

Machine learning models are difficult to employ in biology-related research. On the one hand, the availability of features increases as we can obtain gene expressions and other omics information. On the other hand, the number of available observations is still low due to the high costs associated with obtaining the data for a single subject. In this work we, therefore, focus on the set of problems where the number of observations is smaller than the number of features. We analyse different combinations of feature selection and classification models and we study which combinations work the best. To assess these model combinations, we introduce two simulation studies and several real-world datasets. We conclude that most classification models benefit from feature pre-selection using feature selection models. Also, we define model-based thresholds for the number of observations above which we observe increased feature selection stability and quality. Finally, we identify a relation between feature selection False Discovery Rate and stability expressed in terms of the Jaccard index.