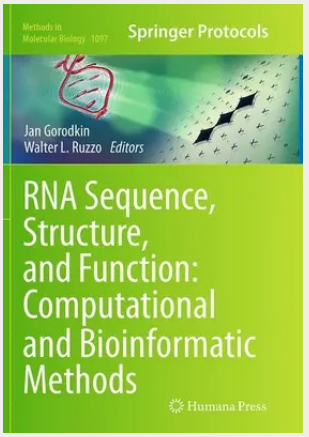
Gorodkin / Ruzzo

RNA Sequence, Structure, and Function: Computational and Bioinformatic Methods



The existence of genes for RNA molecules not coding for proteins (ncRNAs) has been recognized since the 1950's, but until recently, aside from the critically important ribosomal and transfer RNA genes, most focus has been on protein coding genes. However, a long series of striking discoveries, from RNA's ability to carry out catalytic function, to discovery of riboswitches, microRNAs and other ribo-regulators performing critical tasks in essentially all living organisms, has created a burgeoning interest in this primordial component of the biosphere. However, the structural characteristics and evolutionary constraints on RNA molecules are very different from those of proteins, necessitating development of a completely new suite of informatic tools to address these challenges. In *RNA Sequence, Structure, Function: Computational and Bioinformatic Methods* , expert researchers in the field describe a substantial and relevant fraction of these methodologies from both practical and computational/algorithmic perspectives. Focusing on both of these directions addresses both the biologist interested in knowing more about RNA bioinformatics as well as the bioinformaticist interested in more detailed aspects of the algorithms. Written in the highly successful *Methods in Molecular Biology* series format, the chapters include the kind of detailed description and implementation advice that is crucial for getting optimal results.

Thorough and intuitive, *RNA Sequence, Structure, Function: Computational and Bioinformatic Methods* aids scientists in continuing to study key methods and principles of RNA bioinformatics.

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