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Dig deep and dig greedily: what we awaken in omics data analyses

Abstract:

Omics data analyses are among the most powerful analytic techniques available today. The methods and instruments employed provide the capability to acquire data for a very large amount of molecules in a single analysis, while also spanning a broad dynamic range. Of course, this impressive performance is a two-edged blade: omics approaches open up enormous possibilities while creating highly complex issues. Typical problems are the incomplete interpretation of the large amount of data acquired, difficulties in reproducibility especially at the lower end of the dynamic range, and the unavoidable presence of false signals and/or false interpretations. As a result, the downstream integration of results derived from omics datasets is particularly tricky. Not only do these results cover different phases in the flow of biological information (DNA-RNA-protein-metabolites), there are also domain-specific issues with the results that act synergistically (in the bad sense here) to confound efforts to harmonize the findings. Here, a few interesting analyses on omics data are presented, illustrating the promises of omics and across-omics analyses, but also highlighting the issues encountered when attempting to fulfil these promises. The focus will be on metabolomics, proteomics and the combination of genomics and proteomics data.