

---

# Contents

<i>Preface</i> . . . . .	<i>v</i>
<i>Contributors</i> . . . . .	<i>ix</i>

## PART I RNA SECONDARY AND TERTIARY STRUCTURES

1 Free Energy Minimization to Predict RNA Secondary Structures and Computational RNA Design. . . . .	3
<i>Alexander Churkin, Lina Weinbrand, and Danny Barash</i>	
2 RNA Secondary Structure Prediction from Multi-aligned Sequences . . . . .	17
<i>Michiaki Hamada</i>	
3 A Simple Protocol for the Inference of RNA Global Pairwise Alignments . . . .	39
<i>Eugenio Mattei, Manuela Helmer-Citterich, and Fabrizio Ferrè</i>	
4 De Novo Secondary Structure Motif Discovery Using RNAProfile . . . . .	49
<i>Federico Zambelli and Giulio Pavesi</i>	
5 Drawing and Editing the Secondary Structure(s) of RNA . . . . .	63
<i>Yann Ponty and Fabrice Leclerc</i>	
6 Modeling and Predicting RNA Three-Dimensional Structures. . . . .	101
<i>Jérôme Waldispühl and Vladimir Reinharz</i>	
7 Fast Prediction of RNA–RNA Interaction Using Heuristic Algorithm . . . . .	123
<i>Sobeila Montaseri</i>	

## PART II ANALYSIS OF HIGH-THROUGHPUT RNA SEQUENCING DATA

8 Quality Control of RNA-Seq Experiments. . . . .	137
<i>Xing Li, Asha Nair, Shengqin Wang, and Ligu Wang</i>	
9 Accurate Mapping of RNA-Seq Data. . . . .	147
<i>Kin Fai Au</i>	
10 Quantifying Entire Transcriptomes by Aligned RNA-Seq Data . . . . .	163
<i>Raffaele A. Calogero and Francesca Zolezzi</i>	
11 Transcriptome Assembly and Alternative Splicing Analysis . . . . .	173
<i>Paola Bonizzoni, Gianluca Della Vedova, Graziano Pesole, Ernesto Picardi, Yuri Pirola, and Raffaella Rizzi</i>	
12 Detection of Post-Transcriptional RNA Editing Events . . . . .	189
<i>Ernesto Picardi, Anna Maria D’Erchia, Angela Gallo, and Graziano Pesole</i>	
13 Prediction of miRNA Targets . . . . .	207
<i>Anastasis Oulas, Nestoras Karathanasis, Annita Louloupi, Georgios A. Pavlopoulos, Panayiota Poirazi, Kriton Kalantidis, and Ioannis Iliopoulos</i>	

14	Using Deep Sequencing Data for Identification of Editing Sites in Mature miRNAs . . . . .	231
	<i>Shahar Alon and Eli Eisenberg</i>	
15	NGS-Trex: An Automatic Analysis Workflow for RNA-Seq Data . . . . .	243
	<i>Ilenia Boria, Lara Boatti, Igor Saggese, and Flavio Mignone</i>	
16	e-DNA Meta-Barcoding: From NGS Raw Data to Taxonomic Profiling . . . . .	257
	<i>Fosso Bruno, Marzano Marinella, and Monica Santamaria</i>	
17	Deciphering Metatranscriptomic Data . . . . .	279
	<i>Evguenia Kopylova, Laurent Noé, Corinne Da Silva, Jean-Frédéric Berthelot, Adriana Alberti, Jean-Marc Aury, and Hélène Touzet</i>	
18	RIP-Seq Data Analysis to Determine RNA-Protein Associations . . . . .	293
	<i>Federico Zambelli and Giulio Pavesi</i>	
PART III WEB RESOURCES FOR RNA DATA ANALYSIS		
19	The ViennaRNA Web Services . . . . .	307
	<i>Andreas R. Gruber, Stephan H. Bernhart, and Ronny Lorenz</i>	
20	Exploring the RNA Editing Potential of RNA-Seq Data by ExpEdit . . . . .	327
	<i>Mattia D'Antonio, Ernesto Picardi, Tiziana Castrignandò, Anna Maria D'Erchia, and Graziano Pesole</i>	
21	A Guideline for the Annotation of UTR Regulatory Elements in the UTRsite Collection . . . . .	339
	<i>Matteo Giulietti, Giorgio Grillo, Sabino Liuni, and Graziano Pesole</i>	
22	Rfam: Annotating Families of Non-Coding RNA Sequences . . . . .	349
	<i>Jennifer Daub, Ruth T. Eberhardt, John G. Tate, and Sarah W. Burge</i>	
23	ASPicDB: A Database Web Tool for Alternative Splicing Analysis . . . . .	365
	<i>Mattia D'Antonio, Tiziana Castrignandò, Matteo Pallocca, Anna Maria D'Erchia, Ernesto Picardi, and Graziano Pesole</i>	
24	Analysis of Alternative Splicing Events in Custom Gene Datasets by AStalavista . . . . .	379
	<i>Sylvain Foissac and Michael Sammeth</i>	
25	Computational Design of Artificial RNA Molecules for Gene Regulation. . . . .	393
	<i>Alessandro Laganà, Dario Veneziano, Francesco Russo, Alfredo Pulvirenti, Rosalba Giugno, Carlo Maria Croce, and Alfredo Ferro</i>	
	<i>Index</i> . . . . .	413

RNA Bioinformatics

Picardi, E. (Ed.)

2015, XII, 415 p. 102 illus., 73 illus. in color., Hardcover

ISBN: 978-1-4939-2290-1

A product of Humana Press