\*Note for general setup

<https://www.rosettacommons.org/manuals/archive/rosetta3.4_user_guide/db/d3c/database.html>

* Download database directory to computer

<https://www.rosettacommons.org/manuals/archive/rosetta3.4_user_guide/d4/d4a/make_symmdef_file_denovo.html> (plus see DiMaio article)

Denovo Symmetry Definition File

OPTIONS

* (Point AKA NCS AKA noncrystallographic default) symmetry type: cyclic or dihedral
  + Alternatively, helical (rotation & transition along one symmetry axis), or wallpaper & crystal (subunit forms repeating 2D or 3D pattern)
  + Expect 3-6 DoF, where dofs are torsion angles of the backbone and side-chains along with the rigid-body transformations between peptide segments, only with regards to the master subunit (surrounded by all interaction partners needed to calculate total energy)
    - Jumps control the position of each subunit relative to its reference frame (wrt rigid body symmetry)
      * Reference frame coordinates (AKA virtual residue coordinates) can be set manually through X & Y axis unit vectors (start & stop) or rotation & translation of a single virtual residue
    - 3 rotational, 3 translational variables describe the rigid-body transformation between start and end coordinates of the jump, then further restricted by axes
* Number of subunits
* Simulate subsystem
* Slide\_type
  + How multidimensional slide should be performed: randomly for each step, random for first step but sequential through both, or order manually
* Slide\_criteria\_type
  + Abandon slide if: (don’t understand options other than number of contacts)
* Slide\_criteria\_val (use if type is CONTACTS)
  + Value when a slide move is abandoned, given criteria
    - In principle, a protein complex with identical symmetry can be used as the starting point to generate a SDF using the make\_symmdef\_file.pl script. The resulting SDF has to be modified by hand to remove any dependence on the rigid body position of the analyzed complex and to completely randomize the symmetric rigid body space.

Example Symmdef File Denovo from DiMaio article:

symmetry\_name c2

subunits 2

recenter

number of interfaces 1

E = 2\*VRT0001 + 1\*(VRT0001:VRT0002)

* subunit connected to virtual residue 0001 is the scoring subunit, with internal energies multiplied by 2 to get total system energy, with intermolecular energies from subunits connected to VRT0002 added with a factor of 1)

anchor residue COM

virtual transforms start

start -1,0,0 0,1,0 0,0,0

rot Rz 2

virtual transforms stop

connect virtual JUMP1 VRT0001 VRT0002

set\_dof BASEJUMP x(50) anglex(0:360) angle\_y(0:360)

angle\_z(0:360)

* A 2nd virtual residue is generated by application of twofold rotation around the Cartesian Z axis
* For the jump BASEJUMP, translation along x axis initialized at value of 50 and rotation around x, y, and z axes allowed
  + Two subunits at (50, 0, 0) and (-50, 0, 0) for non-contact
  + All angles 0-360 degree, so random & uniformly sampled
* make\_symmdef\_file\_denovo.py -symm\_type cn -nsub 2 > C2.symm generates the file
* Reference frames have axis pointing towards (0, 0, 0), translational dof along x-axis; recenter to ensure that anchor residues align with x-axis such that translating along the x-axis causes atomic contact between subunits

<https://www.rosettacommons.org/manuals/rosetta3.1_user_guide/symmetry.html>

FAQ: <http://www.robetta.org/faqs.jsp>

Q. What are Fragment Libraries?

Fragment Libraries are the pieces of experimentally determined structures that Rosetta uses to guide the search of conformational space when predicting structures using the ab initio protocol, as well as longer loop conformations in homology models.

Q. What is the difference between Ab Initio and De Novo Modeling?

Ab initio structure prediction classically refers to structure prediction using nothing more than first-principles (i.e. physics). De Novo is a more general term that refers to the greater category of methods that do not use templates from homologous PDB structures. Since Rosetta uses fragments from existing PDB structures in order to guide the search in conjunction with energy functions, there is a semantic argument as to whether it is truly "ab initio" (although the same could be said for any statistically derived energy function). Long story short: call it what you want, but be prepared for a debate!

[http://getit.library.utoronto.ca/index.php/access?http://myaccess.library.utoronto.ca/login?url=http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PMC&cmd=Search&term=21731614[pmid](http://getit.library.utoronto.ca/index.php/access?http://myaccess.library.utoronto.ca/login?url=http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PMC&cmd=Search&term=21731614%5bpmid)]