Alexander Kel[1,2] received his Ph.D. in Bioinformatics, Molecular Biology and Genetics in 1990. He studied biology and mathematics at Novosibirsk State University and obtained his M.S. in biology with special focus on mathematical biology in 1985. He worked for 15 years at the Institute of Cytology and Genetics, Russia (ICG) holding positions as a programmer, scientist, senior scientist and Vice-Head of the Laboratory of Theoretical Molecular Genetics. In 1995, he won the Academician Belaev Award. In 1999 he received an independent funding from the Volkswagen foundation and organized a Bioinformatics group at ICG. From 2000 to 2010, he has been the Senior Vice President Research & Development of BIOBASE GmbH, Wolfenbüttel, Germany.

The scientific career of Dr. Kel includes numerous research stays in the USA (e.g. 1993: Supercomputer Center, Tallahassee; 1997: University of Pennsylvania, Philadelphia; 1999, 2000: Cold Spring Harbor, NY), in Italy (1991, 1992: ITBA, Milan), and in Germany (1994, 1995, 1996, 1997-1998: GBF; 1997: MPI of Molecular Biology, Berlin).

The research experience of Dr. Kel in Bioinformatics totals more than 20 years. During his career, he has worked in almost all branches of current bioinformatics including: theoretical models of molecular genetic information systems, sequence analysis, gene recognition, promoter analysis and prediction, analysis of protein secondary structure, prediction of RNA secondary structure, theory of mutation and recombination process, molecular evolution, databases and gene expression studies.

Alexander Kel is the author of more than 90 scientific publications. He is also an author of several chapters in books on bioinformatics, tutorials and education materials.

Tutorial at BITS 2017 - Modeling transcription regulation for system medicine of common human diseases.

Transcription regulation is of central importance for nearly all processes in a living system, and erroneous transcription control is causative for numerous diseases. To enable a systems approach to transcription, we still have to struggle with the very first step that is to infer underlying wiring diagrams. Empirical information about the interaction of regulators (transcription factors) and the regulated target genes, obtained by either conventional or high-throughput methods, has been collected in the TRANSFAC database since 28 years, and

1) GeneXplain GmbH, Am Exer 10B, D-38302 Wolfenbüttel, Germany
2) Institute of Chemical Biology and Fundamental Medicine, Novosibirsk, Russia

statistical models inferred from this information have been included as positional weight matrices (PWMs) and made available for the prediction of regulatory sites as well. New extension includes syntax (relevant combinations) and semantics (regulated processes) of regulatory sites. Extended annotation of gene-disease associations is available in the Human Proteome Survey Database (HumanPSD), connected with signaling pathways that control the activity of TFs (TRANSPATH database). All this carefully curated information can be used in full power to analyze disease related multi-omics data using recently created geneXplain platform (http://www.genexplain.com/genexplain-platform), which helps to decipher the molecular mechanisms of disease often on very early stages of its progression. First of all, differentially expressed genes revealed by microarray or RNA-seq analysis are combined with ChIP-seq/ATAC-seq and DNA methylation assays to find disease-related enhancers. Next, genetic algorithms reveal TFs synergistically acting in those enhancers. Finally, topology analysis of signal transduction networks upstream of transcription factors identifies master-regulators of the disease progression, which proposed as perspective therapeutic targets.

Acknowledgements (including grant agreement numbers and sponsors)
SysmedIBD (EU FP7, Grant Agreement no. 305564); MyPathSem (Germany BMBF, Grant no.: 031L0024 B); Grant №14.604.21.0101 of Targeted Federal Program of Russian Federation.