Clinical and genomic data integration in support of biomedical research and clinical practice

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Alexander Kel studied biology and mathematics at Novosibirsk State University and obtained his MS in 1985. He worked for 15 years at the Institute of Cytology and Genetics, Russia (ICG) finally holding the position of Vice-Head of the Theoretical Molecular Genetics Lab. In 1990 he received his PhD in Bioinformatics, Molecular Biology and Genetics. In 1999 he organized a Bioinformatics group at ICG.

From 2000 to 2010, he has been the Senior Vice President Research & Development of BIOBASE GmbH.

During his career, he has worked in many branches of current bioinformatics. He is a prolific author of scientific publications, as well as of tutorials and education materials.

In the tutorial, he will approach the analysis and modeling of biological systems from several practical angles. First, he will introduce into systems biology and modeling from a network-based perspective. He will introduce several pathway databases and describe how to use them for pathway analysis. Next, he will describe computational methods for analysis of pathway information and for reconstruction of signal transduction and gene regulatory pathways using gene expression data and knowledge from the pathway databases. This will be followed by methods of analysis of topological properties of biochemical and regulatory networks. This will lead to the application of such methods for revealing key nodes in networks as potential biomarkers or drug targets. He will then show examples of application of these methods for identification of disease related biomarkers and drug discovery.

The attendees of the tutorial will get demo of the online system geneXplain with the aim to enable them to use it in their lab.