Lecture 1, Tuesday, Aug. 22. **Homewrok 1 is due on Thursday, Sept. 7.**

Reading homework: section 4.1, page 116-121.

Chapter 1: Introduction

The purpose of science to society is to produce *useful models of reality*. While it is virtually impossible to make inferences from human senses which actually describe what "is," we can form hypotheses based on *observations*. By analyzing a number of related hypotheses, scientists can form general theories. Specifically, scientists apply skeptical, methodical evaluation of the body of evidence that seeks to establish alternative working hypotheses, and then reject some hypotheses, while retaining others (the remainder are still subject to re-evaluation in the light of new data or theory). Such processes are the internal organs of sciences which are vital but usually not revealed in manuscripts, books, or presentations.

Frequently, the goal of a mathematical bioscience effort is to obtain an **integrative understanding** of some biological issues with the help of mathematical tools (often models). **In most of such cases, models are our purposes and our products.** The models shall be biologically well motivated, mathematically carefully (painfully) formulated and numerically thoroughly tested (they shall produce plausible dynamics when parameters are plausible). *Models must be built on the basis of a solid and preferably a comprehensive understanding of the relevant existing biology literature/knowledge.* This often requires the collaboration of bio-scientists. Lack of such solid understanding contributed to the proliferation of many imaginary and absurdly formulated ad hoc models in the literature. To succeed in a modeling effort is very much like to succeed in an experimental effort: learn from failures and keep improving on the model at hand.

Once a model is satisfactorily formulated, mathematicians may devote substantial effort to systematically study the fine and often rich dynamics of the model, such effort often calls for advanced training in mathematics and is often labeled as biomathematical research. In some senses, biomathematics is an important part of the broadly defined area of mathematical biosciences.

As biosciences continue to strengthen their dominance of sciences, mathematical biosciences are doing the same in the broad areas of applied mathematics and applications of mathematics. In addition, mathematical biosciences' reaches are expanding rapidly into the hearts of all areas of biosciences.

This course seeks to lay a basic foundation for mathematical biosciences research.

Science as simplification: Observation, modeling and experiment can each be seen as a way of organizing, ordering and simplifying our understanding of the natural world.

Observations can simplify by focusing on critical components and highlighting similarities and differences among phenomena. Modeling simplifies by exposing the effects of a few model parameters, ignoring many or most of the complexities of the real world. Experiment simplifies by holding all but a few factors constant (by the use of replicates and controls).

Why use mathematical models or mathematical approaches?

1) To expose faulty assumptions.

Consider the Malthus (http://www.marxists.org/reference/subject/economics/malthus/) exponential growth (x'=ax) as an example. The assumption there is that growth is independent of population size/density. According to Malthus, "…Population, when unchecked, increases in a geometrical ratio. Subsistence increases only in an arithmetical ratio. A slight acquaintance with numbers will show the immensity of the first power in comparison of the second. By that law of our nature which makes food necessary to the life of man, the effects of these two unequal powers must be kept equal. This implies a strong and constantly operating check on population from the difficulty of subsistence. This difficulty must fall somewhere and must necessarily be severely felt by a large portion of mankind…." In truth, Malthus model, while useful in some physical applications, it almost never applies to natural populations except for a short time following introductions or invasions. We are forced to incorporate density dependence, leading to many density dependent growth models, including the logistic equation (x'=rx(1-x/K)), regrowth model (x'=b-ax, for perennials) and Gompertz model (x'=r_0e^{-at}x, or x' = rx – ax ln x=-axln (x/d), r=r_0+a ln x_0). A more mechanistic approach involves the employment of Droop (growth rate) model ($\mu = \mu_{\max}\left(1-\frac{q}{Q}\right)$).

logistic.m

```
function [Ydot] = LogisticCont(t,Y, r, K)
r=1; K=1.4;
Ydot(1) = r*Y(1)*(1-Y(1)/K);
Ydot=Ydot';
```

regrowth.m

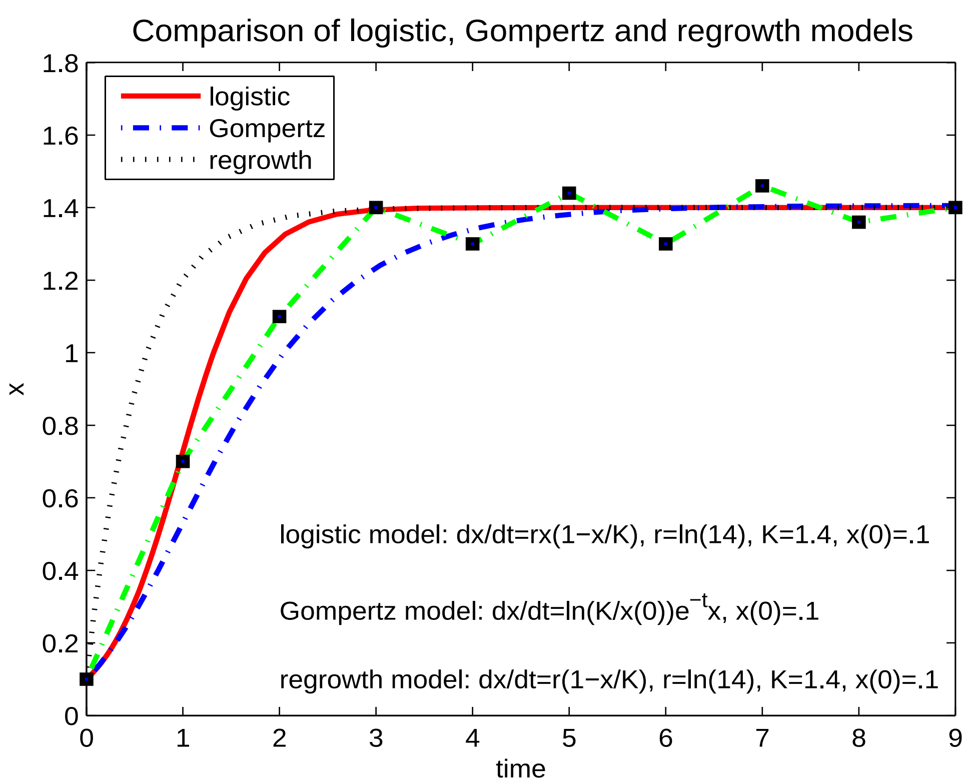
```
function [Ydot] = regrowth(t,Y, r, K)
r=1; K=1.4;
Ydot(1) = r*(1-Y(1)/K);
Ydot=Ydot';
```

Gompertz.m

```
function [Ydot] = Gompertz(t,Y)
Ydot(1) = Y(1)*Y(2);
Ydot(2) = -Y(2);
Ydot=Ydot';
```

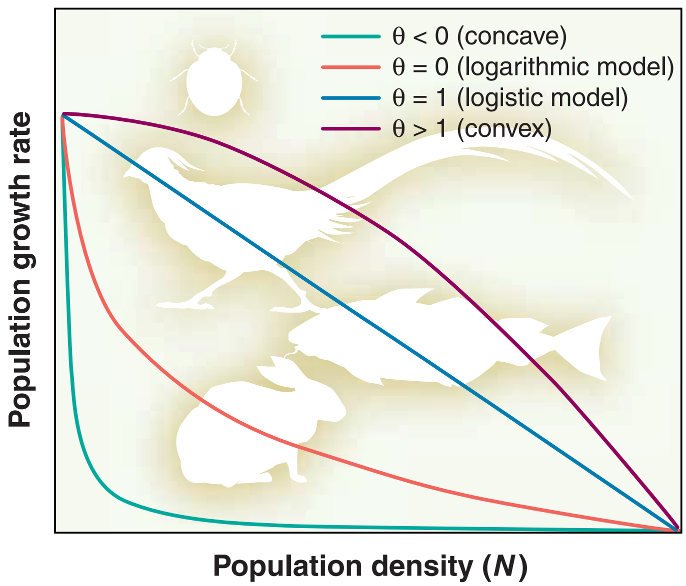
OneSpeciesPlot.m

```
figure
time=9; fs=10;
[T1,Y1] = ode23s('logisticCon',[0 time],[.1]);
[T2,Y2] = ode23s('Gompertz',[0 time],[.1, log(14)]);
[T3,Y3] = ode23s('regrowth',[0 time],[.1]);
x = 0:1:9;
y = 0.2*[0.5 3.5 5.5 7 6.5 7.2 6.5 7.3 6.8 7]';
option=odeset('AbsTol',1e-9,'RelTol',1e-9);
plot(T1(:,1),Y1(:,1),'r',T2(:,1),Y2(:,1),'b-.',T3(:,1),Y3(:,1),'k:',x,y,'-.gs','LineWidth',2,...
          'MarkerEdgeColor','k','MarkerFaceColor','b','MarkerSize', 4);
text(2,0.5,'logistic model: dx/dt=rx(1-x/K), r=ln(14), K=1.4, x(0)=.1','FontSize',fs);
text(2,0.3,'Gompertz model: dx/dt=ln(K/x(0))e^{-t}x, x(0)=.1','FontSize',fs);
text(2,0.1,'regrowth model: dx/dt=r(1-x/K), r=ln(14), K=1.4, x(0)=.1','FontSize',fs);
legend('logistic','Gompertz','regrowth',2)
title('Comparison of logistic, Gompertz and regrowth models','FontSize',12)
xlabel('time'); ylabel('x'); xlim([0 time]); ylim([0 1.8]);
```



Different shapes for the relationship between population growth rate and density.

The growth rate–density relationship can be modeled by the *a*-logistic equation per capita growth rate (pgr) = $r_1[1 - (N/K)^a]$: r_1 is the rate of population growth at density 0 [$r_1 = r_0/(1 - K^{-a})$, where r_0 is the maximal rate of population growth from low density]; K is the carrying capacity of the environment, or equilibrium; *a* controls the shape of the relationship and depends on the ways that members of a population interact at different densities. Sibly *et al.* (Science, 2005) find that mammals, birds, fish, and insects do not generally grow exponentially to carrying capacity, as had been widely thought due to logistic model. Instead, population growth decelerates well before carrying capacity is achieved, as illustrated by the concave

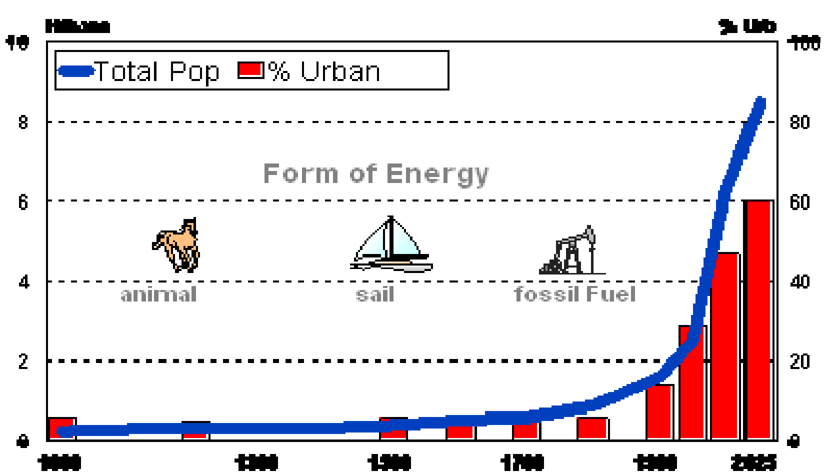


curve.

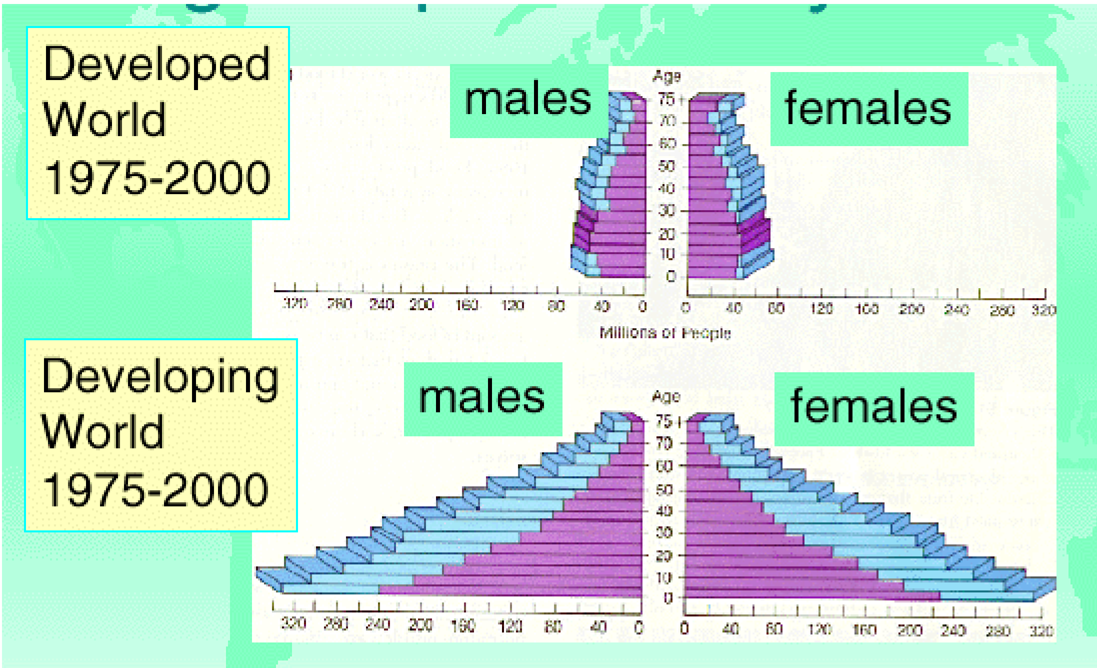
Exercise 1.1: Show that the solution of $x' = r_0 e^{-at} x$, $x(0)=x_0$ is the same as the solution of $x' = rx - ax \ln x$ with $x(0)= x_0$.

2) To provide testable statement or new insights.

Models can guide our thinking, provide the basis for critical tests or experiments and clarify our thinking about a problem. Consider again the logistic equation. The maximum growth rate shall occur at x=K/2. This statement can be tested by some specific population growth experiments. For example, by inspecting the following figure, one may estimate the earth's carrying capacity for human is 9-10 billions. DO NOT BELIEVE THIS.



Age structure is a very important aspect of population dynamics.



<u>Science is progressive, and subject to test and falsification.</u> We seek a better, more comprehensive view of interrelationships. In the arts, no one can improve on Shakespeare or Beethoven -- a new artist may be revolutionary, perhaps, but not progressive in the same sense.