7. SUMMARY AND CONCLUSION

The developed snake database is used to provide the information about snakes. It gives the information about the characteristics of various venomous and non-venomous snakes in India including its images. The developed software tool used to analyze the protein sequence in order to predict venomous and non-venomous snakes using PI and Molecular Weight of protein sequences. This is accurate way of analyzing the snake venom. The software tool gives the accurate results quickly. The Phylogenetic tree generated by the developed software tool with protein sequences using through Neighbor Joining and UPGMA algorithms. This phylogenetic tree can be used to understand the relationship between the species. The Phylogenetic tree also generated by the developed software tool with nucleotide sequences through Neighbor Joining and UPGMA algorithms.

Thus the software tool ‘mcompu’ is a comprehensive software tool used to provide vast information about all Indian snakes and to analyze protein & nucleotide sequences in various views. This software gives the details of snakes with photos. It is used to analyze protein and nucleotide sequences of any species in the world. This software is used to compare the given input protein sequences in order to find out venomous and non-venomous species. Also it is used to find out the close relationship between species using protein and nucleotide sequences. So this is a useful software tool to research scholars, educators, students and general public.