View metadata, citation and similar papers at core.ac.uk

brought to you by CORE

provided by Repositorio Institucional de la Universidad de Córdoba

*PL10*

# QUALITY CONTROL OF PROTEOMICS DATA: PERFORMING LOCAL AS WELL AS GLOBAL ANALICES

***L. Martens*** *(1)*

(1) Department of Medical Protein Research, VIB, Gent, Belgium

The field of mass spectrometry based proteomics has been developing at a rapid pace into a high-throughput field for proteome identification and quantification. With a strong focus on method development, and increasingly powerful instruments allowing leaps in performance, the main focus of the field has so far been on future developments. Yet with quantification now fast becoming routine, and the application of proteomics to biological and clinical samples becoming more mainstream, there is now also a growing need to work towards a consolidation of the field as a true analytical discipline. Perhaps the first and most important step towards the establishment of proteomics mass spectrometry as a (clinical) analytical discipline is the pervasive usage of quality control. Such quality control applies to both the wet-lab work, as well as the data processing, and will need to be simple, automated and informative. Here, several analyses of proteomics data are provided that can be used to ascertain several aspects of data quality easily. The methods shown are tailored for use in one of three settings: within-lab, evaluating publicly available data, and meta-analysis of large-scale data. The first setting, within a lab, yields methods that provide direct feedback on the quality of the acquired data as well as its processing. The second setting is relevant to researchers that wish to re-use publicly available data, and allows the detection of outlying datasets when compared to a large body of heterogeneous data. Finally, because there are increasing amounts of publicly available data, quality control can also be applied at the level of large-scale data obtained across many high-throughput experiments, providing valuable feedback on the strengths, weaknesses and nuances of the methods and technologies used in mass spectrometry driven proteomics.