

## **Biological Interpretation of high-throughput expression data using ExPlain™**

Ryota Kunita (BIOBASE Japan, Ph.D.)

Recent advances in sequencing technology have facilitated the production of great amounts of high-throughput expression data, but still, the biological interpretation of the expression profiles obtained in these experiments remains a challenge in many cases.

ExPlain™, an expression data analysis platform, provides tools to aid the interpretation of these profiles accurately. By using ExPlain™ algorithms a researcher can make gene ontology and functional analysis on the gene expression profiles, and also identify possible upstream causes and/or regulators that explain the observed expression. ExPlain™ algorithms can easily help to generate hypothesis on master regulators of intracellular gene regulation and signal transduction processes. This becomes relevant both in basic research and applied science; ExPlain™ can directly facilitate the identification of perspective drug targets, causal biomarkers, and elucidation of cell differentiation mechanisms.

ExPlain™ analyses supports various types of high-throughput data, such as transcriptomics, proteomics and phosphoproteomics data, ChIP-chip and ChIP-seq data, as well as data on protein-protein interactions.

This presentation will include an analysis work flow using ExPlain™, and a description of the extensive data library supporting it, which includes the databases TRANSFAC (transcription factors and position weight matrices), TRANSPATH (signal transduction networks) and TRANSPRO (whole genome promoters).

Examples of ExPlain™ applications, involving various processes and diseases such as viral infection, inflammatory processes, cell differentiation and cancer, will be provided.