

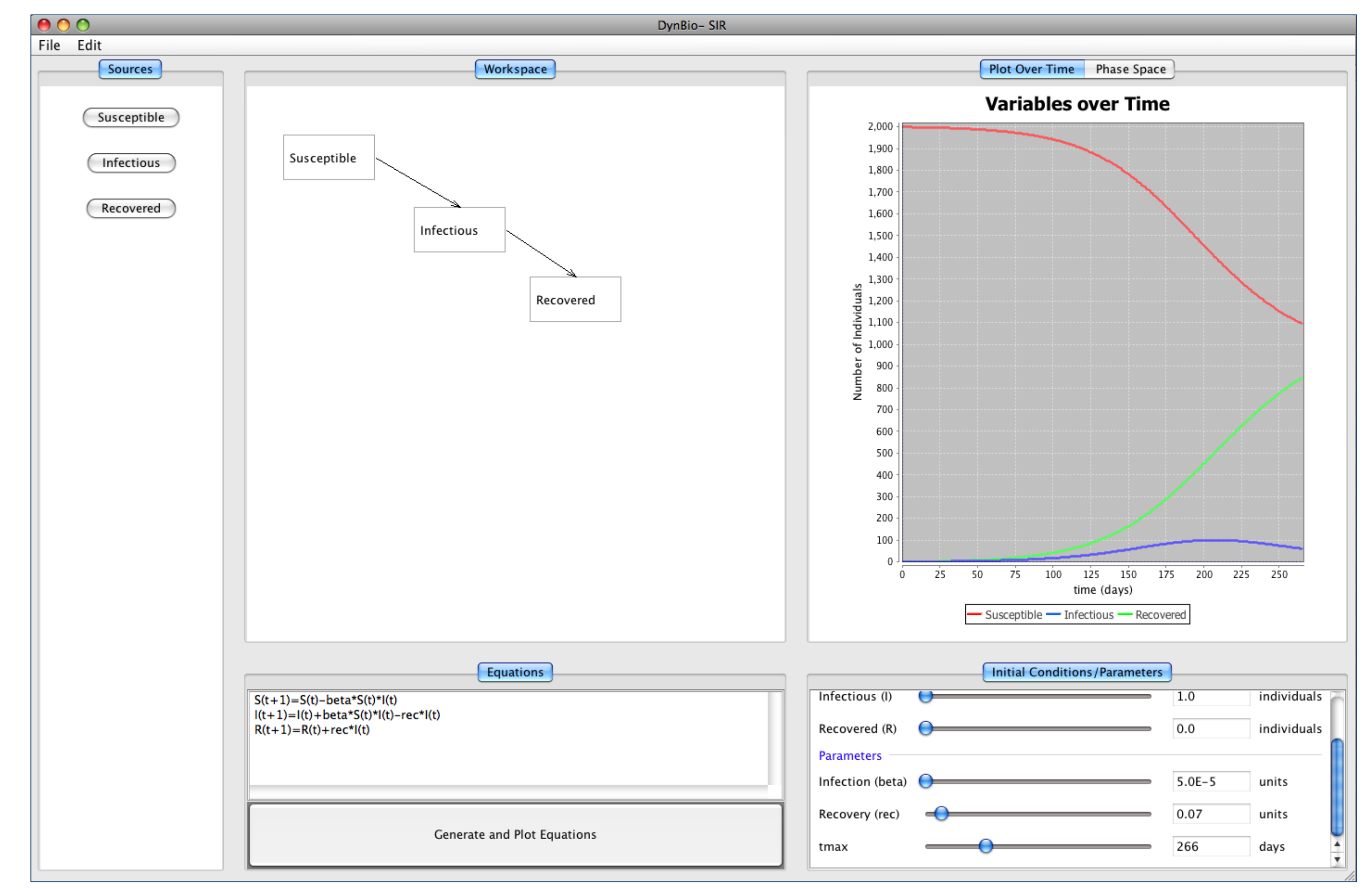
## Introduction

Mathematical biology is to a large extent the modeling of interaction networks and their formulation as differential equations. Teaching mathematical biology on an undergraduate level presents a two-fold problem:

1. Students are uncomfortable with the formalism of differential equations.
2. Educators face the problem of being limited in the concepts that they can teach students with little formal background.

To date, various modeling software exist [1] to model interaction networks, predominantly targeted at scientists [2-5]. None of the existing software puts emphasis on the student and educator relation. Thus, we have developed an application called DynBio that is geared to facilitate easy modeling of networks. Direct visual feedback of the network, plot over time and phase diagram of the network and its equations are presented to the student. Additionally, DynBio contains a flexible data structure which allows detection of modeling errors for the student and the easy extension to various network types for educators.

## Screenshot of DynBio with an Epidemiological Model



1. Click sources to be included in the model (they are added to the workspace).
2. Connect sources with arrows (representing interactions or events).
3. Generate the equations corresponding to the model in the workspace, then plot those equations.
4. Change values of initial conditions and/or parameters, and re-plot the equations.

## Case Study (SIR model)

Biol 2400: Mathematical Models in Biology  
- geared towards sophomores with little programming experience

### CASE STUDY (from Biol 2400, Spring 2009)

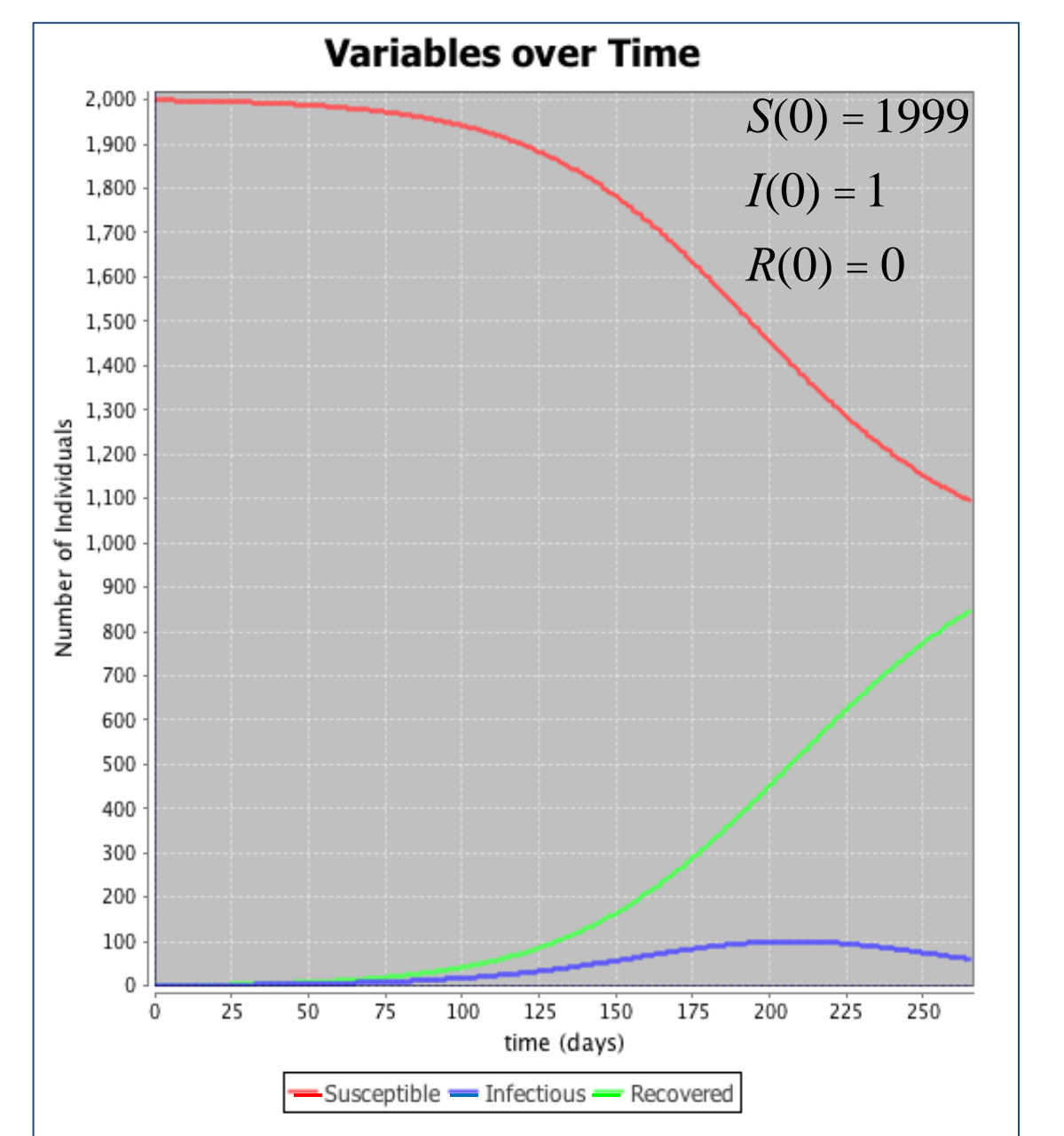
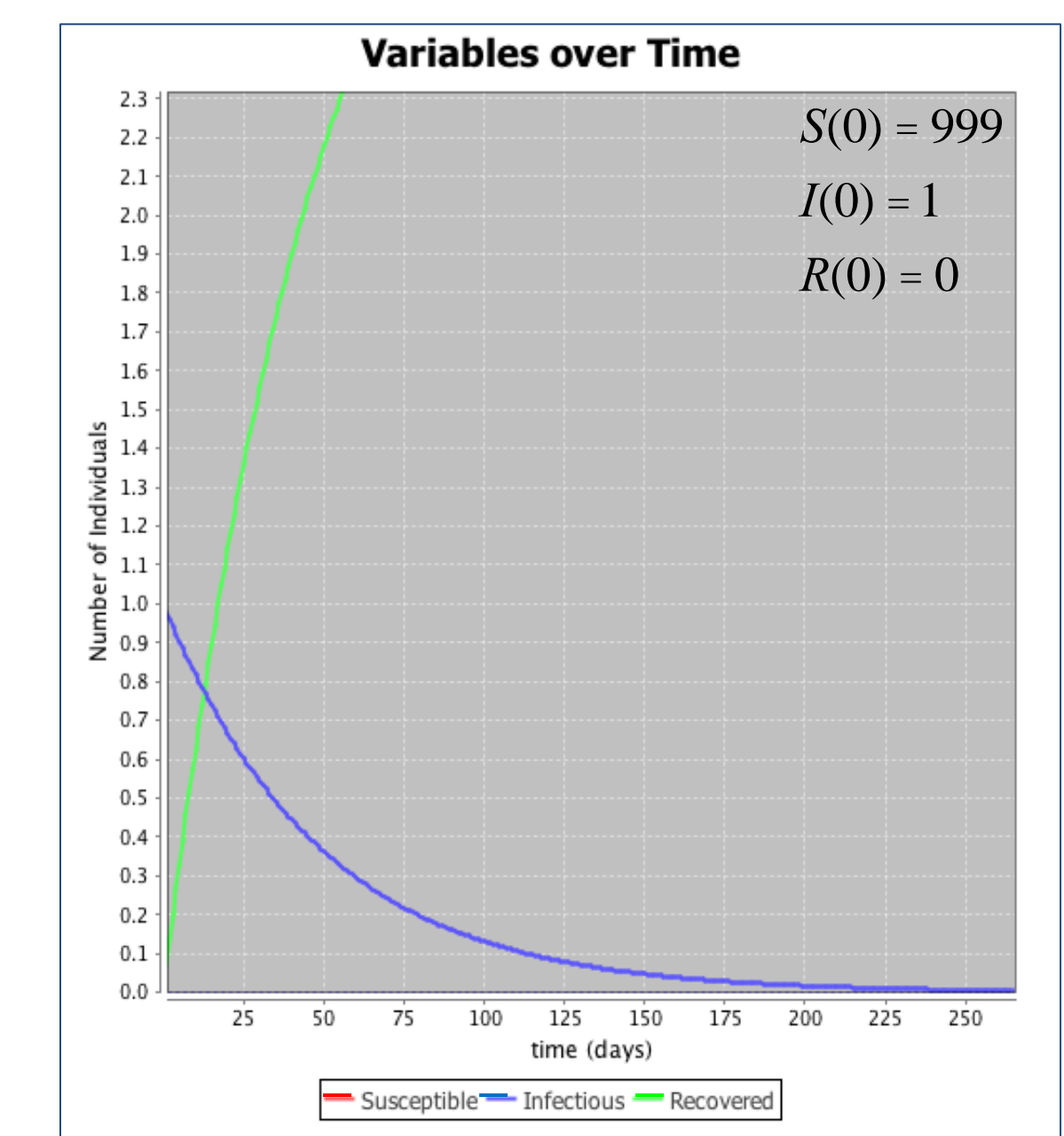
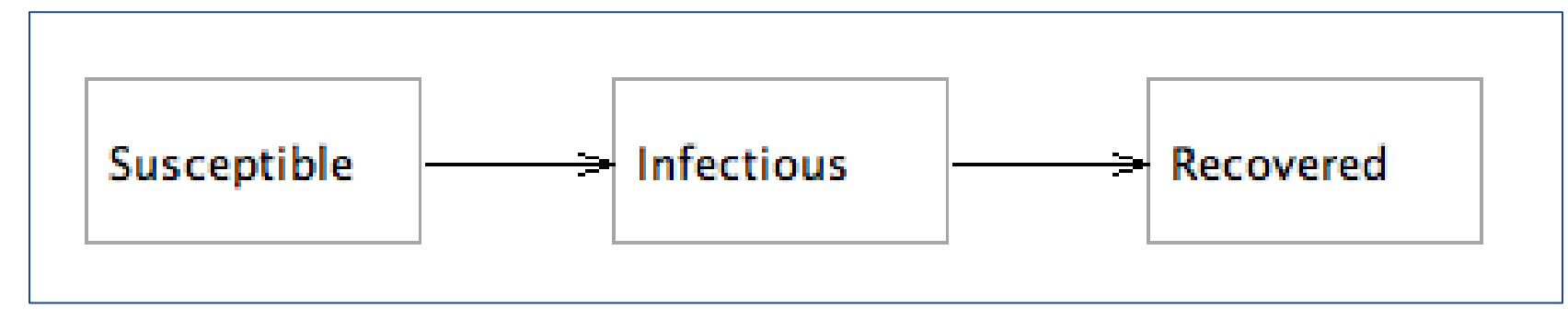
“Imagine there is an outbreak of a disease similar to the avian flu in Northeast Malaysia. There are a number of villages affected by the disease, although it seems that epidemic outbreaks only occur in the largest villages. Your job is to understand why.

- There are between 500 and 5000 people in each village.
- The suspected outbreak involves, initially, a single infected individual.
- The typical villager interacts with ~1% of their village in a typical day.
- It takes approximately 2 weeks to recover once ill (according to prior cases).
- The probability of infection given a contact is very low, .5%.

Does the epidemic depend on village size?”

$$b = 0.005 * 0.01 = 0.00005$$

$$1/r = 14 \supset r = 0.0714$$

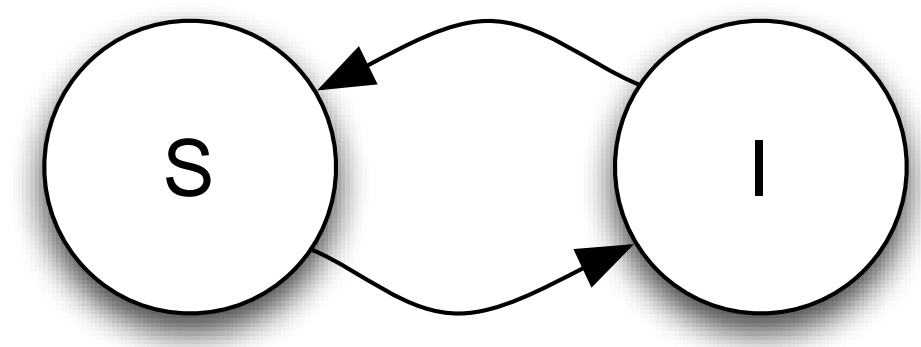


Yes, an epidemic occurs when  $S(0) > r/b = 0.0714/0.00005 \gg 1428$

## DynBio Pedagogical Pipeline

### Graphically build model of biological system

Given susceptible individuals,  $S$ , and infected individuals,  $I$ , a rate of infection,  $\beta$ , and a rate of recovery,  $r$ , we can graphically model the system in the following way:

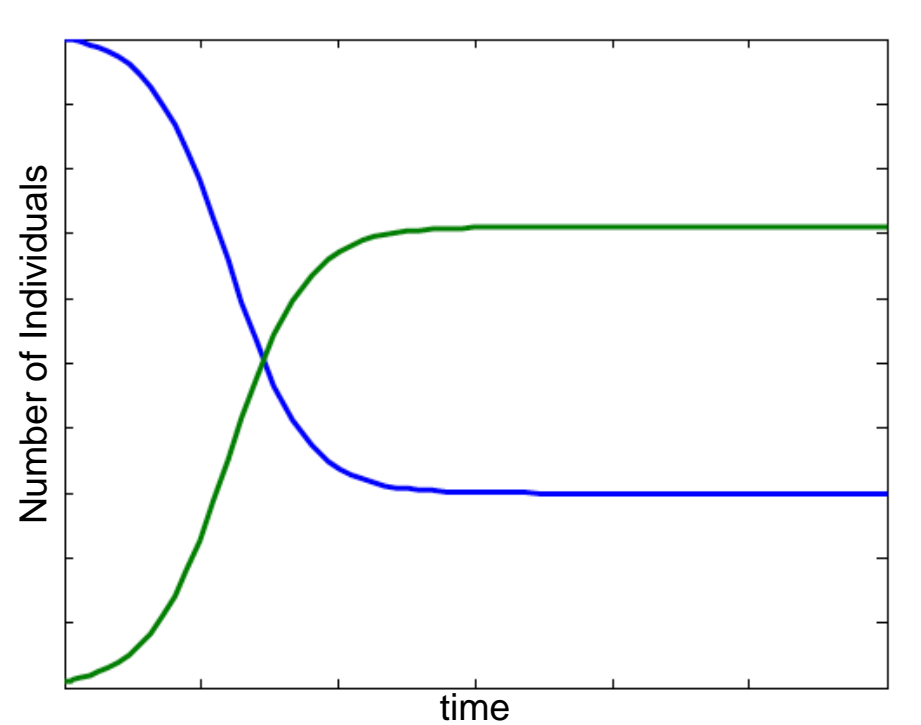


### Turn model into equations

$$S(t+1) = S(t) - \beta S(t)I(t) + rI(t)$$

$$I(t+1) = I(t) + \beta S(t)I(t) - rI(t)$$

### Analyze dynamics of system



## Dynamic Equations Generated from Graphical Models

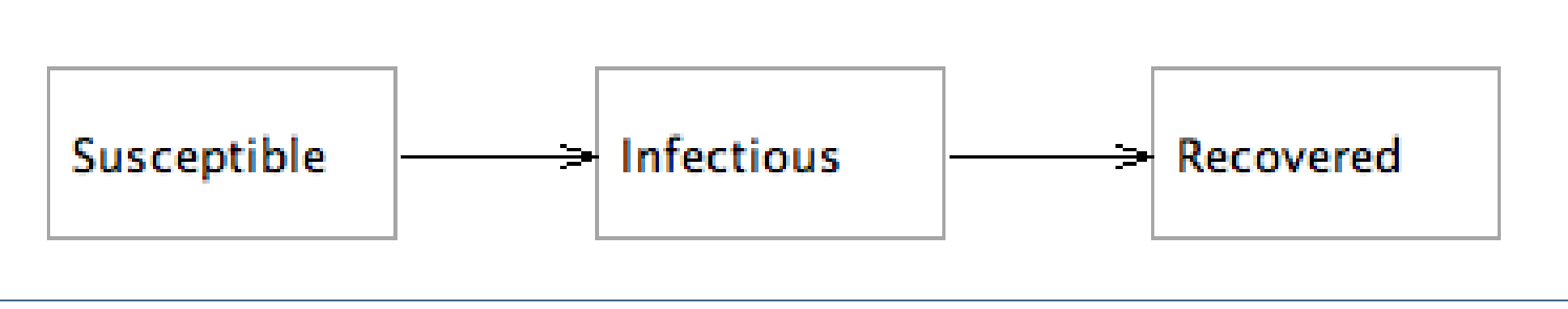
Once a module is added and all possible and equations are defined, students can build models graphically. Equations are then generated for the student's model in 2 steps:

1. The graph is translated into an interaction matrix using the matrix of all possible interaction (SIR model is shown to the left).
2. The entries in the interaction matrix point to columns in the equation matrix, resulting in terms for each interaction.

All possible interactions

	S	I	R	$\emptyset$
S	5	1	4	6
I	0	7	2	8
R	3	0	9	10

Graphical model



Interactions from graph

	S	I	R	$\emptyset$
S	5	1	0	6
I	0	7	2	8
R	0	0	9	10

All possible terms

	$\emptyset$	$\beta$	$r$	$i$	$v$	$b_s$	$d_s$	$b_I$	$d_I$	$b_R$	$d_R$
$S(t+1)$	$\emptyset$	$-\beta * S * I$	$\emptyset$	$i * R$	$-v * S$	$b_s * S$	$-d_s * S$	$\emptyset$	$\emptyset$	$\emptyset$	$\emptyset$
$I(t+1)$	$\emptyset$	$\beta * S * I$	$-r * I$	$\emptyset$	$\emptyset$	$\emptyset$	$\emptyset$	$b_I * I$	$-d_I * I$	$\emptyset$	$\emptyset$
$R(t+1)$	$\emptyset$	$\emptyset$	$r * I$	$-i * R$	$v * S$	$\emptyset$	$\emptyset$	$\emptyset$	$\emptyset$	$b_R * R$	$-d_R * R$

$$S(t+1) = S(t) + b_s S(t)$$

## Conclusions and Future Work

- DynBio facilitates the learning of dynamical systems as a result of direct visual feedback. DynBio's modularized extensibility to a wide range of interaction networks underlines its relevance from an instructors perspective.
- Future work is focused on increasing the extensibility of DynBio, incorporating differential versus difference equations, providing the option to compare the simulation to available data, and the modeling of interactions between two interaction networks.

Thanks to the Burroughs Wellcome Fund, James S. McDonnell Foundation & Bioinformatics Masters Program for financial support.

## References

- [1] Alves R, Antunes F, Salvador A (2006) Tools for kinetic modeling of biochemical networks. Nature Biotechnology 24:667-672.
- [2] <http://www.cbs.umn.edu/populus/>.
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