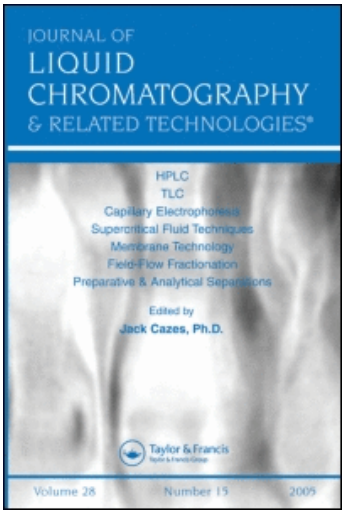

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The Book Corner

INTRODUCTION TO ENVIRONMENTAL ANALYSIS, R. N. Reeve, John Wiley & Sons, Ltd., West Sussex, England, 2002, 301 pp.

Introduction to Environmental Analysis is volume number three in the Analytical Techniques in the Sciences series, D. J. Ando, series editor. The other two published volumes in this series are Analytical Instrumentation: Performance Characteristics, and Quality and Fundamentals of Electroanalytical Chemistry. Interest in the environment continues to expand and develop. It is now very much a part of our everyday lives. As a consequence, the need for chemical analysis of the environment continues to grow.

This book is a revision and expansion of the ACOL text "Environmental analysis" which was first published in 1994. It is an introduction into how chemical analytical techniques are applied to the environment. Global awareness of the importance of monitoring and protecting our environment has grown considerably over the last ten years. Environmental concerns are now an integral part of today's legislation, product design and development, waste minimization and disposal. As well as background monitoring of the environment, scientists are involved in monitoring liquid and gaseous discharges and surveying contaminated land and landfill sites—very topical issues due to concern over waste duping and potential problems with reuse of old industrial sites.

Introduction to Environmental Analysis introduces the reader to the methodology required to monitor our environment and to safeguard it. The present book is made up of eight chapters which are well presented and clearly written. The techniques discussed develop in complexity, starting with simple volumetric measurements for water quality and finishing with ultra-trace analysis. Chapter 1 introduces the reader to simple concepts needed in the study of the environment, to what we mean by the term "pollution" and

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the role of analytical chemistry. Chapter 2 starts by discussing pollution dispersion, reconcentration and final degradation—important concepts to understand when setting up a monitoring scheme. This chapter then goes on to describe simple concepts about sampling and the subsequent analysis, the choice of laboratory or field analysis, and also introduces quality assurance and quality control. The remaining six chapters, in turn, cover the analysis of water, solid, and atmospheric samples. Where there is a choice of techniques available, the questions (SAQs and Dqs) guide the reader into understanding why one specific technique is often preferable. One of the main themes of this book is to demonstrate how an understanding of the principles of the analytical techniques is vital for good analytical choice. Chapters 3 and 4 are devoted to water, while Chapter 5 is concerned with solids and the techniques used to extract pollutants for subsequent analysis. This is an area of great current interest due to concern over waste dumping and potential problems with the reuse of old industrial sites. Chapters 6 and 7 are concerned with sampling and analysis of gases and particulates in external atmospheres, buildings and flues (chimneys or exhausts). Many of the techniques may already be familiar to laboratory personnel, although they will often find in the instruments very novel applications. Chapter 8 is concerned with the special problems of ultra-trace analysis.

A book of this length can only be seen as an introduction to environmental analysis. A bibliography is provided to guide the reader into more specialized texts in the area and to where one can find the various standard methods. It also gives examples of current usage of the techniques.

This book is recommended for environmentalists and analytical chemists.

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ON-LINE LC–NMR AND RELATED TECHNIQUES, K. Albert, Ed., John Wiley & Sons, Ltd., West Sussex, England, 2002, 290 pp. $105.00

This book deals with a topic (NMR) that has grown in the last twenty years from 200 MHZ to 900 MHZ instruments that are used in the chemical; for analysis, and biomedical; metabonomics, and medical; diagnosis. On the other hand, HPLC is an essential separation technique that is available in almost every analytical laboratory. The marriage of both techniques is a successful combination. In the preface of the book Dr. Albert writes and I agree with him.

It has been more than 20 years since the very first HPLC–NMR experiments were conducted, employing iron magnets for the registration of ^{1}H NMR spectra. Since then, an enormous increase in sensitivity has been accomplished by the combined use of cryomagnets, new NMR coil designs and materials, together with effective pulse sequences for solvent suppression. In the last 1970s, only model separations with mg amounts could be performed, but nowadays LC–NMR is an established analytical technique in biomedical, pharmaceutical, environmental, drug metabolism and natural product analysis. The newest development of capillary NMR shows detection limits beyond 10 ng.

Whereas LC–NMR was considered to be an exotic technique in the late 1970s, today over 200 LC–NMR systems are installed world-wide. The success of LC-NMR is due to the enthusiastic work of people in both industry and academia, who have combined their skills and efforts to continuously improve the reliability of this coupled technique. Some of the early pioneers of LC–NMR are coauthors of this book and thus ensure a guarantee for competent contributions.

The aim of this text is to introduce the fascinating topic of the hyphenation of chromatographic separation techniques with nuclear magnetic resonance spectroscopy to an interested readership with a background either in organic pharmaceutical or medical chemistry. The book does not discuss basic principles of NMR spectroscopy, or of separation science, and should previously be known to the reader.

This book gives a comprehensive overview of the basis and the current applications of LC–NMR and related techniques. It deals with the practical aspects of the hardware and software set-up for a successful performance of on-line coupling experiments. It covers the solution of real-world problems from the fields of biomedical, pharmaceutical, and environmental studies as well as the analysis of natural products and polymeric compounds. Thus guidelines for an efficient application of the powerful hyphenated technique LC–NMR in combination with LC–MS are presented. Besides LC–NMR, important techniques such as the on-line coupling of gel permeation chroma-

tography and supercritical fluid chromatography, together with ^{1}H NMR spectroscopy, are described in detail.

The specific constraints and requirements of continuous-flow NMR is explained in the first chapter, whereas specific applications, such as biomedical and natural product analysis, LC–NMR–MS and LC–NMR in an industrial environment, together with polymer analysis, is discussed separately. Thus, the reader will obtain a broad overview of the application power of LC–NMR and the benefits of its use. The reader is also introduced to the pitfalls of this technique. Special attention is given to the exciting newer coupled techniques such as SFC–NMR and capillary HPLC–NMR. However, new emerging future developments are also discussed thoroughly.

This book is clearly written and illustrated. It is highly recommended.

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SINGLE MOLECULE DETECTION IN SOLUTION, **Methods and Applications**, Ch. Zander, J. Enderlein, and R. A. Keller, Eds., Wiley-VCH, Berlin, 2002, 371 pp.

The detection of single molecules opens up new horizons in analytical chemistry, biology, and medicine. This discipline, which belongs to the expanding field of nanoscience, has been rapidly emerging over the last ten years. The first, indirect detection of a single molecule in solution was performed by Rotman when detecting the multiple reaction products of a single enzymatic molecule and was reported in the Proc. Natl. Acad. Sci, USA in 1961. This was followed in 1976 by the direct optical detection of a single although multiply labeled molecule by Hirschfield (Appl. Optics 1976, 15, 2965–2966 and same volume pages 3135–3138).

The field of single molecule detection is not a trivial matter. However, since the pioneering work of Rotman and Hirschfield many studies have been published. The present book discusses in a clear manner and easy to follow format the advances and basics of single molecule detection.

In chapter 8 of the book Sauer and Zander state that an important feature of single molecule detection is that it can provide information about distributions and subpopulations, i.e., phenomena that are hidden in ensemble measurements. In other words, experiments at the single molecule level allow one to observe whether a spectroscopic or biological property, like non-exponential fluorescence kinetics or turnover rates, arise from large variations between different individuals or whether each individual exhibits the same behavior. In combination with fluorescence resonance energy transfer (FRET), an extreme detection sensitivity is feasible that allows the study of biological processes on-line at the molecular level.

Besides more fundamental oriented studies, single molecule detection and identification in solution can also serve to develop new powerful tools for diagnosis with increased sensitivity. This may lead to benefits in diagnosis of viral or bacterial infection, or early-stage observation of tumor development.

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In chapter 2 the general and optimized conditions for successful detection of single molecules is discussed. Obviously, it is essential for single molecule detection in solution that the probability of finding a molecule in the applied detection volume is significantly smaller than unity. This can be achieved by sufficiently diluting the sample of interest or by restricting the detection to a sufficiently small detection volume. Furthermore, an observable has to be chosen which allows one to differentiate between the molecule of interest and its environment. Fluorescence has proven to be an appropriate observable to detect individual molecules because many organic dyes have a relatively large absorption cross section and a high fluorescence quantum yield, whereas most solvents do not show fluorescence in the visible range. In nearly all reported single-molecule experiments (except experiments using surface enhanced Raman scattering), compounds with a conjugated π-electron system (i.e. an organic dye) have been used. Usually, detection of these molecules has been performed by sensitive detection of their laser-induced fluorescence.

Different aspects of single molecule detection are discussed in this timely book. This book discusses the basics of Single Molecule Detection and provides the latest applications and topical research results. The result is a modern, timely handbook for advanced researchers, specialists and company professionals in physics, biotechnology, chemistry, and medicine.

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PROTEOMICS IN PRACTICE, A Laboratory Manual of Proteome Analysis, R. Westermeier and T. Naven, Wiley-VCH, Weinheim, 2002, 316 pp.

In the Forword of the book Dr. Hanash of the University of Michigan, Ann Arbor, states:

Proteomics is in an extraordinary growth phase. This is due to a great extent to the fact that the major undertaking of sequencing the human and other important genomes has largely been accomplished, which has opened the door for proteomics by providing a sequence-based framework for mining the human proteome and that of other organisms. It is evident that proteomics has attracted a substantial following, with an influx of investigators and of biotechnology and pharmaceutical companies that are taking an active interest in the field, as well as an influx of a new generation of scientists in training. There is undeniably a pressing need for training in proteomics and much need for textbooks that facilitate the use of related methodology. This book makes a valuable contribution by providing a clear presentation of some of the most widely utilized methods in this field.

The field of proteomics can be divided in practice into three major areas: expression proteomics, functional proteomics, and proteome related bioinformatics. This book focuses primarily on methodology utilized for expression proteomics, an important component of proteomics which deals with global quantitative analysis and identification of proteins encoded in genomes and expressed to a varied extent in different tissues and cell populations. Expression proteomics relies on a mix of, on the one hand, high-tech approaches and on the other, a harvest of know-how in protein chemistry and biochemistry gained over the past half-century.

The objective of Proteomics in Practice, according to the authors, is to provide the reader with a comprehensive reference and manual guide for the successful analysis of proteins by 2-D electrophoresis and mass spectrometry. The idea for the book has come from the continuing success and favourable responses received from the scientific public for our on-going proteomics seminar and practical courses we have delivered in the past twelve months.

The book will include a theoretical introduction, comprehensive practical section complete with worked examples, a unique troubleshooting section designed to answer many of the frequently asked questions regarding proteome analysis and a thorough reference list to guide the interested reader to further detail.

The theoretical section will introduce the fundamentals behind the techniques currently being used in proteomics today and describe how the techniques are used for proteome analysis.

However, the practical aspects of the book will not address many of these methods, but will instead focus on the main stream methodology of 2-D electrophoresis and mass spectrometry. 2-D electrophoresis is still the most successful method of resolving a proteome with increasing reproducibility and automation. All aspects for the successful performance of 2-D electrophoresis and image analysis will be addressed in practical detail. Subsequently, the importance of mass spectrometry, sequence databases and search engines for successful protein identification will be discussed.

Dr. Hanash and the authors realize and understand the limitation of 2D-PAGE, and the advantages of liquid phase separations in the detection and identification of proteins and peptides. Another area of proteomics that is emerging is "diagnostic proteomics" an important area for the diagnosis of disease such as cancer.

I am glad to see, and it is commendable, that the authors understand and wholly appreciate that the analysis of post-translational modifications such as phosphorylation and glycosylation is an integral aspect of proteomics. As such the theoretical, technical, and practical issues involved will be addressed in great detail in a subsequent edition. Approaches for functional proteomics are still varying and many procedures are under development. These methods will be added in a laster edition.

As the technical developments in this field are proceeding so fast, the contents of the book need to be updated every few months. The reader can have access to a web-site at Wiley-VCH: http://www3/interscience.wiley.com/XXXXXX, which will contain the updated chapters and recipes.

The book is a result of a course that has been taught by the two authors and is mainly devoted to 2-D gel electrophoresis.

Proteomics in Practice is a combined review, manual and reference for the successful analysis of proteins using the classical approach of 2-D gel electrophoresis, mass spectrometry and related sequence database inquiries. The first section, written in a textbook style, introduces the entire technology, while the second section represents a comprehensive laboratory manual spanning the full range of methods from sample preparation to protein identification. Alternative methods and procedures are only suggested for those cases where the "default" procedure would fail to deliver adequate

results. The third section is a unique troubleshooting guide, designed to answer many of the frequently asked questions regarding proteome analysis. The final section contains a thorough reference list to guide interested readers towards further detail.

Intended for all those wishing to go beyond the theoretical aspects of proteome analysis, this book is targeted at research groups within academia and industry, course instructors, research assistants and graduate students.

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