Risks & benefits of the use of computational methods

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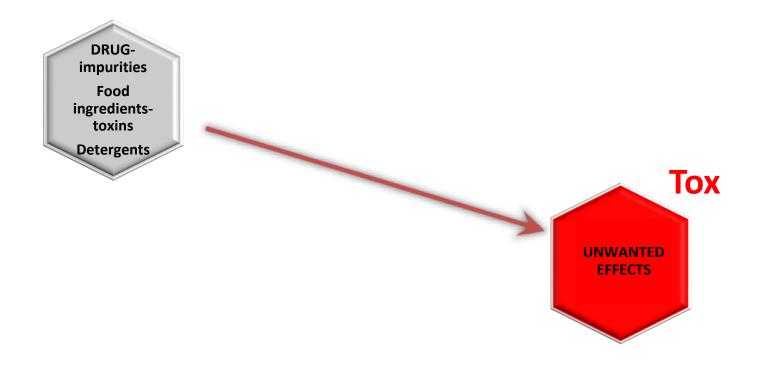






Outline

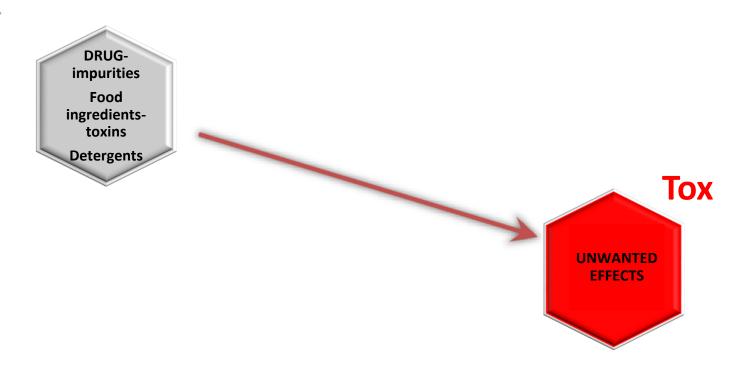
- 1. Approaches for structure-property relationships
- 2. Limits of QSAR (QSPR) methods
- 3. Phenotype descriptors using *-omics* approach
- 4. Examples



Risk-benefit assessment of medicinal products (A. Kouroumalis)

Chemical description 01100011100010101

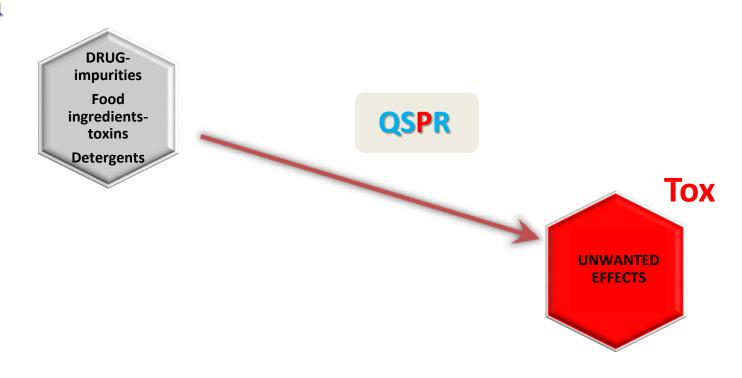
xenobiotics



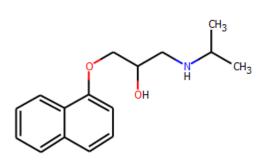
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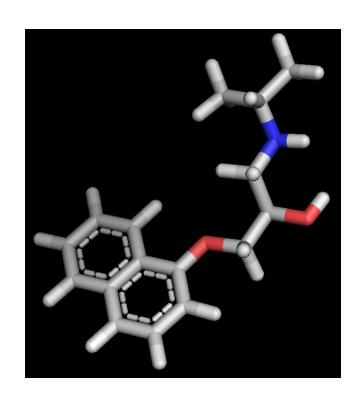


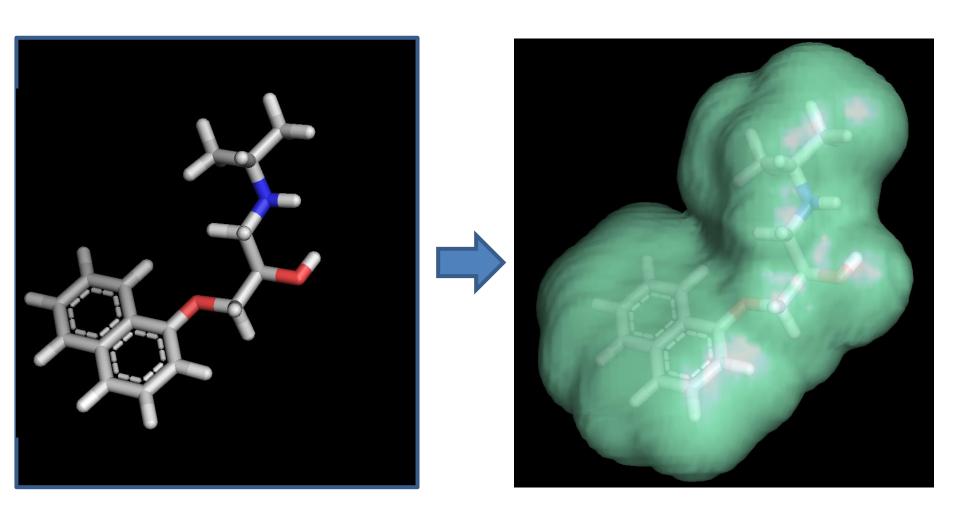
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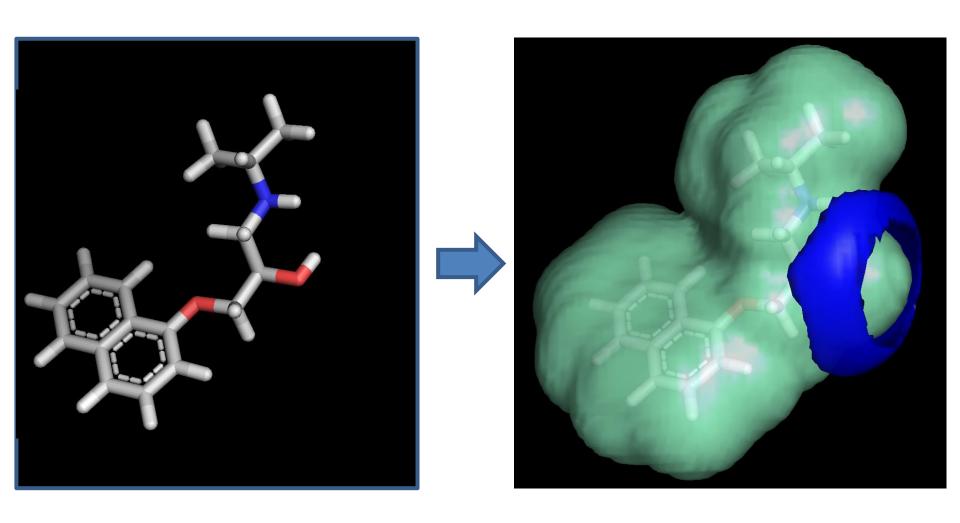


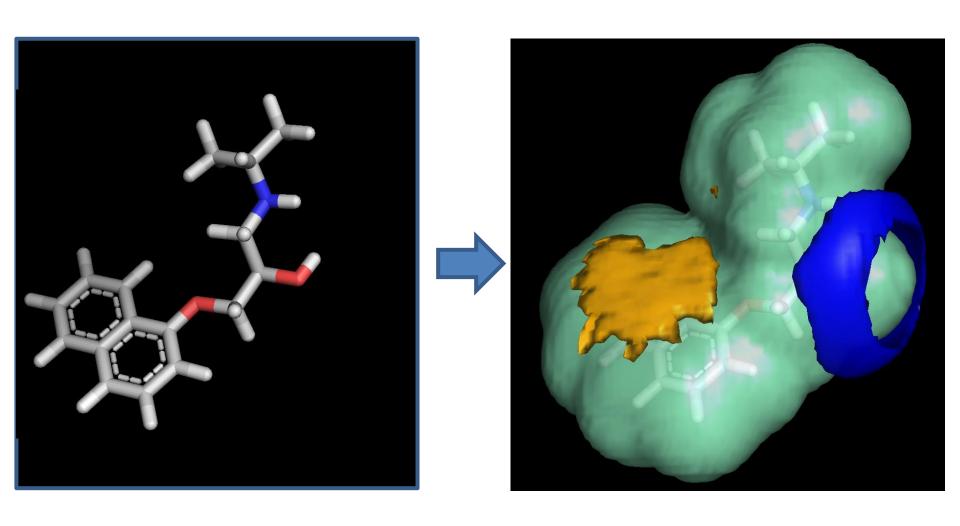
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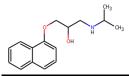


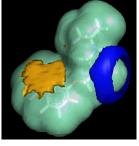




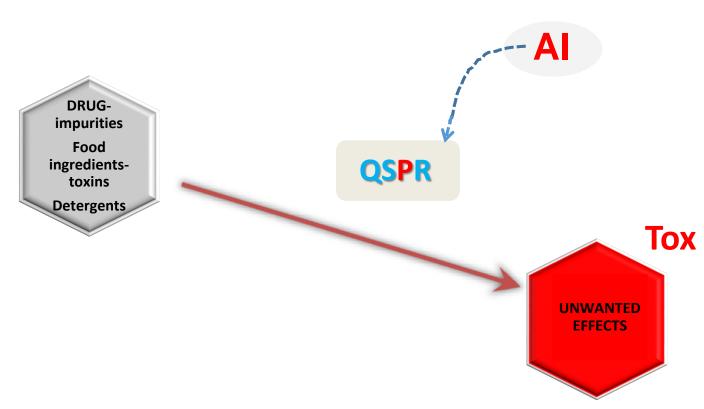


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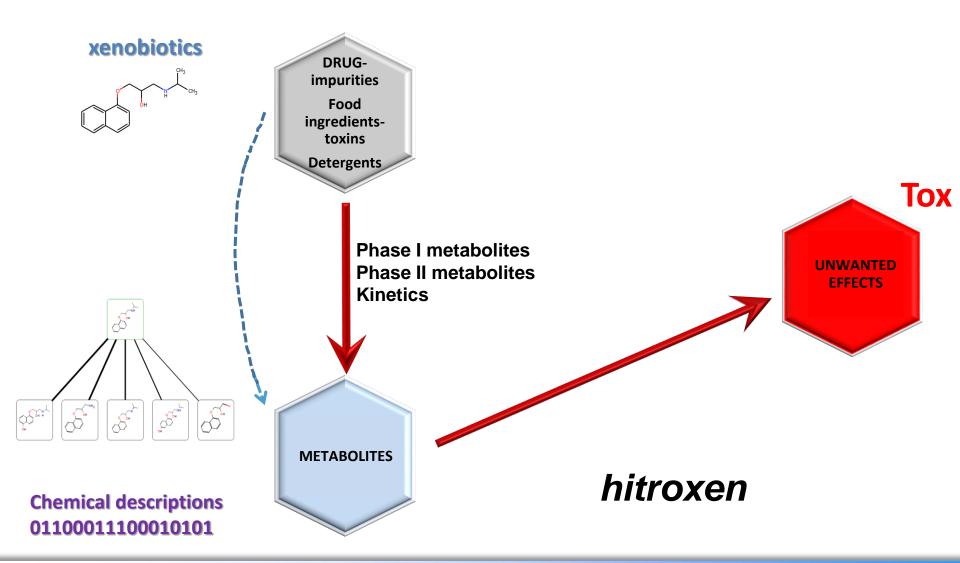




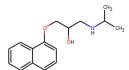
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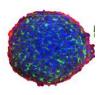
2nd approach: Structure-Property Relationships



xenobiotics



organoids



DRUGimpurities
Food
ingredientstoxins
Detergents



METABOLITES

Phase I metabolites Phase II metabolites Kinetics



METABOLOMICS
LIPIDOMICS

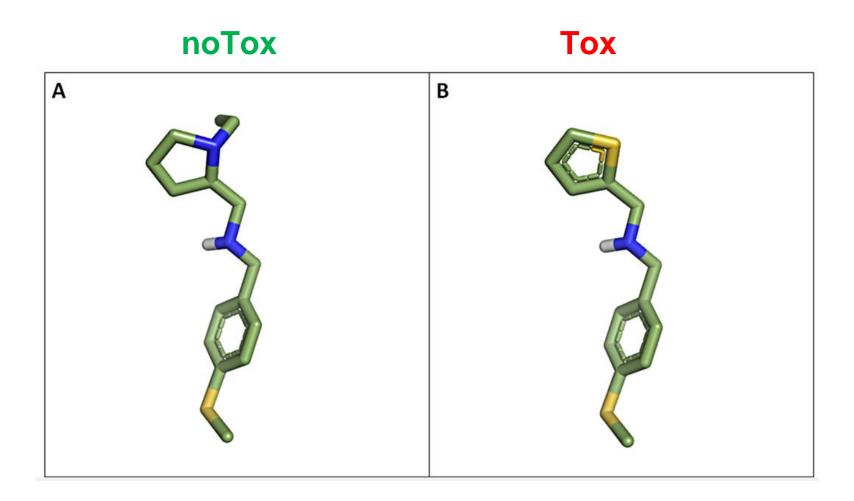


phenotype description 01100011100010101

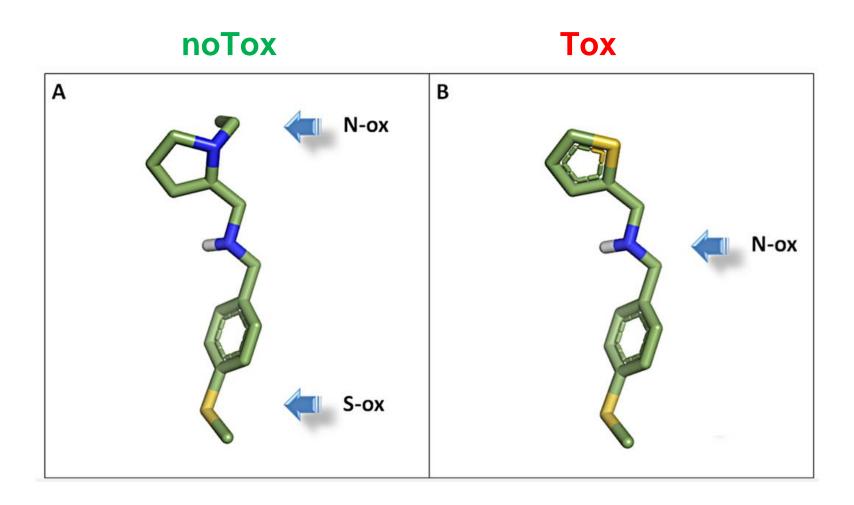


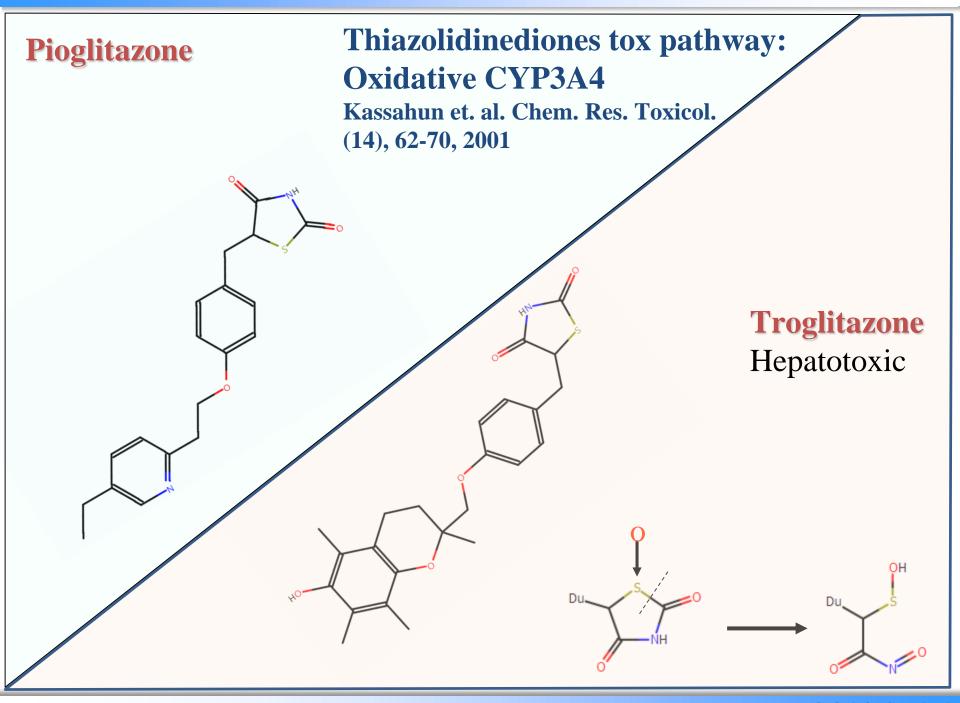
Gabriele Cruciani

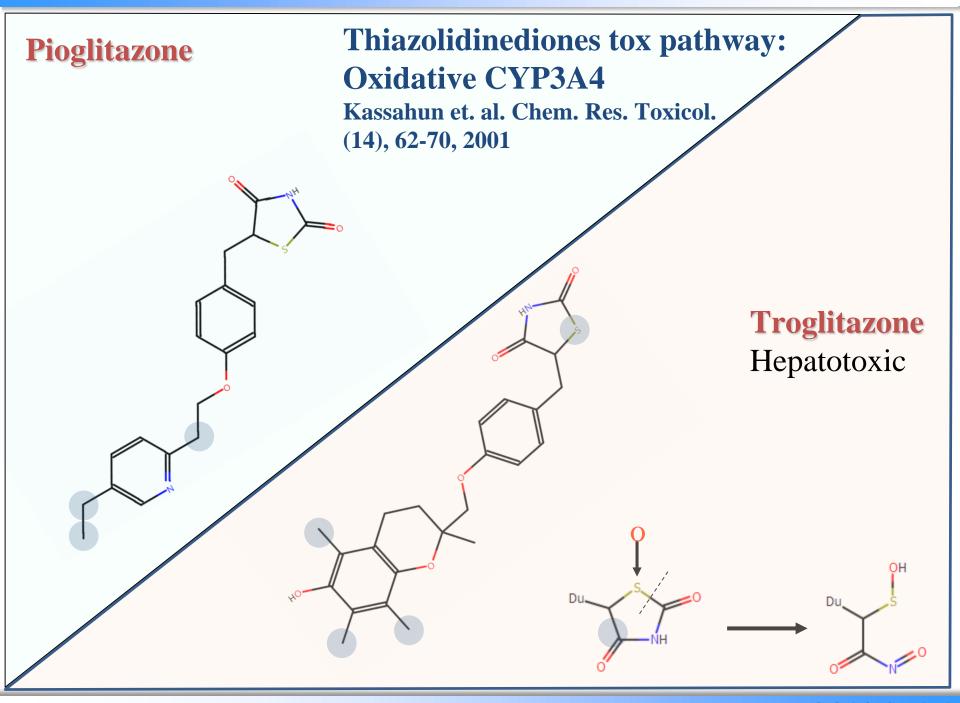
example



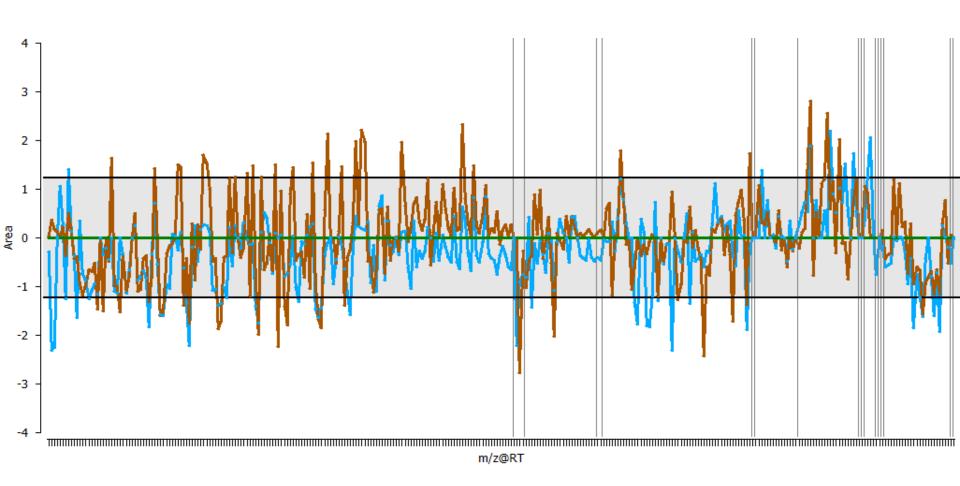
example



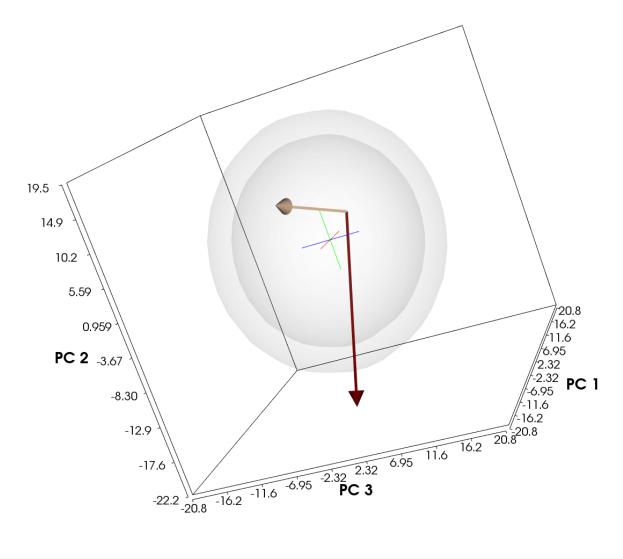








Pioglitazone Troglitazone 12 days human MIT hepatocyte



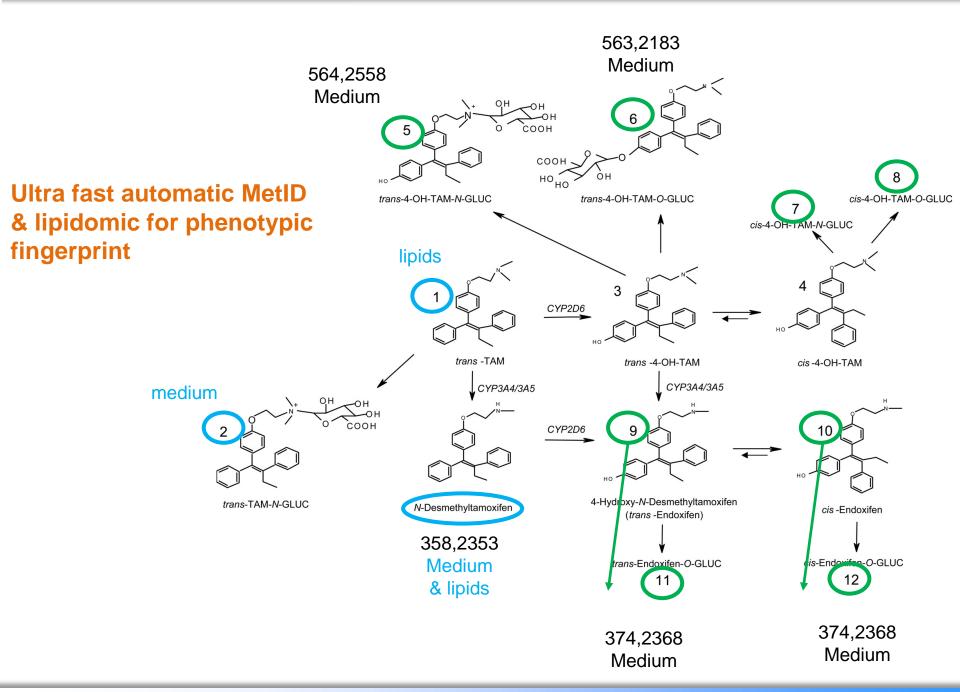
Benefit: prevent breast cancer

Risk: increased risk of uterine cancer, stroke

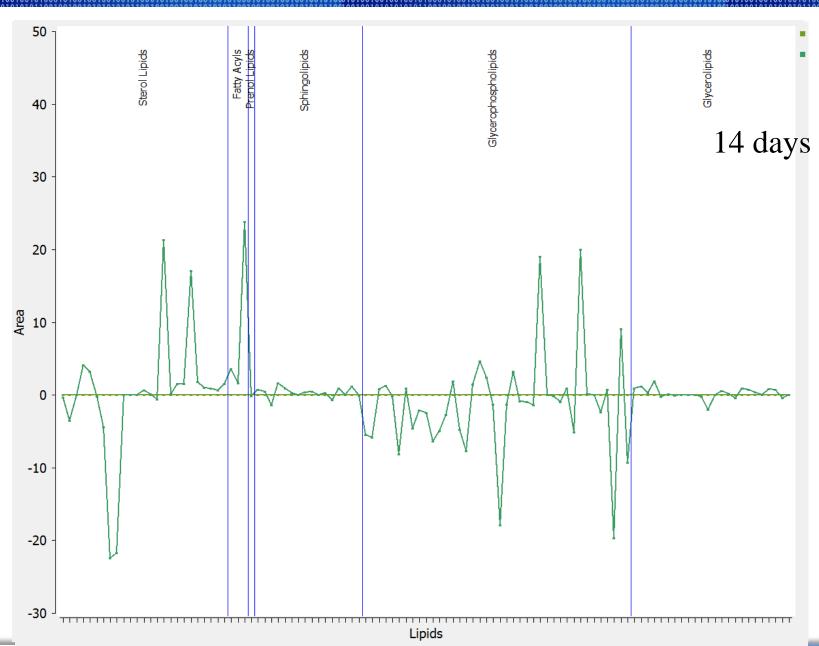
Risk / Benefit ??

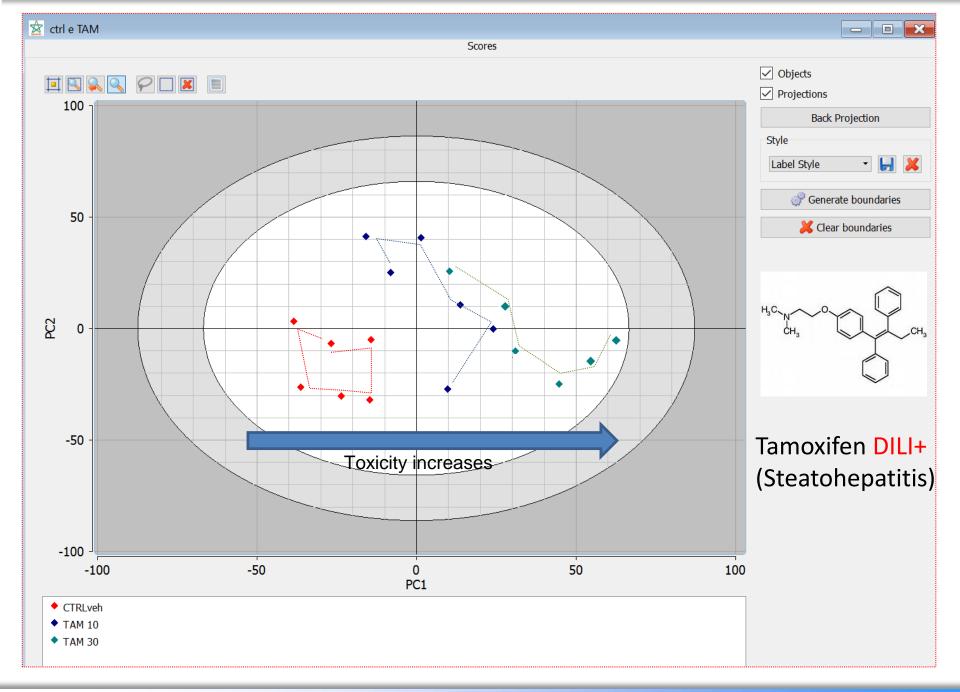
Tamoxifen DILI+ (Steatohepatitis)

Personalised approach



LipoTox Technology Platform





What Can We Do With LipoTox Profile Data?

- Analyze overall toxicity profiles
 - Profile characteristics
 - Unsupervised and supervised approaches to compare profiles
- Focus on individual endpoints
 - Correlate to external data
 - Build an understanding of clinical mechanisms

Applications

- Compound characterization
 - ADME Property profiles
 - Pathways, possible clinical indications
- Mechanism of action
 - Unexpected off-targets (toxicity)
- Support therapeutic hypotheses
 - Compare to competitor molecules, clinical standards of care
 - Identify translational biomarkers

Drug Combinations

- Challenges for studying drug combinations:
 - System may include more drugs
 - Suitably robust to capture combination effects

MALDI (DESI) Metab-Lipid-omics (looking for locations in space)

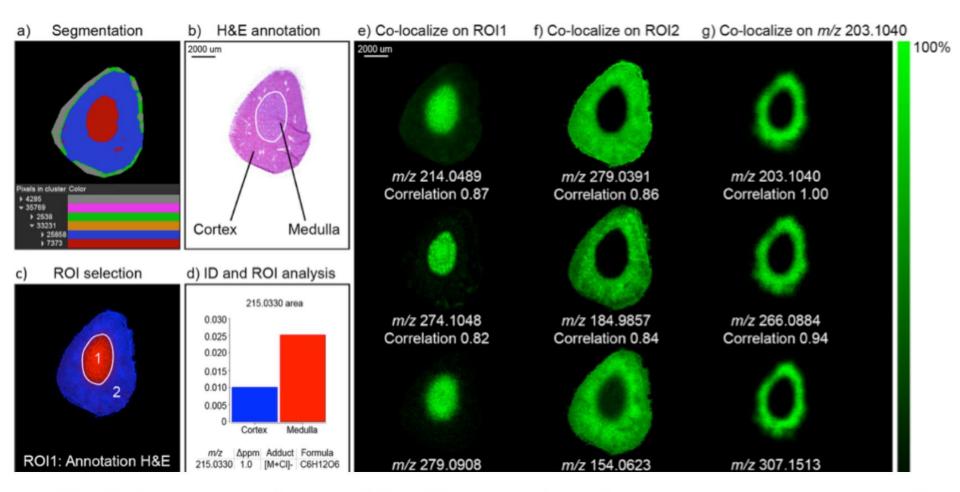


Figure 2. Example data analysis pipeline for metabolite MSI of rat kidney tissue. (a) Bisecting k-means segmentation is performed and enables differentiation of medulla (red) and cortex (blue). (b) Optical image of the analyzed tissue section following MSI acquisition and stained with H&E. The medulla region is annotated with a white circle. (c) Regions-of-interest (ROIs) are defined using both annotated regions from stained tissues (ROI1, red) and from bisecting k-means segmentation shown (ROI2, blue). From the regions a variety of univariate and multivariate analyses can be performed for both inter- and intra-sample comparisons. (d) The peak area for an ion at m/z 215.0330 within ROI1 and ROI2. This ion is automatically identified as the [M+Cl] ion of an analyte with molecular formula $C_6H_{12}O_6$, most likely a sugar. Finally, automatic identification of ion signals that co-localize with ROI's (e, f) and m/z values (g) is performed. The scale bar on the right indicates relative intensity.

Thanks to ...

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