



2D MODELLING AND ANALYSIS OF SPATIALLY DISTRIBUTED CELLS TYPES OF PRIMARY SHOOT APICAL MERISTEM (SAM) OF ARABIDOPSIS THALIANA

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Development of organisms is a very complex process for understanding of that there are used methods of system computer biology along with experimental methods. It is well known that postembryonic development of the above-ground part of higher plants depends on the expression of apical shoot meristems, a dynamic structure which forms leafage, flowers and scape. The apical shoot meristem (SAM) is stem cells reservoir of plants and it regulates processes of growth and development in response to both incoming external signals (light, temperature) and internal signals (phytohormone, signal molecules). Therefore development rules of plant above ground level depend on mechanisms of meristem development in many respects. Object of our research is the apical shoot meristem of *Arabidopsis thaliana* during embryonic vegetative of developmental stages. Choice of the object as model object is determined by *Arabidopsis thaliana* is one of the most strongly studied of higher plant. There are strongly accumulated data both about molecular genetic processes and about spatial structures rules of the plant on the different stages his life cycle. In particular, there were revealed numerous genetic mutations which responsible for phenotypic anomalies in plant development. The cumulative experimental data allow starting construction of spatial distributed hierarchical model that will describe both molecular genetic processes and processes on the level of cell-cell interactions simultaneously. Development of this model allows to ascertain cause-and-effect relations between intracellular processes which are regulated gene networks and morphological characteristics of the plant and his separate parts (tissues, cell groups, individual cells). The cellular automaton was developed to model the development of shoot meristems of the *Arabidopsis thaliana* in embryogenesis on basis of experimental data from AGNS database (Arabidopsis Genenet Supplementary Database) (<http://wwwmgs.bionet.nsc.ru/agns>). Modeling covers the initiation of SAM, the formation of the SAM complex structure and its further functioning (Akberdin et al., 2007). Here the embryo is described as a two-dimensional array of cells, the rates of division of which depend on the cellular environment. The cells in the model may receive and, depending on the cell type, produce signals that should

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be received by other cells in the model. The biological meaning of signals is the concentration of certain diffusing substances, or morphogenes, which provide a specific influence on the cell.

Creation of a cellular automaton that imitates morphodynamics of embryo development by means of regulation of signals produced by different embryonic cells is a first step in modelling the process of development in general and in modelling the gene network for morphogenesis in particular. The formation of plant meristems in embryogenesis is characterized by a combination of a violent development of differentiating tissue and a stable development of its stem cells. Both processes were modeled in the cellular automaton being reported. Not only is this automaton a tool for predicting the dynamics of the division process and the cell differentiation process which underway in the systems being considered, but also for the examination of how real mutations influence the system.

1. Akberdin I.R., Ozonov E.A., Mironova V.V., Gorpinchenko D.N., Omelyanchuk N.A., Likhoshvai V.A., Kolchanov N.A. (2007). “A cellular automaton to model the development of shoot meristems of *Arabidopsis thaliana*”, *Journal of Bioinformatics and Computational Biology* (in publication).

INTERLOCKS IS A CHARACTERISTIC FEATURE OF SANDWICH-LIKE DOMAINS

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Sandwich-like domains form a large group of protein domains with a similar architecture – two beta-sheets packed against each other – but rather different topologies. For their characterization and classification it is important to identify characteristic elements of their topology, i.e. elements contained in almost all sandwich-like domains and rarely contained in other classes of domains.

It was shown [1] that interlocks – two pairs of neighboring strands from two beta-sheets with special “interlocked” topology of the strands – are typical structural elements of sandwich-like domains. There are no publications on interlock occurrences in domains of other architectures. To investigate interlock spread in all solved protein structures, we have designed a computer aided procedure to classify all families in the SCOP 1.69 database into 3 groups: IL+ (all domains in the family contain an interlock), IL- (all domains are interlock-free) and IL+/-

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