

Preface

Transcriptomics consists of the mathematical, statistical and computing methods that aim to solve biological problems using nucleotides and amino acid sequences and related information. Transcriptomics is about searching biological databases, comparing sequences, looking at protein structure and more generally, asking biological question with a computer. Biological or genetic information is the fundamental concept of Transcriptomics. Transcriptomics, a genome-wide measurement of mRNA expression levels based on DNA microarray technology is one of the prominent fields of study. This is the term given to the set of all transcripts or messenger RNA (mRNA) molecules produced in cells. It can also be applied to the specific subset of transcripts present in a particular cell or the total set of transcripts in a given organism. Transcriptomics has evolved from a variety of already present technologies and areas. These areas include proteomics, genomics, and environmental science. Transcriptomics is the symbiotic relationship between computational sciences.

Transcriptomics concepts provide a distinct knowledge layer for biologists, especially when they become interested in high throughput experimental analyses. Modern biology is becoming an information science and such transcriptomics classification can provide skeletons for well defined fields. It is a scientific field that studies how the genome is involved in responses to environmental stresses. It combines studies of gene expression, cell and tissue-wide protein expression and to understand the role of gene-environment interactions in disease. One of the important aspects of transcriptomics research is the development and application of bioinformatics tools and databases in order to facilitate analysis, mining, visualization and sharing of the vast amount of biological information being generated in this field. This rapidly growing area promises to have a large impact on many other scientific and medical disciplines as scientists could now generate complete descriptions of how components of biological systems work together in response to various stresses and drugs. This book content finds out more information about key technologies for transcriptomics, analytical technologies, separation techniques, transcriptomics in practices, technology development, applications, current research and their approaches. The wide area covered by this issue articles gives an idea of how diverse the field is. We worked together to bring high quality articles to this book.

We worked hard to take the book to well organized format. We have not only given knowledgeable information but also guided in putting this knowledge for the benefit of the society in the form of book. Transcriptomics are increasingly driven by research integration, the ability to pull together seemingly unrelated branches of basic and applied sciences to produce in a timely fashion innovative and

efficacious solutions to multidisciplinary human health problems. The rising healthcare costs in most developed countries can probably be reduced by enlarging the fraction of variety of most sophisticated supramolecular-based drug formulations offered on the global pharmaceutical markets. Further advancements in research targeted delivery of macromolecular drugs and transcriptomics could be expected by combining contemporary technologies and enable to achieve optimal new drug development. Hoping that, such promising views will soon be changed into reality in new drug findings. Also with help of our publishing efforts, we would like to extend our appreciations, as the authors of this book.

Virendra S. Gomase

Somnath Tagore