Maastricht University

The way forward in multi-omics data analyses

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Thesis title: The way forward in multi-omics data analyses
Thesis sub-title: From the methylome to the transcriptome and the proteome in drug-induced cardiotoxicity and hepatotoxicity

Summary:

Drug side effects play an important role in not only drug safety but also drug discovery and development. High throughput (omics) technologies are the modern and powerful approaches to discover drugs' toxic mechanisms. This thesis has explored and analyzed 3 different omics data types (MeDIp-seq, RNA-seq, proteomics) derived from human cardiac and hepatic microtissues models exposed to 4 drugs including doxorubicin, epirubicin, idarubicin, and rifampicin. We demonstrated substantial changes in DNA methylation, transcriptome, and proteome, as well as parts of their inter-dependences regarding drug-induced cardiotoxicity and hepatotoxicity. Particularly, this thesis emphasized the aspects of the biological system such as DNA methylation and lncRNAs, which so far, have been rarely investigated in toxicology. All these genomic features can help to understand the drug's toxic mechanism and become biomarkers to diagnose the particular drug side effects. Furthermore, the outcome of this thesis is to not only contribute to drug side effects and the toxicology field but also partially tackle the omics analysis obstacle and enrich the analysis toolbox. The omics analysis approaches in this thesis can be used and improved by other researchers. This will also support the effective usage of omics data and promotes the transparency of omics analysis.