

INFORMATIONAL MODELLING IN INFECTIOUS PROCESS

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Correlating a great number of bibliographical data with our own investigations we reached the conclusion that the infectious process (in general) and implicitly each separate infectious diseases (in particular) are fulfilling the characteristics of an informational model, which we have prioritarly proposed. The elements of the informational model are the followings: R = reception of the pathogenetical signal by means of the adhesine-receptor (A-R) system, thus specifying the preferential sites of insertion ($R=1,...,n$); CS = cellular signals carried by the infectious agent which are characterized by the mode of action of the factors of virulence, toxins, enzymes and so on, on the host's cells; DCS = decoding process of the cellular signals, i.e. the cellular restructurations by means of which the signals are assimilated; SCS = supracellular signals or the actions of the pathogenes leading to liberation of endogenous mediators of infection - i.e. biochemical, neuropathogenetical or immunopathogenetical mediators; DSCS = decoding process of the supracellular signals that is realized through liberation of citokynes, arachidonic acid metabolites (prostaglandines and leukotrienes) and also of cathecholamines, activation of adenylcyclase-cyclic AMP system, liberation of mediators of immunopathological reactions and so on; E = exit, or the outcome representing: the infectious disease with its various forms of manifestation (autolimitating, severe or complicated ones). As a result of the collaboration with specialists in informatics, we realized that by substituting each of the steps (R, S, D, E) with adequate medical items for each particular disease, one is able to design medical graphs that can be converted into an expert system (ES) on the IBM-PC 486 computer, using C++ language, a language that proved by its nature and quantum of informations to be best suited for this purpose in neural network.