ )  
 $\pi^*$  ( $b_2$ )

Transition	$\langle S^2 \rangle$	Root	Strength	Energy/eV		$R_{C-O}/\text{\AA}$
				Vertical	Adiabatic	
GS	0	0				1.209
$n \rightarrow \pi^*$	2	1	0.000	3.347	2.670	1.311
$n \rightarrow \pi^*$	0	2	0.000	4.067	3.344	1.317
$\pi_b \rightarrow \pi^*$	2	3	0.000	5.835	2.787	1.455
$\pi_b \rightarrow \pi^*$	0	15	0.171	9.956	8.538	1.337



# The PES

The potential energy surface (PES) arises as a direct results of making the Born-Oppenheimer approximation.

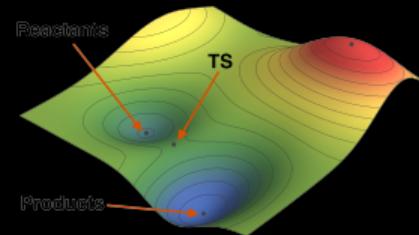
$$\hat{H} = \hat{H}_e + \hat{H}_n$$

$$\hat{H}_e = \hat{T}_e(\mathbf{r}) + \hat{V}_{ee}(\mathbf{r}) + \hat{V}_{ne}(\mathbf{r}; \mathbf{R}) + \hat{V}_{nn}(\mathbf{R})$$

$$\hat{H}_n = \hat{T}_n(\mathbf{R}) + \hat{V}_{eff}(\mathbf{R})$$

Although fictitious, it helps us understand and rationalize much of chemistry including:

- ▶ Structures
- ▶ Reaction barriers
- ▶ Reaction mechanisms



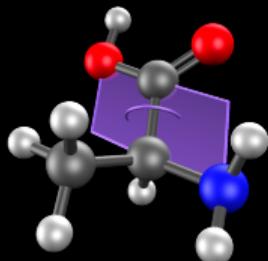
# Q-CHEM Job Types

Q-CHEM can perform several different kinds of calculation to explore and characterize the PES:

- ▶ Optimization
- ▶ Optimization with constraints
- ▶ PES scan
- ▶ Transition state search
- ▶ Frequencies (both harmonic and anharmonic)
- ▶ Intrinsic reaction pathways



# Exercise — Alanine PES Scan

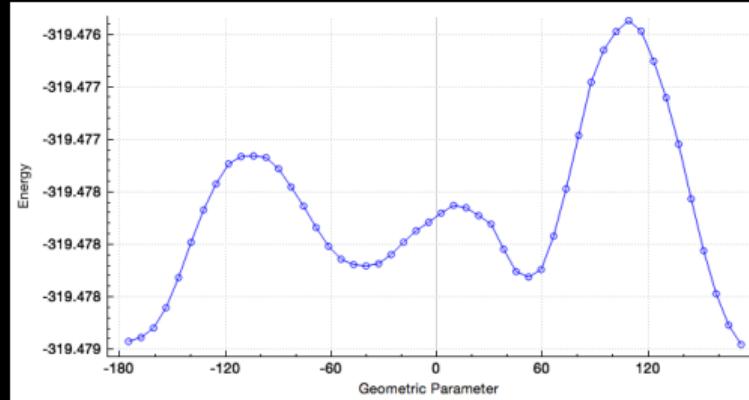


1. Use the Molecule Library to build alanine and optimize the structure using molecular mechanics.
2. Set up a B3LYP/STO-3G PES scan calculation:
  - ▶ Select the O-C-C-N atoms (in that order!)
  - ▶ Set a dihedral scan coordinate using the Build ▶ Set Geometric Constraint menu option.
  - ▶ Scan between -179 to 155 using 10 steps.
  - ▶ Turn off the checkpoint file!
3. How many minima do you expect to see on the PES?
4. What is the barrier to rotation of the C—C bond?



# Results — Alanine PES Scan

- ▶ The PES has three minima:



- ▶ The barrier to rotation at B3LYP/STO-3G is about 5.3 kJ/mol ( $\approx 2 \text{ mE}_h$ ) (more points are required to see this)
- ▶ The relative stability of the two minima around 0° changes when dispersion is incorporated.



# MP2 Methods

- ▶ MP2 theory provides one of the cheapest wave-function based methods that accounts for the correlation energy.

$$E^{(2)} = -\frac{1}{4} \sum_{ab}^{\text{virt}} \sum_{ij}^{\text{occ}} \frac{|\langle ab||ij\rangle|^2}{\varepsilon_a + \varepsilon_b - \varepsilon_i - \varepsilon_j}$$

- ▶ The required MO integrals result in a  $\mathcal{O}(N^5)$  cost.
- ▶ Q-CHEM has optimized direct (energies only) and semi-direct (energies+gradients) implementations MP2.
- ▶ The semi-direct method requires only  $ONV$  memory.



# MP2 Methods

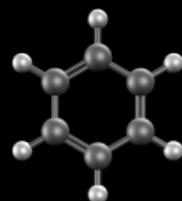
Q-CHEM also has a range of fast MP2 methods that can be cheaper, but introduce some approximations.

- ▶ RI-MP2 makes use of an auxiliary basis to approximate basis function pairs  $|\mu\nu\rangle = \sum_P C_{\mu\nu}^P |P\rangle$  - this significantly lowers the  $N^5$  cost prefactor.
- ▶ Local-MP2 restricts the double substitutions such that the occupied and virtual orbitals involved must be on the same atom - this requires first extracting local polarized atomic orbitals (PAOs) from the HF wave function.
- ▶ SOS-MP2 uses empirical scaling of the opposite spin component of  $E_c$  - this lowers the cost to  $\mathcal{O}(N^4)$ .



# Benzene Dimer

Benzene dimer has three main structures of interest; T-shaped (T), sandwich (S) and parallel-displaced (PD):



(T)



(PD)

Because dispersion is important in weakly bound systems regular DFT is unsuitable  $\Rightarrow$  MP2-based methods.



# Exercise — Benzene dimer

1. Download the structure files:

<https://www.iqmol.org/workshop/benzene.xyz>

<https://www.iqmol.org/workshop/benzene-dimer-T.xyz>

<https://www.iqmol.org/workshop/benzene-dimer-PD.xyz>

2. What point-group symmetry do these structures have?
3. Compute the MP2, RI-MP2, Local-MP2 and SOSMP2 energies using the cc-pVDZ basis. The auxiliary basis should be set to rimp2-cc-pVDZ.
4. What fraction of the correlation energy is recovered by each method?
5. Do all these levels of theory predict the same relative stability?



# Results — Benzene dimer

	Binding Energy (kJ/mol)		Ratios (T-struct)	
	PD ( $C_{2h}$ )	T-Shaped ( $C_{2v}$ )	$E_c$	Time
Regular MP2	-17.43	-15.62	100.00	100%
RI-MP2	-17.47	-15.64	99.99	16%
TRIM-MP2	-15.91	-13.00	101.49	190%
SOS-MP2	-7.63	-9.79	95.71	17%

Note: BSSE and relaxation effects are not accounted for

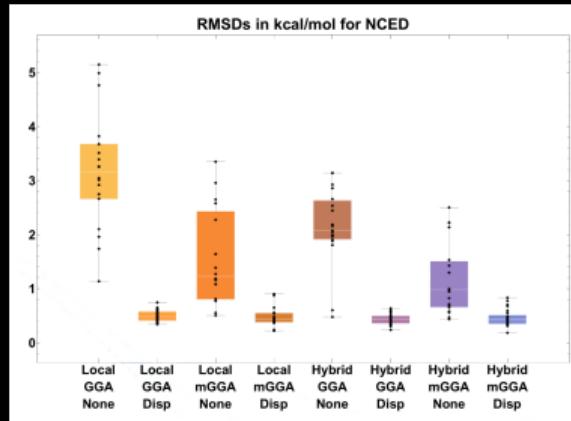
Raw energies:

	Monomer	PD	T-shape
MP2	-231.50485534	-463.01634774	-463.01566085
RIMP2	-231.50476161	-463.01617634	-463.01547986
TRIM-MP2	-231.51709580	-463.04024993	-463.03914459
SOS-MP2	-231.47227531	-462.94745711	-462.94827790



# Dispersion DFT

Traditional DFT methods are unsuitable for non-covalent interactions due to the absence of long-range electron correlation.



RMSD over 1744 non-covalent dimers.

Empirical Dispersion corrections, such as Grimme's DFT-D approach, significantly improve DFT calculations.



# DFT-D3

The D3 correction to KS-DFT relies only on the relative positions of the nuclei:

$$E_{\text{D3}} = - \sum_{A < B}^{\text{atoms}} \sum_{n=6,8} s_n \frac{C_{n,AB}}{R_{AB}^n} f_n(R_{AB})$$

$f_n$  are damping functions and give rise to the principle differences between the various flavours of D3 corrections.

These are controlled by the `DFT_D rem` variable:

- ▶ `D3_ZERO`: the original zero damping
- ▶ `D3_BJ`: the Becke-Johnson damping
- ▶ `D3_OP`: the ‘optimal power’ damping by Witte *et al.*



Basis set superposition error (BSSE) arises from the inconsistent treatment of the monomers and super-system:

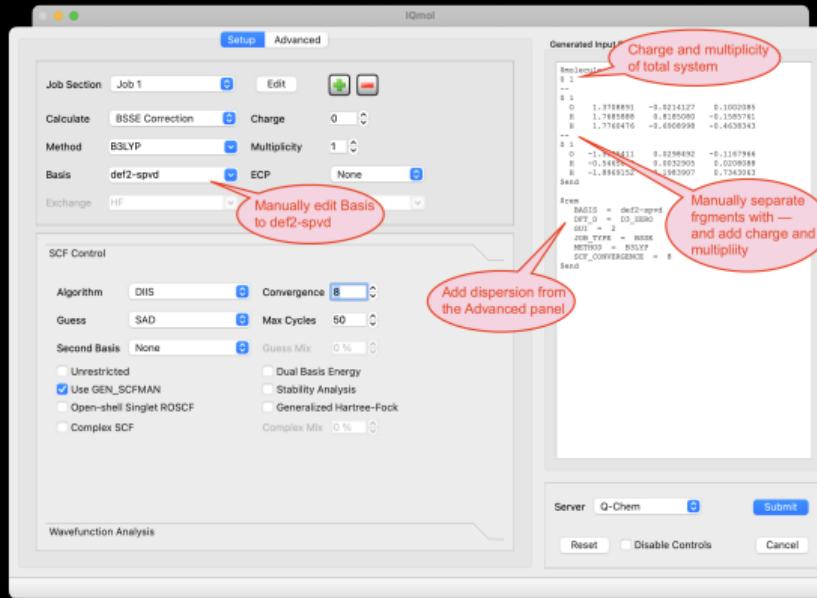
$$E_{\text{int}} = E(AB) - E(A) - E(B)$$

The dimer is over-stabilised, leading to [over-binding](#).

- ▶ For non-covalent interactions def2-QZVPPD roughly represents the CBS limit.
- ▶ The performance of aug-triple- $\zeta$  (def2-TZVPPD) is close.
- ▶ The use of smaller basis sets (e.g. def2-SVPD) can introduce much larger BSSE errors.



# Fragment Job Setup



You will need to manually edit the fragment specification in the generated input panel.



# Exercise — Water Dimer



1. Optimize the structure of the water dimer using BLYP-D3(0) and the def2-SVPD basis.
  - ▶ Use the MMFF94 forcefield to pre-optimize your structure.
  - ▶ BASIS=def2-SVPD will need to be manually edited.
  - ▶ The checkpoint file should be turned off with GUI=0
  - ▶ The D3(0) correction can be found in the Advanced panel.
2. What length do you get for the hydrogen bond?
3. Compute the interaction energy your equilibrium structure using the same level of theory.
  - ▶ Use JOB\_TYPE=BSSE and
  - ▶ You will need to edit the fragments in the QUI panel.
4. How does the D3(0) correction affect your results?



## Exercise — Water Dimer

Energy decomposition analysis (EDA) can be used to breakdown the binding energy in to physically interpretable components:

- ▶ Frozen density (no relaxation)
  - ▶ Polarization (intrafragment relaxation)
  - ▶ Charge transfer (interfragment relaxation)
1. Use the EDA to determine the breakdown of the binding energy of the water dimer.
  2. Which component contributes the most to the binding energy?

Note: You will need to specify the separate fragments in the same way as for the BSSE calculation.



# Results — Water Dimer

Indicative results (depending on initial geometry).

	Units	w/ D3	w/o d3
Hydrogen bond-length	Å	1.9261	1.9353
Binding energy	kJ/mol	-24.491	-21.471
Binding energy (CP)	kJ/mol	-22.589	-19.563
Frozen	kJ/mol	-8.956	-6.315
Dispersion	kJ/mol	-8.153	-4.950
Polarization	kJ/mol	-5.071	-4.944
Charge transfer	kJ/mol	-10.464	-10.212

The bond-length is less effected by dispersion than the energies.  
Charge transfer gives rise to the largest contribution to binding.

