

with the computed Morse decompositions. The power of the developed method is illustrated with an application to the two-dimensional, density-dependent, Leslie population model.

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The origin of the tRNA molecule

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A model has been proposed suggesting that the tRNA molecule must have originated by direct duplication of an RNA hairpin structure [Di Giulio, M., 1992. On the origin of the transfer RNA molecule. *J. Theor. Biol.* 159, 199-214]. A non-monophyletic origin of this molecule has also been theorized [Di Giulio, M., 1999. The non-monophyletic origin of tRNA molecule. *J. Theor. Biol.* 197, 403-414]. In other words, the tRNA genes evolved only after the evolutionary stage of the last universal common ancestor (LUCA) through the assembly of two minigenes codifying for different RNA hairpin structures, which is what the exon theory of genes suggests when it is applied to the model of tRNA origin. Observations strongly corroborate this theorization because it has been found that some tRNA genes are completely separate in two minigenes codifying for the 5' and 3' halves of this molecule [Randau, L., et al., 2005. *Nanoarchaeum equitans* creates functional tRNAs from separate genes for their 5'- and 3'-halves. *Nature* 433, 537-541]. It is shown that these tRNA genes codifying for the 5' and 3' halves of this molecule are the ancestral form from which the tRNA genes continuously codifying for the complete tRNA molecule are thought to have evolved. This, together with the very existence of completely separate tRNA genes codifying for their 5' and 3' halves, proves a non-monophyletic origin for tRNA genes, as a monophyletic origin would exclude the existence of these genes which have, on the contrary, been observed.