

生物信息学

用一个相对简单的方法来探测核苷酸替代模型的异质性

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收稿日期 2004-8-30 修回日期 2005-4-19 网络版发布日期 接受日期

摘要 对于可观察到的分子序列进化模型的不同, 提出一个相对简单的方法—卡方检测, 来检测在DNA序列间替代过程的同质性。这个卡方检测方法不管在座位间下列3个条件是否满足皆是成立的: (1) 替代率的异质性; (2) 进化率/模型的相关性; (3) 替代模型的变异。计算机模拟也显示出卡方检测在各种生物学条件下的序列进化模型是非常有效的。在真实数据中, 用11种节肢动物线粒体DNA的比较中发现, 水蚤或卤虫与其他9种节肢动物以高百分比违背了同质性进化模型假设, 显然是由于AT含量高而引起的, 且在两种蚊子的线粒体DNA比较中发现, 其满足同质性假设仅有7.69%。还比较了卡方检测与Kumar and Gadagkar的ID检测之间的效能差异: 在较为复杂的模型下, 卡方检测效率在许多情况下较ID检测方法略高; 并且在犯I-型错误以及卡方测验的效率曲线中清楚地表明我们的方法是保守的, 而Kumar等的方法是不保守的。

关键词 [同质性](#); [替代模型](#); [卡方检测](#); [效能](#)

分类号

A Simple Method to Detect the Heterogeneity of Nucleotide Substitution Processes by Asymmetry in Paired Comparison

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Abstract

A simple method is presented, which uses a χ^2 statistic to measure asymmetry of substitution matrix between two DNA sequences to test a homogeneity hypothesis of their substitution processes. In theory, this χ^2 test holds irrespective of whether there is among-site (i) heterogeneity in substitution rates, (ii) correlation in evolutionary rates/models, and (iii) variation in substitution models. Computer simulations showed that the χ^2 test is powerful under a variety of models of sequence evolution. An application of the test to the comparisons of the eleven sequenced arthropod mtDNAs revealed that most of the observed evolutionary models were homogeneous between the two mosquitoes but not between *Daphnia pulex* or *Artemia Franciscana* and the other arthropod, probably due to shifts to a high AT content. And a comparison to Kumar and Gadagkar's test by computer simulation as well as empirical data analysis is given.

Key words [homogeneity](#) [substitution model](#) [\$\chi^2\$ test](#) [power](#)

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