<p>The department combines two modern directions of study in the field of biology: bioinformatics and computational biology. The main objective of the department is to develop and analyze the efficiency of data structures and algorithms, the visualization and communication tools to integrate a large amount of information and create models of biological systems, both at macro and micro - structural levels. This approach involves the use of computer simulations for analysis and visualization of complex connections of cellular processes.</p>   <p>The department combines two modern directions of study in the field of biology: bioinformatics and computational biology. The main objective of the department is to develop and analyze the efficiency of data structures and algorithms, the visualization and communication tools to integrate a large amount of information and create models of biological systems, both at macro and micro - structural levels. This approach involves the use of computer simulations for analysis and visualization of complex connections of cellular processes.</p> <p>The research team includes young researchers among whom PhD students and postdoctoral fellows, a system administrator and technical staff, to which we add the undergraduate and master students involved in research projects.</p> <p>The Department will be equipped with a computer network and a high performance cluster for parallel computing, databases servers and servers for data visualization, as well as a significant software package that should provide the possibility of analyzing a variety of data simultaneously. The department will also have available, several work points, each with the possibility of simultaneous implementation of several directions of study.</p> <p>The Department structure consists of three laboratories modules which will ensure the performance of research in the following areas:</p> Biosystems dynamics modeling Module of molecular bioinformatics Analysis and data visualization <h2>Biosystems dynamics modeling</h2> <p>The study of systems dynamics is a branch of systems theory, a method of understanding the dynamic behavior of complex systems. Modeling biosystems dynamics study deals with deciphering the functioning and evolution of biological systems in time and it enables the prediction of static and dynamic properties depending on how the components interact. The information obtained through dynamics calculations illustrate the time dependence and the scale of fluctuations in the system parameters, states of dynamic equilibrium or instability.</p> <p>We are able to modele and simulate processes of ecology, physiology, biochemistry, molecular modeling of dynamics, etc. Examples of research themes: modulation of receptor for TRPA1compounds pollutants: role in states of chronic pain, effects of insecticides on the activity and excitability of sensory neurons present in the peripheral nervous system.</p> <p>The module ensures the mathematical modeling of ecological systems, one of the fastest growing fields worldwide. At the national level, the field is extremely underrepresented, there is no tradition in shaping these highly complex systems. Creating this new method will ensure an increased scientific competitiveness in the field and it will ensure the use of a very valuable tool in developing response scenarios for ecological systems to the action of various control factors, especially in the case of climate change.</p> <p>Module of molecular bioinformatics</p> <p style="line-height: 15.8079996109009px;">Molecular bioinformatics module ensures a multidisciplinary approach including molecular biology, biochemistry and genetics on the one hand and computer science, on the other. This approach will use areas in the field of computer science such as algorithms, combinatorial optimization,

linear programming, formal language theory, neural networks, database systems and simulation data.</p> <p style="line-height: 15.8079996109009px;">The Module will apply computer techniques for conceptualizing biology in terms of molecules,in order to understand and organize information associated with these molecules on a large scale. Computational modeling techniques consist in building structural models based on homology with the amino acid sequence and three-dimensional structure of a known homologous protein ("Matrix").</p> <h2>Analysis and data visualization</h2> <p>It is a branch of bioinformatics directed towards the application of computer graphics, scientific visualization and visualization of information in various areas of life. It includes viewing of sequences, genomes, alignments, phylogenies, macromolecular structures, biological systems.</p> <p>The main direction approached is the development and application of integrated computational methods to understand and analyze biological data on the systemic scale.</p> <p>It combines theoretical methods and computational techniques with experimentation in order to verify assumptions and to obtain more information in the study of biological systems. At the molecular level, we perform molecular modeling studies, molecular dynamics, parameterization, normal modes analysis, sequence analysis, and molecular mechanics studies using laws of traditional mechanics and / or quantum mechanics to obtain findings regarding the state of the system and its changes over time.</p> <p>�</p> <p>Thus, the Department creates the framework for the development of programmes to meet the requirements of the fields of environment and environmental studies. Additional directions are focused on providing software solutions to environmental problems as well as consultancy regarding their implementation, providing for computing time.</p> <p>The Department also ensure the computer network management for the entire building.</p>