

Finding Inverse Kinematics Solutions of Short Robotic Chain

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Introduction

Forward kinematics and Inverse kinematics are classical problems in robot control and motion planning. They are important tools for studying the motion of robotic structures



Fig 1. Takana robot arm made by Neuronics [1]

Project Goal

- Create a generic model to represent robot arms
- Find inverse kinematics parameters for small models
- Apply robotic methods on protein polypeptide chains

Analogy of Robotic Chain

We model a robot arm as a chain of rigid bodies connected by hinge-like mechanical joints

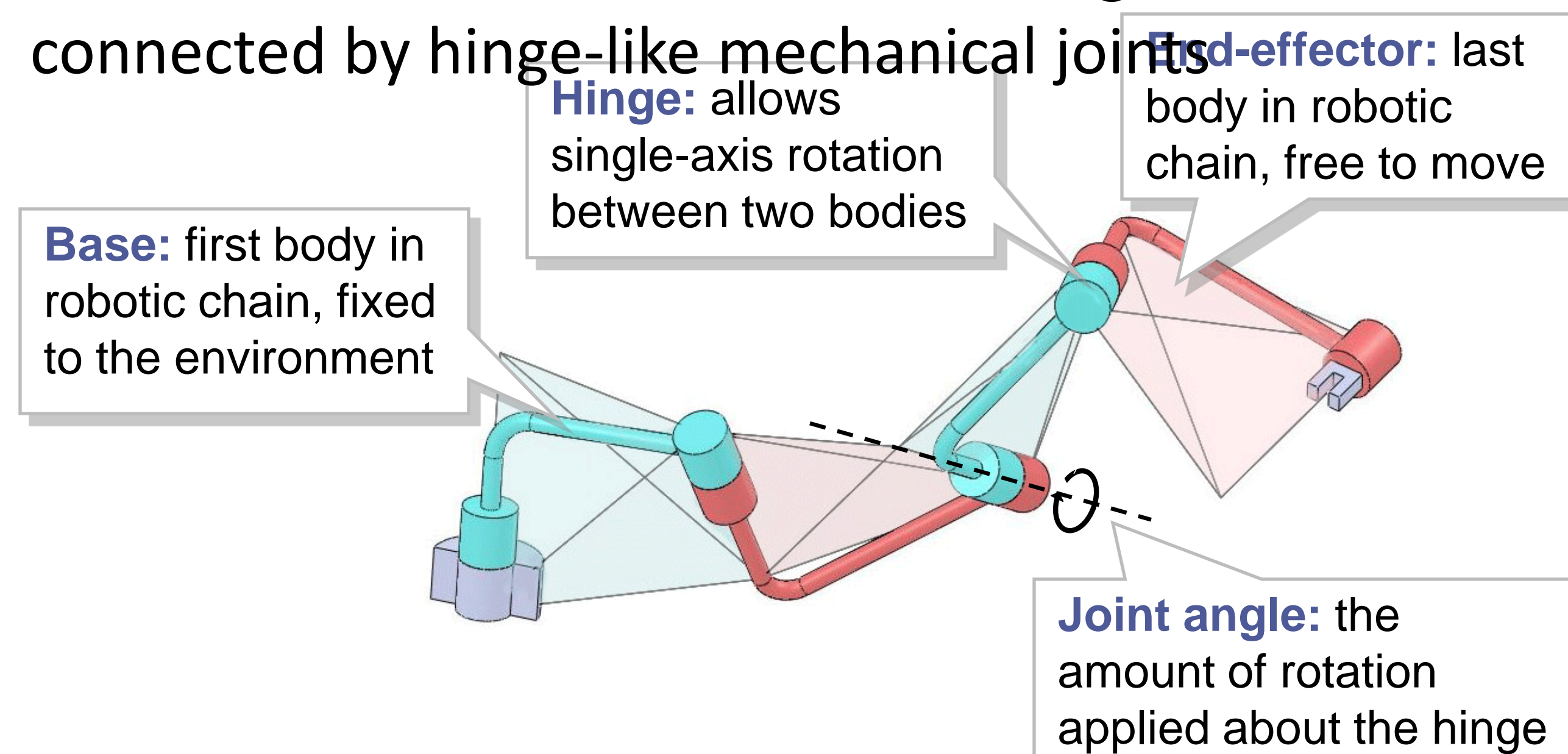


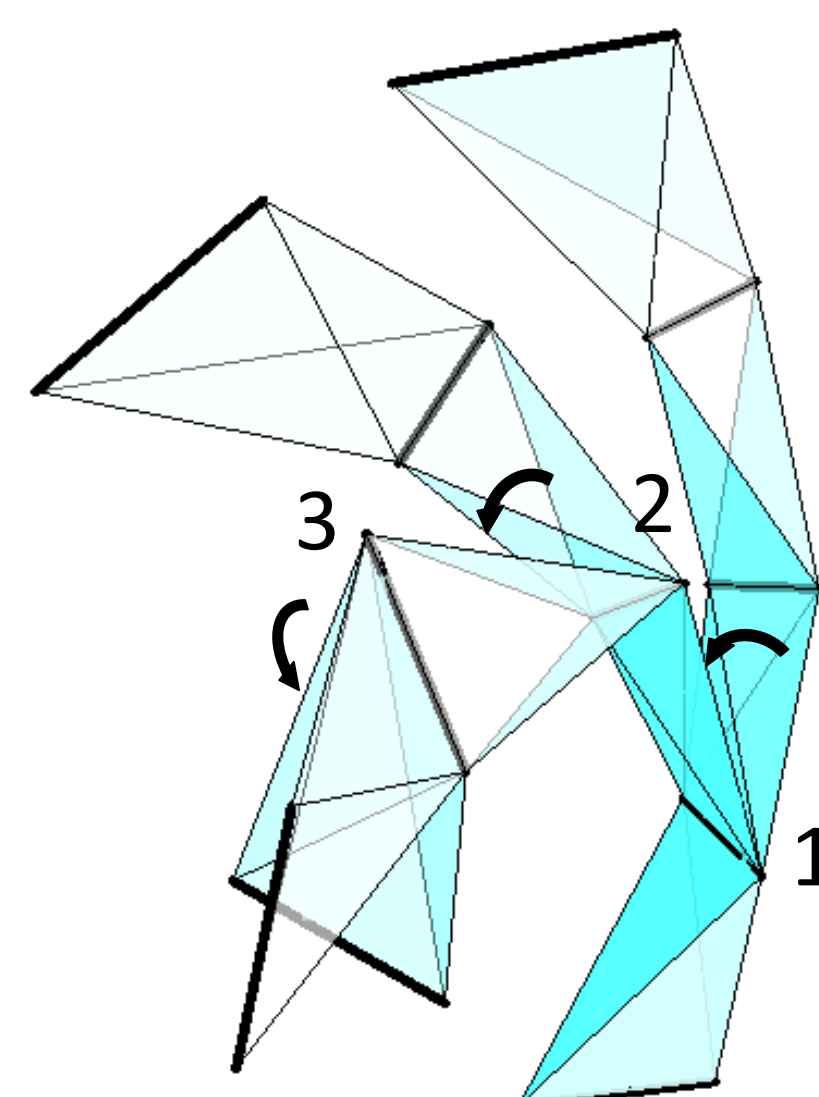
Fig 2. A 3-hinge revolute (3R) chain

The 3R chain consists of 4 rigid bodies and three hinges. Each rigid body can be visualized as a tetrahedron whose opposite edges are hinges.

Forward Kinematics

“Given a joint angle at each hinge, where is the end-effector?”

Fig 3. Forward kinematics on 3R chain
Step by step illustration of iteratively rotating chain about all three hinges. Joint angles are 30°, 60°, and -90° respectively.



- Used for controlling robot configurations
- Solved by applying transformation matrices iteratively to points in each rigid body

Inverse Kinematics

“Given the desired position of the end-effector, what must be the angles at all hinges?”

- Sets of angles are finite if chain contains at most 6 joints
- Used in motion planning, game design and computer animation
- Chains with one or two hinges can be solved easily using geometric methods.

Inverse Kinematics on 3R Chain

The Challenge: Conventional methods using forward kinematics require solving transcendental equations of three unknowns for three joint angles

Approach

- Break 3R chain into upper chain and lower chain
- Transform lower chain to coincide hand with target
- Fix the hand and the base, compute rotations about first and the last hinge that is needed for merging upper and lower chain

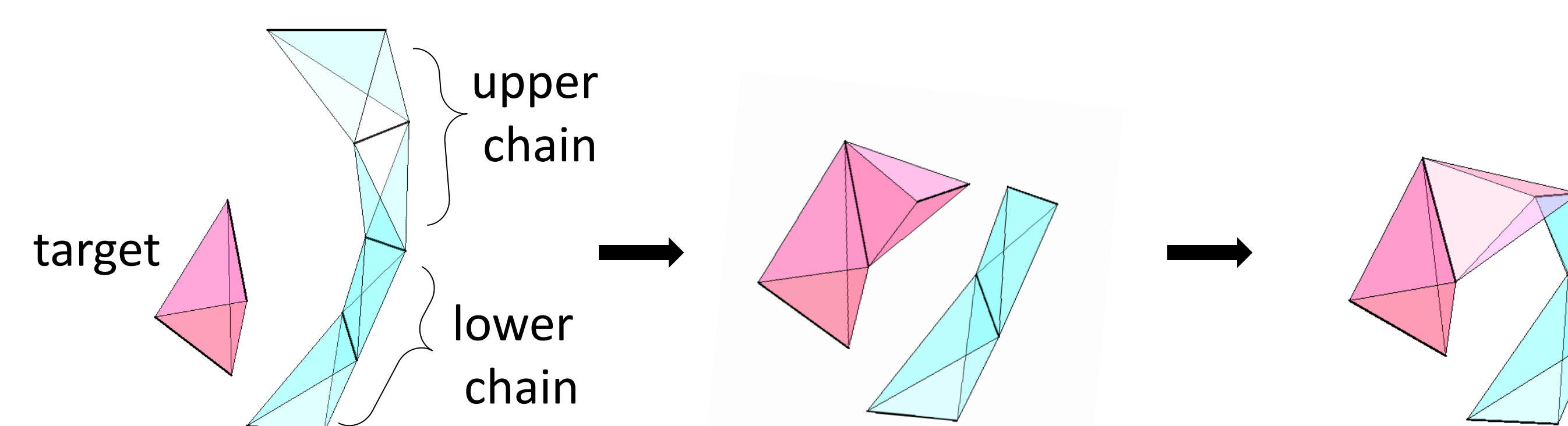


Fig 4. Solving Inverse Kinematics of a 3R chain

Left: initial configuration of a 3R chain (blue) and target (red); Middle: lower chain (blue) and transformed upper chain (red); Right: upper chain and lower chain merges at second hinge.

Results

- Solution is unique and can be obtained by solving a system of linear equations.
- Developed a Mathematica module that computes inverse kinematics solutions and intermediate configurations

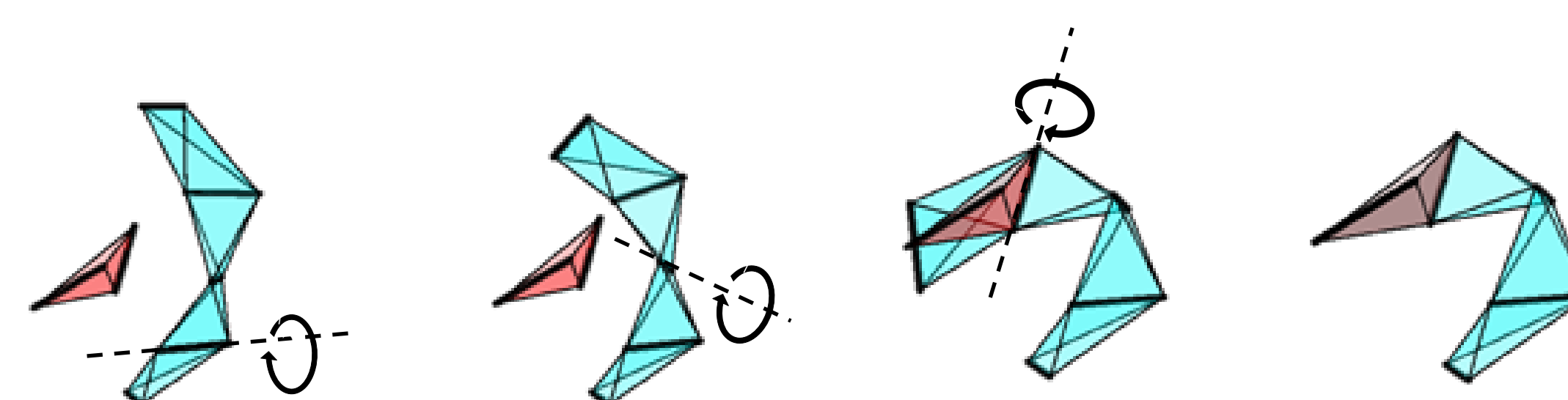


Fig 5. A 3R chain (blue) reaching to a target (red) by rotating around each hinge by the solved joint angles

Proteins and Robotic Chains

Modeling Protein Polypeptide Chains

- Proteins are chains of peptide units
- Each peptide unit is a planar rigid body
- Peptide bonds N-C α and C α -C' are hinges; dihedral angles Φ and Ψ by the peptide bonds are joint angles

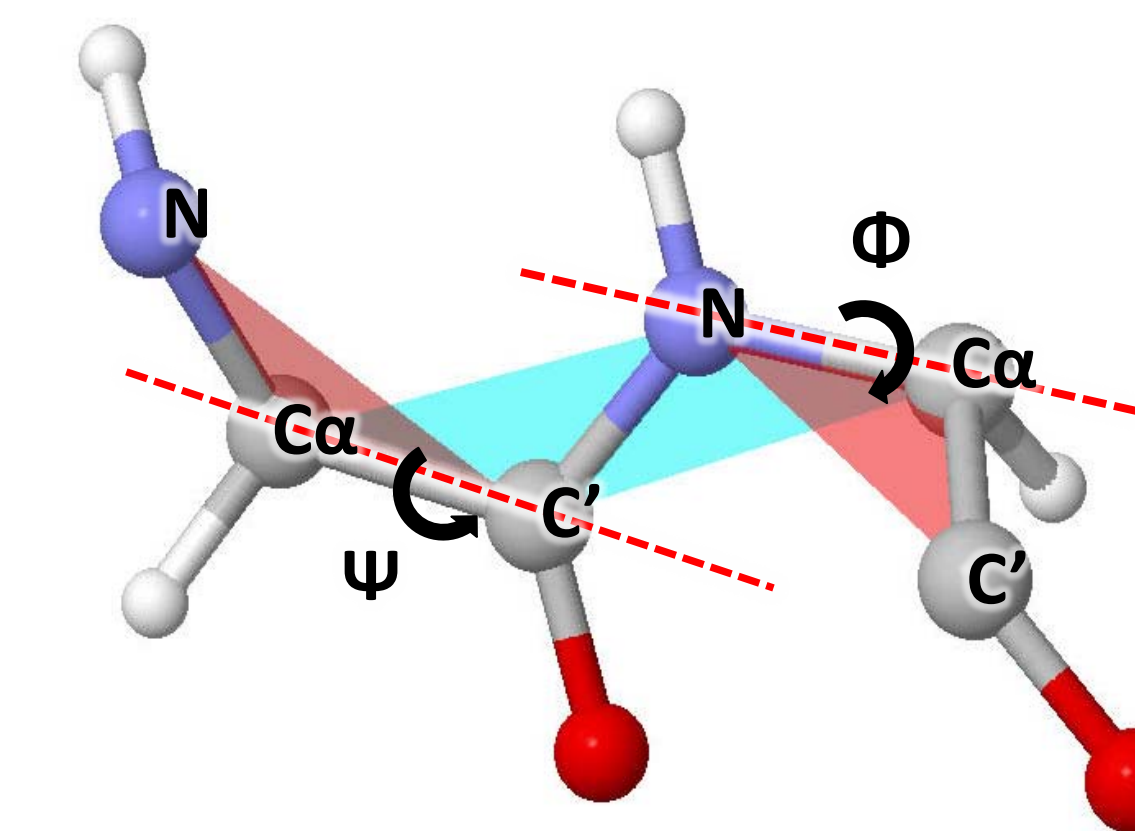


Fig 6. peptide units and dihedral angles

Fig 7. Forward kinematics on Amphiphilic Octadecapeptide (1PEF)
Blue: original polypeptide chain of 1PEF;
Red: transformed chain obtained by rotating 6° at each hinge

Forward Kinematics

- Compute the new spatial locations of atoms given a set of dihedral angles [2]
- Used for manipulating protein configurations in computer simulations

Inverse Kinematics

- Find the dihedral angles so that protein polypeptide chains satisfy certain spatial constraints [3]
- Used for finding missing loops or searching for alternative configurations of polypeptide chains [3]

Acknowledgements

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Images were created with Mathematica, Solidworks and Jmol.

References

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- [2] L. Kavraki, “Representing Proteins in Silico and Protein Forward Kinematics”, Connexions, Jun. 11, 2007. [Online]. Available: <http://cnx.org/content/m11621/1.15/>.
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