MODELS FOR CHIRAL AMPLIFICATION IN SPONTANEOUS MIRROR SYMMETRY BREAKING.

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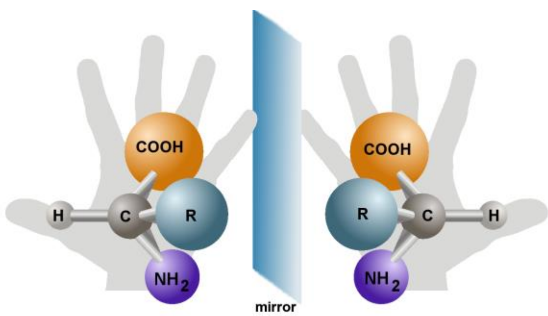
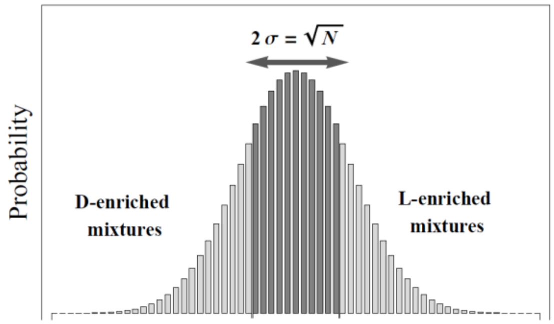
Introduction: It is an empirical fact that there is an absolute chiral imbalance (or mirror symmetry breaking) in all known biological systems, where processes crucial for life such as replication, imply chiral supramolecular structures, sharing the same chiral sign (homochirality). These chiral structures are proteins, composed of amino acids almost exclusively found as the left-handed enantiomers (L); and DNA, and RNA polymers and sugars, with chiral building blocks composed by right-handed (R) monocarbohydrates.



The degree of chiral imbalance in a given sample is defined as $ee=(L-D)/(L+D)$, and it is called enantiomeric excess. Based on the fact that a perfect racemic mixture is chemically impossible to achieve on purely statistical grounds alone, we assume the presence of an unavoidable tiny enantiomeric excess even in a 'perfect' racemic mixture. Thus, there is a need to amplify this initial stochastic enantiomeric excess, ee_{st}, though any efficient mechanism of amplification.



Knowing the total number of particles present in the mixture, N, we can calculate the expected initial enantiomeric excess, ee_{st}, in a racemic mixture (inexorable to the system and due to stochastic fluctuations over the ideal racemic system). Our purpose here is to test the ability of some different models to amplify a tiny initial enantiomeric excess, ee_0, even lower than the expected imbalance (i.e., using $ee_0 < ee_{st}$).

References:

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