Rigidity, Flexibility, and Motion in Biomolecules Workshop 2006

FIRST: A Look Under The Hood

By Don J. Jacobs

Physics and Optical Science, University of North Carolina at Charlotte

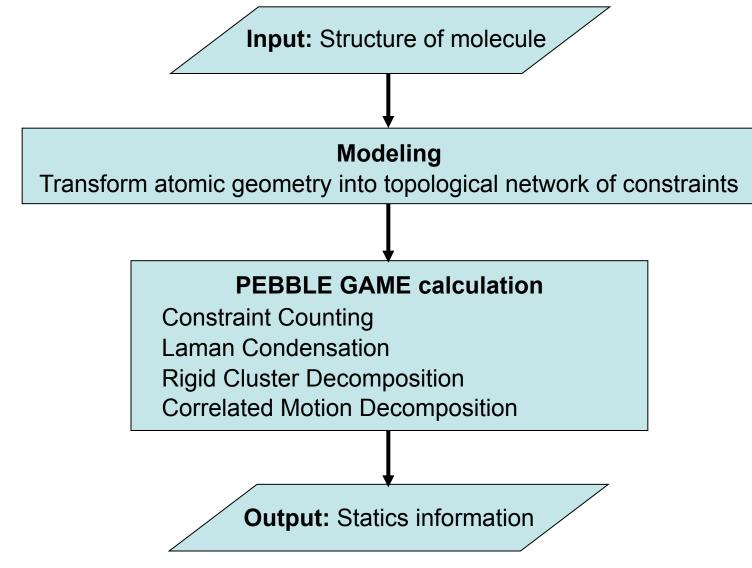
FIRST(biomolecular structure) \rightarrow Detailed mechanical information



- 2. Over constrained regions
- Rigid cluster decomposition
 Correlated motions

Floppy Inclusion and Rigid Substructure Topography

FIRST Workflow Schematic



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Input Biomolecular structures and Modeling

Input structure Modeling

Pebble game Constraint counting Laman Condensation Rigid Cluster Decomposition Correlated Motion Decomposition Output

X,Y,Z coordinates of **all** atoms Use **empirical** rules to convert geometrical information to a topological **body-bar** network.

List of microscopic interactions to <u>consider</u>

- Covalent bonding
- Hydrogen bonding and Salt bridges
- Torsion forces
- Hydrophobic interactions
- Metallic interactions
- Solvent interactions
- van der Waals interactions

Input Biomolecular structures and Modeling

Input structure Modeling

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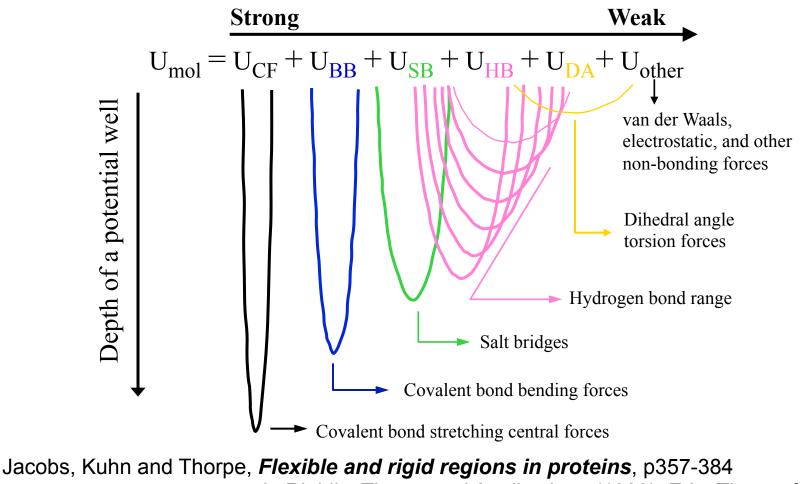
X,Y,Z coordinates of all atoms Use **empirical** rules to convert geometrical information to a topological **body-bar** network. List of microscopic interactions in FIRST

- **Covalent bonding**
- Hydrogen bonding and Salt bridges
- **Torsion forces**
- Hydrophobic interactions
- **Metallic interactions**
- **Other (user defined)**

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Modeling Interactions as Constraints A Tricky Business

Schematic Microscopic Interaction Strength Scale

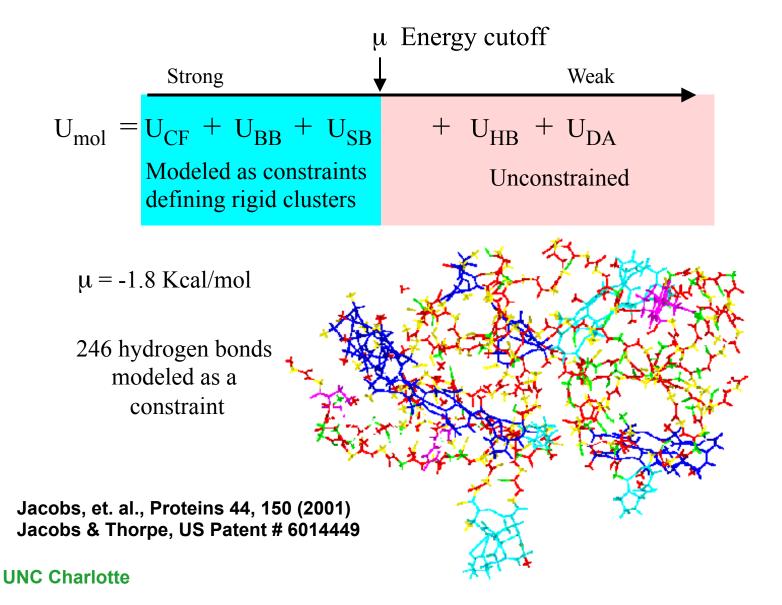


in Rigidity Theory and Applications (1999) Eds. Thorpe & Duxbury

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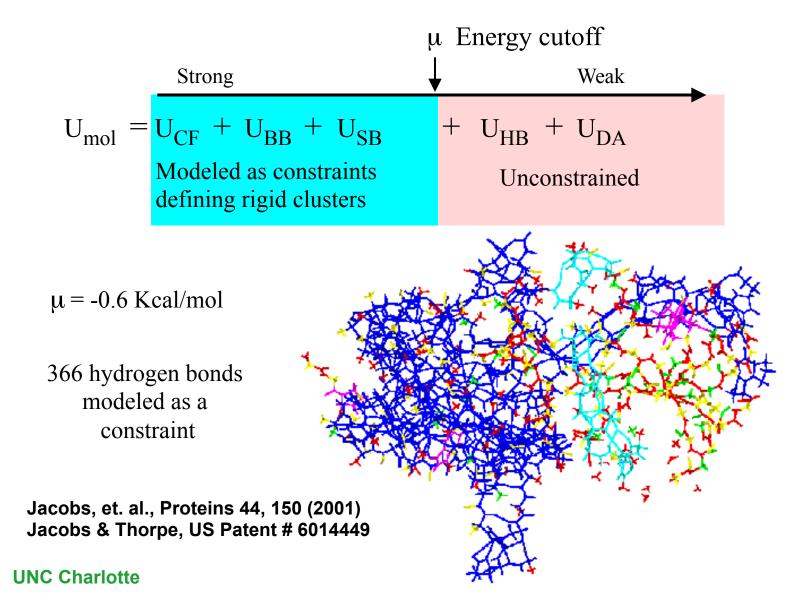
Network Rigidity: Applied to Proteins

To be or not to be a constraint?



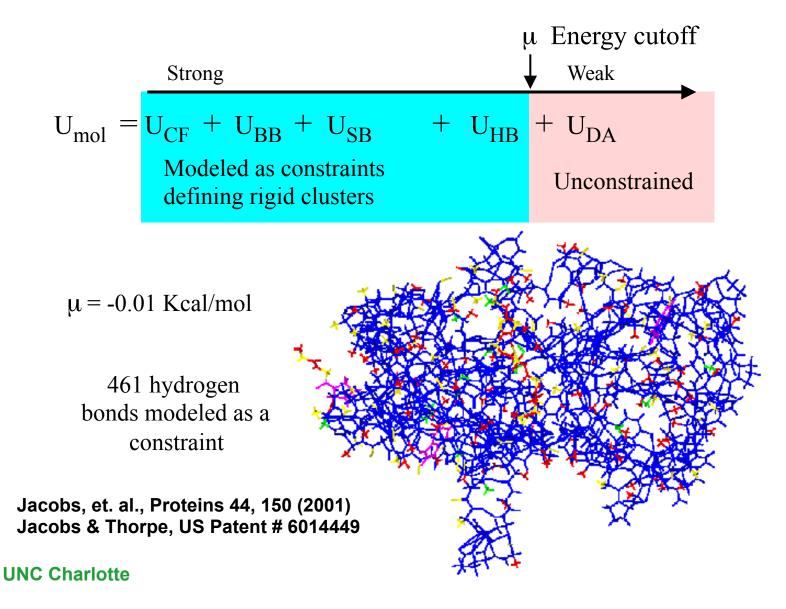
Network Rigidity: Applied to Proteins

To be or not to be a constraint?



Network Rigidity: Applied to Proteins

To be or not to be a constraint?



Modeling Covalent Bonds

Input structure Modeling

Pebble game Constraint counting Laman Condensation Rigid Cluster Decomposition Correlated Motion Decomposition Output

> **Covalent bonding** Central force interactions

Represented as a bar-joint network graph G

Jacobs, J. Phys. A 31, 6653 (1998)

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Modeling Covalent Bonds

Input structure Modeling

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> Covalent bonding Central force interactions Bond-bending interactions

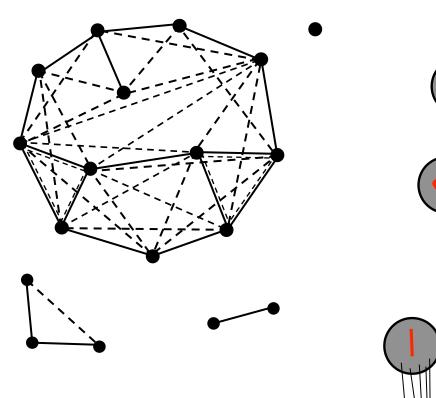
Represented as a bar-joint network graph G²

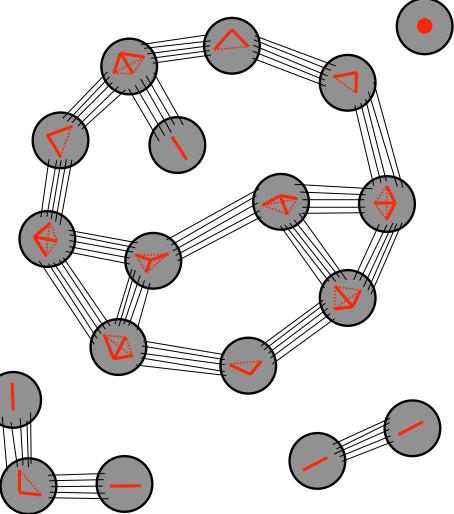
Jacobs, J. Phys. A 31, 6653 (1998)

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Modeling Covalent Bonds

Bar-joint graph $G^2 \longrightarrow Body$ -Bar multigraph

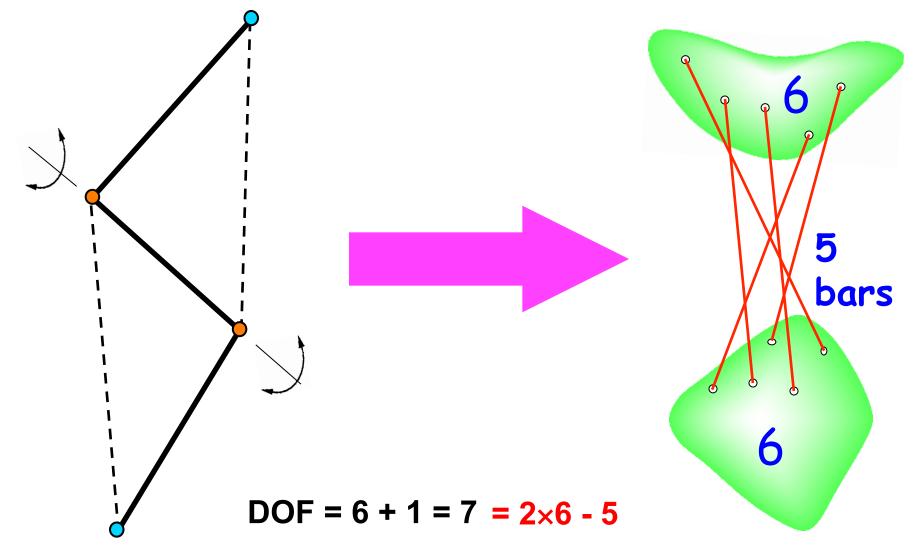




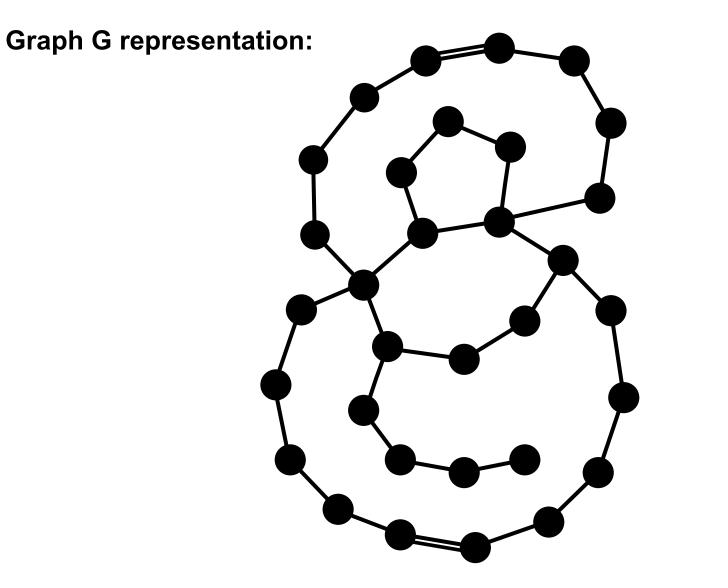
Jacobs, J. Phys. A 31, 6653 (1998) Tay & Whiteley, *Struct. Topol.* 9, 31 (1984) **UNC Charlotte**

Body-bar representation

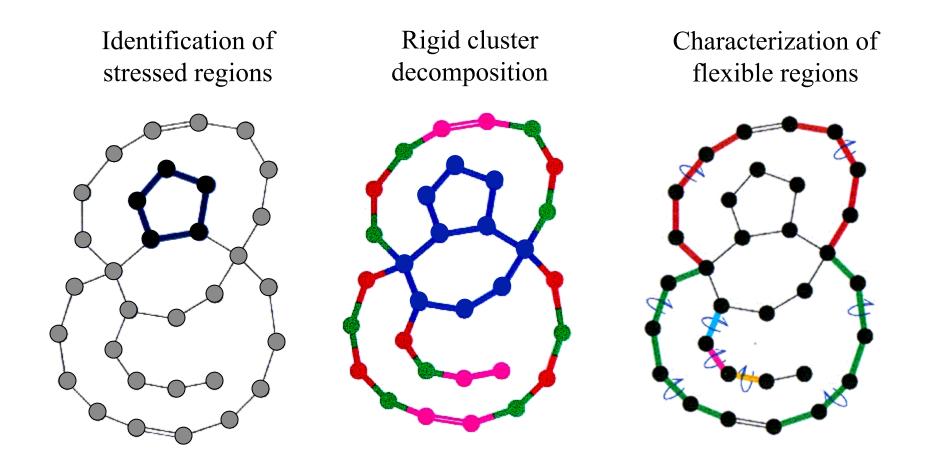
Covalent bond



Simple Covalent Bonded Ring System

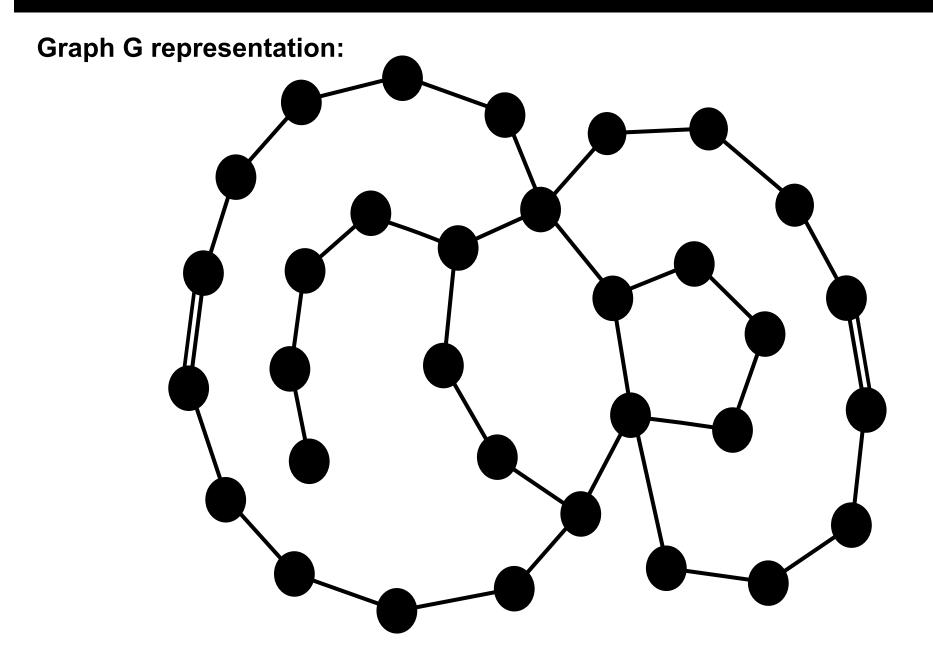


Network Rigidity of a Simple Ring System

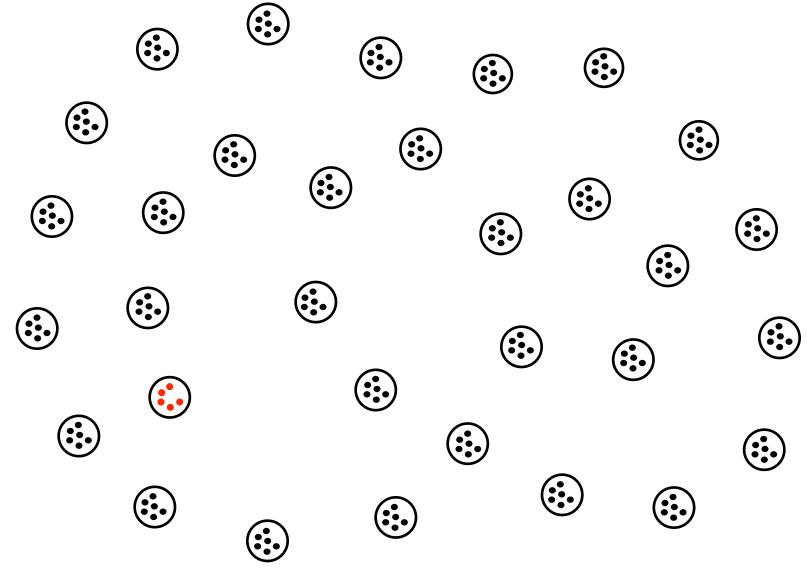


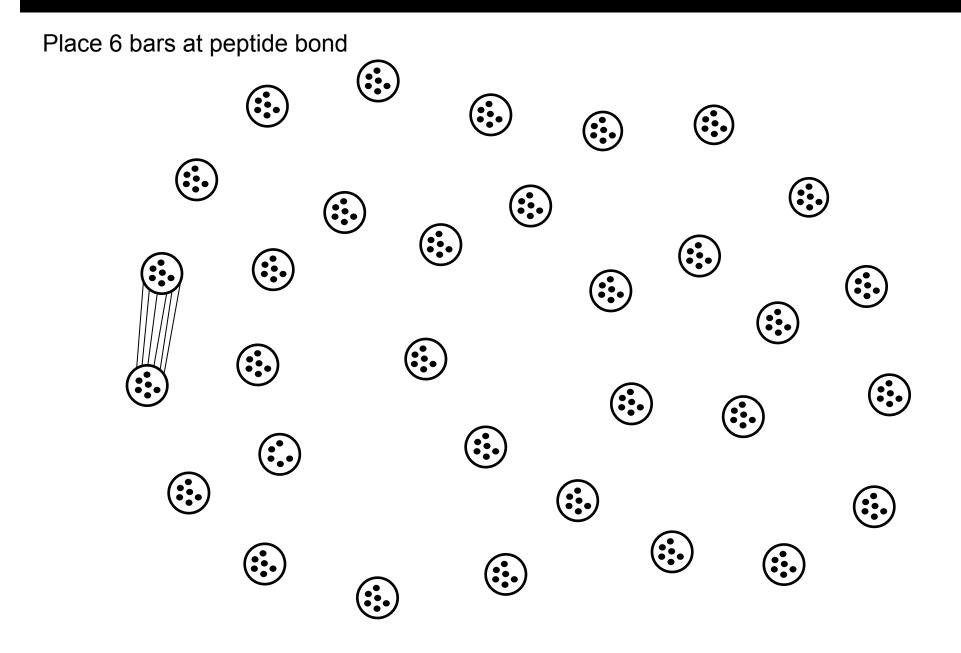
Jacobs, Kuhn and Thorpe, *Flexible and rigid regions in proteins*, p357-384 in Rigidity Theory and Applications (1999) (Eds. Thorpe & Duxbury

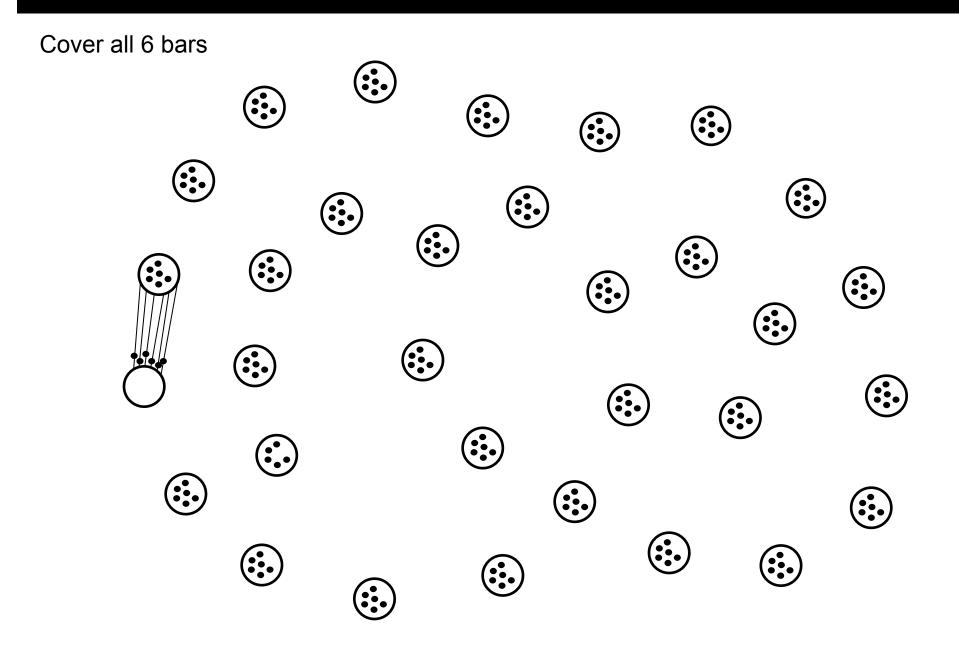
Simple Covalent Bonded Ring System

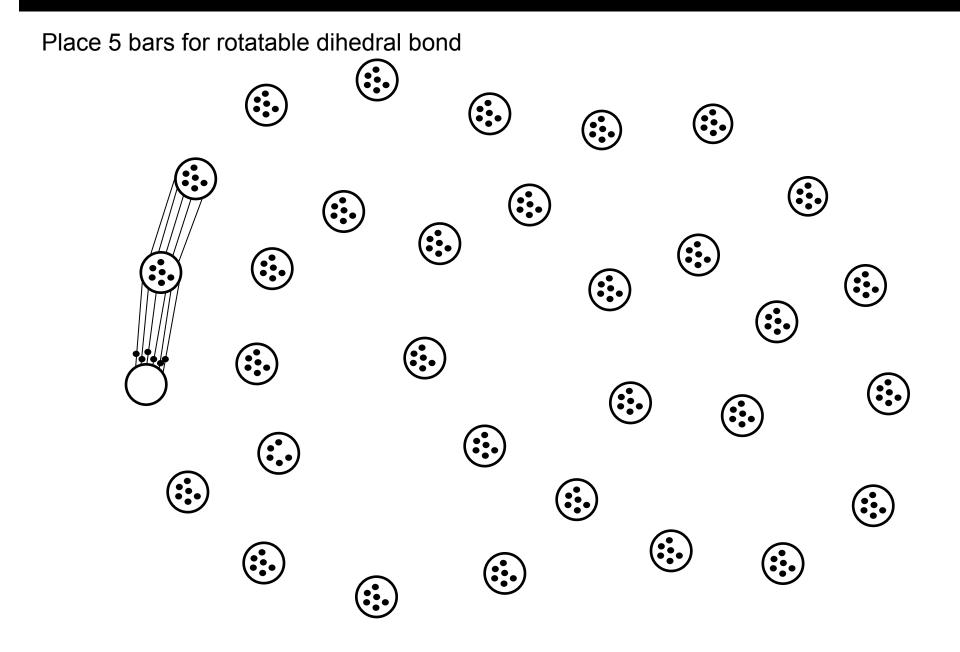


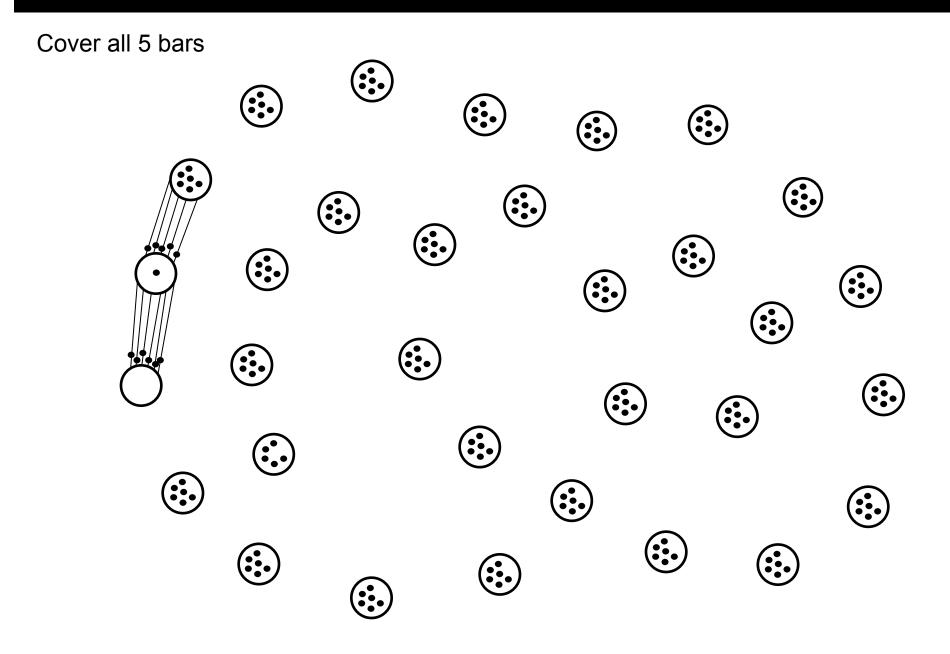
Place 6 pebbles on n-connected bodies (n>1) & 5 pebbles on 1-connected bodies

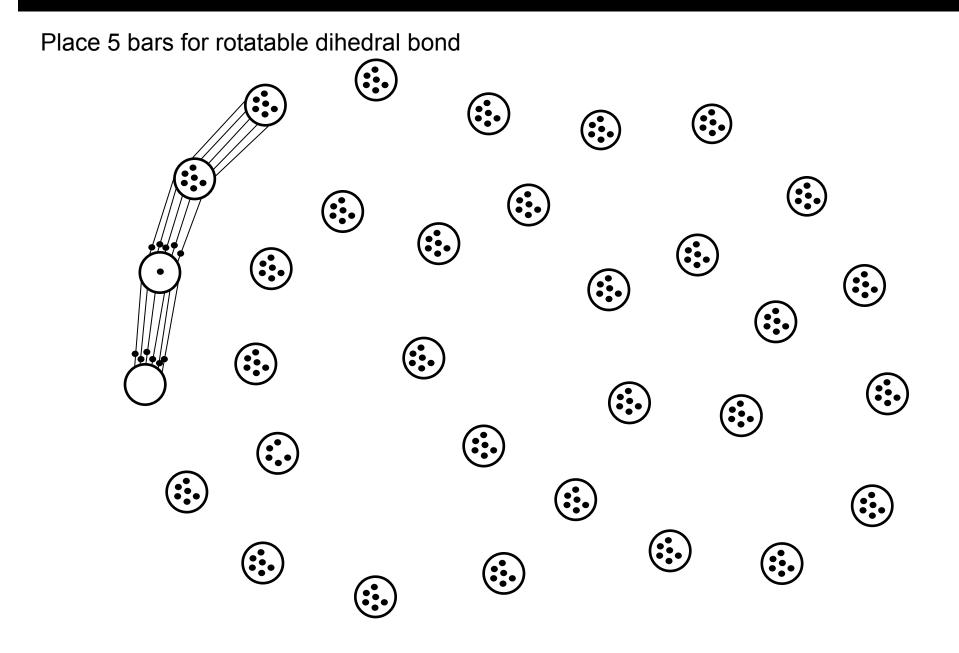


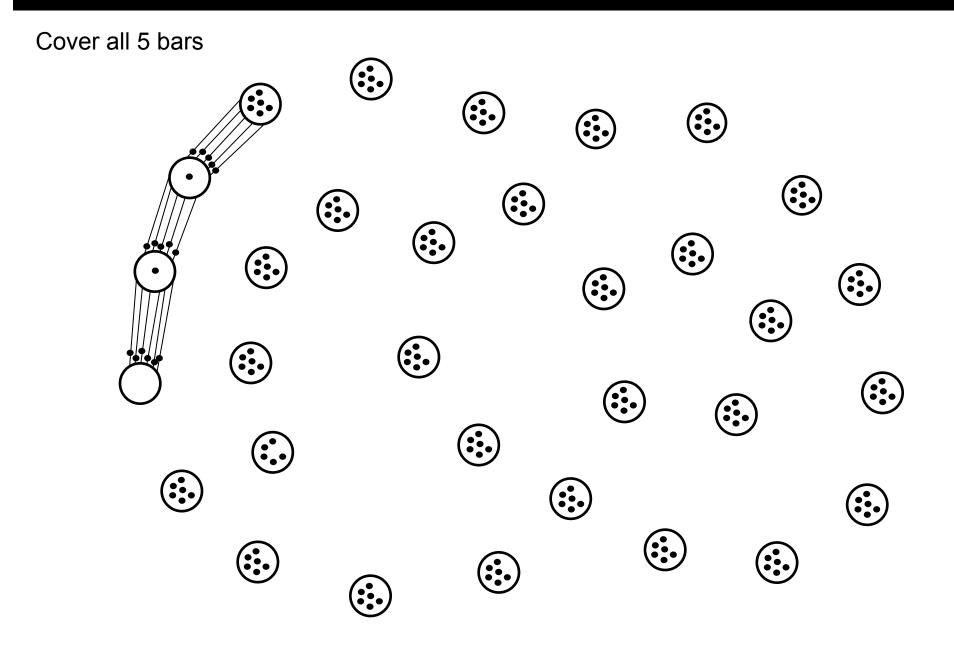




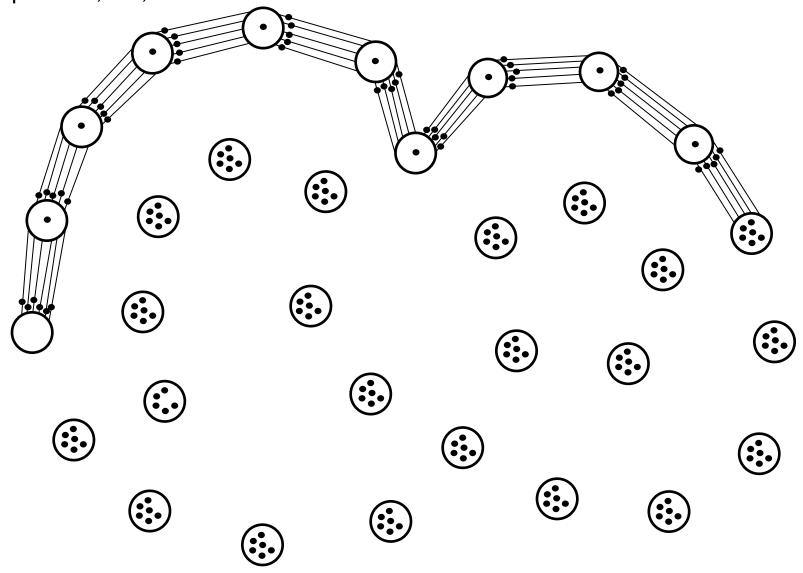


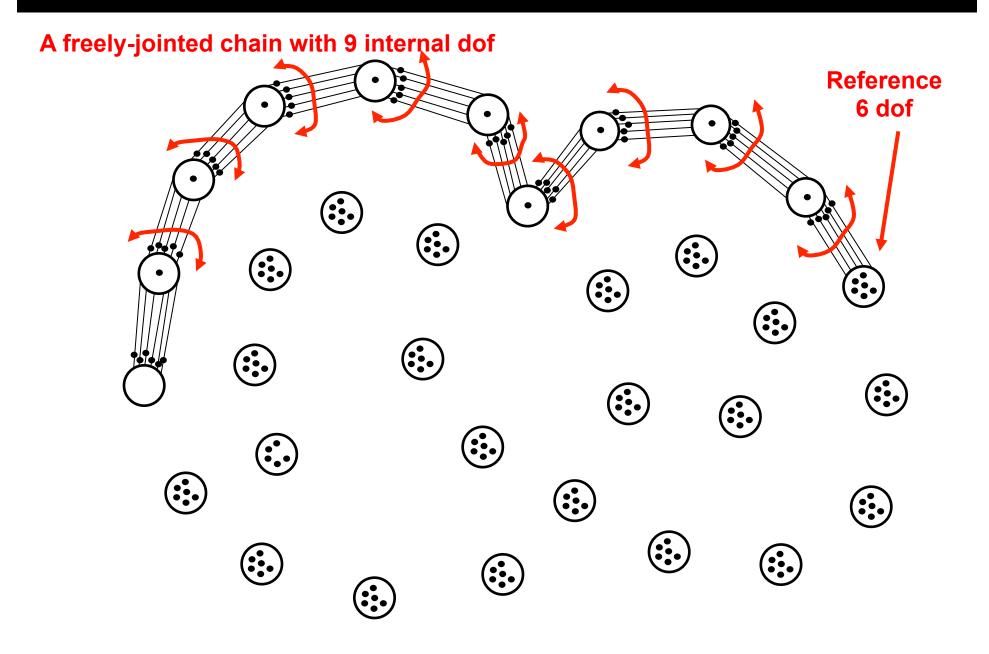




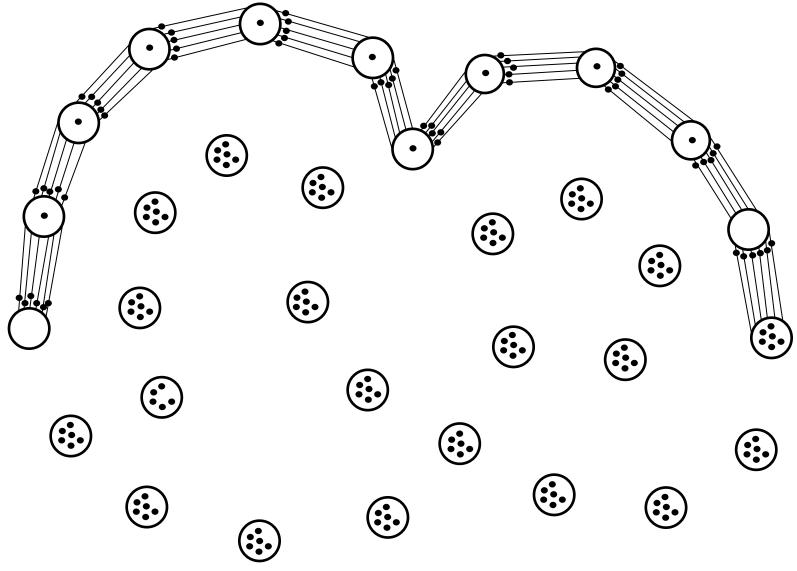


Repeat process, etc, ...

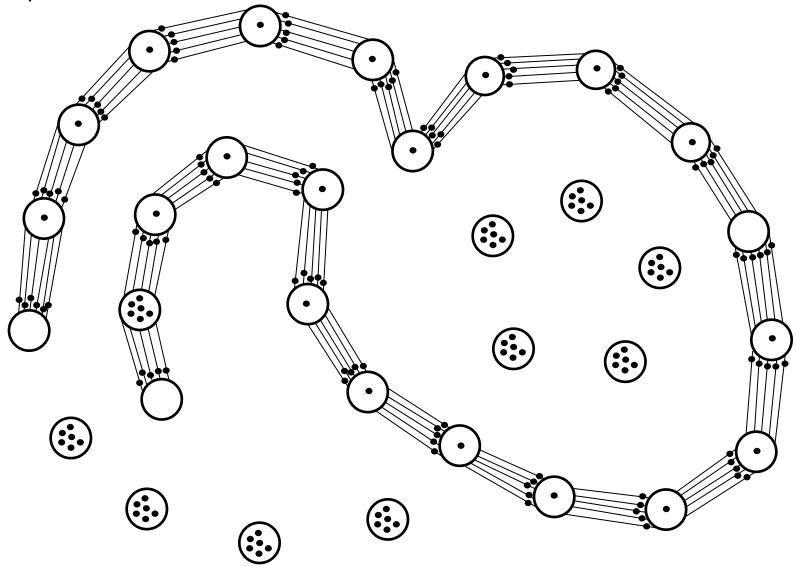


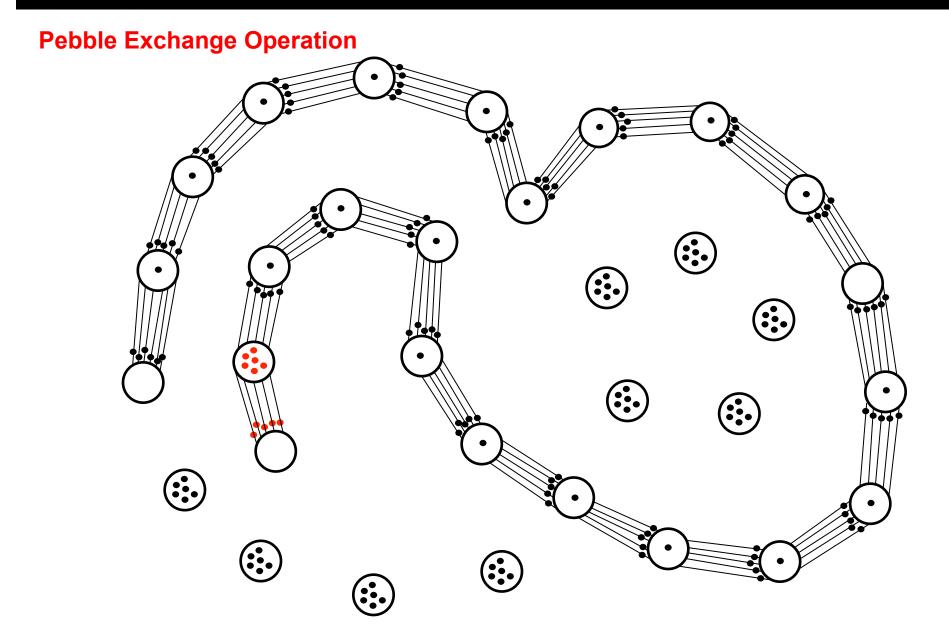


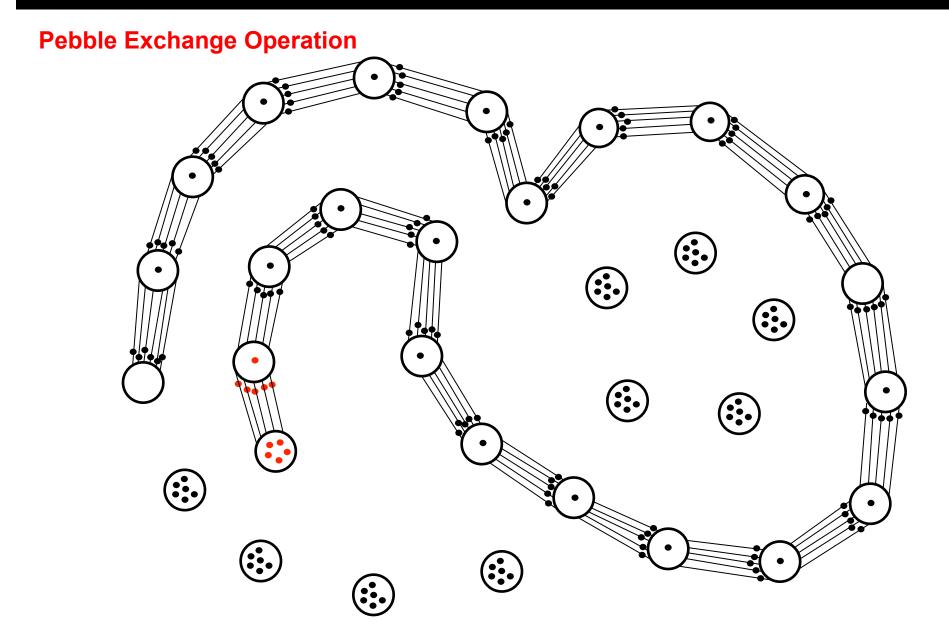
Place 6 bars at the other peptide bond and then <u>cover</u> all of them

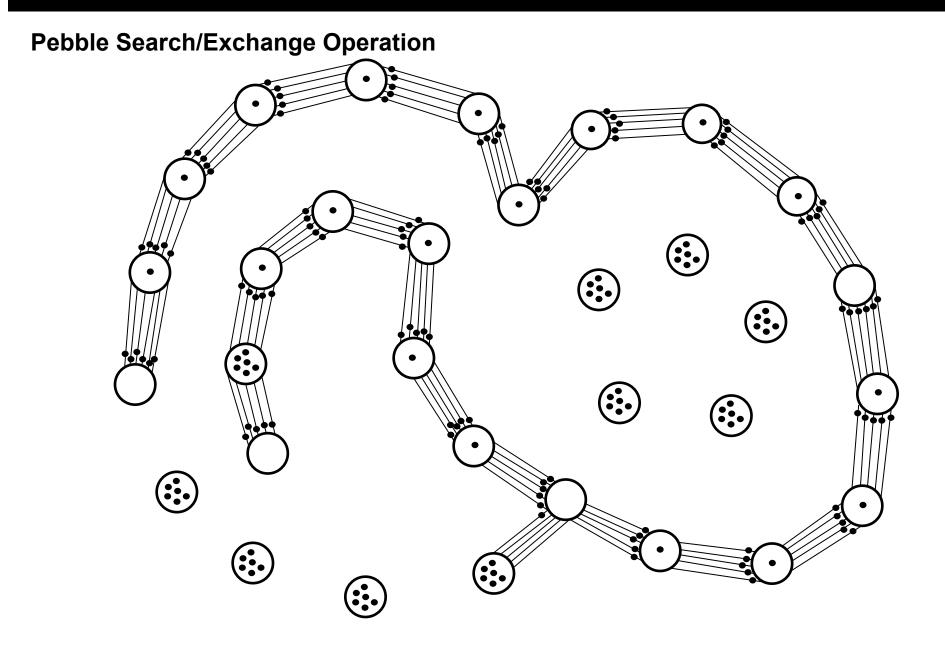


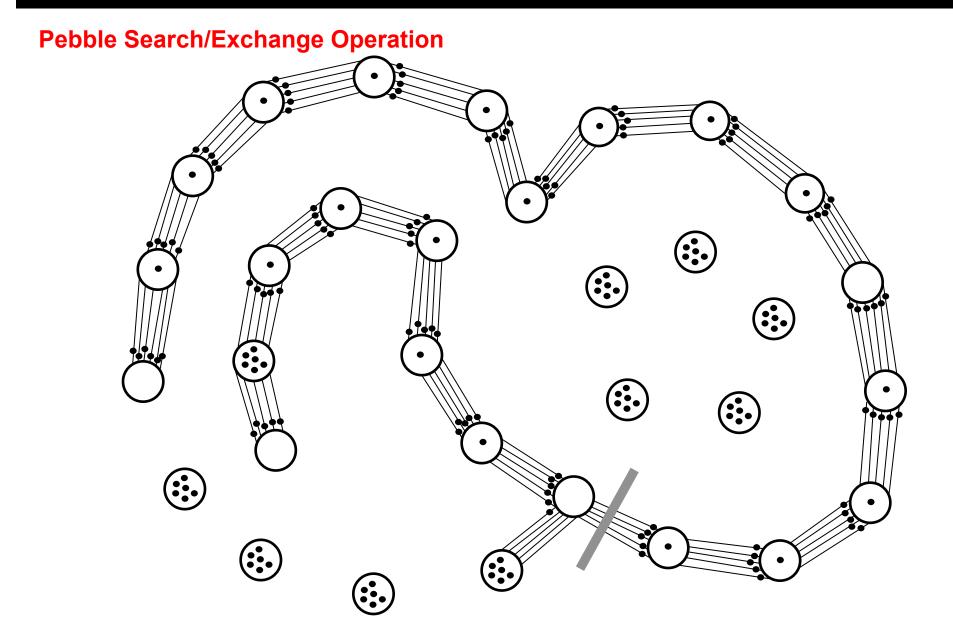
Continue process, etc, ...

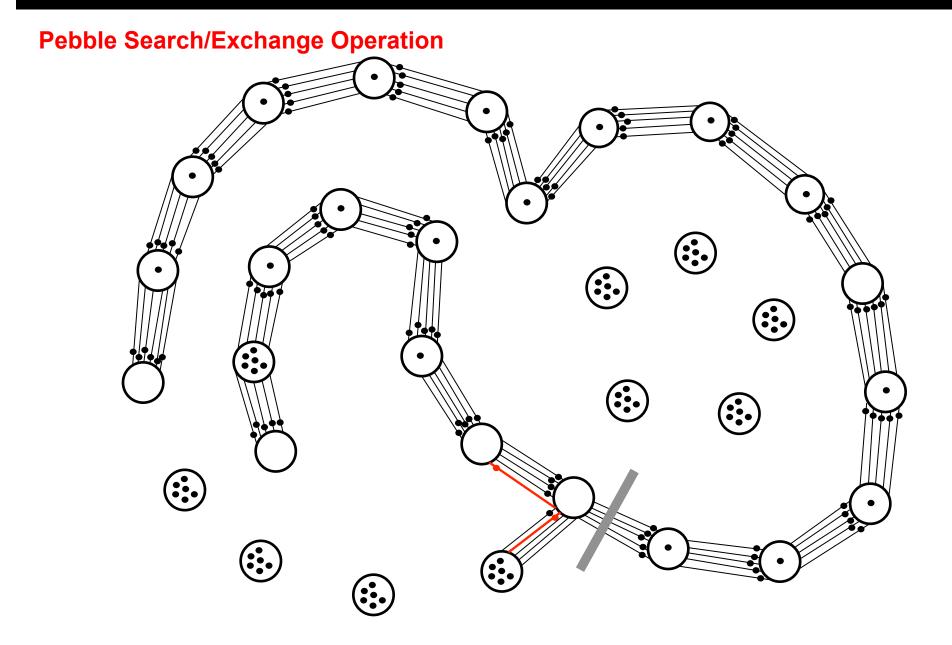


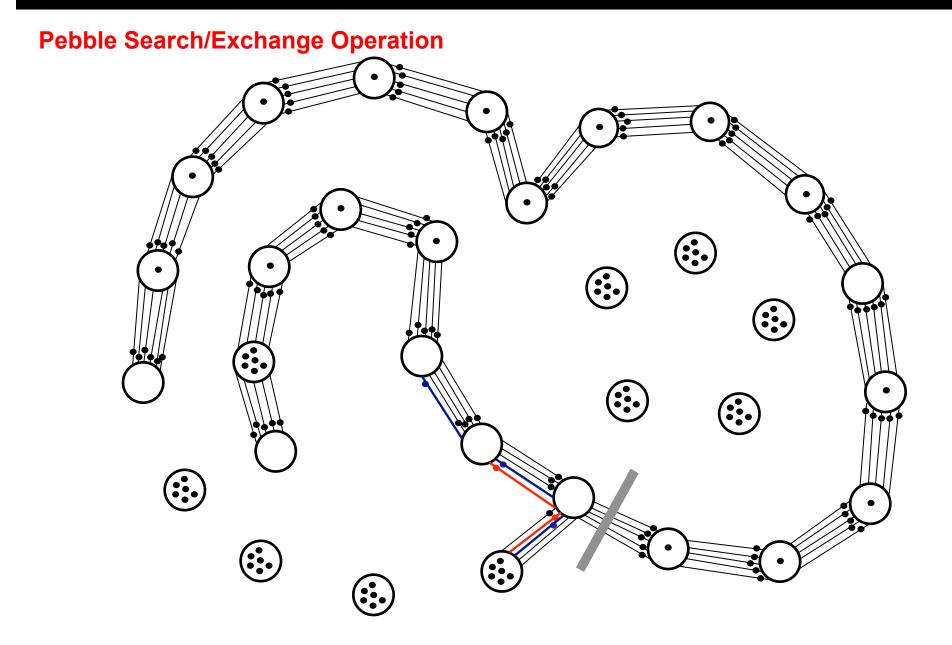


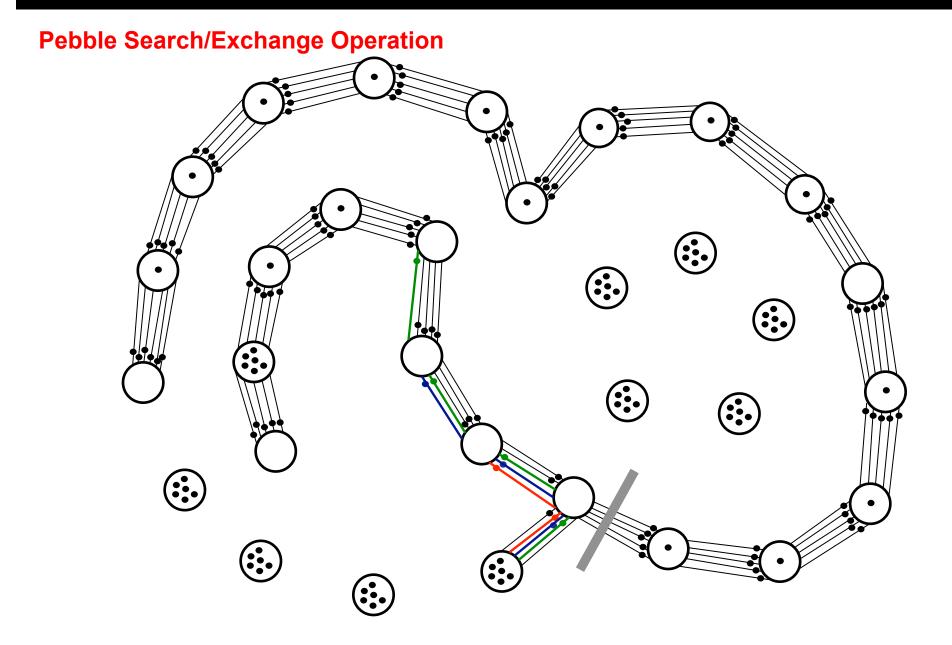


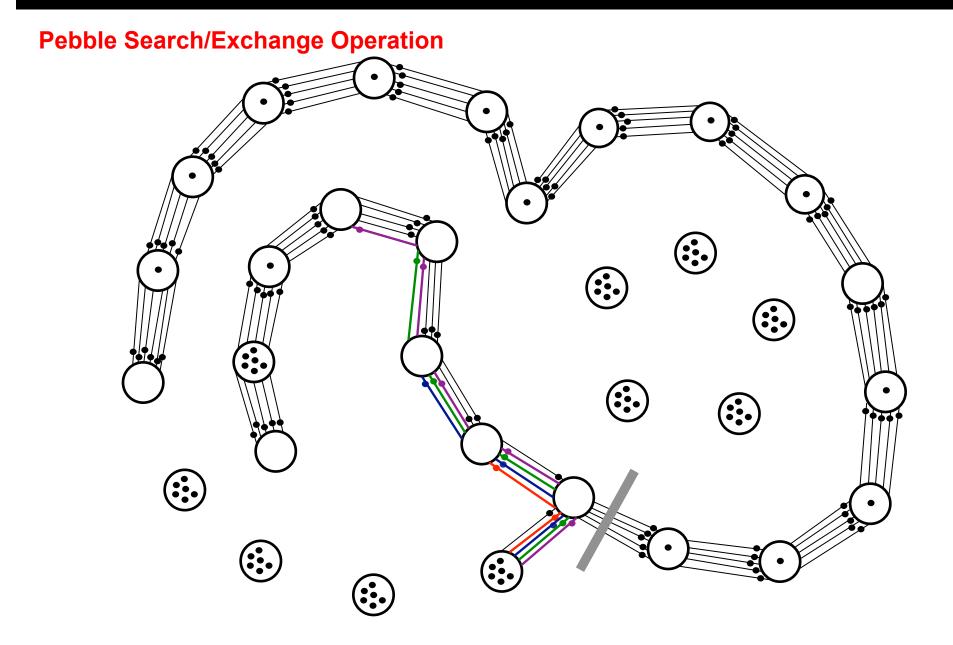




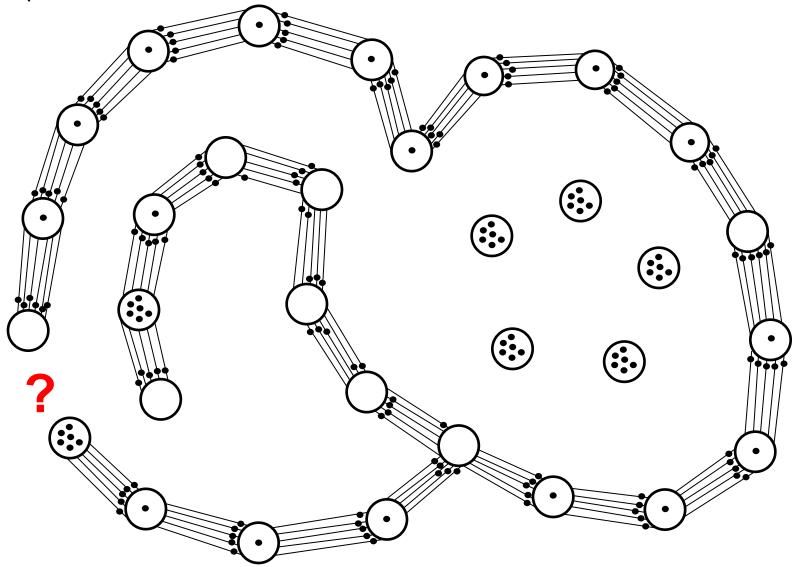


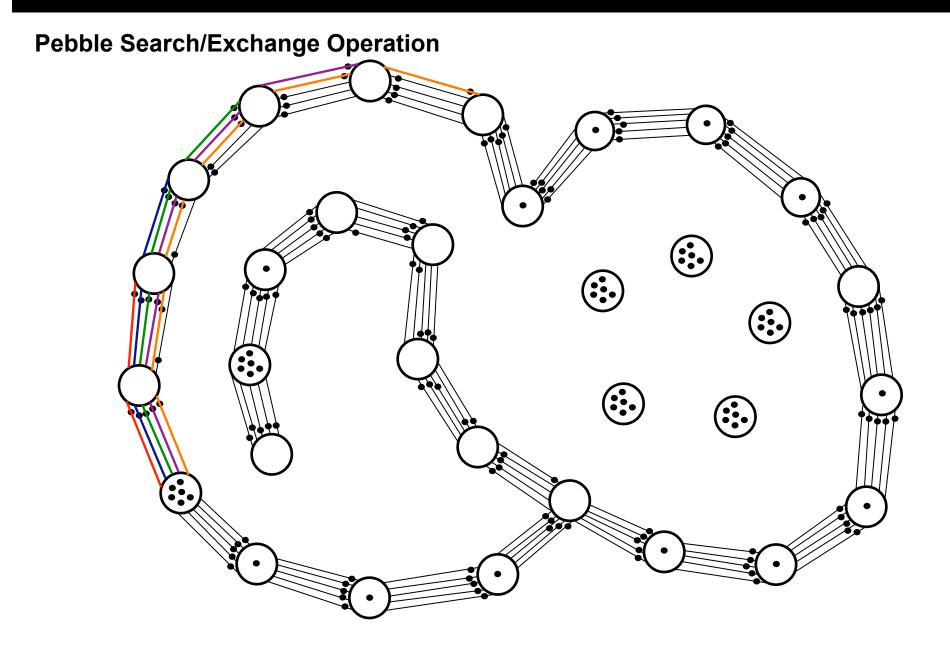




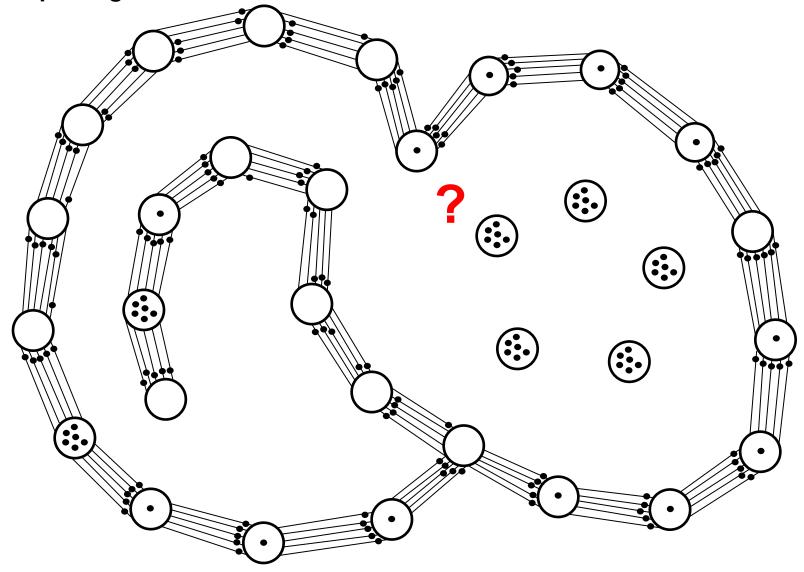


Continue process, etc, ...

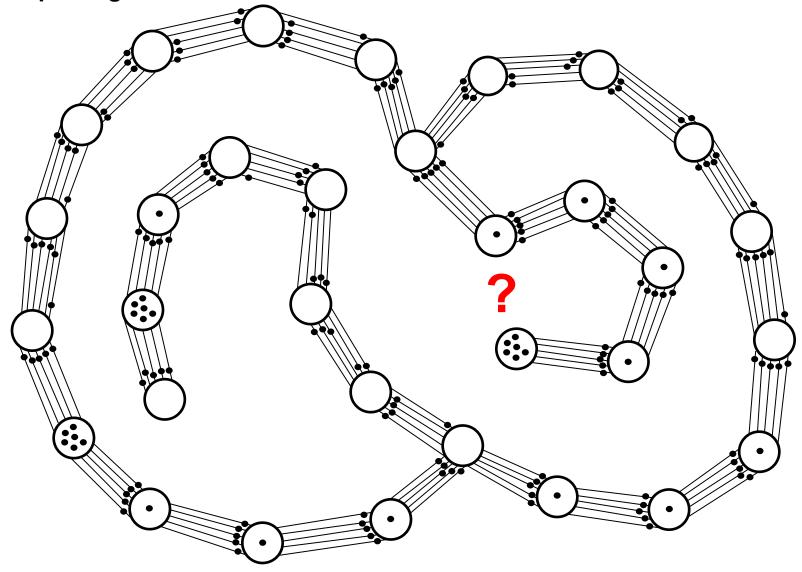




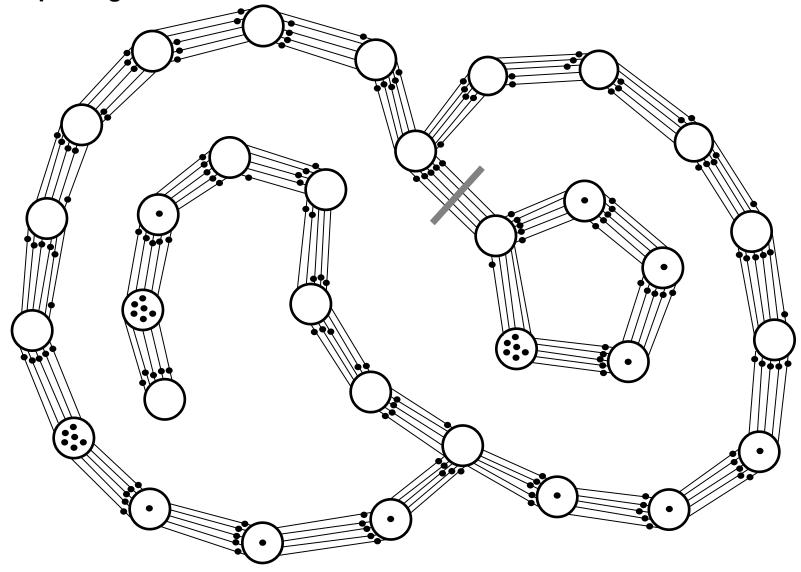
Continue placing 5 bars at rotatable bonds

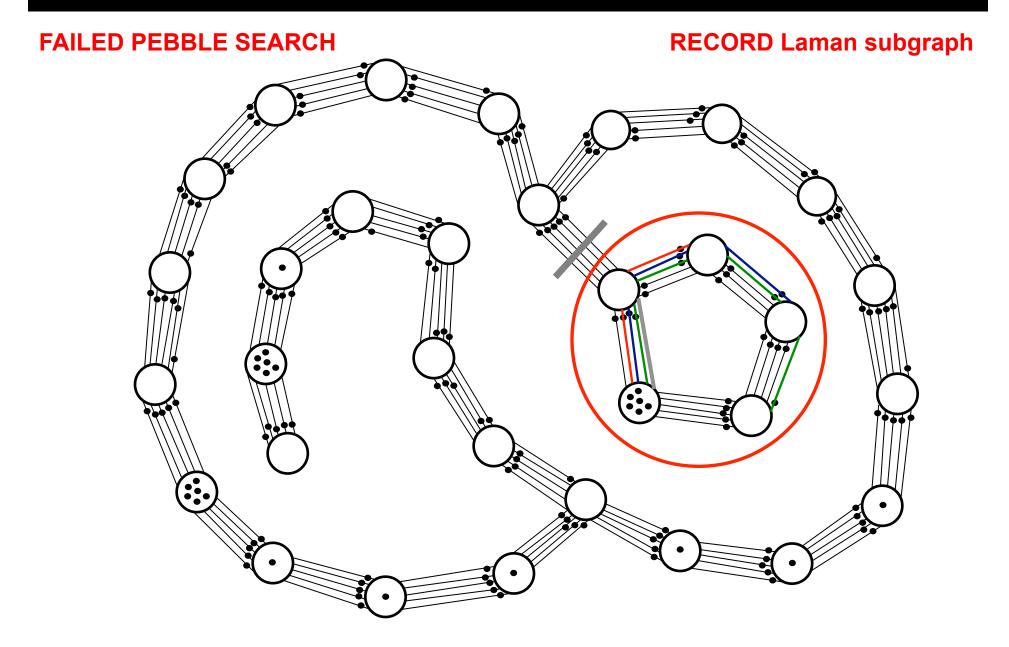


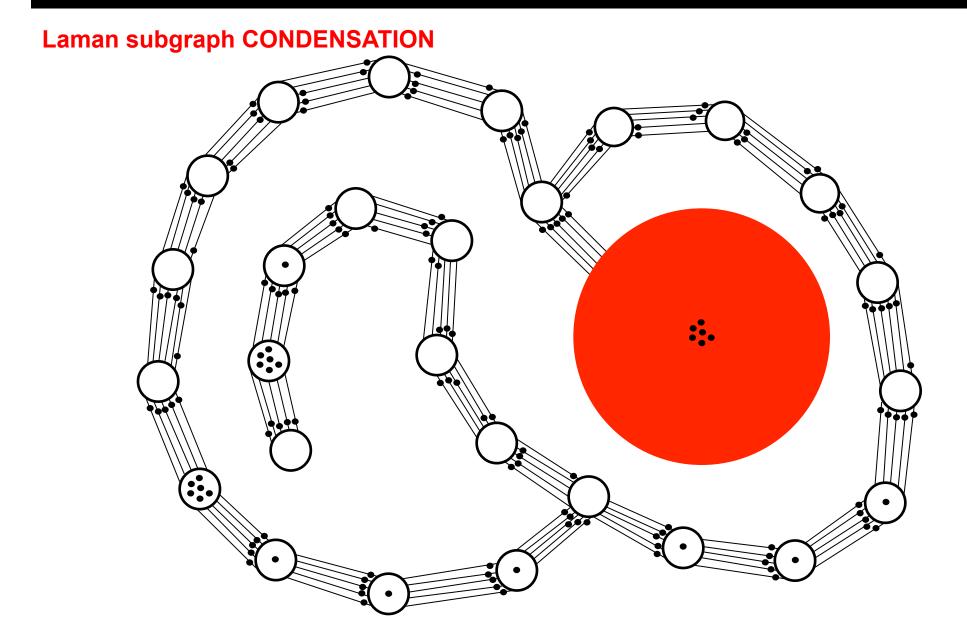
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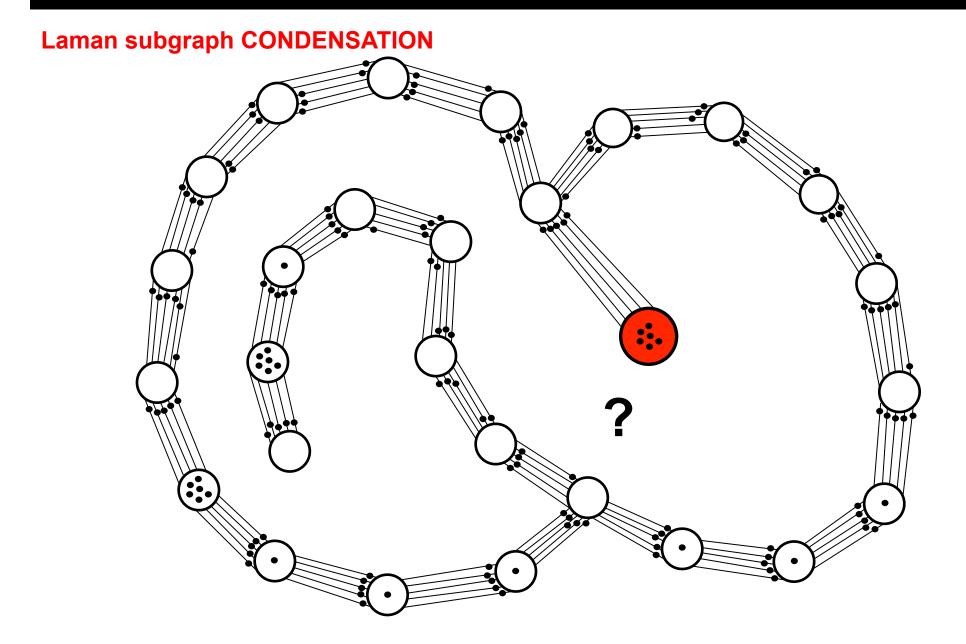


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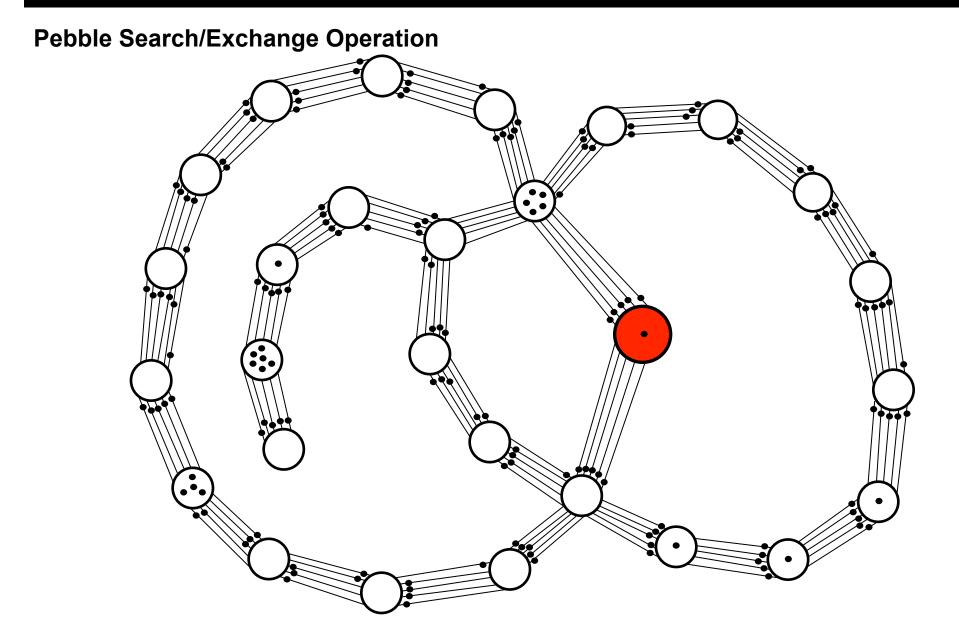


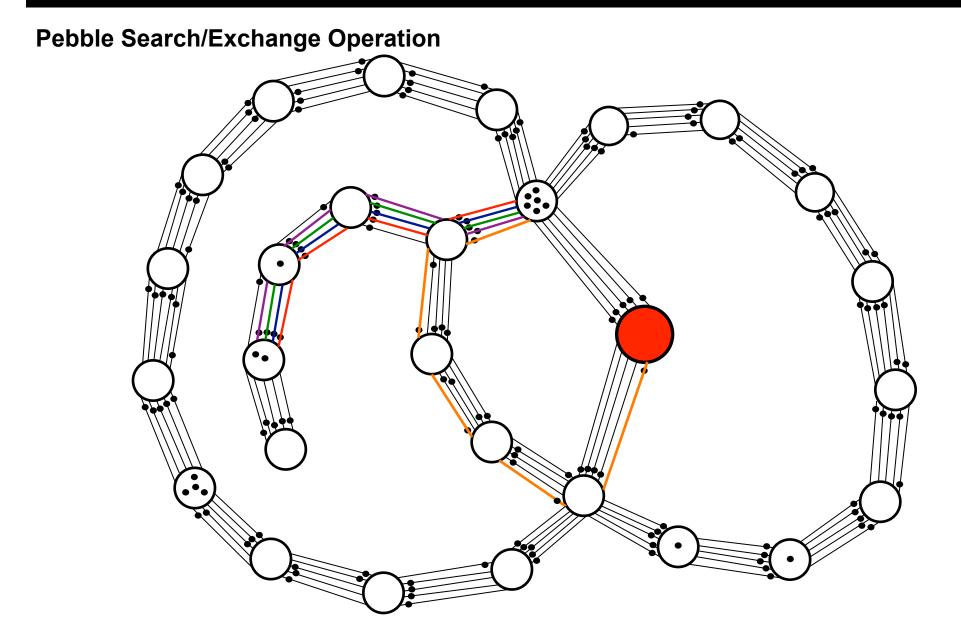


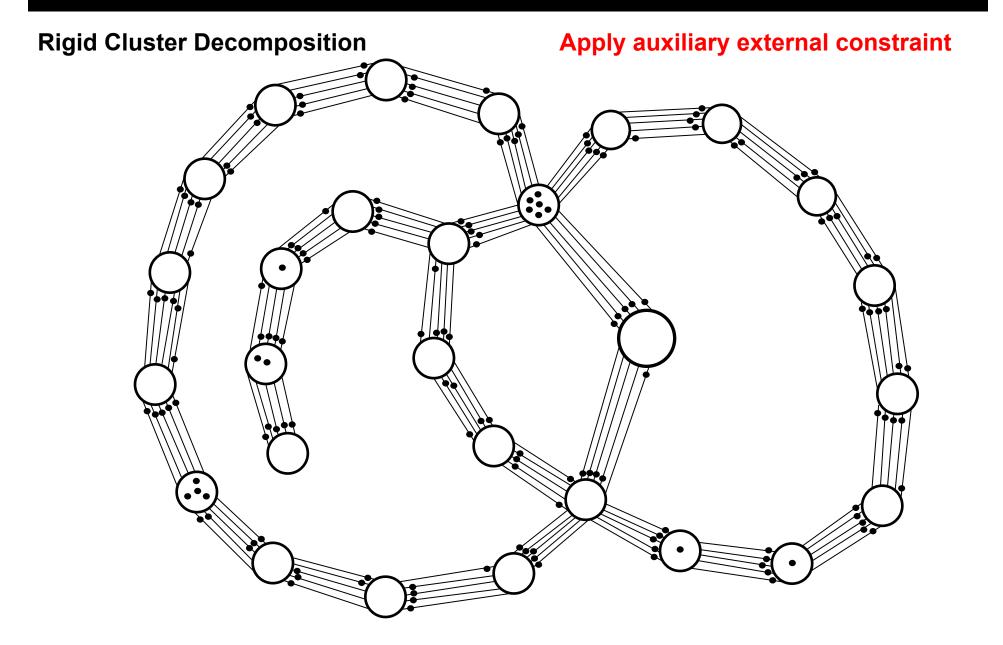


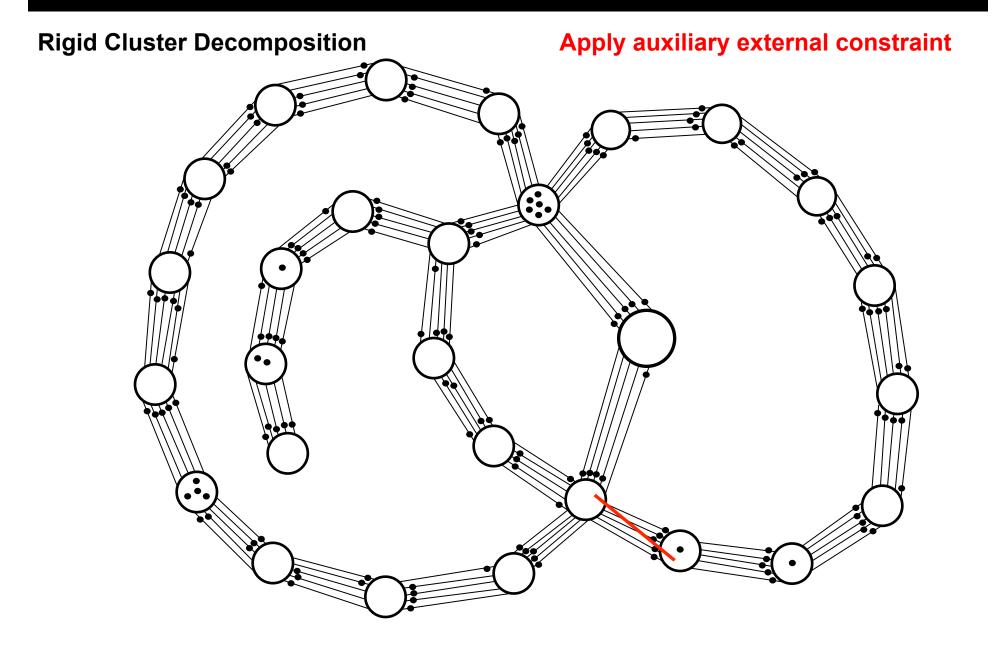
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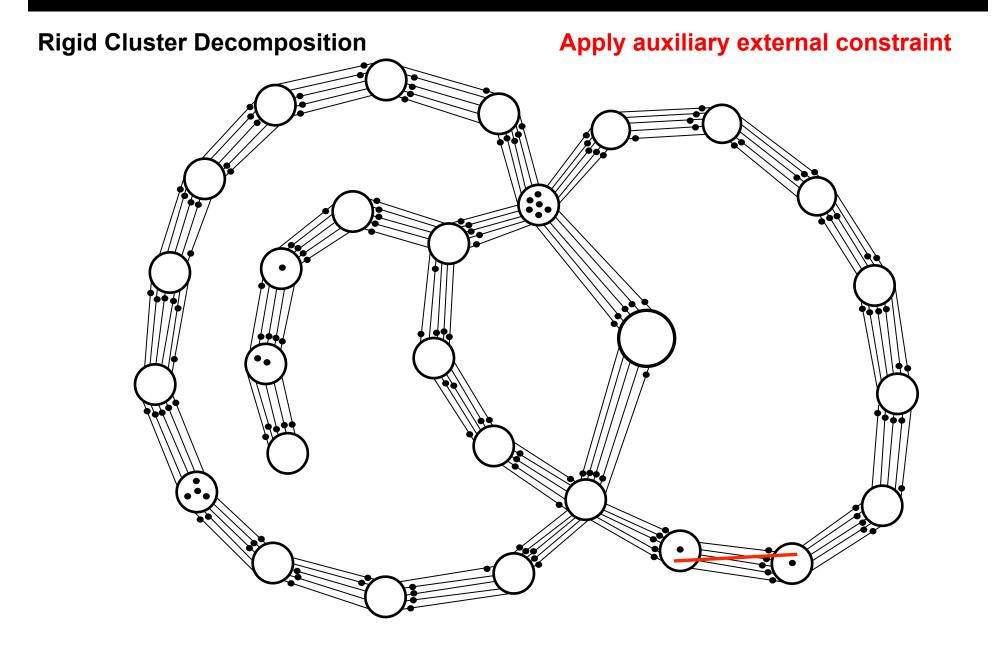
Continue placing 5 bars at rotatable bonds ::.

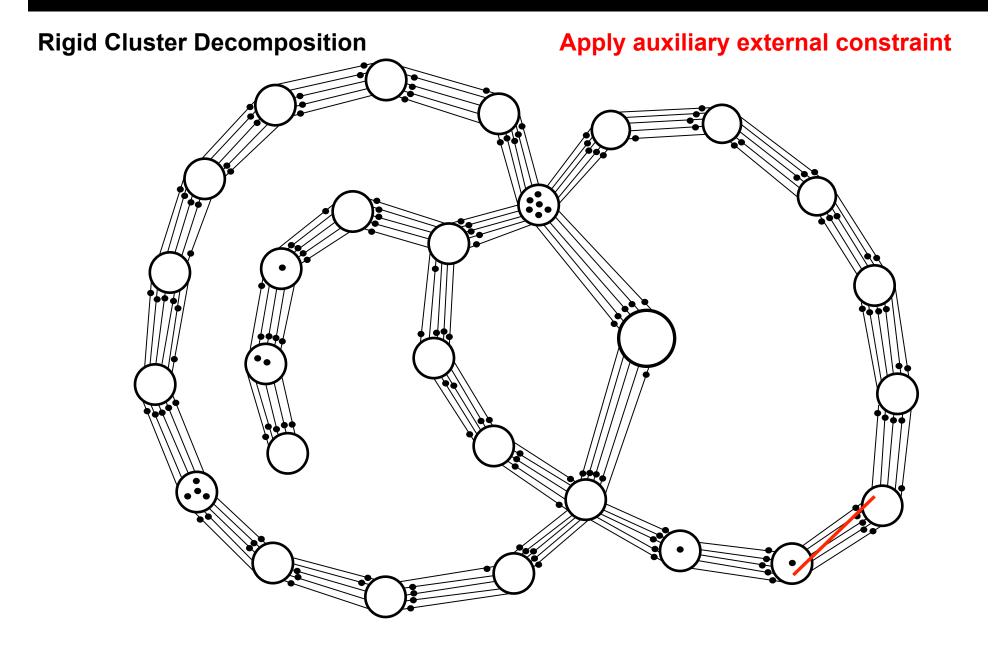


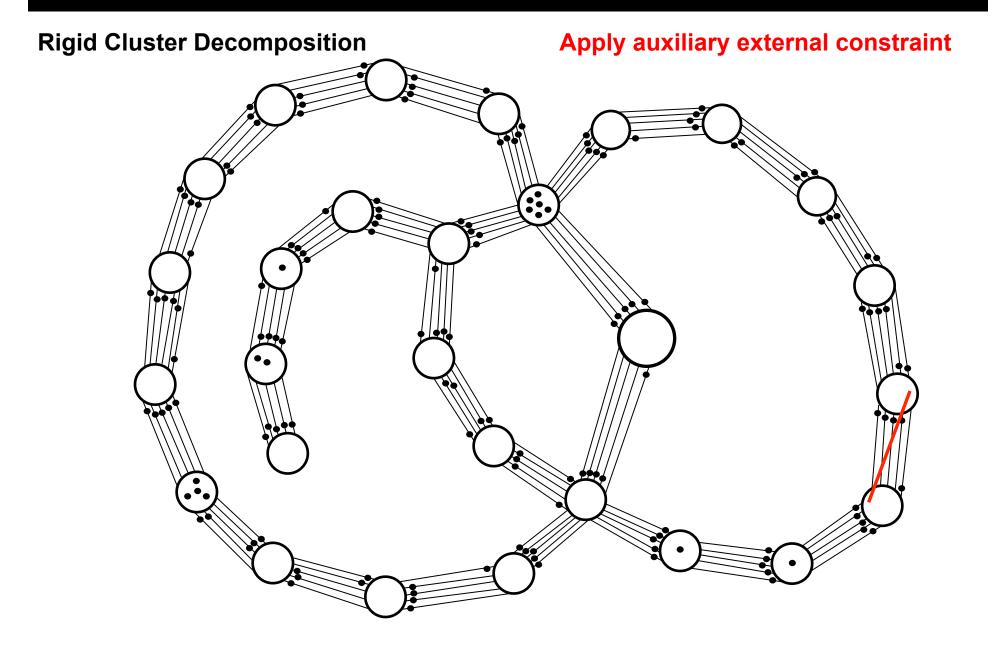


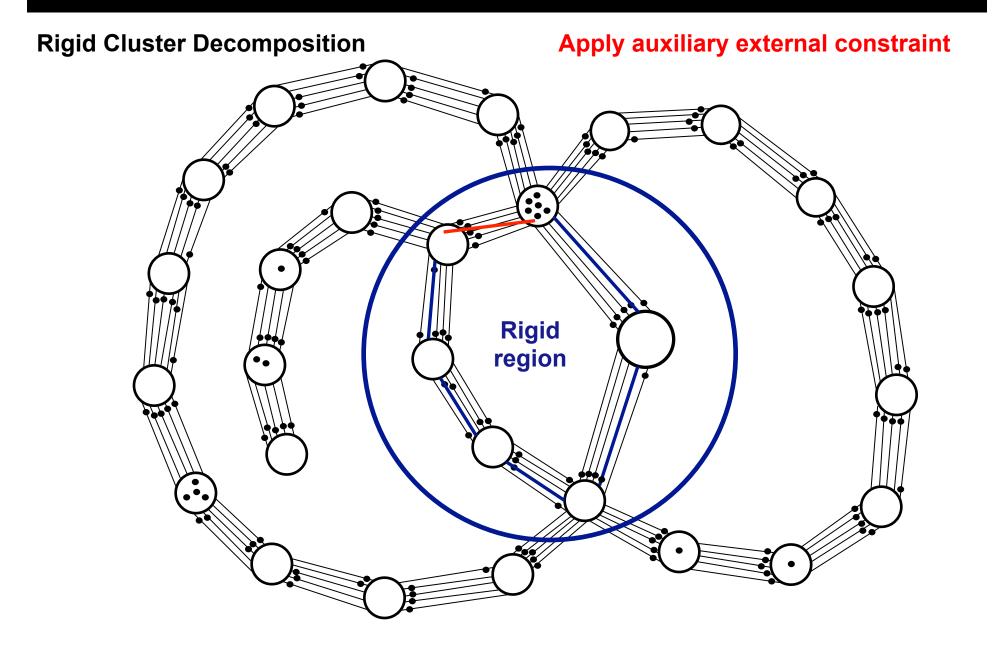




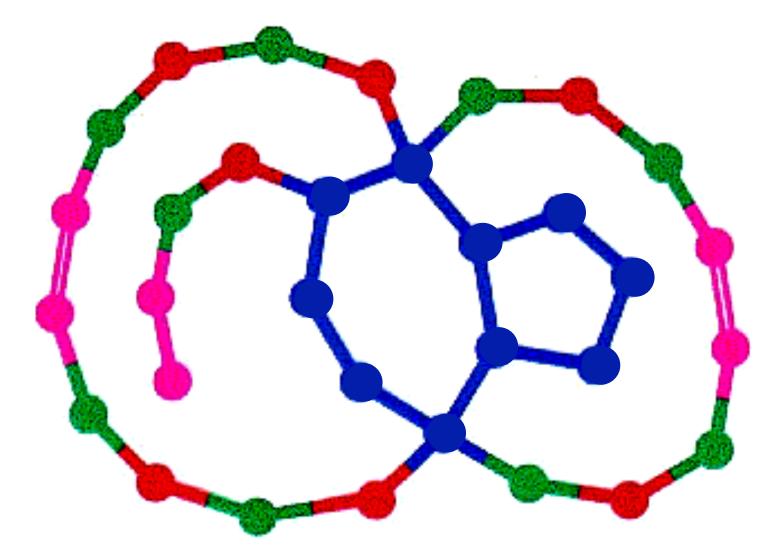


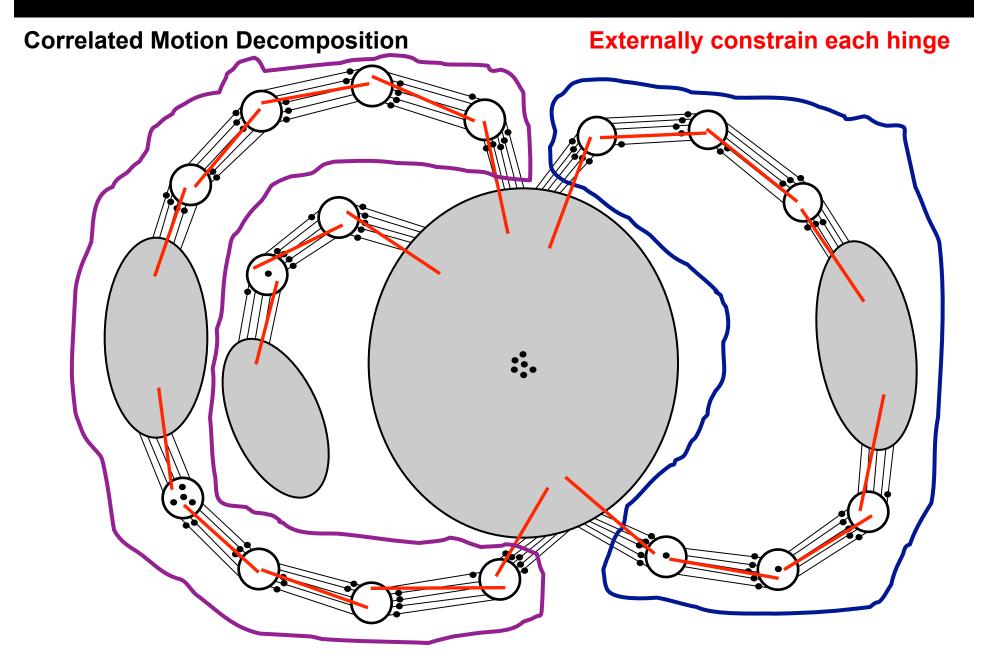


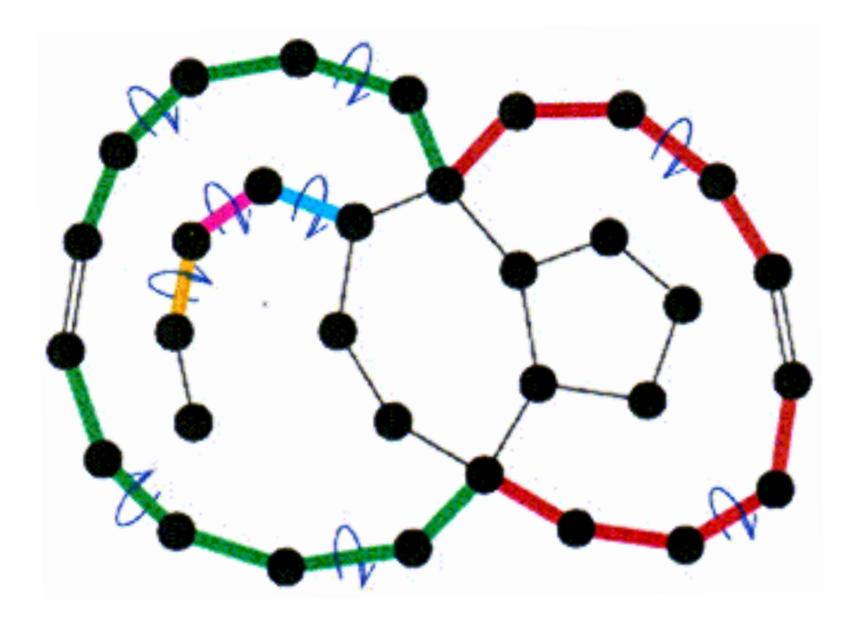




Each Rigid Body (circle) can belong to one and only one rigid substructure





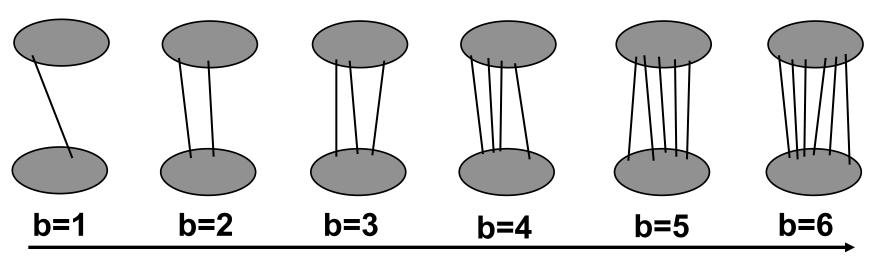


Modeling Molecular Interactions

Input structure Modeling

Pebble game Constraint counting Laman Condensation Rigid Cluster Decomposition Correlated Motion Decomposition Output 0-connected bodies: assign 3 dof 1-connected bodies: assign 5 dof n-connected bodies: assign 6 dof for n>1

Increase in mechanical relevance of a constraint



Increase in number of bars within a constraint

Body-bar representation

FIRST Applications

Input structure Modeling Pebble game Constraint counting Laman Condensation Rigid Cluster Decomposition Correlated Motion Decomposition Output

FIRST provides a stand-alone software that gives virtually instantaneous output for BIOLOGICAL INSIGHT.

But it is quite limited in utility

ADDED VALUE APPLICATIONS

- 1. ROCK uses FIRST to pre-identify correlated flexible rings
- 2. ENM/FIRST allows very large spring networks to be analyzed
- 3. FRODA uses FIRST to partition protein into rigid substructures
- 4. MD analysis uses FIRST to post priori analyze atomic trajectories
- 5. DCM uses FIRST to construct accurate free energy decomposition

Conclusion

FIRST has proven to be a useful tool, and has complemented many applications.

Acknowledgements:

Pre-FIRST work on rigidity

Debbie Franzblau Bruce Hendrickson Phil Duxbury

Key people involved in FIRST origins:

Mike Thorpe Walter Whiteley Leslie Kuhn Mykyta Chubynsky Andrew Rader Brandon Hespenheide