The *Caenorhabditis elegans* genome: a multifractal analysis

P.E. Vélez[1], L.E. Garreta[2], E. Martínez[3], N. Díaz[3], S. Amador[3], I. Tischer[2], J.M. Gutiérrez[4] and P.A. Moreno[2]

[1]Departamento de Biología, Universidad del Cauca, Popayán, Colombia
[2]Escuela de Ingeniería de Sistemas y Computación,
Universidad del Valle, Santiago de Cali, Colombia
[3]Escuela de Ingeniería de Sistemas y Computación,
Universidad del Cauca, Popayán, Colombia
[4]Instituto de Física de Cantabria,
Universidad de Cantabria-CSIC, Santander, Spain

Corresponding author: P.A. Moreno
E-mail: pedro.moreno@correounivalle.edu.co

ABSTRACT. The *Caenorhabditis elegans* genome has several regular and irregular characteristics in its nucleotide composition; these are observed within and between chromosomes. To study these particularities, we carried out a multifractal analysis, which requires a large number of exponents to characterize scaling properties. We looked for a relationship between the genetic information content of the chromosomes and multifractal parameters and found less multifractality compared to the human genome. Differences in multifractality among chromosomes and in regions of chromosomes, and two group averages of chromosome regions were observed. All these differences were mainly dependent on differences in the contents of repetitive DNA. Based on these properties, we propose a nonlinear model for the structure of the *C. elegans* genome, with some biological implications. These results suggest that examining

differences in multifractality is a viable approach for measuring local variations of genomic information contents along chromosomes. This approach could be extended to other genomes in order to characterize structural and functional regions of chromosomes.