## Project: proton transfer in mixed dimers and trimers of HF and H<sub>2</sub>O

This project deals with the interactions of HF 1 with  $H_2O$  2 within their dimers (HF)<sub>2</sub> 3 and ( $H_2O$ )<sub>2</sub> 4, the mixed dimer  $H_2O$ –HF 5 and the mixed trimers  $H_2O(HF)_2$  7 and ( $H_2O$ )<sub>2</sub>HF 9, as well as the degenerate multiple proton transfer in the mixed dimer (5 to 5') via the transition structures ( $H_3O$ )F 6 and in the mixed trimers (7 to 7') and (9 to 9') via the transition structures ( $H_3O$ )( $H_2O$ )F 10, respectively. The calculations will be performed using the density functional assigned to you, as follows (detailed instructions below):

- 1. compute the structures with Gaussian 16 using the **Def2SVP** basis set and refine using the **Def2TZVP** basis set. Include **Pop=NBORead** and the \$NBO keyword line in the refinement calculation to obtain the gas phase NPA charges. Use a checkpoint file for each system.
- 2. perform counterpoise calculations for the minima after refinement, using the Def2TZVP basis set.
- 3. recompute the structures (use the checkpoint files) using **SCRF=PCM** (water is the default solvent). Include **Pop=NBORead** to obtain the NPA charges in the implicit solvent.
- 4. calculate high-level energies (single points) with Orca at the **DLPNO-CCSD(T)** aug-cc-pVTZ level using the gas-phase structures computed in step 1 with the Def2TZVP basis set.

In the first optimization (with the Def2SVP basis set), use **Opt Freq=NoRaman** for the minima and **Opt=(TS,CalcFC) Freq=NoRaman** for the transition structures. In the refinement step (with the Def2TZVP basis set), use **Opt=ReadFC Freq=NoRaman** and **Opt=(TS,ReadFC) Freq=NoRaman**, respectively, and include the keywords **Guess=Read Geom=Check**. You can use Molecule to generate the inputs for the refinement step or copy the input files and use an editor like nedit; in the latter case, make sure that no coordinates are present in the input and be careful to position the \$NBO keyword line correctly. A starting structure for a TS can easily be constructed from the corresponding minimum by moving the hydrogen atoms to obtain a symmetrical (C<sub>s</sub> or C<sub>2</sub>) structure; no interpolation is required.

The structures for **3**, **4**, **7** and **9** may change significantly when re-optimizing (larger basis set or inclusion of implicit solvent). This may cause the optimization to stop (check the output), due to a linear arrangement of atoms. Should this happen, then restart the calculation using **Opt=Cartesian** (without ReadFC) which is slower but less sensitive to this problem.

## Write a concise report:

- · Introduction, methods, results, discussion, conclusions, as usual.
- Include tables of total energies (a.u.) and relative energies (kcal/mol or kJ/mol).
- Evaluate the interaction energies within the dimers and trimers 3, 4, 5, 7 and 9 at each level.
- How serious is BSSE for these systems?
- Compute the activation energies for proton transfer at each level.
- How does the implicit solvent model affect the structures, the charge distribution and the interaction and activation energies?
- Provide pictures of the computed structures. Pro-tip: use "constrain proportions" when scaling.
- Include relevant distances in the pictures (in Molecule: double-click a bond or add a "line" bond)
- Give literature references where appropriate.

## Structures:

