Geometrical Simulation compared to Molecular Dynamics and Elastic Networks:
C. David and D.J. Jacobs, *Characterizing protein motions from structure*,
J. Mol. Graph Model, 31:41-56 (2011)
Geometrical Simulation (GS)
An example of Rigid Cluster Decomposition (RCD)

molecular structure

Identification of rigid clusters using graph rigidity analysis

Geometrical Simulation (GS)
An example of Rigid Cluster Decomposition (RCD)

molecular structure $\rightarrow$ RCD creates multiple copies of atoms

Geometrical Simulation (GS)
Virtual potentials maintain molecular structure

\[ V_{POINT} = \frac{1}{2} A \sum_{(ab)} |\vec{r}_a - \vec{r}_b|^2 \]

\[ V_{MAX} = \frac{1}{2} A \sum_{(ab)} \begin{cases} \left( |\vec{r}_a - \vec{r}_b| - d_{ab}^{MAX} \right)^2 & \text{for } |\vec{r}_a - \vec{r}_b| \geq d_{ab}^{MAX} \\ 0 & \text{otherwise} \end{cases} \]

\[ V_{MIN} = \frac{1}{2} A \sum_{(ab)} \begin{cases} \left( |\vec{r}_a - \vec{r}_b| - d_{ab}^{MIN} \right)^2 & \text{for } |\vec{r}_a - \vec{r}_b| \leq d_{ab}^{MIN} \\ 0 & \text{otherwise} \end{cases} \]

Relaxation Step: Energy minimization method brings constraint network to ZERO energy.

Geometrical Simulation (GS)

**Example**

Ramachandran plots as well as rotamers are reproduced using distance inequality potentials.

GS parameters were optimized** to keep local geometries that are sampled statistically equivalent to structures from X-ray crystals and that generated by MD simulation.


**Figure from:** S.C. Lovell, J. M. Word, J. S. Richardson and D. C. Richardson. The penultimate rotamer library. Proteins 40:389-408 (2000)

Geometrical Simulation (GS)
Exploration of conformations for fixed constraint topology

High Level Overview

1. Identify constraint topology
2. Identify all rigid clusters using network rigidity

Input initial protein structure

Relaxation Step
Restore constraints that connect rigid clusters

Monte Carlo Step
Randomize position and orientation of all rigid clusters in the network.

finished?

no

yes

stop