
Preface

RNA is a versatile nucleic acid polymer with a structure analogous to single-stranded DNA even though it has a backbone composed of ribose sugar and the organic base thymine (T) is replaced by uracil (U). In contrast to DNA, RNA molecules are less stable and characterized by secondary and tertiary structures, which underline their different function. According to the central dogma of molecular biology, RNA is directly involved in the flux of genetic information from the DNA to the proteins. However, recent developments in molecular biology indicate that RNA molecules have a plethora of functional roles and are indispensable for living organisms and cell homeostasis. Indeed, on the basis of their functions, RNA molecules can be divided into two groups, coding and noncoding. While the coding fraction is represented by messenger RNAs (mRNAs), noncoding RNAs (ncRNAs) include at least two main classes: (1) structural ncRNAs as transfer RNAs (tRNAs), ribosomal RNAs (rRNAs), and small nucleolar RNAs (snoRNAs); (2) regulatory ncRNAs as micro RNAs (miRNAs), piwi-interacting RNAs (piwiRNAs), and long noncoding RNAs (lncRNAs).

A large fraction of eukaryotic transcriptomes consists of ncRNAs that play relevant biological roles as the regulation of gene expression in normal as well as pathological conditions. NcRNA functions are generally mediated by interactions with other RNA molecules or DNA regions or proteins. In all cases, RNA secondary and tertiary structures are basic for a correct function and interaction. However, the characterization of RNA molecules is a challenging task and, thus, during past decades a variety of bioinformatics tools have been developed. Nowadays, RNA bioinformatics represents one of the most active fields of bioinformatics and computational biology.

The interest towards RNA bioinformatics has increased rapidly thanks to the advent of recent high-throughput sequencing technologies that enable the investigation of complete transcriptomes at single nucleotide resolution.

The present book has been conceived with the aim of providing an overview of RNA bioinformatics methodologies, starting from “classical” technologies to predict secondary and tertiary structures, to novel strategies and algorithms based on massive RNA sequencing. Indeed, the content of the book is organized as follows:

- Part I—RNA secondary and tertiary structures. This section includes chapters devoted to main computational algorithms to predict, draw, and edit secondary and tertiary RNA structures or infer RNA-RNA interactions.
- Part II—Analysis of high-throughput RNA sequencing data. The aim of this section is to provide a global overview of current methodologies to handle and analyze large sequencing dataset generated by next-generation sequencing (NGS) technologies. Indeed, the section includes chapters about quality control of RNA sequencing data or the mapping of RNA-Seq reads on complete reference genomes or the gene expression profiling. In addition, methodologies to investigate posttranscriptional events as alternative splicing or RNA editing and entire meta-transcriptomes are also described in detail.

- Part III—Web resources for RNA data analysis. Finally, this section provides chapters about several available web resources to work with RNA data without specific computer requirements (hardware and software) or specialized bioinformatics skills.

Hoping that the book content meets the reader expectations, I would like to acknowledge those who helped make this book possible: all chapter authors for their work and excellent contributions; the Series Editor, John Walker, for his constant support and suggestions; my wife Angela and daughter Adele for their patience and encouragement.

A special thanks is addressed to my mentor Graziano Pesole for his always indispensable paternal suggestions.

Finally, I would to dedicate this effort to my parents since they have always believed in me and to the memory of my first supervisor Carla Quagliariello who introduced me for the first time to the wonderful and fascinating world of RNA bioinformatics.

Bari, Italy

Ernesto Picardi

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