# caLIBRAte
nano risk governance

Do environmental model organisms exposed to nanoparticles exhibit a common toxicological response?

Background

The use of innovative methods, such as 'omics' technologies (e.g. transcriptomics) are gaining importance in the field of nano-ecotoxicology; an increasing number of studies are aiming to investigate the effects of engineered nanomaterials (ENMs) in this way. However, systematic synthesis of the outcome of such studies regarding common responses and toxicity pathways is currently lacking. The caLIBRAte project performed a meta-analysis for environmentally relevant transcriptomic studies of engineered nanomaterials (ENMs) in order to study the molecular mechanisms in an unbiased way.

Outcome 1: Development of a pipeline

caLIBRAte built an R-scripted pipeline to process semi-automatically data from different microarray technologies and organisms. The pipeline includes functional enrichment analysis, performed either with a list of differentially expressed genes (DEGs) or fold change rank ordering statistics (FCROS). The use of the pipeline ensures unified and coherent statistical analysis as well as reliable output. The package will be made available upon publication.
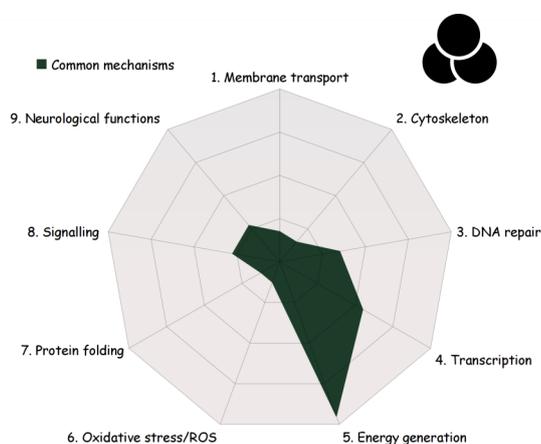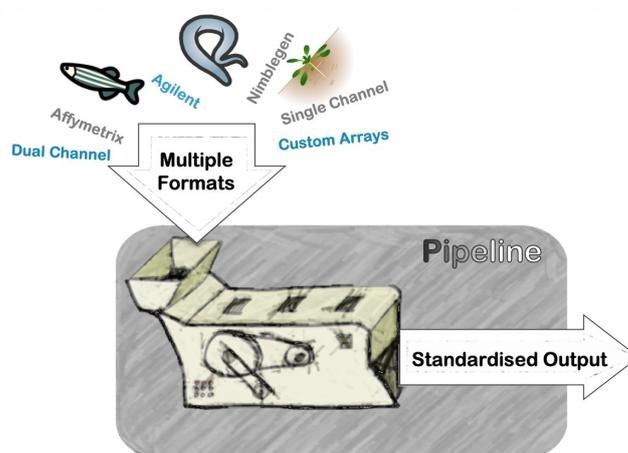
Outcome 2: Common mechanisms of nanotoxicity

The project was able to determine common mechanisms of nanotoxicity, such as disturbed energy balance, across extremely variable datasets which included different organisms (*A.thaliana, C.elegans and D.rerio*). Furthermore, caLIBRAte identified mechanisms beyond commonly described paradigms of nanotoxicity such as DNA methylation, protein folding and interference with neurological function.

Conclusion

caLIBRAte's work demonstrates not only the possibility to identify more rarely described toxicity mechanisms, commonly only detected in specifically focussed studies, but also highlights the importance to use a unified analysis strategy in order to process diverse data formats to obtain transferable conclusions.

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