

Poincaré Recurrence Time Theorem as a Unifying Element Towards the Understanding of Coding/Noncoding Prediction Algorithms for DNA

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Abstract. A coarse-grained version of the Poincare recurrence time theorem for the symbolic dynamics of some special cases of chaotic maps has been outlined by G. Nicolis and co-workers in a J. Stat. Phys. paper (1997). A detailed study of the recurrence times for the logistic map have been advanced by K. Karamanos and co-workers in a series of articles, and mainly in the journal Kybernetes (2012). Strangely enough, these studies allow one to put together in a unified picture and finally to better understand the coding/noncoding prediction algorithms for DNA strings (developed in the context of the Human Genome Project (HGP)), under the light of modern Statistical Physics and Complexity Science. We point out that our main contribution is conceptual, that is a direct link between Chaos, Linguistic Processes, and DNA Complexity considerations is established. This is achieved through the identification of word-length series encountered in the symbolic dynamics of one-dimensional maps (such as the logistic map), as the coding/noncoding segments' duality in DNA strings