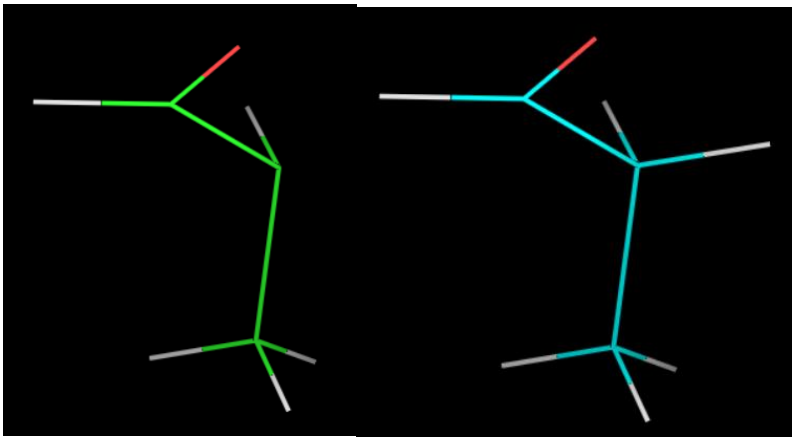
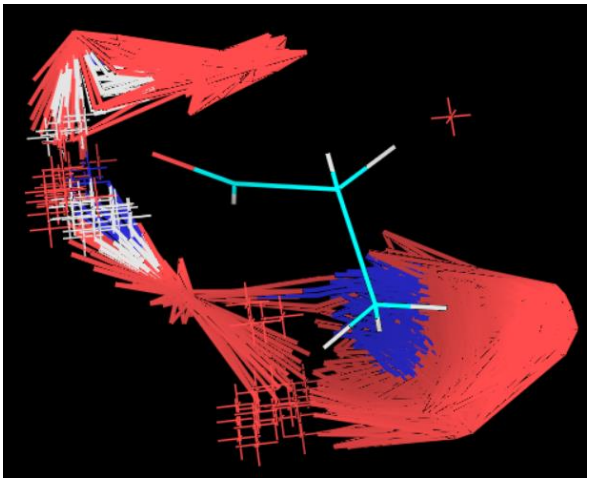
Files can be found: https://github.com/MiloCheng17/RINRUS/tree/master/examples/mesh

1. Select the .pdb file from which you want to extract a small amino acid residue. (It can be any number of residue). We have selected template44.pdb from the example.
2. Use the same pdb from which. probe file is generated because if. probe and .pdb have not same coordinates then newly trimmed pdb will not create mesh around it.
3. We will trim ALA 474 for this tutorial from template44.pdb.
4. Open template44.pdb and locate coordinates lines for ALA 474.
5. Keep these lines and delete other lines. Save it. Name as ala.pdb
6. If that amino acid is attached to some residue in protein then we need to add hydrogen using pymol, reduce or any other program.
   python3 ~/git/RINRUS/bin/pymol_scripts.py (this pymol script can add hydrogen)
7. Make sure that while adding new Hydrogen, remaining protein structure should not change coordinates. Save as ala_h.pdb
8. We have created trimmed .pdb



9. You can see difference after hydrogen addition.
10. Once we generate mesh around this pdb then it looks as below.

```
probe_mesh_rin.py -model ala_h.pdb -data 4urh_CS_A_h.probe
```



probemesh_rin.xyz