

# The Systems Biology: integration of experimental and computational approaches

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The last 15-20 years in development of biology were marked with accumulation of unprecedentedly huge arrays of experimental data. The information amassed with exclusively high rates due to the advent of highly efficient experimental technologies. The new technologies provided for high throughput genomic sequencing, analysis of gene expression, protein compositions, determination of metabolite concentrations within the cell. The new paradigm of description and analysis of these data is the Systems Biology. Systems biology largely focuses on the study of the organization and operation of the biological systems at various levels: molecular genetic entities, cells, tissues, organs and organisms on the basis of information encoded in their genomes. The analysis of information based on the efficient computer storage of data, integration and analysis based on the “network” models, representing molecular entities and interactions between them.

The gene network is one of such model within the systems framework. It represents groups of genes that function in coordination with each other and control the development of particular phenotypic characteristics of an organism: molecular, biochemical, physiological, morphological, behavioral etc. This model allows integrating large part of the biological information from molecular level to the level of cells and tissues.

The report present the results of gene network approach developing at the Institute of cytology and genetics SB RAS. The work is based on the integration of the experimental data and theoretical and computer models of interaction of DNA and proteins in the regulatory regions of genes (computational genomics), the RNA functioning (computational transcriptomics), protein structure, protein-protein and protein–metabolite interactions (computational proteomics). The large part of work represents approaches for biological database development and maintaining.

The report also presents the fundamental aspects of the theory of hypothetical gene networks. The advantage of the approach is the possibility for computational modeling of the genetic network dynamics. Several examples of network modeling presented (host-viral interaction, plant tissue development, bacterial metabolism, bacterial genosensor response to stress conditions).

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