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of the Modeling
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Definition:

Descriptively
realistic

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to show how the
application of
models to

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describe real

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The three
principles of
mathematical
modeling

illustrated here
are. (1)

Identify the
known and

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variables that are present in the problem. (2)

Identify the relationships between the known and

unknown variables in the problem.

(3) Assess the effect of any assumptions made

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$s = (r - 1) = r$ is an
stable steady
state since
 $|f'(r) = r| = r < 1$. In
Figure 1.3 we
plot this
information on a
diagram of
steady states,
as a function of
 r , with stable

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indicated by
solid lines and
unstable steady
states by dashed
lines. When $r = 1$
we have $(r - 1) = 0$, so both
steady states
are at u .

**Mathematical
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Notes

1.1 What is
mathematical
modelling?

Models describe
our beliefs
about how the
world functions.

In mathematical
modelling, we
translate those
beliefs into the
language of
mathematics.

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This has many advantages 1. Mathematics is a very precise language. This helps us to formulate ideas and identify underlying assumptions. 2.

**An Introduction to
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Let $y(n+1) = 2.2y(n) - (y(n))^2 + 0.3(y(n))^2$. give the state of the heart at time n , measured by some sort of potential obtained from Electrocardiograms, (ECGs). If we start the heart at $y(0) = 0.4$, it converges rapidly to a

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stable oscillation. This is shown in Figure 4.12.

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...

where. c =number
of contacts in
the time unit,

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of one contact
with an
infective, $N(t)$
 $= S(t) + I(t) + R(t)$
 $=$ total
population. (2)

Moreover,
the removal rate
 $\rho(t)$ is usually
assumed to be a
constant. $\rho(t)$
 $= \rho = 1$. (3)

where ρ is the

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average time
spent as an
infective, i.e.
the average
duration of the
infection.

THE MATHEMATICAL MODELING OF EPIDEMICS

Assume that the
number of
offspring
produced per

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individual per unit time is a constant $b > 0$. Similarly assume that the death rate (number of deaths per unit time per individual) is a constant $d > 0$.

$$x(t + \Delta t) = x(t) + bx \Delta t - dx \Delta t$$

Divide by Δt and take the limit as $\Delta t \rightarrow 0$. $\frac{dx}{dt}$

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$\frac{dx}{dt} = (b - d)x = rx$
where $r = b - d$:
Solution is $x(t)$
 $= x_0 e^{rt}$.

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mathematics
major and minor
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biology and
medicine. There
exist a large
number of
mathematical
methods and
procedures that
can be brought
in to meet these
challenges and
this book
presents a
palette of such

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population based
models described
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equations to
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equations
representing

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and space-
dependent
continuous
processes. Both
stochastic and
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methods are
employed to
analyze
biological
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various temporal
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settings. This book illustrates the breadth and depth of research opportunities that exist in the general field of mathematical biomedicine by highlighting some of the fascinating

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that continue to develop between the mathematical and biomedical sciences. It consists of five parts that can be read independently, but are arranged to give the reader a broader picture of

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research topics and the mathematical tools that are being applied in its modeling and analysis. The main areas covered include immune system modeling, blood vessel dynamics, cancer modeling

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and
epidemiology.
The chapters
address topics
that are at the
forefront of
current
biomedical
research such as
cancer stem
cells,
immunodominance
and viral

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aggressive forms
of brain cancer,
or gene therapy.

The Modelling In

presentations
highlight how
mathematical

modeling can
enhance

biomedical

understanding

and will be of

interest to both

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the mathematical
and the
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communities
including
researchers
already working
in the field as
well as those
who might
consider
entering it.
Much of the
material is

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pulled from the
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equations,
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probability.

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modeling of gene-
networks in
bacteria. As an
entry point to

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the field, we

focus on the

analysis of

simple gene-

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with an

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the

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reference to
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presence of
noise—either
arising from low
numbers of
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three well

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by considering

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minimum), as
well as with
basic notions of
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State of the art
approaches using
parameter
sensitivity are
discussed for
enhancing model
identifiability
through joint
analysis of
model structure
and data.
Practical
examples
illustrate model

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development at various levels of complexity based on given physiological information. The sensitivity-based approaches for examining model identifiability are illustrated by means of specific

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examples. The themes presented address the current problem of patient-specific model adaptation in the clinical setting, where data is typically limited.

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processes
includes a wide
selection of
biological
topics that
demonstrate the
power of
mathematics and
computational
codes in setting

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rigorous and
predictive
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spread of
disease,
harvesting
bacteria,
competition
among live
species,

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oscillations,
transport of
neurofilaments
in axon, cancer
and cancer
therapy, and
granulomas.

Complete with a
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the biological
background and
biological
question that

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this book is
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students and
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