

Sorting the signals: meta-analysis of transcriptome data of zebrafish embryos after chemical exposure

ANDREAS SCHÜTTLER^{1,4}, KRISTIN REICHE^{2,3}, ROLF ALTENBURGER^{1,4}, WIBKE BUSCH¹

¹Department Bioanalytical Ecotoxicology ²Department Proteomics, Young Investigators Group Bioinformatics & Transcriptomics
UFZ Helmholtz-Centre for Environmental Research, Permoserstr. 15, 04318 Leipzig (Germany)

³Bioinformatics Research Unit, Department of Diagnostics and New Technologies
Fraunhofer Institute for Cell Therapy and Immunology, Perlickstr. 1, 04103 Leipzig (Germany)

⁴Institute for Environmental Research (Biology V), RWTH Aachen, Worringerweg 1, 52074 Aachen (Germany)

Adverse effects of chemicals on cells and organisms are in many cases either preceded by or result in gene-expression changes. This makes transcriptome analysis a promising tool in ecotoxicological research, e.g. as future bioassay or diagnostic tool for biomonitoring. There are several advantages in comparison to established tools, e.g. the non-targeted approach, allowing assessment of several modes-of-action at the same time, or the possibility to combine assessment of adverse effects with identification of effect-drivers, which will also be helpful in the establishment of adverse outcome pathways (AOPs).

During recent years several studies analysed global gene expression in *Danio rerio* embryos after exposure to chemicals. Many of those studies claim to show specific gene-expression changes in zebrafish embryos after exposure to chemicals and claim to offer a proof of concept of the suitability of microarray analysis as potent bioassay. To put the so far published results into context, and analyze the quality and comparability between the studies, we perform a meta-analysis of published transcriptome data. The analysis will combine the data of nearly 40 published studies using different chemicals, concentrations and exposure times. The aim is to get an overview of the regulation of genes and biologically relevant gene sets. Signals will be grouped into sets which are commonly regulated under certain conditions. Those conditions will include factors of experimental design like array design or exposure time, but also potential biological informative factors as chemical class, effect group or effect concentration. Later on, this should also help to determine if there are general stress answers and developmental disturbances on the transcriptome level, which can be separated from specific effects of chemicals.