

Research

The proposed line of bioinformatics for genetic diversity is to conduct a study of nucleotide variation of a considerable number of species and genera for describing the patterns of nucleotide variation and the elucidation of the weight of the phylogeny, ecology, demography, functional elements in the genome and recombination of partons observed. For this reason, the line has achieved the following objectives

- Develop a mining software, PDAs for the collection, processing, filtering and quality control of DNA sequences 31-32.
- Construction of two databases of nucleotide diversity from a broad spectrum of species of *Drosophila* genes (DPDB25-26) and mammals (MamPol33).
- Establishing a web server for the test of McDonald and Kreitman generalitzada³⁴ standard
- Description of the patterns of nucleotide variation within and between species and verifying the importance of phylogenetic factors, demographic and genomic organ for explaining the observed patterns.

Among other things it has tried to answer the questions:

- Does covariation between levels of polymorphism of the coding sequences and not codificadores⁴⁷?
- How evolving regulatory sequences of genes (Hox genes) and their derivatives⁴⁸⁻⁴⁹?
- What weight is the effective size of populations (N_e), the phylogenetic inertia, ecological variables and life histories and the functional elements of genome variation observed on the 50-51?
- Does it depend on the efficiency of purifying selection of population size as explained by the theory?
- Is there purifying selection in the non-coding conserved regions and 29?

These responses have been presented in both national and international conferences and published in leading international journals in the field.