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Foreword

Coupled-column systems in the biosciences

Analytical procedures which involve more than one separation step are being developed and used in many areas of application for already many years: the efficient analysis of complex samples requires the combination of different separation principles. Multidimensional systems are especially useful when quantification of analytes has to be performed at the trace level. For biological samples, such systems have demonstrated their practicality in terms of, e.g., speed and reliability since the 1980s. In most instances, a single fraction—the one which contains the analytes of (most) interest—is transported, preferably on-line, from the first- to the second-dimension column. This approach enables the design of fully automated systems that provide a high selectivity.

In the past decade, increasing attention has been devoted to the development of so-called comprehensive separation procedures, where each subsequent fraction eluting from the first column is subjected to the second separation or, in other words, where LC–LC and GC–GC are converted into the more powerful LC × LC and GC × GC combinations, respectively. The comprehensive set-ups are more demanding because the second separation should be relatively fast to enable on-line, real-time analysis. Even if this is not possible, and some parallel second-dimension columns or storage loops are introduced to solve the problem, a rapid second separation is of primary interest. For the rest, best results are of course obtained when the two separation modes are orthogonal and complementarity is, consequently, ensured. Today, comprehensive systems are in vogue in fields as divergent as the profiling of peptides in proteomics research and the identification of flavours and fragrances in food analysis.

Summarizing the above, powerful multidimensional systems for both target analysis and profiling and pattern-recognition studies are available to solve the various types of complex questions, which, at present, dominate the discussion in the biosciences. One illustrative example is that there is a general and widespread interest to participate in plenary sessions and panel discussions, such as are continually organized during, e.g., the HTC, Capillary Chromatography, HPLC and HPCE symposia. Many of us no doubt were and/or are active contributors to stimulating discussions on the potential and limitations of various ways of interfacing, the merits of a comprehensive over a heart-cut approach and, certainly, also about the most efficient way to handle the dramatically increasing amount of data generated by these modern analytical systems—specifically if hyphenation to a variety of mass spectrometers is taken into account.

This Special Issue comprises several interesting reviews and research papers on coupled-column systems and related topics in the biosciences. Developments in the field of instrumentation and automation are discussed and due attention is given to real-life applications. In the field of on-line clean-up and trace enrichment, it is shown that, also during sample pre-treatment, selectivity often is a key aspect. Moreover, next to LC- and/or GC-based coupled systems, the role of electro-driven separations is highlighted. In addition, the overriding importance of mass spectrometry is demonstrated. Much attention is devoted to quantitative bioanalysis and to modern disciplines, such as proteomics and metabolomics. We hope that the information contained in this Special Issue will convince our readers of the important and multi-faceted role of the separation sciences in solving the challenging problems encountered today in the life sciences.

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