

國立東華大學應用數學系  
專題演講

主講人：Professor Shu-Chuan Chen

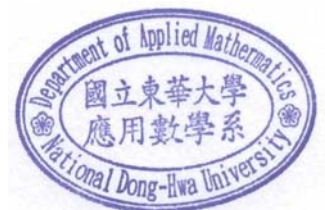
School of Mathematical and Statistical Sciences,  
Arizona State University

講題：Mixture Clustering and its Applications in  
Bioinformatics

時間：100年1月7日(星期五)15:10-16:50

摘要

A new method based on an ancestral mixture model for building a gene tree from Single Nucleotide Polymorphism (SNP) data was developed by Chen and Lindsay, 2006. The sieve parameter in the model plays the role of time in the evolutionary tree of the sequences. By varying the sieve parameter, one can create a hierarchical tree that estimates the population structure at each fixed backward point in time. A software, called MixtureTree, was developed for this purpose. In this talk, we will review the model and present an application to the clustering of the mitochondrial sequences using the mixture tree software. Different optimization algorithms will be discussed. We will also simulate real SNPs sequences with known ancestral history to compare the mixture trees with true trees to evaluate how well the mixture tree method performs. Comparison with some existing methods will be presented as well.



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