Basin-Hopping Simulation of Alanine Dipeptide

In this exercise you will perform several **Basin-Hopping (BH) simulations** with **GMIN** using the **CHARMM19** force field with the implicit **EEF1** solvent model. We we will work on **JUBIO**. Necessary files are available from "/home/strodel/ala-gmin/".
The **GMIN program** can be invoked via
/home/strodel/bin/CGMIN >& charmm.out
Required input: a data file and an input stucture
Output: GMIN_out and structure files (*dbase.*.pdb, aftermove.pdb*)

Task: Follow the exercises and report the chosen commands and parameters for each step in your protocol. Check your Monte-Carlo moves after each change in the data file by looking at the system using VMD.

1) **Copy the input structures *input.pdb* and *input.crd* for all subsequent GMIN runs from /home/strodel/ala-gmin/highT/.**
   CHARMM works with *.crd* files as input (as Gromacs can use *.gro* files). This input structure was generated via a short high temperature MD run.

2) **Perform a local minimization of the starting structure using the given data input**

   /home/strodel/ala-gmin/local_minimization/data.

   a) How many steps are needed to decrease the root mean square force to RMSF < 10^{-6} kcal/(mol*Å)?

   b) Show and align the minimized structure (*dbase.1.pdb*) together with the starting structure (*input.pdb*) in one picture with different colors.

   c) What is the RMSD between both structures?

3) **Perform one Basin-Hopping step using Cartesian moves with a maximum step size of 2 Å.**

   Use the *data* file from /home/strodel/ala-gmin/cartesian_moves/data.

   a) Show and align *input.pdb*, *aftermove.pdb* and *dbase.1.pdb* with VMD in one picture with different colors. Report the changes in **2-3 sentences**!

   b) How many minimization steps were required till convergence after the BH step?

4) **Perform one Basin-Hopping step using dihedral moves with a maximum step size of 60°.**

   Use the *data* file from /home/strodel/ala-gmin/diheral_moves/data.

   a) Show and align *input.pdb*, *aftermove.pdb* and *dbase.1.pdb* with VMD in one picture with different color and file name. Report the changes in **2-3 sentences**!

   b) How many minimization steps were required till convergence after the BH step?

   Compare with 3b) in **few sentences**.

5) **Perform a Basin-Hopping simulation with 1000 steps using Cartesian moves with a maximum step size of 2 Å.**

Save the **10 lowest energy structures**. Use the *data* file from step 3 and make the necessary changes:

STEPS 1000 1.0
SAVE 10
Remove DEBUG

a) How many final structures were found? What is the smallest and what the largest energy for these structures?

b) Analyze the Ramachandran angles ϕ and ψ of these structures (provide a table)? Compare these structures with those obtained from your MD runs in the previous exercises using Gromacs.

c) Show the Markov energy (*markov*) and the energy (*energy*) after each step. Use *Gnuplot* for that.* What is the difference between these two energies? (**2-3 sentences)**

6) **Perform a Basin-Hopping simulation with 1000 steps by using dihedral moves with a maximum step size of 60°.**

Save the **10 lowest energy structures**. Use the *data* file from step 4 and make the necessary changes:

STEPS 1000 1.0
SAVE 10
Remove DEBUG

a) How many final structures were found? What is the smallest and what the largest energy for these structures?

b) Compare these structures with those obtained in 5). Why are more structures found using Cartesian moves?

c) Show the Markov energy (*markov*) and the energy (*energy*) after each step.
Compare with 5c). Use *Gnuplot* for that.*

7) **Discussion of the results by answering the following questions.**

a) Which global optimization was more efficient and why: the one with Cartesian or with dihedral moves? (**2-3 sentences)**

b) What is the difference between local and global optimization? (**2-3 sentences)**

***Help:**

```
set terminal png font "arial,12" size 1200,1200
set output 'energies.png'
set xlabel "Schritt"
set ylabel "Energie [kcal/mol]"
```

```
set multiplot layout 1,2
plot 'energy' u 1:2 with lines title 'Energie' ,\
plot 'markov' u 1:2 with lines title 'Markov'
unset multiplot
```