From numbers to decisions - data processing in omics-driven approaches

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In Life Science and Medicine, researchers strive to understand the mechanisms of life and disease. The human body contains 3.7×10^{13} cells, each equipped with about 20,000 genes, encoding an estimated 1,000,000 protein variants making the disentangling of cause and effect arbitrarily difficult [1].

To tackle this situation various omics-approaches like genomics, transcriptomics, proteomics, lipidomics using molecular biology and chemical analytics on the molecular level are used and generate massive data sets. In plasma medicine, the subject of clinical application of cold physical plasmas (CAP) and the related fundamental research, researcher seeks to unveil the impact of the treatment on signaling processes in cells or tissues. As of now, reactive species delivered by the discharge are the main suspects [2]. In an effort to understand their individual impact and quantities deposited, terabytes of mass spectrometry data from cellular proteins, isolated peptides or proteins, and small molecule tracers have been acquired. The latter acting as modifiable beacons were investigated for covalent changes inflicted by CAP treatment [3]. The task remaining is data analysis to condense the information content alleviating a valid conclusion. This comprises bioinformatics workflows: raw data conversion, data curation (normalization etc.) and annotation, and multivariate analysis using statistical approaches such as cluster analysis or principal component analysis. Ultimately, analysis of the biological network follows.

In a second line of approach, public repositories that allow a data re-evaluation disconnected from the original contributor may provide a chance to a) disseminate data, and b) allow the comparison between CAP derived changes in the proteome with other physical or chemical entities, e.g. radiation or pulsed electric fields.

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