Homework 21

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PREAMBLE:

> **#Question to self: but what if two text files have the same name of a procedure but do completely different things? is the procedure from the first txt file ignored because the procedure from the second file replaces the first?**

> **read `C:/Users/cgrie/Dynam Models Bio/Homeworks/HW21/DMB.txt` ;**

read `

First Written: Nov. 2021

This is DMB.txt, A Maple package to explore Dynamical models in Biology (both discrete and continuous)
accompanying the class Dynamical Models in Biology, Rutgers University. Taught by Dr. Z. (Doron Zeilbeger)

The most current version is available on WWW at:
http://sites.math.rutgers.edu/~zeilberg/tokhniot/DMB.txt .
Please report all bugs to: DoronZeil at gmail dot com .

For general help, and a list of the MAIN functions,
type "Help();". For specific help type "Help(procedure_name);"

For a list of the supporting functions type: Help1();
For help with any of them type: Help(ProcedureName);

For a list of the functions that give examples of Discrete-time dynamical systems (some famous),
type: HelpDDM();
For help with any of them type: Help(ProcedureName);

IMPORTANT INFO FOR
When doing all the time series stuff, leave at least a couple of the parameters as symbols, otherwise the TimeSeries commands

####################
PROBLEM 1: Carefully read, and understand, the Maple code for the following procedures (type **Help (ProcedureName)**; for instructions)

ChemoStat, GeneNet, Lotka, Volterra, VolterraM

For each of them, experiment with three randmom choices of parameters, and random initial conditions, using **TimeSeries (with h = 0.01)**, of each of the quantities in question, and (if applicable,i.e things take place in R2) also **PhaseDiag**.

Part 1: CHEMOSTAT

What chemostats in real life do:
A Chemostat is a device that microorganisms grow/live inside, and delivers nutrient in a controlled manner

about the chemostat model:

```
> Help(ChemoStat);
```
ChemoStat(N,C,a1,a2): The Chemostat continuous-time dynamical system with N=Bacterial
poplulation densitty, and C=nutient Concentration in growth chamber (see Table 4.1 of
Edelstein-Keshet, p. 122)
with paramerts a1, a2, Equations (19a_, (19b) in Edelestein-Keshet p. 127 (section 4.5, where they
are called alpha1, alpha2). a1 and a2 can be symbolic or numeric. Try:
$$ChemoStat(N,C,a1,a2);$$
$$ChemoStat(N,C,2,3);$$ **(2)**

```
> CS := ChemoStat(N,C,3,4);
```
$$CS := \left[\frac{3\,C\,N}{C+1} - N, \ -\frac{C\,N}{C+1} - C + 4 \right]$$ **(3)**

> **Help(TimeSeries);**

TimeSeries(F,x,pt,h,A,i): Inputs a transformation F in the list of variables x

The time-series of x[i] vs. time of the Dynamical system approximating the the autonomous
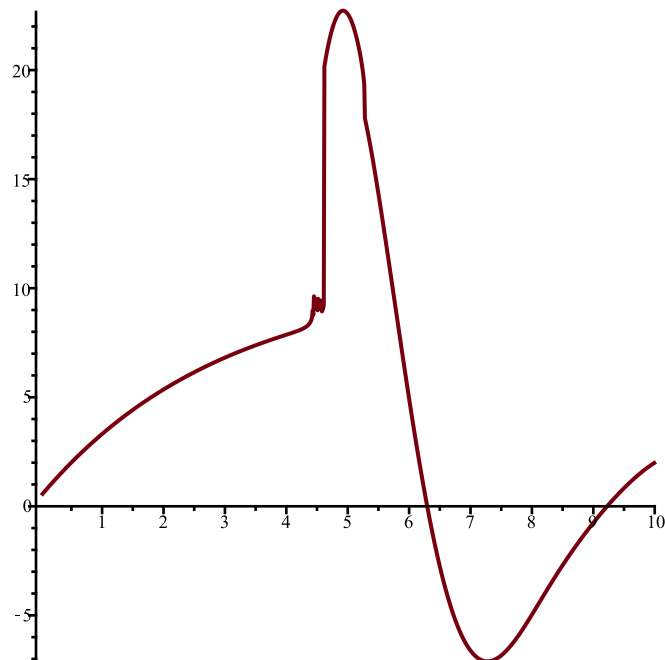
continuous dynamical process

$dx/dt=F(x(t))$ *by a discrete time dynamical system with step-size h from t=0 to t=A*

Try:

TimeSeries([x*(1-y),y*(1-x)],[x,y],[0.5,0.5], 0.01, 10,1);   **(4)**

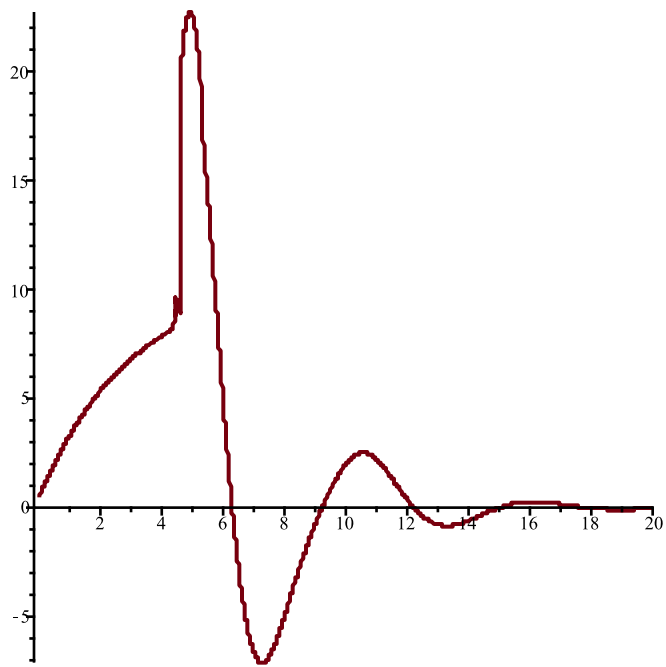> **TimeSeries(CS,[C,N],[0.5,0.5],0.01,10,2);**
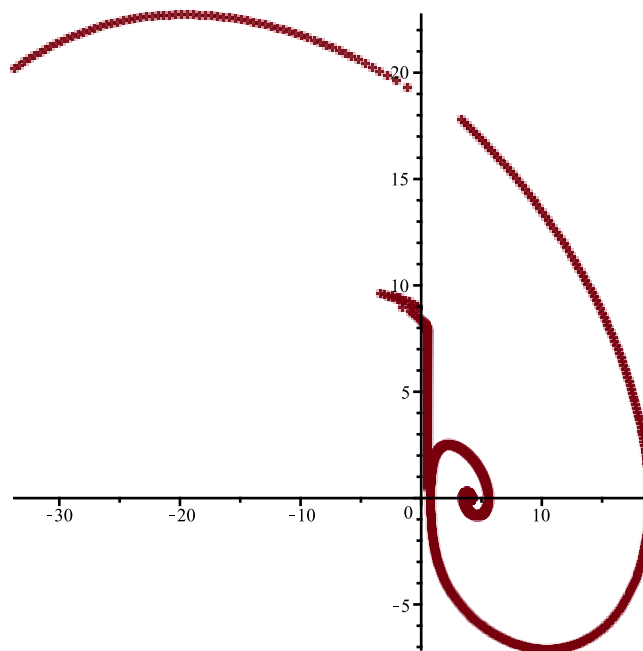

Whats with the weird spikiness?

I will see what happens long term

> **TimeSeries(CS,[C,N],[0.5,0.5],0.01,20,2);**

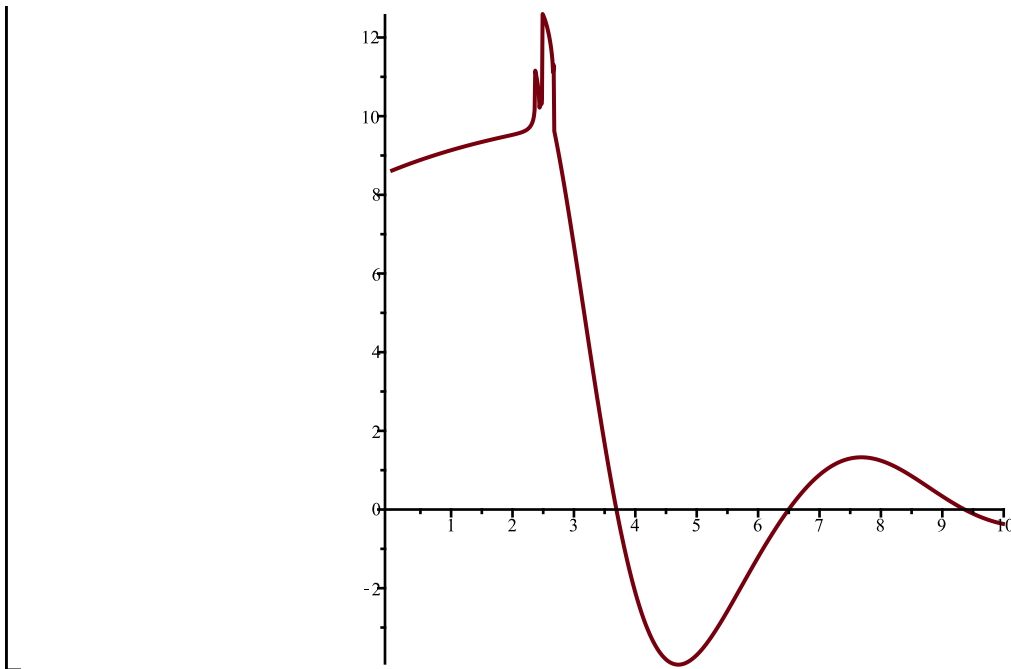> **PhaseDiag(CS,[C,N],[0.5,0.5],0.01,20,1);**

Move initial conditions so y-value starts near a 9

> **TimeSeries(CS,[C,N],[0.5,8.6],0.01,10,2)**

The volatility location actually got nudged up to above 10
#############################
PART 2: GeneNet

what Gene net does:
There is an oscillatory network

gene regulation network- whet is the regulation?

people are Doing Synthetic biology by creating that correspond to simple models.

one type of model can be a clock

Another type of model can be a switch.

GeneNet is a clock-type model.

```
> Help(GeneNet);
```
GeneNet(a0,a,b,n,m1,m2,m3,p1,p2,p3): The contiuous-time dynamical system, with quantities m1,
   m2,m3,p1,p2,p3, due to M. Elowitz and S. Leibler
      described in the Ellner-Guckenheimer book, Eq. (4.1) (chapter 4, p. 112)
   and parameers a0 (called alpha_0 there),a (called alpha there), b (called beta there) and n. Try:
         GeneNet(0,0.5,0.2,2,m1,m2,m3,p1,p2,p3);   **(5)**

It appers that gene net describes how concentrations of protien repressors (p1 corresponds to P_lacI , p2
corresponds to P_tetR, p3 corresponds to P_cI)
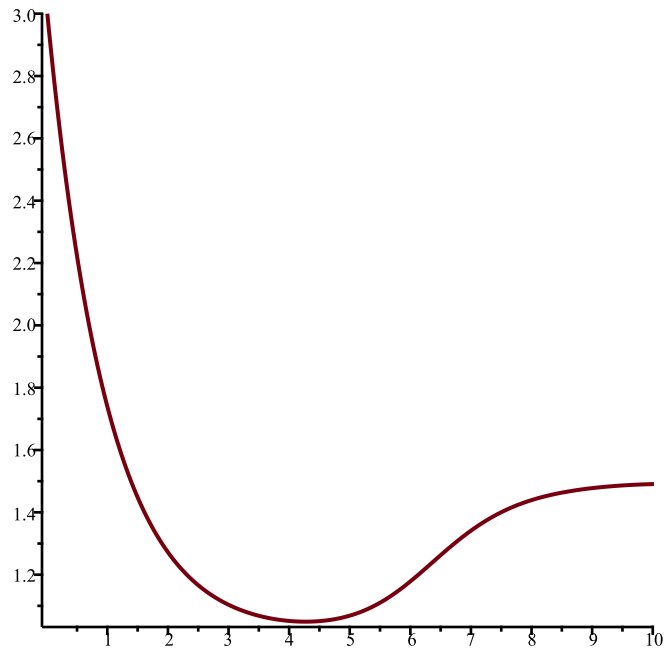interact with MRNA
MRNA :(m1 corresponds to M_lacI , m2 corresponds to M_tetR, m3 corresponds to M_cI)
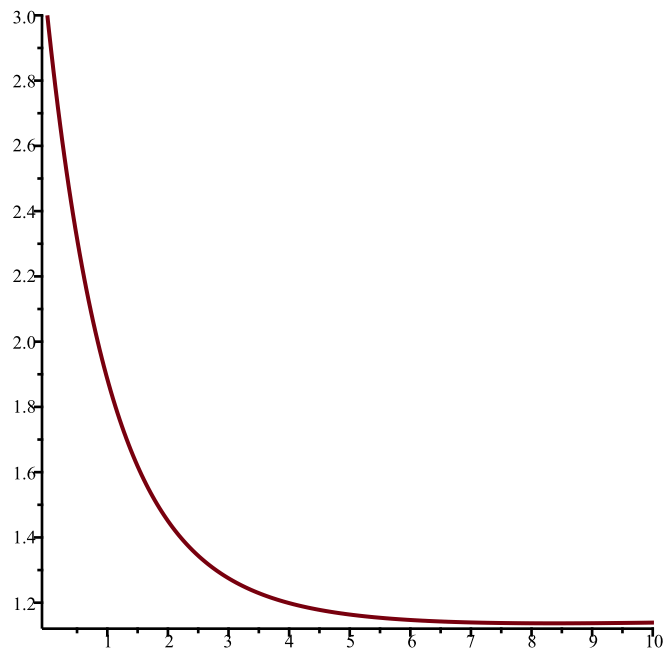
```
> GN := GeneNet(1,0.5,0.2,4,m1,m2,m3,p1,p2,p3);
```

$$GN := \left[-m1 + \frac{0.5}{p3^4 + 1} + 1, \ -m2 + \frac{0.5}{p1^4 + 1} + 1, \ -m3 + \frac{0.5}{p2^4 + 1} + 1, \ -0.2\,p1 + 0.2\,m1, \right. \quad \textbf{(6)}$$

$$\left. -0.2\,p2 + 0.2\,m2, \ -0.2\,p3 + 0.2\,m3 \right]$$

```
> TimeSeries(GN,[m1,m2,m3,p1,p2,p3],evalf([1.3,3,1,-6,0.1,0.1]),
  0.01,10,2)
```



```
> TimeSeries(GN,[m1,m2,m3,p1,p2,p3],evalf([1.3,3,1,1,0.1,0.1]),
  0.01,10,2)
```

                                                                                 (7)

```
> #We must represent some part of GN in R2 (even if there is not
  all the information). #Maybe just show relationship between 2 v
  m1 and p1.

  #THIS IS WHY DR. Z Mentioned if applicable, because a problem
  with more than 2

  Slice_GN := [GN[1], 0.5*p3];
  Slice_GN2 := [GN[1], p3];

  PhaseDiag(Slice_GN,[m1,p3], evalf([0.1,0.1]),0.01,10,2);

  PhaseDiag(Slice_GN2,[m1,p3],evalf([0.1,0,1]),0.01,10,2);
```
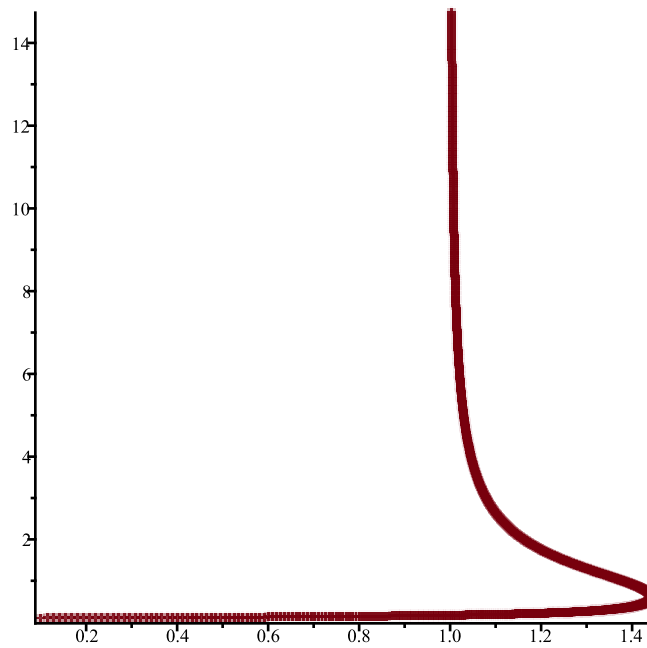
$$Slice\_GN := \left[-m1 + \frac{0.5}{p3^4 + 1} + 1, \, 0.5 \, p3 \right]$$

$$Slice\_GN2 := \left[-m1 + \frac{0.5}{p3^4 + 1} + 1, p3 \right]$$

bad input

FAIL   (8)

PART 3: Lotka

what lotka does:

The Lotka-Volterra model depicts competition between two species (higher population of N1 with respect to N2 will decrease the growth rate of N2)
 This is known as **competitive exclusion**

h

```
> Help(Lotka);
```
Lotka(r1,k1,r2,k2,b12,b21,N1,N2): The Lotka-Volterra continuous-time dynamical system, Eqs.
   (9a),(9b) (p. 224, section 6.3) of Edelstein-Keshet
with popoluations N1, N2, and parameters r1,r2,k1,k2, b12, b21 (called there beta_12 and beta_21)
                                          Try:
                          Lotka(r1,k1,r2,k2,b12,b21,N1,N2);
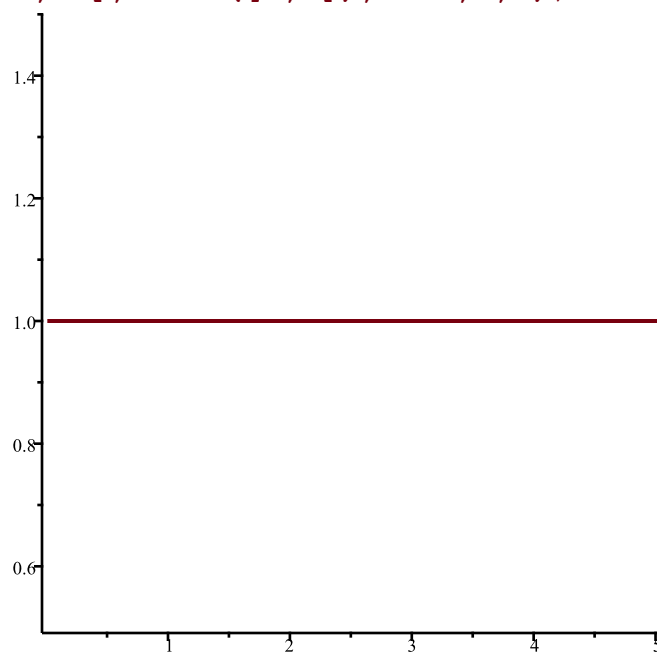   *Lotka(1,2,2,3,1,2,N1,N2);*   (9)

```
> L := Lotka(r1,k1,r2,k2,b12,b21,N1,N2);
```

                                                                                    (10)

$$L := \left[\frac{r1\ N1\ (-b12\ N2 - N1 + k1)}{k1},\ \frac{r2\ N2\ (-b21\ N1 - N2 + k2)}{k2} \right] \tag{10}$$
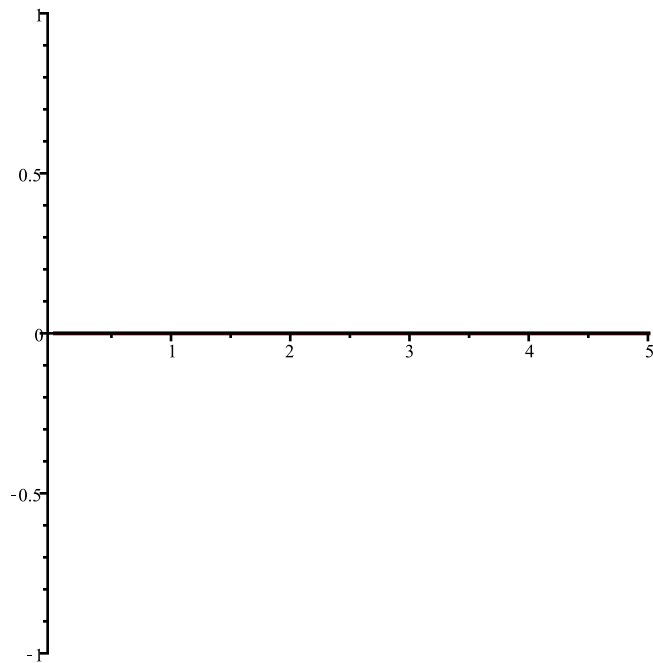
```
> LI := Lotka(1,2,2,3,1,2,N1,N2);
```

$$LI := \left[\frac{N1\ (2 - N1 - N2)}{2},\ \frac{2\ N2\ (3 - N2 - 2\ N1)}{3} \right] \tag{11}$$

```
> #Equilibrium
  TimeSeries(LI,[N1,N2],evalf([1,1]),0.01,5,1);
```
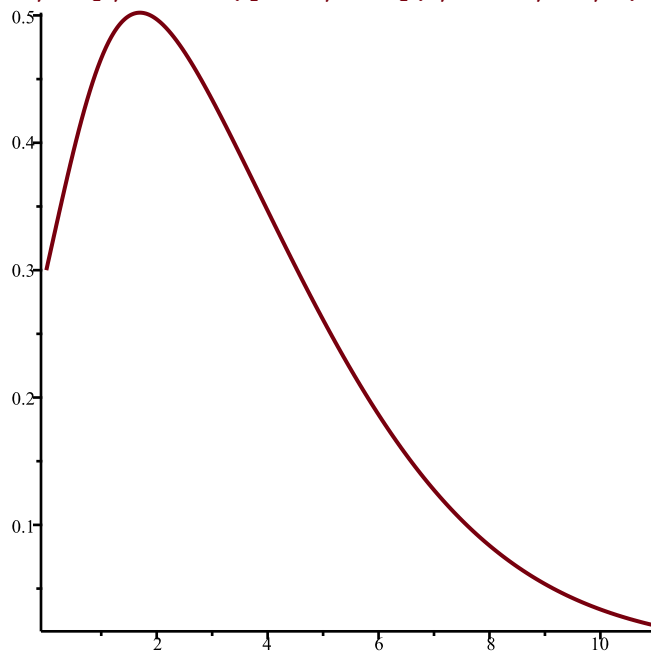

#It appears that initial condition [1,1] is an equilibrium (by inspection of plugging those values into a transformation)
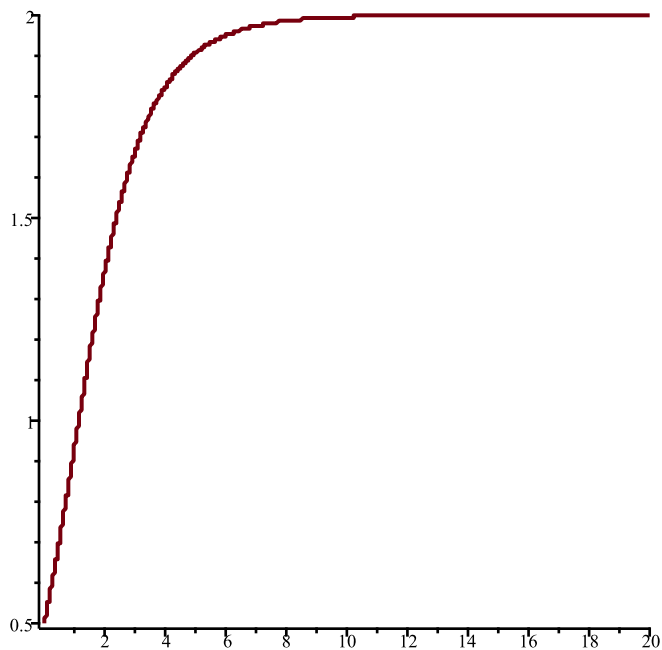
```
> #another equilibrium
  TimeSeries(LI,[N1,N2],evalf([0,0]),0.01,5,1);
```

`#Not an equilibrium. here, initial condition of N1 < N2`
`TimeSeries(LI,[N1,N2],evalf([0.3,0.4]),0.01,11,1);`

`#an example where n2 is smaller than n1 enough that there appears`
`to be stability and nobody dies off`
`TimeSeries(LI,[N1,N2],evalf([0.5,0.02]),0.01,20,1);`

> #Test out the phase diagram
  Help(PhaseDiag);
  #PHASE DIAGRAM HAS

PhaseDiag(F,x,pt,h,A): Inputs a transformation F in the list of variables x (of length 2), i.e. a
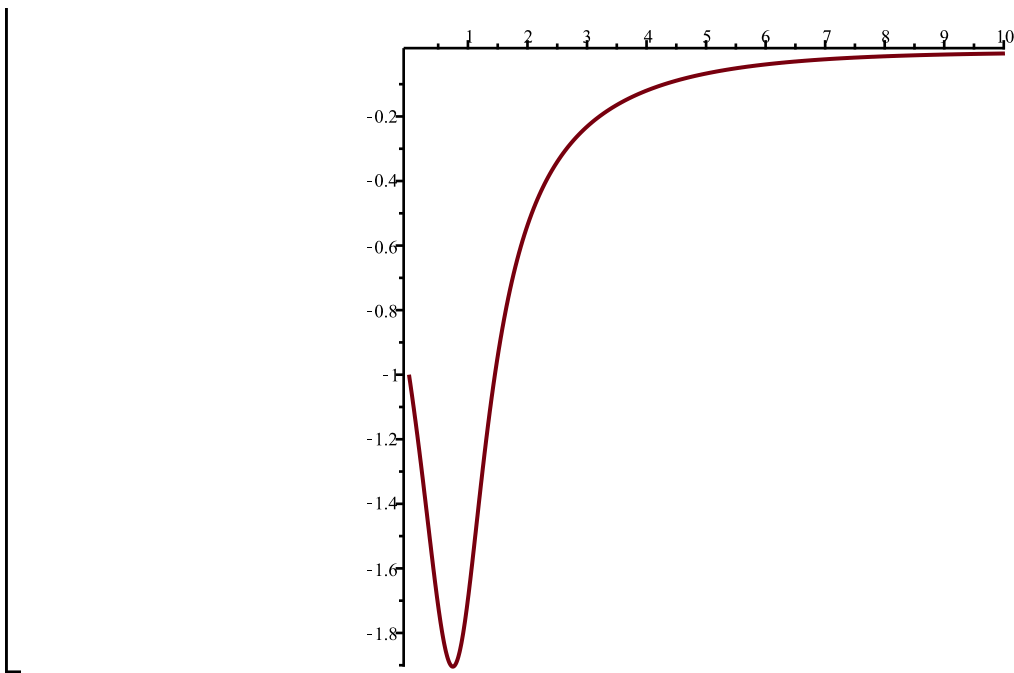
mapping from R^2 to R^2 gives the

The phase diagram of the solution with initial condition x(0)=pt

dx/dt=F[1](x(t)) by a discrete time dynamical system with step-size h from t=0 to t=A

Try:

PhaseDiag([x(1-y),y*(1-x)],[x,y],[0.5,0.5], 0.01, 10);*   **(12)**

> #N2 can still be smaller than N1 and
  TimeSeries(LI,[N1,N2],evalf([-1,0.5]),0.01,10,1);

Part 4: Volterra

> **Help(Volterra);**

Volterra(a,b,c,d,x,y): The (simple, original) Volterra predator-prey continuous-time dynamical

    system with parameters a,b,c,d

        Given by Eqs. (7a) (7b) in Edelstein-Keshet p. 219 (section 6.2).

        a,b,c,d may be symbolic or numeric

        Try:

        Volterra(a,b,c,d,x,y);

        Volterra(1,2,3,4,x,y);   **(13)**

what Volterra does:

> **#SYMBOLIC**
> **Volterra(a,b,c,d,x,y);**

$$[-b\,x\,y + a\,x, \, d\,x\,y - c\,y]$$ **(14)**

> **#NUMERIC**
> **Volterra(2,1,2,7,2,7);**

$$[-10, 84]$$ **(15)**

PART 5: VolterraM

What makes VolterraM different than Volterra?

```
> Help(VolterraM);
```
VolterraM(a,b,c,d,x,K,y): The MODIFIED Volterra predator-prey continuous-time dynamical
    system with parameters a,b,c,d,K
           Given by Eqs. (8a) (8b) in Edelstein-Keshet p. 220 (section 6.2).
           a,b,c,d ,Kmay be symbolic or numeric
           Try:
           VolterraM(a,b,c,d,K,x,y);
           VolterraM(1,2,3,4,3,x,y);   **(16)**

```
> print(Volterra);
```
$$\mathbf{proc}(a, b, c, d, x, y)\ [a*x - b*x*y,\ -c*y + d*x*y]\ \mathbf{end\ proc} \qquad \textbf{(17)}$$

```
> print(VolterraM);
```
$$\mathbf{proc}(a, b, c, K, d, x, y)\ [a*x*(1 - x/K) - b*x*y,\ -c*y + d*x*y]\ \mathbf{end\ proc} \qquad \textbf{(18)}$$

VolterraM itroduces attenuation to (provided that the values of K are within bounds)

   -K probably represents a carrying capacity constant   (Probably positive, because