

Abstract

Kinematics is the branch of mechanics that is concerned with the motion of a 'tool' at the end of a system comprising of rigid links connected by joints. 'Inverse kinematics' refers to the situation when we know the position and orientation of the tool and wish to calculate the set of system states that effect this position and orientation. A system state can be described in terms of the set of angles at the joints. Inverse kinematics problems are noted for their difficulty in solving. 'Loop closure' is an inverse kinematics problem. It is studied in Biology, Computer Science, and Mechanical Engineering. We can consider the 'protein backbone' to be a kinematics system. Loops play an important role in proteins. The 'protein loop closure' problem is an inverse kinematics problem. This paper describes the state of the art in solving the protein loop closure problem. Several methods exist for solving the problem; however, there is scope for improvement.