**The role of modern statistical methodology in toxicological research**

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The statistical analysis of experimental data is crucial part of research in toxicology. This applies to classical low-dimensional data generated by many widely used toxicological assays, but even more so to high-dimensional data such as gene expression or proteomic measurements.

In the first part of this talk, we briefly discuss statistical methods for low-dimensional data analysis. Many suitable approaches are available, but often, not sufficient statistical expertise is available in the toxicology teams. This even concerns the presentation of results with respect to visualization as well as summary measures. For example, instead of confidence intervals, only providing p-values is still common. In studies with different increasing concentrations and a negative control, we discuss testing each concentration against the control versus modelling the dose-response curve with continuous functions. We also contrast the insights with common practice observed in toxicological publications. In the second part of the talk, we give an overview of typical necessary steps in the analysis of high-dimensional data in toxicology. First, preprocessing and normalization steps are of great importance and require statistical expertise. Then, the more complex data structures require tailor-made statistical approaches, including estimation of interaction effects, penalization techniques in high-dimensional regression and classification, and enrichment tests to identify important biological processes and molecular functions that are common to gene or protein lists identified in toxicological experiments. Also for this topic, we will compare common practice in toxicology with the great possibilities offered by modern statistical methodology.