

國立中山大學跨領域及數據科學研究中心

國立中山大學應用數學系

學術演講

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講題：Alignment-free Genome Comparison with
Trinucleotide Usage Profile (TUP)

時間：2016/12/29（星期四）14:10 ~ 15:00

地點：理學院四樓理 SC 4009-1 室

茶會：15:00 於理 SC 4010 室（系辦公室）

摘要

We propose a new method, called Trinucleotide Usage Profile (TUP), to build a genome-wide phylogenetic tree for a large group of species. Each species contains a large number of genes and each gene has a long nucleotides sequence. The key issue is to find a macroscopic statistics to represent and characterize the whole-genome DNA information. The most popular method, called feature frequency profile (FFP), is finding the frequency distribution for all words of certain length over the whole genome sequence using (over-lapping) window of the same size. Unfortunately, in order to characterize the genome-wide information, the word length is often much larger than 3 (codon length). We propose an essential modification on the popular FFP method while maintaining typical word length of 3. The main idea is to summarize the sequence in a matrix of three rows corresponding to three reading frames and each row is the distribution on the (non-overlapping) words of length 3 for the corresponding reading frame. Based on the proposed TUP method, the empirical study showed that phylogenetic trees with strong biological support can be built.

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