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A winding road of metabolic stability predictions

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The prediction of favourable metabolic, pharmacokinetics and physicochemical profile during the investigation of the new potential drugs is not less important than finding a scheme of activity towards the therapeutically targeted proteins. The numerous *in silico* tools are available for the evaluation of the possible metabolic pathways, indication of the sites the most prone to being metabolised and estimation of probability of interaction with the specific cytochrome P450 subtype(s) [1].

In this study, the set of approaches for direct and indirect examination of compounds metabolic stability were evaluated and compared with our *in-house* machine learning-based predictive models. Two data sources were used in the study – compounds from the ChEMBL database [2] and the series of long chain arylpiperazines with metabolic stability verified in our labs [3]. The obtained results revealed significant differences in the outcome of the tools. The complexity of the metabolic pathways and our still limited knowledge about them, make the predicting of the fate of compounds in the organism indeed challenging task.

References

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