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problems and

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to program but
also how to
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several biological

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demands and
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these data are
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application of
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analysis,*

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as well as for
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approaches
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goal in machine
learning is to
extract useful
information from
a body of data
by building good
probabilistic

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*models—and to
automate the
process as much
as possible. In
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approaches and
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*equation can
explain the
process to
obtain the
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by determining
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analysis, in
the continuum
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one. It
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presents both
fundamental
conservation
principles
(mass, charge,
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relevant
fluxes
resulting from

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driving
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forces, which
are important
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systems. It
includes the
concept of

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conservation,
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an important
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equations,
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*Kniha je zaměřena
na regresní modely,
konkrétně
jednorozměrné
zobecněné lineární
modely (GLM). Je
určena především
studentům a
kolegům z*

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*biologických oborů a
vyžaduje pouze
základní statistické
vzdělání, jakým je
např.*

*jednosemestrový
kurz biostatistiky.*

*Text knihy obsahuje
nezbytné minimum
statistické teorie,
především však
řešení 18 reálných
příkladů z oblasti*

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*biologie. Každý
příklad je
rozpracován od
popisu a stanovení
cíle přes vývoj
statistického modelu
až po závěr. K
analýze dat je použit
populární a volně
dostupný statistický
software R. Příklady
byly záměrně
vybrány tak, aby*

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*upozornily na
leckteré problémy a
chyby, které se
mohou v průběhu
analýzy dat
vyskytnout. Zároveň
mají čtenáře
motivovat k tomu,
jak o statistických
modelech přemýšlet
a jak je používat.
Řešení příkladů si
může čtenář*

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vyzkoušet sám na
datech, jež jsou
dodávána spolu s
knihou.

*R is the most widely
used open-source
statistical and
programming
environment for the
analysis and
visualization of
biological data.*

Drawing on Gregg

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*extensive
experience teaching
biostatistics and
modeling biological
systems, this text is
an engaging,
practical, and lab-
oriented introduction
to R for students in
the life sciences.*

*Underscoring the
importance of R and*

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*RStudio in
organizing,
computing, and
visualizing biological
statistics and data,
Hartvigsen guides
readers through the
processes of
correctly entering
and analyzing data
and using R to
visualize data using
histograms,*

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boxplots, barplots, scatterplots, and other common graph types. He covers testing data for normality, defining and identifying outliers, and working with non-normally distributed data.

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two-sample tests as well as one- and two-way analysis of variance (ANOVA), correlation, and linear and nonlinear regression analyses. This volume also includes a section on advanced procedures and a chapter outlining algorithms and the

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*art of programming
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using R. This
second edition has
been revised to be
current with the
versions of R
software released
since the book's
original publication.
It features updated
terminology,
sources, and
examples

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throughout.

*This book
addresses the
difficulties
experienced by wet
lab researchers with
the statistical
analysis of
molecular biology
related data. The
authors explain how
to use R and
Bioconductor for the*

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*analysis of
experimental data in
the field of molecular
biology. The content
is based upon two
university courses
for bioinformatics
and experimental
biology students
(Biological Data
Analysis with R and
High-throughput
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R). The material is divided into chapters based upon the experimental methods used in the laboratories. Key features include:

- *Broad appeal--the authors target their material to researchers in several levels, ensuring that the*

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*approaches,
therefore novel
methods are*

*available early for R
users.*

*This richly illustrated
book provides an
overview of the
design and analysis
of experiments with
a focus on non-
clinical experiments
in the life sciences,*

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including animal research. It covers the most common aspects of experimental design such as handling multiple treatment factors and improving precision. In addition, it addresses experiments with large numbers of

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*treatment factors
and response
surface methods for
optimizing
experimental
conditions or
biotechnological
yields. The book
emphasizes the
estimation of effect
sizes and the
principled use of
statistical arguments*

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*in the broader
scientific context. It
gradually transitions
from classical
analysis of variance
to modern linear
mixed models, and
provides detailed
information on
power analysis and
sample size
determination,
including 'portable*

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*power' formulas for
making quick
approximate
calculations. In turn,
detailed discussions
of several real-life
examples illustrate
the complexities and
aberrations that can
arise in practice.*

*Chiefly intended for
students, teachers
and researchers in*

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*the fields of
experimental biology
and biomedicine, the
book is largely self-
contained and starts
with the necessary
background on
basic statistical
concepts. The
underlying ideas and
necessary
mathematics are
gradually introduced*

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*in increasingly
complex variants of
a single example.*

*Hasse diagrams
serve as a powerful
method for
visualizing and
comparing
experimental
designs and deriving
appropriate models
for their analysis.*

Manual calculations

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*are provided for
early examples,
allowing the reader
to follow the
analyses in detail.*

*More complex
calculations rely on
the statistical
software R, but are
easily transferable to
other software.*

*Though there are
few prerequisites for*

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*effectively using the
book, previous
exposure to basic
statistical ideas and
the software R
would be advisable.*

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Complex Biological Data provides relevant and to the point content for those who need to understand the different types of biological data and the techniques to process and interpret them. The book includes feedback the editor received from

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students studying at both undergraduate and graduate levels, and from her peers. In order to succeed in data processing for biological data sources, it is necessary to master the type of data and general methods and tools

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for modern data processing. For instance, many labs follow the path of interdisciplinary studies and get their data validated by several methods. Researchers at those labs may not perform all the techniques

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themselves, but
either in
collaboration or
through
outsourcing, they
make use of a
range of them,
because, in the
absence of cross
validation using
different
techniques, the
chances for
acceptance of an

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article for
publication in high
profile journals is
weakened.

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interpret enormous
amounts of data
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approaches in
simple terms, thus
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and physics at the

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data files and

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