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This book discusses in detail molecular, mycobiont culture, biomonitoring and bioprospection of lichens, providing insights into advances in different fields of lichenology by applying modern techniques and approaches and examining how their application has enhanced or changed classical approaches. It offers a valuable resource, especially for beginners, students and researchers from different academic backgrounds interested in the study of lichens. In recent years, the introduction of modern analytical techniques and approaches has significantly improved our understanding of the environment, including lichens. Lichens are unique organisms which possess untapped potential as effective and reliable bioindicators, sources of therapeutic phytochemicals, and as excellent extremophiles. The unique and peculiar characteristics of lichens underline the need for a multidimensional approach to explore their potential in various fields of environment science, botany and chemistry. Modern techniques, especially molecular techniques, have greatly enriched the field of lichen taxonomy and its position in the plant kingdom, revealing little-known species and exploring their evolutionary history, while multivariate analysis and GIS approaches have established lichens as an ideal and reliable tool for monitoring air pollution. Advanced culture techniques have expanded the pharmacological applications of lichens, which was formerly restricted due to their small biomass. The advent of sophisticated analytical instrumentation has now facilitated the isolation and characterization of lichens' bioactive constituents, even in lower concentrations, as well as the estimation of their stress responses at different levels of pollution. As lichen diversity is adversely affected by increasing air pollution, there is a pressing need to develop effective management practices to conserve, restore and document lichen diversity.

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Crick and Watson's discovery of the structure of DNA fifty years ago marked one of the great turning points in the history of science. Biology, immunology, medicine and genetics have all been radically transformed in the succeeding half-century, and the double helix has become an icon of our times. This fascinating exploration of a scientific phenomenon provides a lucid and engaging account of the background and context for the discovery, its significance and afterlife, while a series of essays by leading scientists, historians and commentators offers uniquely individual perspectives on DNA and its impact on modern science and society.

Recent advances in genomic studies have stimulated synergetic research and development in many cross-disciplinary areas. Processing the vast genomic data, especially the recent large-scale microarray gene expression data, to reveal the complex biological functionality, represents enormous challenges to signal processing and statistics. This perspective naturally leads to a new field, genomic signal processing (GSP), which studies the processing of genomic signals by integrating the theory of signal processing and statistics. Written by an international, interdisciplinary team of authors, this invaluable edited volume is accessible to students just entering this emergent field, and to researchers, both in academia and in industry, in the fields of molecular biology, engineering, statistics, and signal processing. The book provides tutorial-level overviews and addresses the specific needs of genomic signal processing students and researchers as a reference book. The book aims to address current genomic challenges by exploiting potential synergies between genomics, signal processing, and statistics, with special emphasis on signal processing and statistical tools for structural and functional understanding of genomic data. The first part of this book provides a brief history of genomic research and a background introduction from both biological and signal-processing/statistical perspectives, so that readers can easily follow the material presented in the rest of the book. In what follows, overviews of state-of-the-art techniques are provided. We start with a chapter on sequence analysis, and follow with chapters on feature selection, classification, and clustering of microarray data. We then discuss the modeling, analysis, and simulation of biological regulatory networks, especially gene regulatory networks based on Boolean and Bayesian approaches. Visualization and compression of gene data, and supercomputer implementation of genomic signal processing systems are also treated. Finally, we discuss systems biology and medical applications of genomic research as well as the future trends in genomic signal processing and statistics research.

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This book covers the past, present and future of the intra-cellular trafficking field, which has made a quantum leap in the last few decades. It details how the field has developed and evolved as well as examines future directions.

4.1.1 Demographic significance Confined populations grow more rapidly than populations from which dispersal is permitted (Lidicker, 1975; Krebs, 1979; Tamarin et al., 1984), and demography in island populations where dispersal is restricted differs greatly from nearby mainland populations (Lidicker, 1973; Tamarin, 1977, 1978; Gliwicz, 1980), clearly demonstrating the demographic significance of dispersal. The prevalence of dispersal in rapidly expanding populations is held to be the best evidence for presaturation dispersal. Because dispersal reduces the growth rate of source populations, it is generally believed that emigration is not balanced by immigration, and that mortality of emigrants occurs as a result of movement into a 'sink' of unfavourable habitat. If such dispersal is age- or sex-biased, the demography of the population is markedly affected, as a consequence of differences in mortality in the dispersive sex or age class. Habitat heterogeneity consequently underlies this interpretation of dispersal and its demographic consequences, although the spatial variability of environments is rarely assessed in dispersal studies.

The Carabidae form one of the largest and best studied families of insects, occurring in nearly every terrestrial habitat. The contributions included in this book cover a broad spectrum of recent research into this beetle family, with an emphasis on various aspects of ecology and evolution. They deal both with individual carabid species, for example in studies on population and reproductive biology or life history in general, and with ground beetle communities, as exemplified in papers treating assemblages in natural habitats, on agricultural land and in forests. Disciplines range from biogeography and faunistics, over morphology, taxonomy and phylogenetics, ecophysiology and functional ecology, to population, community, conservation and landscape ecology. This volume is the result of the 8th European Carabidologists' Meeting, 2nd International Symposium of Carabidology, September 1-4, 1992, Belgium.

As one of the most dynamic fields in contemporary science, bioinorganic chemistry lies at a natural juncture between chemistry, biology, and medicine. This rapidly expanding field probes fascinating questions about the uses of metal ions in nature. Respiration, metabolism, photosynthesis, gene regulation, and nerve impulse transmission are a few of the many natural processes that require metal ions, and new systems are continually being discovered. The use of unnatural metals - which have been introduced into human biology as diagnostic probes and drugs - is another active area of tremendous medical significance. This introductory text, written by two pioneering researchers, is destined to become a landmark in the field of bioinorganic chemistry through its organized unification of key topics. Accessible to undergraduates, the book provides necessary background information on coordination chemistry, biochemistry, and physical methods before delving into topics that are central to the field: What metals are chosen and how are they taken up by cells? How are the concentrations of metals controlled and utilized in cells? How do metals bind to and fold biomolecules? What principles govern electron transfer and substrate binding and activation reactions? How do proteins fine-tune the properties of metals for specific functions? For each topic discussed, fundamentals are identified and then clarified through selected examples. An extraordinarily readable writing style combines with chapter-opening principles, study problems, and beautifully rendered two-color illustrations to make this book an ideal choice for instructors, students, and researchers in the chemical, biological, and medical communities.

With an increasing human population and a decreasing amount of arable land, creative improvements in agriculture will be a necessity in the coming decades to maintain or improve the standard of living. In Plant Chromosome Engineering: Methods and Protocols, expert researchers present techniques for the modification of crops and other plant species in order to achieve the goal of developing the much needed novel approaches to the production of food, feed, fuel, fiber, and pharmaceuticals. This volume examines vital topics such as transformation procedures, chromosome painting, production of engineered minichromosomes, gene targeting and mutagenesis, site specific integration, gene silencing, protein expression, chromosome sorting and analysis, protocols for generating chromosomal rearrangements, enhancer trapping, and means of studying chromosomes in vivo. As a part of the highly successful Methods in Molecular Biology™ series, the methodological chapters include brief introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and professional tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, Plant Chromosome Engineering: Methods and Protocols highlights the spectrum of tools currently available for modifying plant genomes and chromosomes and provides the foundation for crucial future developments.

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