

# Chapter 2

## The Modeling Process

### 2.1 Models Are Problems

We are faced with insurmountable opportunities. — Walt Kelly (doubtful)

WHEN WE EMBARK on a modeling project, we immediately have a problem. We want something that we don't have: a model. The modeling process is a semi-formal set of rules that guides us through a solution to this problem. The rules are not mechanical instructions, not like a set of computer instructions we can step through one at a time and be guaranteed of arriving at the correct answer at the end. Modeling is real-world problem solving; it's hard and fraught with many opportunities for failure (or, if you're an optimist, opportunities for new insights). So, it is useful to begin by noting George Polya's four steps to solving mathematical problems (Polya 1973). Associated with each step is a question that we must answer. (1) *Understand the problem* (i.e., What is the question?) (2) *Devise a plan* for solving the problem (i.e., How do we solve it?) (3) *Execute the plan* (i.e., What is an answer?) (4) *Check the correctness of the answer* (i.e., Was it right?).

Certainly, these instructions are very general, perhaps only heuristically plausible, but they work on all problems, including the problem of producing a model. In this and the remaining chapters, we will see some more specific rules and tools that work in the more restricted domain of mathematical and computer models of biological systems. Ford (2000) elaborates in wonderful detail these four steps in the context of practical scientific activities taking examples from, but not limited to, ecological research.

As a problem to solve, then, the modeling process consists of the steps we take to produce a model, implement it in some formal language, derive consequences (predictions) from the model, and evaluate these based on the desired uses of the model. Since the statement of the model inevitably requires making assumptions, comparing model consequences with observations is a major test of the adequacy of the assumptions to "explain" the observations. In its broadest form, then, modeling is the hypothetico-deductive approach to science and vice versa (Nagel 1961; Romesburg 1981). Here, we will describe this process in a way that emphasizes several important quantitative and computational procedures that are relevant to computer simulation.

Is Levins' reply that models are "relativistic" and not be evaluated in terms of their context relevant? Does this imply models can not describe truth?

Which of the Levins' triad does the MacArthur-Wilson theory of island biogeography emphasize more: realism, precision, or generality?

The regression equations for immigration and extinction rates (Fig. 1.5 and Eq. 1.2) violate some of the assumptions of the basic island biogeography model. What are they and how would you correct them in the parameter estimates? [Think about the maximum number of species that can be on the island and about extinction rates when no species are present.]

Derive an equation for the equilibrium number of species on an island.

The net rate of change in a person's knowledge is a balance of learning and forgetting. Suppose in humans the rate of learning increases as a fraction of the square root of age and the rate of forgetting increases as a fraction of the square of age. Write a finite difference equation that describes the amount of knowledge a person has as he ages and solve for the age at which his knowledge peaks at 64 years. Choose values for the two parameters so that knowledge the person achieves in any one year?

Rakata is a small island between the islands of Sumatra and Java in the South Pacific. It is famous for being the largest remnant of Krakatau Island after the notorious 1883 eruption. Whitaker et al. (1989) and Thornton et al. (1993) compiled historical plant and animal surveys of Rakata from 1886 to 1992; the approximate data for vascular plants species numbers ( $R$ ), immigration rate ( $I$ ) and extinction rate ( $E$ ) are:

$R$	0	36	80	155	210	240
$I$	8.0	3.0	5.0	6.5	4.0	2.5
$E$	0.0	0.05	0.10	0.5	1.75	1.75

- Use linear regression to estimate the immigration and emigration rates.
- Re-write Eq. 1.2 using these Rakata data.
- Estimate the equilibrium number of vascular plant species on Rakata.
- How many species are in the mainland pool?

Use the code supplied on the MBS-CD, simulate the species dynamics using the parameters you estimated and starting with no plants. Also simulate a scenario representing the pre-explosion condition in which the initial number of plant species is 500. Assuming only that the island size changed, how long would it take to achieve the current projected equilibrium level of about 250 species?

## 2.2 Two Alternative Approaches

The classical description of the modeling process is shown in Fig. 2.1. This basic approach is presented in many texts (Shannon 1975; Spriet and Vansteenkiste 1982; Grant 1986). Its essential feature is that models should be constructed one at a time, and the quality of each is evaluated sequentially. Another model is not constructed until the current model is shown to be inadequate. For many biological systems, this is an appropriate methodology, but for others, a slightly modified view of this modeling process will be effective.

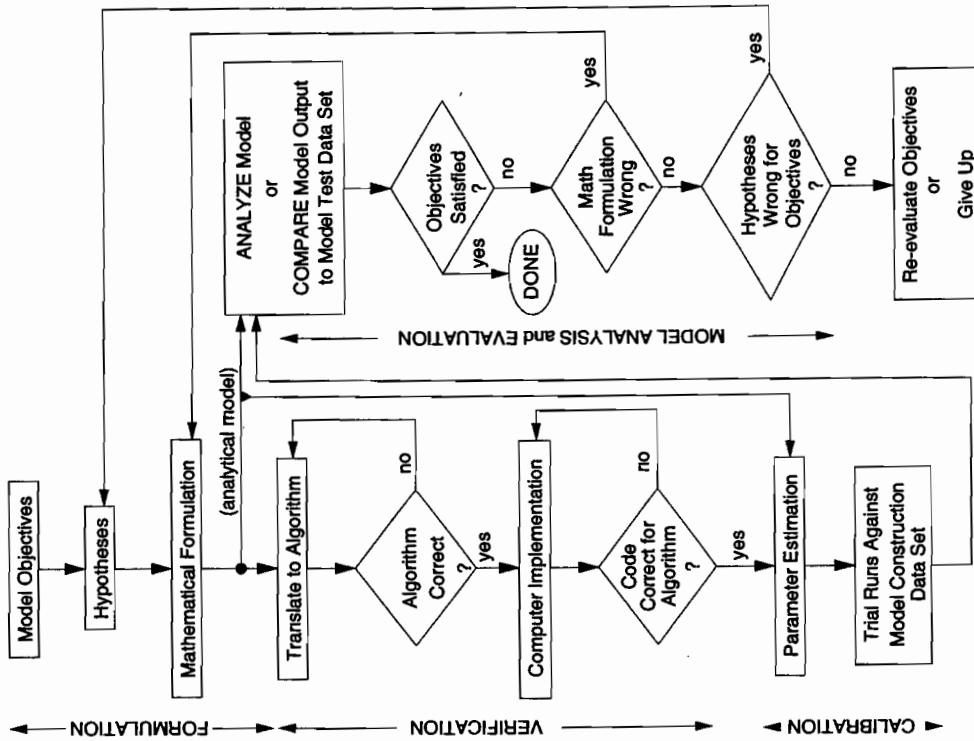
### 2.2.1 The Classical View

**Objectives** The beginning of the process is a statement of the objectives or purposes of the model. At this stage, we demonstrate our understanding of the problem (Green 1979). If we cannot give a clear statement of the reasons for building a model, then we do not understand the problem. If we do not understand the problem, then we are unlikely to discover the solution. Consequently, substantial detail should be provided in the statement of the objectives to answer the following questions:

- What is the system to be modeled?
- What are the major questions to be addressed by the model? (How will the model be applied?)
- What is the *stopping rule* for the modeling activity? (How good must the model be? To what will it be compared?)
- How will the model output be analyzed, summarized, and used?

Because of the importance of a clear statement of objectives, we will discuss this aspect of modeling in more detail later in this chapter. Here we note that the objective statement is a document that defines the reasons for producing the model in the first place. In cases of large, complicated modeling projects, it can ensure that the goal is well defined and achievable. Even when exploring theoretical concepts with small models, by answering the four questions above, the theoretician is forced to evaluate the scope and importance of the original questions.

**Hypotheses** The second stage is to translate the objectives and current knowledge of the system into a list of specific hypotheses. These are usually verbal statements. For example, a simple idea in population ecology is that crowding increases as numbers of individuals in the population increase and this, in turn, reduces the reproductive capacity of females. This can be qualitatively stated as: "increasing density decreases per capita growth rates." Hypotheses may also use more quantitative relationships. For example, in simple models of blood circulation, the heart chambers expand as they fill with blood, but the rate of expansion decreases at large volumes because heart wall elasticity is limited. More quantitatively, we can say that the degree that chamber volume increases with a unit increase in blood volume decreases linearly as total volume increases. At this stage, we can also describe the complete model qualitatively with a graphical formalism that pictorially shows the objects modeled and their relations (e.g., flow of blood between organs). However it is accomplished, the function of this stage of modeling is to identify more fully the set of objects in the system and to bound the set of relations that connect the objects. At this stage,



**Figure 2.1:** The classical approach to the modeling process, showing the four basic stages. In this approach, alternative models are developed sequentially, conditional on the failure of a previous model.

the modeler must be cognizant of the fundamental uses of the model articulated in the objectives: understanding, prediction, or control. These have a crucial affect on the nature of the hypotheses.

**Mathematical Formulation** Qualitative hypotheses must be converted into specific, quantitative relations that can be formulated with mathematical equations. In the third stage, the actual equations are defined. This corresponds to Polya's stage to *devise a plan* for solving the problem. This step uses the initial physical, chemical, and biological information available for model construction to derive and check the correctness of the equations we hope will describe the dynamic behavior of system objects. For many beginners, this is the most difficult and frustrating stage. It requires a certain level of mathematical sophistication, but more importantly, it requires that vague concepts and loose relations be made definite in the cold light of mathematics.

**Verification** Many mathematical models cannot be solved analytically, but can only be solved approximately using numerical techniques. Today, this means solving the equations using a digital computer. The fourth stage is a set of activities in which the equations are translated into computer code. At this stage, it is necessary to *verify* that the computer algorithms and code are correct for the mathematical relationships defined. Modeling projects that do not require numerical solution of the equations will replace this step with mathematical verification activities performed during the formulation stage. For example, in Chapter 1 we solved the island biogeography model by a recursive equation. As we will see in Chapter 4, we could (and possibly should) have written the model as a differential equation. There are numerous numerical techniques for solving these equations (e.g., Runge-Kutta), and, depending on the nature of the equation, some methods are inappropriate. Thus, the choice of algorithm is important and can influence the predictions of the model. Similarly, for any algorithm, there are many different ways to write the computer code; some of these will be wrong. Models of biological systems can easily involve scores of dynamic variables and hundreds of parameters. This is especially common in models with explicit spatial processes. In writing a computer program to solve the equations, it is a nontrivial exercise to demonstrate that the computer output is correct. This is a concern of software engineering, and there are some basic programming procedures that can help in this regard (e.g., object-oriented programming).

**Calibration** After the model is correctly implemented on a computer, output can be produced. But before simulations can be performed, numerical values for the initial conditions (e.g., the starting number of species on an island) and constants in the equations must be specified. Calibration is the set of activities by which this is done; the basic problem involved is parameter estimation. Usually, this involves defining relations between observed quantities and the parameters so that statistical methods (e.g., linear regression) can be applied to produce the best estimates for the parameters (e.g., the slope and intercept of a straight line). These relations may require that specific laboratory experiments be performed. For example, in physiological models, one may wish to estimate the parameters for the quantitative effects of temperature on oxygen production in leaves. Laboratory measurements of oxygen at defined, controlled temperatures provide the necessary data. Often experiments cannot be performed, but uncontrolled observations over time are available (e.g., in ecological succession: plant

biomass over several years). If this variable is an output of the model, some parameters can be estimated by curve fitting wherein the model is run repeatedly using different parameter values and compared to the same dynamic data set until a satisfactory fit is obtained. This stage is discussed in more detail in Chapter 7.

**Analysis and Evaluation** Once the model is calibrated, we can use it to produce the answer that our objectives specified. This corresponds to Polya's *execution* of the plan. For numerical models, this involves running a computer program and recording the numbers produced. This is primarily a mechanical exercise that can be automated to a great extent. For analytical models, execution may range from simple computations to complicated mathematical argument and theorem proving. This latter activity can require substantial creativity and may be the most difficult step in the process.

For both numerical and analytical models, the answer should be evaluated for its quality according to the objectives. It should be *checked* (Polya 1973) in some way. Often in purely theoretical studies where the primary objective is to "understand" the system, this involves, at most, only a qualitative comparison of model output and data. For example, in a theoretical plant succession model we may be satisfied if the model shows an initial increase in plant biomass followed by a decline, if this were the observed pattern. Ideally, however, we also desire models that are quantitatively correct as well. To establish this for a particular model, we need to *validate* (or *corroborate*) the model against independent data sets. (For a broader perspective see Hilborn and Mangel 1997, Chap. 2.)

We have already noted the similarities between modeling and the hypothetico-deductive approach to scientific investigation. A component of this method is the doctrine of *falsificationism* (Popper 1968), which states that hypotheses cannot be proved, but only disproved (i.e., falsified). The same framework applies to models, since they are basically collections of hypotheses. Many modelers (e.g., Holling 1978a; Hall and DeAngelis 1985) have adopted this view to the point of stating that the objective is to invalidate the model, that is, discover evidence that contradicts it, not evidence that supports it. There is much philosophical and logical weight behind this view; nevertheless, there is also a real psychological need to be able to point to a model, theory, or body of experiments and say: "We believe this is the way it is." On the one hand, logic permits only falsification; on the other, we desire positive statements that summarize our beliefs, if only at a moment in time. We need an approach that synthesizes these two different approaches. A candidate is proposed below that develops and tests *multiple working hypotheses* as well as the *resultant alternative models*.

If the model passes the validation criteria specified in the objectives, the project, as defined by the objectives, is complete. If it fails, then errors were made earlier in the modeling process and the hypotheses and/or mathematical formulations need to be revised. The entire process is repeated. Finally, depending on the objectives, further analyses of the model through computer simulation or mathematical analyses are performed. These topics are discussed in Chapters 8 and 9.

## 2.2.2 Problems with the Classical View

Many statisticians believe that for statistically rigorous hypothesis testing to occur, prior knowledge should not influence the test. (But the Bayesian school of statistical

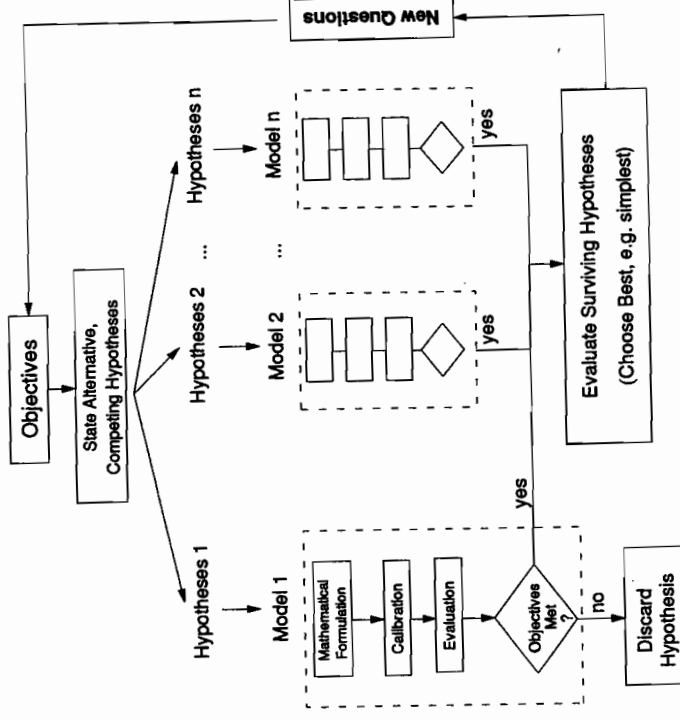
analysis disagrees, and this will be discussed in Chapter 8.) Therefore, sequential passes through the modeling process must use new data for validation. If only one independent data set is available, subsequent comparisons are only exercises in *curve fitting*, since the modeler has become familiar with the validation data during the development of the second and subsequent models. Thus, the major problem with the classical approach is that independent data sets necessary for validation are often difficult or expensive to obtain. A modification of the classical approach, based on multiple hypotheses and models, avoids this problem.

Multiple or alternative models are valuable for another reason. When we are uncertain about the correct equations to use (which we usually are), there is a danger that when we derive a model that we cannot reject, we will believe that this is a correct description. In fact, there may be many other models that would be equally likely to be validated as the one we chose. If we never create these models and their predictions, then we will never know if the original model was unique in its accuracy. If we create them in the sequential method illustrated by the classical view, we risk *overfitting* the model to the data (Burnham and Anderson 1998). That is, we continue the cycle of model refinement to a high degree of precision on a particular dataset using many variables, but with little applicability or accuracy on another system or dataset.

### 2.2.3 Multiple Working Hypotheses

*A man who does not know one answer from another is as ignorant about the question as he can possibly be. The only state of greater ignorance is not to know the question.*  
— Tribus and McIrvine (1970)

An alternative to the sequential approach is a parallel approach that involves implementing and evaluating several different competing hypotheses and models simultaneously (Goodall 1972; Caswell 1976b). This approach is diagrammed in Fig. 2.2. It is based on the ideas of statistical alternative hypotheses. Platt (1964) refers to these *multiple working hypotheses* as a component of *strong inference* and emphasizes the latter's value to incisive scientific analysis in all its forms (not just to modeling). Holling (1978a) and his colleagues (e.g., Walters 1986) have also shown the practical wisdom of using this approach in developing models to assist the management of renewable resources. Some of the philosophical foundations of this view of science as it contrasts with Popperian falsificationism are explored in Hilborn and Mangel (1997, Chap. 2). Among these are scientists' attitudes toward the rejection of a hypothesis. One interpretation of the views of Karl Popper (Popper 1968) holds that scientists will (or should) adhere to the results of an objective hypothesis test (e.g., statistics), regardless of the intellectual context of the test. For example, if an objective test instructs us to reject the only viable explanation for a phenomenon, then we will (should) be able to function in an intellectual milieu in which there is, simply, no explanation for the data. In contrast, the alternative, multiple-hypothesis philosophy of Imre Lakatos would not require, in this situation, that we accept the objective test, if there were no other reasonable alternative hypothesis that replaces the current one. There are many situations in which we might continue to entertain a hypothesis that fails a test, even a stringent one: the data might be flawed, the other situations in which the hypothesis was not rejected carry significant intellectual weight, the hypothesis is useful for

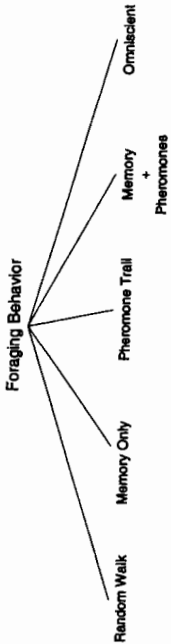


**Figure 2.2:** Another view of the modeling process, in which alternative hypotheses and models are developed and tested independently.

reasons other than scientific understanding, etc.

Using this approach, we formulate several hypotheses and models each with separate computer implementation, verification, and calibration stages. Every model is compared simultaneously (*in parallel*) to all of the validation data that are independent and any models that survive the comparisons can be evaluated further with other quality criteria. A common auxiliary criterion is simplicity, which is the basis for the Principle of Parsimony or Occam's Razor. This approach presupposes that we can uniquely rank models from simplest to most complex, and this is not always so. Another criterion is the likelihood that one of the models is true (regardless of their relative complexity); we will discuss this possibility in Chapter 8. Finally, the model selected suggests new questions or applications. Assuming we are not near retirement age, we pursue these with new objectives and new sets of models.

An example may make this clearer. Many species of seed-harvesting ants will exhibit mass recruitment of large numbers of foragers to rich resources (e.g., large insects or patches of seeds). Under other circumstances, ants forage individually, ignoring other ants and responding only to their local environment. The precise mechanisms required for these ants to perform these actions have not been determined, although experimental evidence indicates that they lay chemical trails and can remember previous



**Figure 2.3:** A family of competing hypotheses on the mechanisms used by ants to find seeds and recruit nest mates.

successful foraging areas.

Suppose we wish to use a simulation model to explore the consequences of the foraging behavior of individual ants for seed consumption rates over the entire ant colony in order to evaluate the relative importance of different mechanisms. We can identify a number of possible candidates (Fig. 2.3; Haefner and Crist (1994)): Random Walk (individual ants walk randomly and independently of other ants), Memory Only (individual ants remember previous successes but do not lay a pheromone trail), Pheromone Trail (ants lay a pheromone trail from the resource but do not use memory), Memory + Pheromone (ants use memory and pheromone trails), Omniscient (ants know the location of all the seeds). The first model serves as a null or random hypothesis in which no significant biological or social behavior is present. The last model represents a “super” ant and (presumably) defines the maximum rate of seed return to the nest. Together these models constitute a continuum of “ant intelligence.” Since we can easily measure the colony’s seed return rate in the field, the purpose of examining such a range of models is to determine where, along the continuum of models, the truth (i.e., real ants) lies. This addresses the question: “How smart does an ant have to be to forage in the way we observe?” We cannot definitively answer such questions with simulation models, but we can identify classes of models and hypotheses that are inadequate.

An important feature of this example, and one that should be used whenever possible, is the construction of a *base* model that incorporates as little of the biology as possible and yet still produces output that can be compared to observations. In this example, the base model eliminated all forms of communication between ants, but moved ants randomly so that they had the possibility of discovering seeds. Thus, the two extreme models, random and omniscient, bound the range of possible explanations.

The base model concept is similar to a null or neutral model (Caswell 1976a): models that exclude biological mechanisms pertinent to a particular hypothesis. The value of including these models is that they are simple explanations. However, we should not stop with these; as Albert Einstein is credited with saying: “a theory should be as simple as necessary, but no simpler.” Or, to put it another way, simple models are good, but getting the right answer for the right reason is also good. Chapter 8 presents methods for choosing the better of alternative models.

### 2.3 An Example: Population Doubling Time

We now summarize the idea of the modeling process applied to alternative models

with a quantitative example. Suppose we wish to answer the question: When will the world’s population double its current numbers? We identify the following objective statement.

*Objective:* Construct a description of the dynamics of the world’s population such that the time when the population size is twice its starting value can be computed.

The above statement has the following desirable properties of an objective statement: (1) It defines the system of interest as the world’s population without mention of spatial heterogeneity. (2) It defines the purpose of the model: determine the doubling time. (3) It indirectly identifies the analysis of the output to be used: a computation of the time at which the population is twice the initial condition. A major deficiency of the objective statement is that it does not mention validation criteria. We cannot tell from this statement when we should stop developing models.

To illustrate the idea of multiple working hypotheses, we will develop two models. One model assumes that per capita growth rate does not vary with increasing population size (density-independent growth) and the other assumes that the growth rate decreases linearly with population size (density-dependent growth). In addition to these assumptions, the two models share the following incomplete set of hypotheses.

1. Per capita growth rate is not influenced by any extrinsic variable (e.g., ozone, UV radiation, temperature).
2. The sex ratio is 1:1 (or we assume there is only a single sex).
3. There are no age differences among individuals (no age classes).
4. There are no geographical differences in growth rates (all countries and regions of the world are the same).

Our objective statement says that we intend to determine the doubling time by following the dynamics of the population. This suggests each of our mathematical models will implement the two hypotheses using equations that project population numbers forward in time. Recalling the Karplus (1977) ESR model of systems from Chapter 1 (Fig. 1.1), our problem is to write an equation for  $S$  that transforms the population numbers at time  $t$  into the population numbers at  $t + 1$ . There are several kinds of mathematical equations we could use here, but for simplicity, we will use recursive finite difference equations (FDE), the same form of equation we used in the island biogeography example of Chapter 1. One way to define a set of alternative models is to define a base model in general functional form:

$$N_{t+1} = N_t + N_t f(N_t). \quad (2.1)$$

The unspecified function,  $f(N_t)$ , is next defined in two or more forms: the alternative models. It is very helpful if these forms can be shown to be a sequence of increasing complexity. For example, from the most complex model, each remaining member of the sequence can be derived by setting parameters to zero. We now illustrate this for the population models.

Our two hypotheses make two different assumptions: (1) the number of offspring produced per female (*per capita rate of increase*) is independent of (i.e., does not



change with) the current numbers in the population, and (2) the per capita rate of increase decreases linearly with increasing numbers. It would appear that (2) is the more complex of the alternatives, so we begin with it.

$$N_{t+1} = N_t + N_t f(N_t) \quad (2.2)$$

$$= N_t + N_t (a - bN_t) \quad (2.3)$$

$$= N_t + N_t [r - (r/K)N_t] \quad (2.4)$$

Equation 2.3 clearly satisfies hypothesis (2), above. When we let the general parameters  $a = r$  and  $b = r/K$  (Equation 2.4), we get the more typical form in ecological contexts:  $r$  is the *intrinsic* (or maximum) *per capita growth rate* of the population;  $K$  is *carrying capacity* of the environment.

If we set  $b = 0$  in equation 2.3, we have the FDE for the density-independent model (hypothesis 1):

$$N_{t+1} = N_t + rN_t \quad (2.5)$$

Note that while the per capita rate of population growth is independent of  $N_t$ , the *absolute* rate of increase ( $rN_t$ ) does change. The per capita rate is constant and equals  $r$ , and the model asserts that the population increases each time step by a constant proportion ( $r$ ) of the current population.

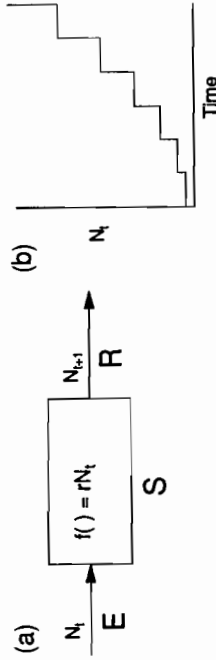
With these two alternatives defined, we can analyze both for their properties, validity, and relative suitability to our objectives. To *calibrate* the simpler of two models (Eq. 2.5), we can solve the model for  $r$ :

$$r = \frac{N_{t+1} - N_t}{N_t}$$

and use population estimates over successive periods of time ( $N_0, N_1, N_2, \dots, N_t$ ) to compute  $r$ . These data would probably be taken from a historical data set, but could be obtained from a field or laboratory experiment. To solve the equation and to predict numbers over time, we specify the numbers at time  $t = 0$  (the initial conditions) and iterate Eq. 2.5 for  $t = 0, 1, 2, \dots, n$  time steps. This model produces the familiar exponential population increase over time (Fig. 2.4). Since the model output is population numbers over time, computing the doubling time is simply a matter of observing the time interval at which the predicted numbers are twice the initial numbers.

The alternative model is handled in a similar way. The key aspect of Eq. 2.4 is that the expression in brackets depends on the current population numbers ( $N_t$ ). This causes the numbers of offspring produced by each female to be reduced as population numbers increase. Although the mechanisms for this phenomenon are not described, they may be due to competition among females for food or child rearing costs. Notice that the relationship between population growth rate and this algebraic expression is similar to that between numbers of species on an island and immigration and extinction rates in Chapter 1 (Eq. 1.1).

Equation 2.4 has two parameters that we calibrate by finding an expression involving  $r$ ,  $K$ , and measurable quantities. Rearranging Eq. 2.4 to again form the realized per capita growth rate on the left-hand side yields:



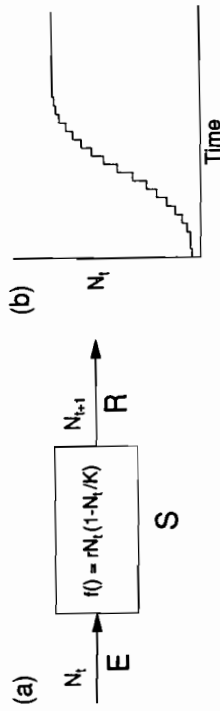
**Figure 2.4:** (a) The ESR scheme and (b) a typical dynamic trajectory for density-independent population growth using Eq. 2.5.

$$\frac{N_{t+1} - N_t}{N_t} = r - \frac{r}{K}N_t.$$

This is a linear equation in which the left-hand side is the  $y$ -axis, or dependent variable, and  $N_t$  is the  $x$ -axis, or independent variable. We can use linear regression to obtain estimates of the intercept ( $r$ ) and the slope ( $-r/K$ ) from which we can calculate  $K$ . The dynamics produced by this model are the classical sigmoidal or S-shaped curve of the *logistic* equation (Fig. 2.5). We will use the same approach to calculating the doubling time for this model as for the first model.

To this point, we have developed alternative hypotheses, their respective mathematical and computational formulations, and a strategy to answer the original question. The next step is to validate the models. Since the model describes the world, we cannot realistically hope to find a similar, alternate system to study (not in this solar system, anyway). We might, however, validate the models by comparing each to an earlier historical record, one not used in the formulation of the model (e.g., from the period 1800–1850). This approach to validation makes some important assumptions about the nature of the system in the past and the present, but it is perhaps as good as we can expect when we cannot replicate the system.

After constructing both models and subjecting them to independent comparisons against the same data set, we may reach the conclusion that either none, one, or both of the models are inadequate to explain the data. Based on the results, we would choose between the two models, if possible (Walters 1986 and Chapter 8). Given that one or more of the models passed our validation test, we could then proceed to analyze the model by calculating the expected doubling time.



**Figure 2.5:** (a) The ESR scheme and (b) a typical dynamic trajectory for density-dependent population growth using Eq. 2.4.

It is natural to ask: "Which alternative hypotheses should a modeling problem compare?" There is no general answer since it depends on the sub-discipline and the objectives of the model. Nevertheless, the two examples given (ants and populations) have something in common among their alternatives. Both examples have a *null* model: a model that hypothesizes that the observed dynamics are not caused by complicated biological processes. In the ant example, the simplest model was one in which seeds were returned to the nest as a result of random movement of individual ants: no interactions between ants were modeled. In the population model, the density-independent model assumed there were no interactions (e.g., competition) between individuals. In my usage here, a null model need not be completely random (e.g., density-independence), although we could have constructed such an alternative. So, it is a matter of degree how far removed from biology one wishes the alternatives to be, but at least one of the models should be as simple as possible; removing biological processes is one method of constructing simple models. As Richard Levins once said: "In order to understand complex systems, it is necessary to study something else instead" (Levins 1970). By this he meant not only models of the system, but also simple models. In the case of biological systems, this may mean models with little or no biological processes in them. The objectives statement should indicate the degree to which biological processes are to be removed from one of the alternatives.

The alternative modeling approach is not useful in all applications. There is an obvious negative correlation between the number of alternative models that can be examined and the effort needed to construct any one model. Even in cases of simple models, in relatively mature disciplines such as physiology, in which either data quality is high or understanding is deep (Fig. 1.2), there will be less debate over the correct form of equations. At some point where a science matures from using models for "what-if gaming" to "recommending action," the equations become less debatable. In these systems, alternative models are less important. However, in the less mature disciplines such as ecology, especially where mechanisms are not understood, there is greater uncertainty, and the effects of using a particular set of equations need to be investigated with alternative models.

## 2.4 Model Objectives

*Never weed your garden in the dark.*

— JWH

We have repeatedly referred to the objective statement and its role in constraining model structure. It is worthwhile to delve a little deeper into this concept and discuss the attributes of a good objective statement. A careful statement of the objectives of a model is important because it defines the problem to be solved and can, therefore, be used to devise the implementation and analysis of the model. The objective statement can also define the domain of applicability of the model. This latter use is important since it can reduce possible misuse of the model and help identify certain kinds of criticism as being directed not to the substance of the model, but to its objectives. These are two different types of criticism. So, while model objectives do not always appear in print, they should be explicitly stated at some point.

Modelers do not agree on the content of a good statement of objectives, but Over-

## §2.4: Model Objectives

ton (1977) contains the most explicit rendition. He emphasizes that effective objectives are those that are stated as *goals with purposes*. For example, "Construct a model of photosynthesis [goal] to determine the effects of elevated UV light [purpose]." But beyond the purpose, an objective statement must provide the following information.

1. The objective *question(s)*.
  2. The *perturbations* and *stimuli* accommodated in the model.
  3. The exact *system* and *environment* which the model addresses.
  4. The temporal and spatial *scales* over which the system is to be described.
  5. The temporal and spatial *scales of extrapolation and prediction*.
  6. The *factual information* and *theoretical concepts* used in model construction (data, assumptions, sources, etc.).
  7. The *criteria of validation* (empirical and theoretical).
- To illustrate one of the best and most complete statements of model objectives, I give an extended quote from Innis (1978). The objective applies to a large, complex model, so this perhaps justifies the lengthy statement.

The objective of this modeling activity was to develop a total-system model of the biomass dynamics for a grassland that, via parameter change, could be representative of the sites in the US/IBP [United States/International Biological Program] Grassland Biome network and with which there could be relatively easy interaction.

There are several key points in this objective that deserve elaboration. First, the term *total-system* model refers to the inclusion of abiotic, producer, consumer, decomposer, and nutrient subsystems. This requirement was imposed to assure that the modeling effort played the integrative role delegated to it . . .

Second, *biomass dynamics* identifies our principal concern with carbon or energy flow through the system. Focus on biomass facilitated the comparison of model and data but turned out to be unfortunate because it is not conserved. The model, therefore, tracks carbon and converts it to biomass (and vice versa) in a number of places. We are concerned with dynamics as part of the general objective of the International Biological Program (IBP).

Third, *representative* expresses our desire to have the model apply, with minimal effort, to sites in the US/IBP Grassland Biome study. Changes of parameters are certainly necessary as these describe site characteristics (among other things). The representation was to depict "normal" dynamics as well as the response of the system to a variety of perturbations.

Finally, *relatively easy interaction* was a desideratum because of the role the effort was to play in program direction . . .

This objective provides only the broadest guidelines to the modelers as to their respective functions. The purpose of the objective is to found the decision making processes that accompany model building. This involves clarification as to how many producers and consumers should be included, the amount of detail required in a representation of a producer, and whether a phosphorus, calcium, or lead model is required [i.e., resource management and research design]. . . In 1970 it was agreed that this objective would stand, with the first model addressing four specific questions:

1. What is the effect on net or gross primary production as the result of the following perturbations: (a) variations in the level and type of herbivory,

- (b) variations in temperature and precipitation or applied water, and (c) the addition of nitrogen or phosphorus?
- How is the carrying capacity of a grassland affected by these perturbations?
  - Are the results of an appropriately driven model run consistent with field data taken in the Grassland Biome Program, and if not, why?
  - What are the changes in the composition of the producers as a result of these perturbations?

These questions were further specified with definitions of terms such as “variations,” “level,” and “type”; acceptance criteria were chosen.

This is a description of a whole ecosystem-level model, and it is quite possible that the reader will not appreciate the motives for or value of building these types of models. Nevertheless, it provides a reasonably clear statement of what the model is intended to do. Other disciplines may not require for publication such a self-conscious and direct statement, but, at some point, the modelers probably do.

## 2.5 Exercises

- Write an objective statement for the island biogeography problem of Chapter 1.
- Design an alternative model for the island biogeography situation that uses curvilinear immigration and extinction functions. Consider a negative exponential and simple quadratic, respectively.
  - Graph the new rates of change against  $R$  and qualitatively sketch the dynamics of colonization from an empty island. Contrast these dynamics with those of the original model.
  - Write a new finite-difference equation and show that the equilibrium number of species satisfies
 
$$\frac{I_x}{E} = R^2 e^{aR}.$$
- Speculate on a biological mechanism that might support this alternative.
- To what extent has Innis incorporated Overton’s criteria for objectives statements?
- How good was the objective statement of the “doubling time” model?
- Using Innis’ statement and Overton’s criteria as guides, write an objective statement for the following problem: “How many cases of AIDS will occur in Utah in 2015?” Would the objectives change if the location had been San Francisco? Why or why not? What role does spatial scale of extrapolation play in this problem?

- Write an objective statement for this problem: “What should be the best grazing pressure on the XYZ National Forest to simultaneously maximize cattle production and forest quality?”
- We noted in the discussion of the model of the world’s population that our abilities to validate the model were limited by our inability to replicate the system. Under what circumstances, if any, is it worth while to model systems that cannot be replicated or tested using rigorous statistical methods?

## §2.5: Exercises

- Read pages 10–13 in Reckhow and Chapra (1983b) and decide if there is a need to distinguish *validation* and *corroboration*.
- Read an article in a current journal describing a model and critique the objective statement. In the models described in the chosen journal, how many discuss validation?