

# STATISTICAL ASPECTS OF THE NON-DARWINIAN THEORY

W. J. EWENS

UNIVERSITY OF TEXAS AT AUSTIN

## 1. Introduction

Quite apart from its possible biological relevance, the non-Darwinian theory of evolution currently under discussion is of considerable interest to statisticians. This is so, of course, because any mathematical formulation of the proposition that a considerable proportion of observed allelic substitutions have no selective significance and have occurred purely by chance, and, hence, any quantitative testing of this theory, must be conducted by statistical methods. The ramifications of the statistical testing which will be required to discuss the half dozen or so major supporting arguments for the theory can hardly be supposed yet to have been analyzed, even superficially; in particular, this is true for those arguments relying on protein sequence data, amino acid frequencies, and the genetic code. It may be that novel forms of statistical tests will be required for these analyses. The main aim of this paper, while going in this direction, though rather restricted, is to devise a statistical test of the non-Darwinian theory based on a form of data currently being obtained in large volume by biologists, namely, the number and frequencies of different alleles at a locus provided by a sample of individuals from one generation of a population. A subsidiary aim is to show that quite simple statistical arguments can cast some doubt on the usefulness of one support for the non-Darwinian theory, namely, the support arising from the principle of substitutional loads. It will be convenient to consider this subsidiary aim first.

## 2. The substitutional load

Our aim is not to question the validity of the concept of substitutional load itself, but rather its usefulness as a support for non-Darwinian evolution. To do this we trace the main outline of the way the substitutional load is calculated.

Consider a diploid population of fixed size  $N$  and suppose that at a certain locus two alleles,  $A_1$  and  $A_2$ , are possible. The three genotypes are supposed subject to differential selection and it is assumed that this selection acts entirely

On leave from the Department of Mathematics, LaTrobe University, Bundoora, 3038, Victoria, Australia.

Written under support of USPHS Grant GM-15769.