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TESTING NEUTRALITY OF mtDNA USING MULTIGENERATION CYTONUCLEAR DATA

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Abstract

The neutrality theory of evolutionary genetics assumes that DNA markers distinguishing individuals and species are neutral and have little effect on individual fitness (Kimura, 1983). Under this hypothesis, the action of genetic drift or genetic drift in combination with mutation or migration can be used to describe the evolution of most DNA markers. In recent years, scientists have set up experiments to collect cytonuclear data over several generations to test whether the empirical evidence is consistent with this theory. In this paper, we review the existing statistical tests for neutrality based on such data and propose a new test that we believe is vastly superior. The new test arises from the likelihood theory after embedding the neutral model in a larger class of selection models, where the selection effect takes place due to a difference in fertility of various gametes. A power study based on Monte Carlo simulation is presented to demonstrate the superior performance of the new test.

1 Introduction

A major debate amongst evolutionary geneticists in recent years is whether most DNA markers distinguishing individuals and species are neutral and have little effect on individual fitness (Kimura, 1983). As a profound application of this theory, DNA sequence differences between extant species have been used to reconstruct the history of life. The classical theoretical developments of random genetic drift is built around this assumption. Under this hypothesis, the action of genetic drift or genetic drift in combination with mutation or migration can be used to describe the evolution of most DNA markers.

The recent attacks on the neutrality theory are twofold. Firstly, it has been pointed out that in some cases non-neutral models can also explain behavior consistent with empirical evidence. For example, Gillespie (1979) showed that his model of selection in a random environment has the same