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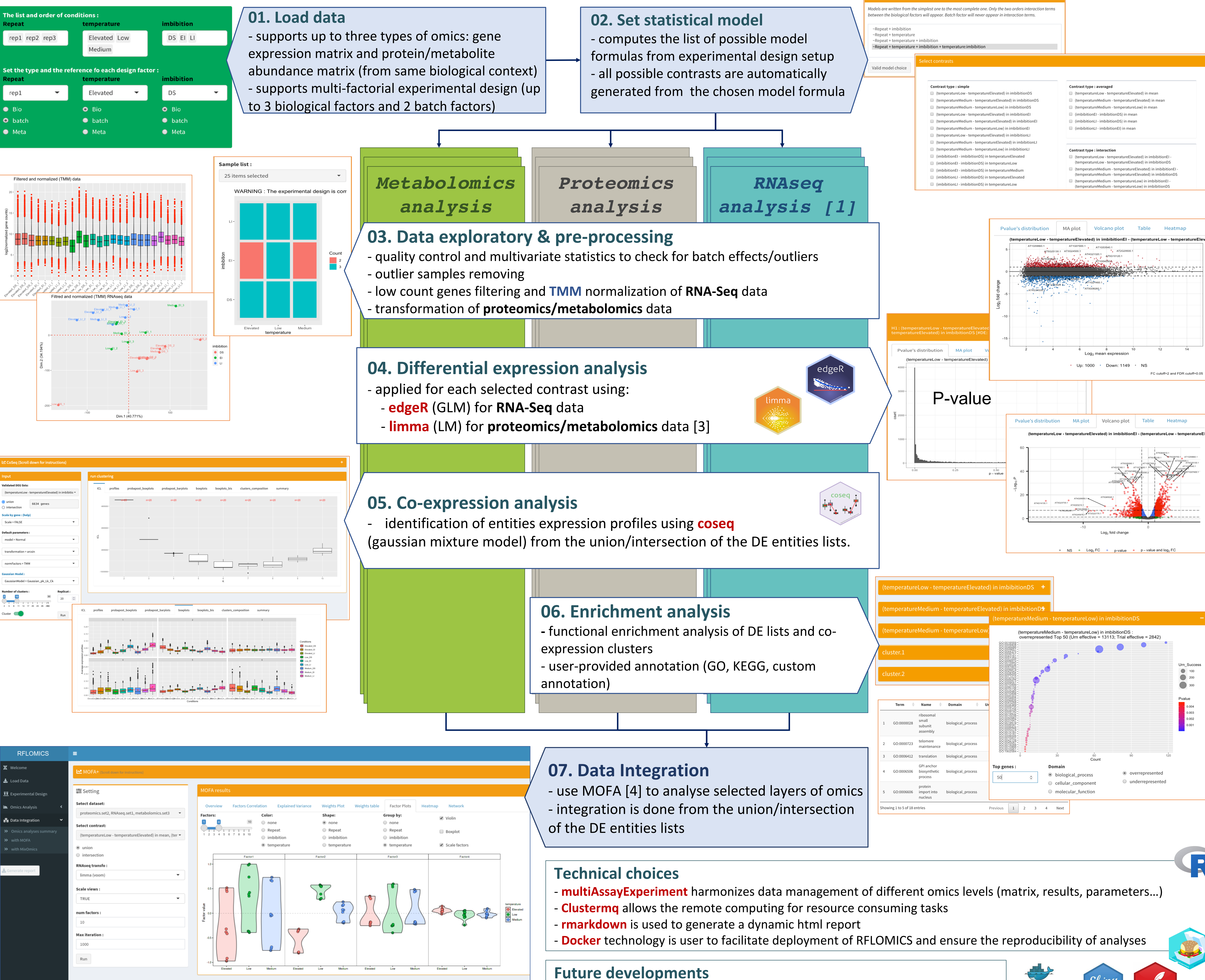
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The acquisition of multi-omics data in the context of complex experimental design is a widely used practice to identify entities and characterise related biological processes. The investigation of each omic layer is a good way to explore and extract relevant biological variability, and restrict statistical integration to only pertinent omics levels and features. The analysis of heterogeneous data remains a technical challenge with the needs of relevant methods and parameters to take into account data specificity. Moreover, applying different statistical methods from several tools could also implies important data management issues. In this context, we developed RFLOMICS, an R package with a shiny interface: it offers a guided, comprehensive and reproducible analysis in a framework which can manage several omics-data. The interface offers an interesting flexibility between the visualization of the results and the data manipulation (filtering, setting).

RFLOMICS is available at : <https://forgemia.inra.fr/flomics/rflomics>



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