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form the basis of what
is often seen as the
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process:

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Biology is concerned

with solutions to

issues that have been

raised by studies in

bioinformatics. In

many cases, the

phrases

“bioinformatics” and

“computational

biology” are used

interchangeably,

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particularly in job
descriptions or
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source and open development software project for the analysis and comprehension of data arising from high-throughput experimentation in genomics and molecular biology.

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and Computational
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sciences,
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And Robert

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computational
methods to
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of the protein
universe, the
knowledge
accumulated on a
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seeks to accomplish what was impossible before its invention, namely the assignment of functions or functional hypotheses for all known proteins. The Ten Most Wanted Solutions in Protein Bioinformatics considers the ten most significant problems occupying

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those looking to
identify the biological
properties and

functional roles of
proteins. - Problem

One considers the
challenge involved
with detecting the

existence of an
evolutionary

relationship between
proteins. - Two and

Three studies the
detection of local

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similarities between protein sequences and analysis in order to determine functional assignment. - Four, Five, and Six look at how the knowledge of the three-dimensional structures of proteins can be experimentally determined or inferred, and then exploited to

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And lastly, Problem
Ten considers ways
to modify the
functional properties
of proteins. After
summarizing each
problem, the author
looks at and
evaluates the current
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utilized, before going
on to consider some
potential approaches.

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This book is the first of its kind to provide a large collection of bioinformatics problems with accompanying solutions. Notably, the problem set includes all of the problems offered in Biological Sequence Analysis (BSA), by Durbin et al., widely adopted as

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A required text for bioinformatics courses at leading universities worldwide. Although many of the problems included in BSA as exercises for its readers have been repeatedly used for homework and tests, no detailed solutions for the problems were available.

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instructors had therefore frequently expressed a need for fully worked solutions and a larger set of problems for use on courses. This book provides just that: following the same structure as BSA and significantly extending the set of workable problems, it will

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facilitate a better understanding of the contents of the chapters in BSA and will help its readers develop problem-solving skills that are vitally important for conducting successful research in the growing field of bioinformatics. All of the material has been class-tested by the

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Authors at Georgia Tech, where the first ever M.Sc. degree program in Bioinformatics was held.

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part covers a wide range of topics, including logging in, working with files and directories, installing programs and writing scripts, and the powerful "pipe" operator for file and data manipulation.

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and a common choice in scientific software development. This part covers the basic concepts in programming (data types, if-statements and loops, functions) via examples of DNA-sequence analysis. This part also covers more complex subjects in software development such as

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objects and classes, modules, and APIs. Programming in R: The R language specializes in statistical data analysis, and is also quite useful for visualizing large datasets. This third part covers the basics of R as a programming language (data types,

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