**Conclusion and Future work**

In this thesis, we introduce slipknotfind, an extended version of already existing knotfind algorithm. We use the knotfind’s approach of removing the atoms which do not intersect with the triangle formed by the chosen triplet of alpha carbon atoms and iteratively extend apply the knotfind algorithm to the increasing length of subsections of the protein chain starting from residual size of three atoms. When a knot is found initially for a subsection and it disappears in a larger subsection in the later iterations using longer subsections of the same protein chain then we report the chain to be slipknotted.

We then have created two different schemes of visualizing knots and slipknots, the first approach was done locally using standalone protein visualizer PyMol and we included a python script to connect the simplified atoms and generate a clean visualization highlighting knots or slipknots in the chain. The second approach was designed to reach limitation of the first approach, accessibility from anywhere. So, we came up with a web interface of analyzing and visualizing knots or slipknots. We have established a web server using Java sever pages to handle the processing of knots and slipknots, and JSmol to handle the visualizations.

In future, this system can be improved in a number of ways to add more functionality.

1. Compute the Alexander polynomial to determine the number of crossings in a given slipknot by connecting the ends of the chain strategically.
2. Have a database of known knots and slipknots and update the PDB list automatically every Wednesday after PDB website gets updated with new set of proteins, this saves time for biochemists who lookup already existing proteins.