

## Dr. Kumudavalli Research details:

**Bioinformatics** is an **interdisciplinary** field which addresses biological problems using computational techniques, and makes the rapid organization and analysis of biological data possible. Bioinformatics and computational biology involve the use of techniques including applied mathematics, informatics, statistics, computer science, artificial intelligence, chemistry, and biochemistry to solve biological problems usually on the molecular level. One of the most key topics in terms of tools, softwares, techniques and exponentially growing challenges is Phylogenetic Analysis. In specific A phylogeny, or evolutionary tree, represents the evolutionary relationships among a set of organisms or groups of organisms, called taxa (singular: taxon) that are believed to have a common ancestor.

The research work is carried out in order to achieve the objectives viz., (i) to construct various forms of Phylogenetic trees, in order to analyse them for their functional and structural behaviours. (ii) to develop a platform independent OS and a software tool (SPGUP) which is a Web interface that allows the user/developer for future scaling, and which follows the open source technology. Making it work without any dependencies of other software programs related to the study of Sequence Alignment and Phylogenetic tree construction. To this end the proposed software tool (**SPGUP**) will demonstrate how a platform independent, portable tool can be used as a quick trick, to produce sequence alignments, Phylogenetic trees and Genome diagrams as compared to few existing tools.