What is the orientation dependence for RNA base-base hydrogen bonds? Can standard force fields mimic this behavior?

**Strategy**

- Scan of functional group interaction energy over HB orientation
- Guanine-Cytosine (GC) Nucleoside - most stable pair
- Large dipole moment of cytosine in F-SAPT
- Explore CC - reaction coordinate
- Entire Watson-Crick (WC) HB
- Comparison of functional form, not parameters - model fitting
- Capability of model - quality of fit

**Methods**

- Guanine-Cytosine Nucleoside
- Mean heavy atom RMSD across six SA replicas
- Carbonyl-Amino HB
- Force Field is Indifferent to Phi
- Guanine-Cytosine Nucleoside
- Mean heavy atom RMSD across six SA replicas
- Guanine-Cytosine Nucleoside
- Mean heavy atom RMSD across six SA replicas
- Guanine-Cytosine Nucleoside
- Mean heavy atom RMSD across six SA replicas
- Light weighted object oriented structure analysis

**Conclusions**

- Need greater diversity of systems
- Cross-validate above fits
- Compare parameter sets to AMBER
- Scan other HBs in GC pair
- Scan all pairs - structures from full nonbonded fit
- Regions very close to WC are more accurately predicted.
- Observed interaction energies in those regions are similar.
- Classic force field functional form cannot match QM.

**Future Directions**

- Need greater diversity of systems
- Cross-validate above fits
- Compare parameter sets to AMBER;
- Scan other HBs in GC pair
- Scan all pairs - structures from full nonbonded fit
- Regions very close to WC are more accurately predicted.
- Observed interaction energies in those regions are similar.
- Classic force field functional form cannot match QM.

**References**