HECSP-NMRScore_P tutorial:

Suppose you put the folder "hecsp" at "/Users/xxx/". Then add the following lines to bash file:

```
## Setting PATH for HECSP NMRScore_P
export PYTHONPATH="/Users/xxx/hecsp:$PYTHONPATH"
export PATH="/Users/xxx/hecsp/calHcsp:$PATH"
export PATH
export HECSPHOME="/Users/xxx/hecsp"
```

Take the Glide docking result of 1J5I model 1 as an example. The pose viewer file generated by Glide docking is "dock_pv.maegz". The first molecule in the file is the receptor, and the following entries are ligand poses.

Step 1: Extract receptor from "dock_pv.maegz" into "receptor.pdb" and ligand poses into "poses.mol2" (scripts available with Schrodinger package)

```
$SCHRODINGER/utilities/pdbconvert -imae dock_pv.maegz -opdb receptor.pdb -n 1
```

Remember to delete the cap residues ACE or NMA if present in the pdb file.

```
$SCHRODINGER/utilities/mol2convert -imae dock_pv.maegz -omol2 poses.mol2 -n 2:
```

Step 2: split the poses.mol2 file into separate mol2 files (script available in HECSP package)

```
splitmol2.py poses.mol2 pose
```

It will give you pose_001.mol2, pose_002.mol2 …….

Step 3: Generate mol2 file with Gasteiger charges by simply run a shell script "run.sh", which needs the antechamber program from the Ambertools package (free)

```
"for file in pose_*.mol2
 do
        base=${file%.mol2}
        num=`echo "$file" | cut -d'.' -f1 | cut -d'_' -f2`
        $AMBERHOME/bin/antechamber -fi mol2 -fo mol2 -i $base.mol2 -o
  gas_pose_"$num".mol2   -j 0 -pf y -c gas -nc 0
done"
```

It will give you gas_pose_001.mol2, gas_pose_002.mol2 …….

Step 4: Prepare "exp_csp.txt" file in the same folder, which contains all the experimental CSPs:

Step 5: Determine the residues or specific protons that are significantly perturbed. The result is used for the NMRScore_P calculation in the next step (script available in the HECSP package).

big_H.py receptor.pdb pose_001.mol2 10

The last integer "10" in the command line is to define the adopted distance cutoff.

Step 6: Calculate NMRScore_P from receptor.pdb and gas_pose_001.mol2 (script available in the HECSP package):

nmrscorep.py -p receptor.pdb -l gas_pose_001.mol2 -s gloocv --resid 4,32,33,34,35,36,43,44,46,47,53,69,75,78,96,97,98,99,102,103,104,106,108

Two files "NMRScore_result.txt " & "receptor_gas_pose_001_csp" will be generated. One can easily write a shell script to calculate hundreds of protein ligand pairs.