

AGENDA OF TRAINING

Course: HANDS ON TRAINING: IDENTIFICATION OF DRUG TARGETS AND BIOMARKERS WITH THE GENEXPLAIN PLATFORM EQUIPPED BY THE INTEGRATED TRANSFAC[®] AND TRANSPATH[®] DATABASES

Riga Stradins University, Riga, Latvia

Course objective: The course aims to provide a hands-on training for identification of drug targets and biomarkers in the geneXplain platform.

Course outcomes and outputs: After the course all the participants will become familiar with the basic functionalities of the geneXplain platform including running the pre-existing workflows for promoter analysis and for pathway analysis as well as the result interpretation. By the end of the course each participant will be able to suggest drug targets and biomarkers in the given expression data set. Each participant will get an online account in the geneXplain platform with 0.5 GB work space for 6 months.

Lecturer: Dr. Alexander Kel, Chief Scientific Officer, geneXplain GmbH

Dr. Olga Kel-Margoulis, Director Applied Life Science Informatics, geneXplain GmbH

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Time schedule	
8:30 – 10:00	<p><i>Intro:</i> Welcome word; brief self-introduction by each of the participants (30 min) AK: Introductory lecture, concept of the upstream analysis for drug target identification in the geneXplain platform (20 min). OKM: Check up of the participants' accounts to start with the hands on exercises. Distribution of the training data sets (20 min). <i>Import of the exercise data into the accounts</i> AK: Demo of data import in several formats (20 min).</p>
10:00-10:15	<i>Coffee break</i>
10:15-12:00	<p>AK, OKM: Hands on exercises: data import in different formats, e.g. raw data in ZIP archive, excel table with normalized data, excel table with genes in focus, ChIP-seq peaks in BED format (30 min) <i>Promoter analysis in the platform</i> AK: Shortly about the methods of identification of transcription factor binding sites, TFBSs (15 min). AK, OKM: Hands on exercises: search for TFBSs in the promoters (1 hour).</p>
12.00-13.00	<i>Lunch break</i>
13:00-15:00	<p>AK: Interpretation of the promoter analysis results and visualization in genome browser of the platform (15 min). AK: Demo for several operations with tracks including intersect tracks (15 min). AK, OKM: Hands on exercises: visualization of tracks in the genome browser, intersect tracks and other operations with tracks (30 min). AK: summarizing promoter analysis, check with the participants if everyone has completed the exercises, questions, comments (15 min).</p>

	<p><i>Pathway analysis in the platform</i></p> <p>OKM: Methods of the pathway analysis in the platform: search for master regulatory molecules as suggested drug targets. Finding clusters in the networks (15 min).</p> <p>AK, OKM: Hands on exercises: the pathway analysis (30 min)</p>
<i>15:00-15:15</i>	<i>Coffee break</i>
<i>15:15-17:30</i>	<p>OKM: Interpretation of the workflow results and selection of the master molecules in focus (15 min).</p> <p>OKM: Demo for visualization on the master molecule diagrams, mapping expression data on diagrams, changing network layouts (15 min).</p> <p>AK, OKM: Hands on exercises: mapping expression data on diagrams, changing network layouts (30 min)</p> <p>OKM: summarizing pathway analysis, check with the participants if everyone has completed the exercises, questions, comments (15 min).</p> <p><i>Functional classifications and GSEA</i></p> <p>AK: Demo for GSEA (gene set enrichment analysis) and functional classifications; interpretation of the results (20 min).</p> <p>AK, OKM: Hands on exercises: GSEA and functional classifications (20 min).</p> <p>Summary, questions and feedback (20 min).</p>
<i>17:30- 19:00</i>	<p><i>Optionally, for those who might be interested:</i></p> <p><i>brief overview of the methods that were not covered by the training, e.g. analysis of RNA-seq data, ChIP-seq data, time course experiments, etc. Possible advices on data analysis for individual participants.</i></p>