

# The way forward in multi-omics data analyses

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## **The way forward in multi-omics data analyses**

From the methylome to the transcriptome and the proteome in drug-induced cardiotoxicity and hepatotoxicity

1. Fundamental research on drug side effects helps to disclose undesired events on the molecular levels, explore their mechanism, and support drug discovery and development progress.
2. Recent high throughput (omics) technologies are powerful and affordable approaches to unveil drug-induced disturbances.
3. Omics data need new approaches and efficient data analyses to filter the noise and suggest potential candidate biomarkers out of thousands of detected molecules.
4. Different analysis approaches for multiple omics data in this thesis have enriched the omics analysis toolbox and can serve as base analyses for other research.
5. Under drug exposure, DNA methylation can be altered and lead to changes in affiliated genes and protein expression.
6. Long non-coding RNA (lncRNAs) play important roles in cell mechanisms and can elucidate the drug mechanisms of action.
7. Besides particular changes per omics data, the inter-dependencies between biomolecules are essential to understand the drug's toxic mechanisms.
8. Being proficient in different single omics approaches serves as a fundamental foundation to accomplish cross-omics analyses. (this thesis)
9. Predictions based on any approach always require experimental validation.
10. Doing PhD is the pregnancy of an elephant. It is heavy and it is long. (from my friend with her collection of wisdom)

Nhan Nguyen, Maastricht, 22<sup>nd</sup> November 2022