Integration of multi-omics data with artificial intelligence

Summary

Novel bioinformatics approaches have been applied to elucidate the function of circular RNAs in the mechanism of action of several cardiotoxicants through their importance in the post-transcriptional regulation. We further our investigation of this regulation via a formulation to predict the quantity of coding transcripts that are available for translation. The complexity of this task makes necessary the introduction of machine learning strategies, which help us predict and impute proteomics values in untreated samples. Finally, we make use of the artificial intelligence methods to classify genes according to their biological relevance based on expert labeling.