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Application of bioinformatics in autoimmune disorders for identifying druggable pathways and promising targets

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Targeted therapy is based on the binding of the target molecule which blocks or modifies the action of the target. The roofs of such a treatment are laid deeply in drug discovery e.g., the process by which drugs are designed or discovered. Creation of product from the original idea takes 12-15 years and costs up to $1 billion. Past records have indicated that the high failure rate (only 8% of success) of drug development can be attributed to the improper target pre-selection. So target discovery is the most crucial step in the modern drug discovery campaign. In this sense, autoimmunity is often caused by concomitant dysfunctions and imbalances at once. Due to the complicated nature of autoimmunity which is manually infeasible when examined on the proteomic level, researchers often employ machine learning methods to identify solutions. Machine learning approach allows to collect a set of samples "training data" which specify the correct output for a given input. A machine learning algorithm takes these examples and produces a program which may work with other sets perfectly. Bioinformatics provides completely new approaches which involve an artificial intelligence to target discovery process. Data mining of available biomedical data has led to a significant increase in target identification. Therefore, data mining would allow for using bioinformatics not only in identifying but also in selecting and prioritizing potential targets.

Biography

Irina Zhegalova is a student I.M. Sechenov First Moscow State Medical University, School of Pharmacy. She is a member of Young Research Team under the aegis of EPMA (Brussels, EU) and ISPM (Tokyo, Japan). She is interested in bioinformatics and performs researches in application of this branch to PPPM model.

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Page 49