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Data reprocessing in omics-driven approaches in plasma medicine[1]

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Omics-approaches like metabolomics, proteomics, and lipidomics generate massive data sets. In plasma medicine, researcher seeks to unveil the impact of the treatment on cells or tissues. It is assumed that reactive species lead to signal processes that ultimately yield to physiological consequences. Two strategies are applied in our lab: the analyzing the direct impact of plasma-generated species on biomolecules (proteins, lipids, amino acids) and the analysis of expression changes in complex targets (skin, cancer models). The subsequent data analysis is the bottleneck, needing improvement. Especially in lipidomics, bottom-up approaches are hard to analyze. We tackle this situation by a number of bioinformatics workflows, engineering new analysis tools to identify phospholipid oxidation products from positive mode Orbitrap data. Additionally, the benefit of public data repositories to disseminate data and the comparison between CAP derived changes in the lipidome/proteome with other physical or chemical entities, e.g. radiation or pulsed electric fields is tested.

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