

Book Review: Microcompetition with foreign DNA and origin of chronic disease. Hana Polansky

Ricardo Bringas

Department of Bioinformatics, Center for Genetic Engineering and Biotechnology (CIGB)
Ave 31 / 158 and 190, PO Box 6162, Havana 10 600, Cuba
E-mail: ricardo.bringas@cigb.edu.cu

Hana Polansky's book, "Microcompetition with foreign DNA: the origin of chronic disease" introduces a new theory based on the competition of the host and exogenous DNA sequences for limited amounts of the host's regulators resulting in chronic diseases. The book provides many examples from the literature that fit this hypothesis. Chronic diseases as diverse as cancer, atherosclerosis and obesity are now explained by the same mechanism, the abnormal behavior of host cells due to the limited availability of host transcription factors that target host as well as foreign DNA regulatory sequences. This theory poses a challenge for scientists dealing with chronic diseases. In the present post genomic era, when a great deal of work is being done in regulatory sequence analysis, with the aid of technologies such as DNA-microarrays and chip-chip (Chromatin immunoprecipitation + DNA microarray) aimed to quantify gene expression levels and to detect the binding of transcription factors to regulatory sequences, respectively, Polansky's theory poses a challenge for experimentalist as well as for bioinformaticians. As a well mathematically formulated theory, it could be tested with experiments designed to combine the analysis of expression profiles and regulatory site

binding by transcription factors with computer models based on the competition for a limited availability of transcription factors. On applying these principles to the analysis of expression profiles and regulatory sequence recognition by transcription factors it would provide bioinformaticians with a new way of looking for biologically relevant patterns in these data. At present most papers look for statistically significant correlations between sets of genes with similar expression profiles and known functional categories or common regulatory motifs in their promoter sequences, based on very simple assumptions such as a positive or negative correlations between the expression of transcription factors and their target genes. Polansky's theory provides the basis for the formulation of much more complex questions in studies that explore correlations between the expression and gene regulatory networks. At present when the system biology paradigm stands as a big challenge for the biological research needed to make sense out of huge amounts of available data, Polansky's theory emerges as a new significant concept, that if proven true, will be of relevant importance to understand the complexity of gene regulatory networks.