

Proteome Profiling: Finding the Proverbial Needle in the Biological Haystack Expression Studies

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Abstract:

Gel-free protein profiling procedures coupling capillary-scale high-performance liquid chromatography to data-dependent tandem MS (LC-MS) present an exciting new paradigm for proteomic screening. In particular, multi-dimensional protein identification technology and isotope-coded affinity reagents now allow for the 'shotgun' sequencing of hundreds of proteins in a single experiment, albeit with a significant expenditure of time and effort. The impact of these methods has been somewhat limited to date, however, in part due to problems associated with the reproducibility of LC-MS, as well as to difficulties in extracting clinically relevant information from the limited number of samples that can practicably analyzed using these specialized methods.

In this talk, I will report on my group's efforts to develop statistical data-mining procedures and software programs with the aim of improving the reliability and utility of protein profiles generated using basic LC-MS procedures and standard instrumentation. I will demonstrate that this informatics toolkit can markedly facilitate the systematic global proteomic comparison and categorization of tissue samples, potentially speeding discovery of biologically and clinically relevant proteomic patterns and biomarkers.