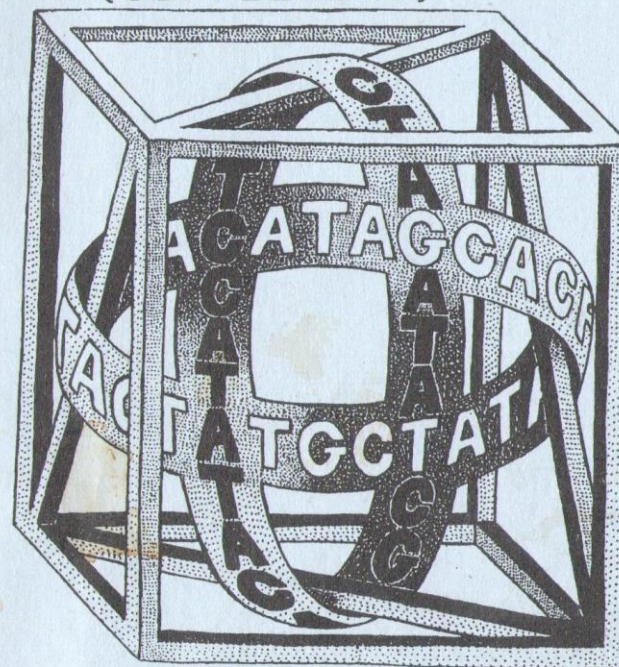The USSR Academy of Sciences
Siberian Branch
Institute
of Cytology and Genetics

MODELLING AND COMPUTER METHODS IN MOLECULAR BIOLOGY AND GENETICS

Abstracts of the International Conference
(SUPPLEMENT)

Novosibirsk. 1990

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resistance to cause also a high G/C contents of the whole region. So far as the more stable DNA double helix prevent from variouns DNA rearrangements(deletions, insertions gene conversion events etc.), which are potentically more typical for eukariotic genes (Solovyev,Kolchanov,1985) and are often provided by the various heteroduplexes forming, when the normal double helix destroys. The fact that many house-keeping genes, executing an important cellular functions has a high G/C contents, correlates to these data.

Having a set of homologous sequenqes of a definite gene and a list of a nucleotide substitutions taking place during the evolution, we can determine an average variability, for an example, a variability of amino acids properties during these substitutions:

$$VA = 1/L \sum \Delta d_{ij} \text{ (summarizing all substitutions),}$$

where Δd_{ij} -value of a distancies between amino acids (Solovyev, Salamov,1990). Taking into account all point mutations in a given gene we can calculate a part of F groups on L size, so having the observed value VA. If VA is lower, than an average value of potential variability MVG for a given gene, then using the formulae obtained by Kimira (1983) we can estimate approximatly such important parameter as a coefficient of stabilizinig selection:

$$S = -\lambda ma = B_1/4N_e, \qquad f/(1-f) = e^{B_1}(V_1/V_2)(2N)^{V_1-V_2}$$

(marks from Kimura, 1983).

Let's apply this methods for estimation of parameters of selection providing unequal usage in highly expressed genes of a difinite synonymous codons.

According to Ikemura (1985) data about genes variability for various bacteria an f/(1-f)=9 relation can be estimated. Then the calculated value S for a single codon will be about 10^{-4}.

1. Ratner VA, 1975, Molecular-genetic systems of management, Novosibirsk.
2. Solovyov V.V., Salamov A.A. 1990, (this abstracts) c.16.
3. Ikemura, 1985, Mol.biol.evol., 2, 13-34.
4. Li et al.,1985, Mol. evol. genes, 1, 1-94
5. Solovyov V.V.,Kolchanov N.A. 1985, VINITI, Mol.biol. т.21, c. 38-80.
6. Kimura M.,1983, The neutral theory of Molecular evolution. NY.