

Conformational Analysis



- Goal: to explore the energy surface of a molecule
- Needed:
 - A definition of conformational space
 - A search method
 - An energy determination method (force field)

Conformational Space



- Cartesian coordinates (x, y, z)
- Internal coordinates (bond lengths, angles, torsions)
- Templates with a joining scheme (cyclohexane can appear as a chair, or two enantiomeric half-chairs, etc)

Conformational Search Methods



- Torsion angle driving
- Monte Carlo
- Artificial Intelligence
- Simulated Annealing
- Poling
- Etc.

Torsion Angle Driving



- Called 'Conformational Search' in MOE (or 'Systematic Search' in newer versions)
 - Compute -> Conformations -> Conformational Search
- Steps a torsion angle from a starting to an ending point by a given increment
 - can be minimized completely at each step to give minima
 - other coordinates can be minimized to derive potential energy surface for torsional rotation
- · Benefit: exhaustive

Torsion Driving Limitations



- Not good for highly flexible molecules (too many torsions requires generation of a large number of conformations for evaluation)
- Explores large regions with high energy
- Ratcheting while exploring PES may result in different start and end points



Class Exercise 1



- · Build an alkane with 5 rotatable torsions and save it
 - Perform 2 torsion angle conformational searches with angle increments of 10° for only 1 dihedral angle, with and without optimization of the conformations
 - Take note of how many conformations are generated, and how many you end up with after minimization
 - Plot the energy for the search done without minimization
 - Perform conformational searches with angle increments of 10° for each dihedral angle, with and without optimization
 - Take note of how many conformations are generated, and how many you end up with after minimization

Monte Carlo



- Uses a random kick of coordinates followed by minimization to find new minima
- · More effective on highly flexible molecules
- Not exhaustive -> heuristics used to define end point:
- if each of the lowest energy conformations has been found ~10 times, the search has probably found all the interesting ones
- if duplicate conformations are found ~20 times in a row, the interesting conformations have probably all been found
- (actual numbers to use depend on the flexibility of the system and your interest in a nearly exhaustive search!)
- In MOE there are two methods that include this
- Compute -> Conformations -> RIPS Conformational Search
- Compute -> Conformations -> Hybrid Monte Carlo

Class Exercise 2

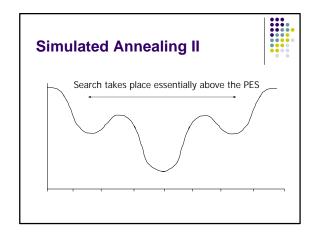


- Perform a RIPS conformational search on the molecule you built for the previous exercise
 - Take note of how many conformations are generated and how many are actually unique
- Perform a Hybrid Monte Carlo conformational search on the same molecules
 - Take note of how many conformations are generated and how many are unique

Simulated Annealing



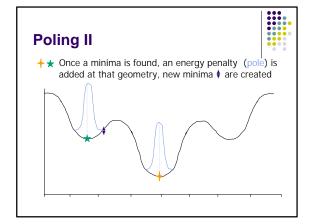
- Variant of molecular dynamics
 - · Provides kinetic energy to the atoms
 - Recalculates atomic positions after a small time step (needs to be more frequent than molecular vibrations to prevent dissociation)
 - Higher temperatures generally used to give molecules sufficient energy to cross energy barriers
 - Cooling cycles used to minimize molecules
- Initially proposed as a way to drive the conformational search to the global minima



Poling



- Goal: to sample accessible conformations, not necessarily only minima
- Justification: interactions between drug molecules and their biological target involve conformational changes in both the drug molecule and the target to generate the COMPLEX structure of lowest free energy – this is not necessarily identical to the lowest energy isolated structure



Reading



 Chapter 8 through the end of 8.8 in Leach (First Edition – probably add one chapter for the Second Edition)