Classification of Neuron Sets from Non-disease States Using Time Series Obtained Through Nonlinear Analysis of the 3D Dendritic Structures

Leonardo Agustín Hernández Pérez[1,2]
José Daniel López Cabrera[2]
Rubén Orozco Morales[3]
Juan Valentín Lorenzo Ginori[2]

[1]Empresa de Telecomunicaciones de Cuba S.A, Santa Clara, Villa Clara, Cuba. leonardo.hernandez@etecsa.cu
[2]Informatics Research Center, Universidad Central, "Marta Abreu" de Las Villas. Cuba
[3]Department of Automatics and Computational Systems, Universidad Central "Marta Abreu" de Las Villas. Cuba

Abstract

The nonlinear dynamic analysis of time series is a powerful tool which has extended its application to many branches of scientific research. Topological equivalence is one of the main concepts that sustain theoretically the nonlinear dynamics procedures that have been implemented to characterize the discrete time series. Based on this concept, in this work a novel way to analyze dendritic trees with high complexity is reported, using features obtained through splitting the 3D structure of the dendritic trees of traced neurons into time series. Digitally reconstructed neurons were separated into control and pathological sets, which are related to two categories of alterations caused by the reduced activity of the adult born neurons (ABNs) in the mouse olfactory bulb. In the first category, a viral vector encoding a small interfering RNA (siRNA) to knock-down sodium channel expression and a second category a naris occlusion (NO) method is applied to reduce the activity of ABNs that migrate to the olfactory bulb. Using the method proposed in this study the mean result of the correct classification was improved in 4.8 and 2.76% for the NO and siRNA sets respectively, while the maximum correct classification rates were improved in 9.53 and 2.5% respectively, when compared to methods based in the use of morphological features.

Keywords: *Neuron trees, Time series, Neuron classification*

Disponible en https://www.springer.com/gp/book/9783030011314