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# Omics-based drug response prediction via machine learning methods

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The amount of publicly available omics and drug data to study anticancer drug response is steadily increasing, and various machine learning methods are emerging to efficiently manage high-dimensional omics data. As each method has its own distinct advantages and disadvantages, we conducted comparative evaluation to determine the most appropriate model for predicting anticancer drug responses. In addition, we investigated which data within the multi-omics dataset offers the most greatest support in predicting drug responses. Furthermore, we evaluated predictive value of utilising drug structure information.