**Course: Advance Bio Informatics**

**Module Title: Automated Tools for Phylogeny Analysis**

**Module No: 60**

Molecular phylogeny captures and visualizes the sequence variation that occurs in homologous DNA, RNA, or protein molecules. Versatile and broad range of approaches for tree generation

Most programs are freeware and can be obtained from the internet. They are designed to address particular questions

Several small programs for the whole analysis are available which may have lots of bugs & restrictions.

**Ape:** R-Project package for analysis of phylogenetics and evolution

Provides a large variety of phylogenetics functions

**BAli-Phy:** Simultaneous Bayesian inference of alignment and phylogeny

Bayesian inference, alignment as well as tree search.

**BayesTraits:** Analyses trait evolution among groups of species for which a phylogeny or sample of phylogenies is available

**BEAST:** Bayesian Eevolutionary Analysis Sampling Trees. Bayesian inference, relaxed molecular clock, demographic history.

**BioNumerics:** Universal platform for the management, storage & analysis of all types of biological data, including tree and network inference of sequence data.

Neighbor-joining, maximum parsimony, UPGMA, maximum likelihood, distance matrix methods

**ClustalW:** Progressive multiple sequence alignment. Distance matrix/nearest neighbor. MEGA: Molecular Evolutionary Genetics Analysis Distance, Parsimony and Maximum Composite Likelihood Methods

**TreeGen:** Tree construction given pre-computed distance data

**TreeAlign:** Efficient hybrid method. Distance matrix and approximate parsimony

**TREE-PUZZLE**: Maximum likelihood and statistical analysis