Julian Herman

Math 336 Final

1.) $x(n)$ = # of rabbits on day "n"

$$x(n) = 2 \cdot x(n-1) - x(n-3), \quad x(0)=1, \quad x(1)=1, \quad x(2)=2$$

$$\frac{x(1000)}{x(999)} = 1.618\ldots \text{ from Maple}$$

2.) $$\frac{dx(t)}{dt} = \frac{5}{2} \cdot x(t) \cdot (1-x(t))(1-0.5 \cdot x(t))$$

a.) EQ. solutions: set underlying function $=0$ and solve.

$$f(x) = \frac{5}{2} x (1-x)\left(1-\frac{x}{2}\right)$$

$$\frac{5}{2} x (1-x)\left(1-\frac{x}{2}\right) = 0$$

$$\boxed{x(t)=0, \quad x(t)=1, \quad x(t)=2}$$

b.) stable? $f'(x(t)=c) < 0$?

Maple: $\boxed{x(t)=1 \text{ is STABLE}}$

c.) If $x(0)=0.1$, $x(t=100) = ?$ MAPLE

3.) $x(n) = \frac{5}{2} \cdot x(n-1) \cdot (1 - x(n-1))\,(1 - 0.5 \cdot x(n-1))$

a.) EQ. solutions: set underlying function = x and solve
(← in this case)

$$f(x) = \frac{5}{2} x\,(1-x)\left(1 - \frac{x}{2}\right)$$

$$\frac{5}{2} x\,(1-x)\left(1 - \frac{x}{2}\right) = x$$

...

Maple

$x(n) = 0, \quad x(n) = 0.47\ldots, \quad x(n) = 2.52\ldots$

b.) Stable? $|f'(x(n) = c)| < 1$?

Maple: $x(n) = 0.47\ldots$

c.) $x(0) = 0.1, \quad x(n=1000) = ?$ MAPLE

```
> #Julian Herman
  #Math 336 Final
> read `/Users/julianherman/Documents/Rutgers/Fall 2021/Dynamical Models In Biology/HW/DMB.txt`
```

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);

For a list of the functions continuous-time dynamical systems (some famous) type: HelpCDM();
For help with any of them type: Help(ProcedureName);

------------------------------ **(1)**

```
> #1)
```

$$> \ evalf\left(\frac{Orbk(3, z, 2\cdot z[1]-z[3], [1,1,2], 1000, 1000)[1]}{Orbk(3, z, 2\cdot z[1]-z[3], [1,1,2], 999, 999)[1]}\right)$$

1.618033989 **(2)**

```
> #THE GOLDEN RATIO IS THE ANSWER! 1.618033989
>
> #2)
```

> #a)

> $EquP\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x]\right)$

$$\{[0],[1],[2]\} \quad (3)$$

> #b)

> $SEquP\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x]\right)$

$$\{[1.]\} \quad (4)$$

> #SAME AS:

> $F(x) := \frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)$

$$F := x \mapsto \frac{5\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)}{2} \quad (5)$$

> $evalb(subs(x=0, F'(x)) < 0)$

$$false \quad (6)$$

> $evalb(subs(x=1, F'(x)) < 0)$

$$true \quad (7)$$

> $evalb(subs(x=2, F'(x)) < 0)$

$$false \quad (8)$$

> #c)

> $dsolve\left(\left\{diff(x(t),t)=\frac{5}{2}\cdot x(t)\cdot(1-x(t))\cdot\left(1-\frac{x(t)}{2}\right), x(0)=0.1\right\}, x(t)\right)$

$$x(t) = \frac{19\,e^{\frac{5t}{2}}}{81\left(-\frac{1}{\sqrt{1+\frac{19\,e^{\frac{5t}{2}}}{81}}}-1\right)\left(-\frac{19\,e^{\frac{5t}{2}}}{81}-1\right)} \quad (9)$$

> $evalf(subs(t=100, \%))$

$$x(100) = 0.9999999999 \quad (10)$$

> #OR DISCRETIZATION:

> $Dis\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x],[0.1],0.01,100\right)[-2]$

$$[100.00, [0.9999999960]] \quad (11)$$

> #When t=100, x(t) is approximately = 0.999

>

> #3)

> #a)

> $FP\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x]\right)$

$$\left\{[0],\left[\frac{3}{2}-\frac{\sqrt{105}}{10}\right],\left[\frac{3}{2}+\frac{\sqrt{105}}{10}\right]\right\} \quad \textbf{(12)}$$

> $evalf(\%)$

$$\{[0.],[0.475304923],[2.524695077]\} \quad \textbf{(13)}$$

> *#SAME AS:*

> $solve\left(\left\{\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)=x\right\},x\right)$

$$\{x=0\},\left\{x=\frac{3}{2}+\frac{\sqrt{105}}{10}\right\},\left\{x=\frac{3}{2}-\frac{\sqrt{105}}{10}\right\} \quad \textbf{(14)}$$

> $evalf(\%)$

$$\{x=0.\},\{x=2.524695077\},\{x=0.475304923\} \quad \textbf{(15)}$$

> ***#b)***

> $SFP\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x]\right)$

$$\{[0.475304923]\} \quad \textbf{(16)}$$

> *#SAME AS:*

> $F(x) := \frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)$

$$F := x \mapsto \frac{5\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)}{2} \quad \textbf{(17)}$$

> $evalb(\mathrm{abs}(subs(x=0.,F'(x)))<1)$

$$false \quad \textbf{(18)}$$

> $evalb(\mathrm{abs}(subs(x=0.475304923,F'(x)))<1)$

$$true \quad \textbf{(19)}$$

> $evalb(\mathrm{abs}(subs(x=2.524695077,F'(x)))<1)$

$$false \quad \textbf{(20)}$$

> ***#c)***

> $Orb\left(\left[\frac{5}{2}\cdot x\cdot(1-x)\cdot\left(1-\frac{x}{2}\right)\right],[x],[0.1],1000,1000\right)[1]$

$$[0.4753049232] \quad \textbf{(21)}$$

>

> **#4)**

> ***#a)***

> $HW(u,v)$

$$\left[u^2+v\,u+\frac{1}{4}v^2,-2\,v\,u-2\,u^2+2\,u-\frac{1}{2}v^2+v\right],[u,v] \quad \textbf{(22)}$$

> $Orb\left(HW(u,v),\left[\frac{1}{3},\frac{1}{3}\right],0,1\right)$

$$\left[\left[\frac{1}{3}, \frac{1}{3}\right], \left[\frac{1}{4}, \frac{1}{2}\right]\right] \quad (23)$$

> #If we start u,v,w (proportions of genotypes AA, Aa, aa respectively) all equal, they must each be 1/3. The proportion of genotype Aa is v in this transformation and v is 1/2 in the second generation as you can see above.

> *#b)*

> $Orb\left(HW(u, v), \left[\frac{1}{3}, \frac{1}{3}\right], 999, 1000\right)$

$$\left[\left[\frac{1}{4}, \frac{1}{2}\right], \left[\frac{1}{4}, \frac{1}{2}\right]\right] \quad (24)$$

> #The whole point of the Hardy–Weinberg Law is that the genotypic frequencies will stabilize given multiple constraints (random mating, no mutations, progeny have equal fitness, no variation in number of progeny from parents of different genotypes) and thus achieve Hardy–Weinberg equilibrium (after one generation). From this, it is obvious that the 1000th generation has the same proportion of genotype Aa (or v) as in the 2nd generation: 0.5. However, I show this above anyways by doing the orbit to the 1000th and 1001th generation (generation n is Orb(...,K1=0,K2=n)[n–1] with the indexing of Orb() in this context).

>

> #5)

> *#a)*

> $Orb\left(HWg(u, v, [[1, 2, 1], [1, 1, 1], [1, 1, 1]]), [u, v], \left[\frac{1}{3}, \frac{1}{3}\right], 0, 1\right)$

$$\left[\left[\frac{1}{3}, \frac{1}{3}\right], \left[\frac{11}{40}, \frac{1}{2}\right]\right] \quad (25)$$

> #If we start u,v,w (proportions of genotypes AA, Aa, aa respectively) all equal, they must each be 1/3. The proportion of genotype Aa is v in this transformation and v is 1/2 in the second generation as you can see above.

> *#b)*

> $Orb(HWg(u, v, [[1, 2, 1], [1, 1, 1], [1, 1, 1]]), [u, v], [0.3333333333, 0.3333333333], 999, 1000)$

[[0.5512669082, 0.3974661814], [0.5512669082, 0.3974661814]] **(26)**

> #0.3974661814 of the 1000th generation would have genotype Aa.

>

> #6)

> $Orb\left(\left[\frac{1+x+y}{2+x+3\cdot y}, \frac{1+x+3\cdot y}{3+x+2\cdot y}\right], [x, y], [100.0, 1000.0], 100000, 100010\right)$

[[0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, **(27)**

0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080],
[0.4705902280, 0.7478789080]]

> $evalf\left(FP\left(\left[\frac{1+x+y}{2+x+3\cdot y}, \frac{1+x+3\cdot y}{3+x+2\cdot y}\right], [x, y]\right)\right)$

{[0.4705902280, 0.7478789082]} **(28)**

> $SFP\left(\left[\frac{1+x+y}{2+x+3\cdot y}, \frac{1+x+3\cdot y}{3+x+2\cdot y}\right], [x, y]\right)$

{[0.4705902280, 0.7478789082]} **(29)**

> **#y(10000000000000000000000000000000000000000000000000000000) would be somewhere between 0.7478789080 and 0.7478789082 (rounded of course) because the system converges towards the stable equilibrium solution [x(n)=0.4705902280, y(n)=0.7478789082] but never actually equals the stable solution EXACTLY. Although, the stable equilibrium solution output of SFP() is still a decimal approximation!**

>

> **#7)**

> ***#a)***

> $Dis(SIRS(s, i, 0.05, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

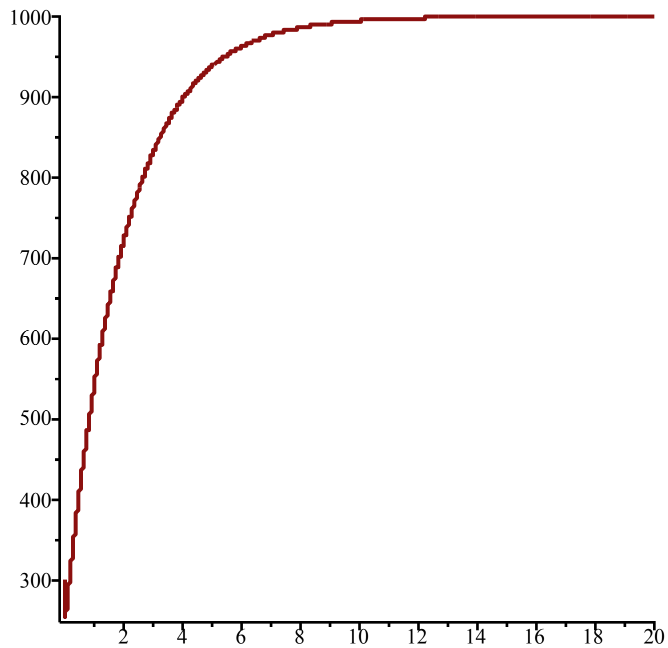
$[100.01, [999.9999900, 4.000205542 \times 10^{-3094}]]$ **(30)**

> $1000 - 999.9999900 - 4.000205542 \times 10^{-3094}$

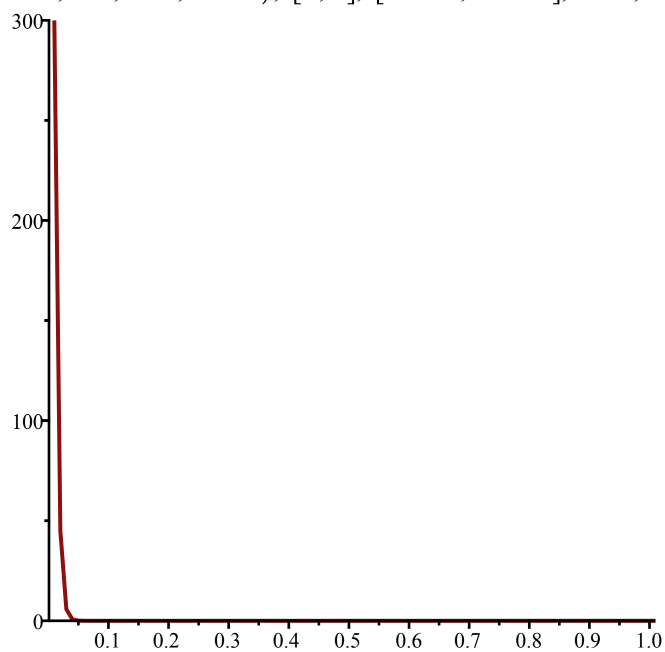
0.0000100 **(31)**

> **#By discretizing the continuous system (representing the SIRS model), we can study what happens with different parameters. From the above, it is apparent that the removed individuals at t=1000 is 0.0000100... Or in other words, as we continue through more and more time steps of this discretization (i.e. in the long run), the removed approaches 0. This can be visualized by the TimeSeries below where susceptible (variable 1) is shown to go to N=1000. The second TimeSeries below shows how infected (variable 2) goes to 0. Therefore, since** $N = s + i + r \Rightarrow r = N - s - i \Rightarrow r = 1000 - 1000 - 0 = 0.$

> $TimeSeries(SIRS(s, i, 0.05, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 20, 1)$



> *TimeSeries*(*SIRS*(*s*, *i*, 0.05, 0.5, 100, 1000), [*s*, *i*], [300.0, 300.0], 0.01, 1, 2)

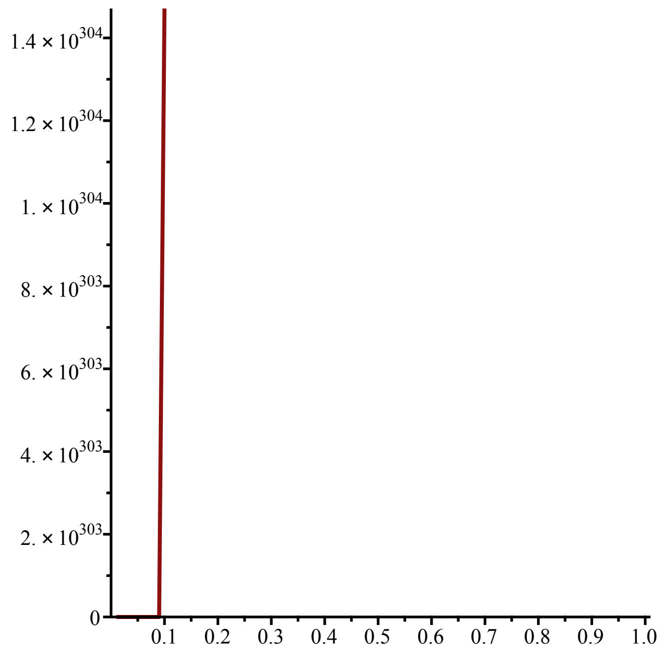


> ***#b)***

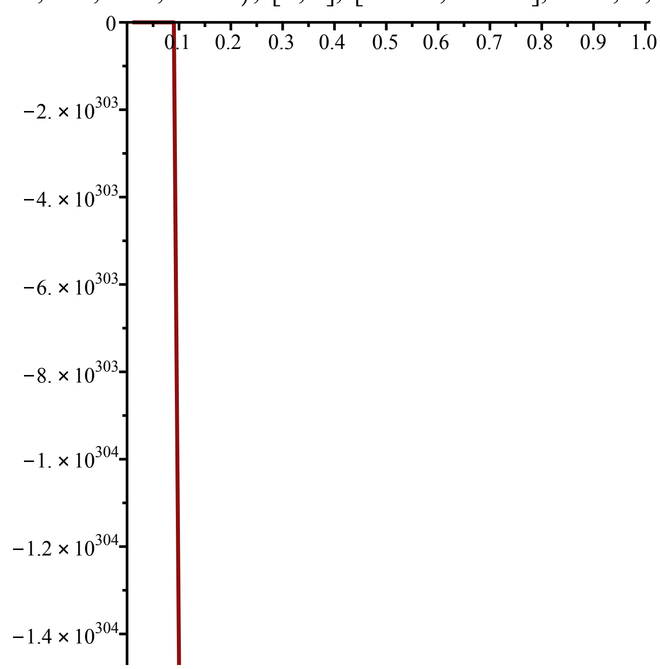
> *Dis*(*SIRS*(*s*, *i*, 1.4, 0.5, 100, 1000), [*s*, *i*], [300.0, 300.0], 0.01, 100)[-1]

[100.01, [Float(∞), Float(-∞)]] **(32)**

> *TimeSeries*(*SIRS*(*s*, *i*, 1.4, 0.5, 100, 1000), [*s*, *i*], [300.0, 300.0], 0.01, 1, 1)



> $TimeSeries(SIRS(s, i, 1.4, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 1, 2)$



> **#In the long run, susceptible goes to infinity and infected goes to negative infinity, therefore, THIS MODEL (with Beta=1.4) IS NONSENSE... Susceptible clearly explodes past N=1000 and infected goes negative... you cannot have a negative count for the number of people that are infected, it simply makes no sense in this context! NONSENSE!**

> ***#c)***

> **#The cutoff for when (in the long run) there would be a non-zero number of infected people is obtained below by running multiple discretization approximations with different beta values and numerically checking when the infected start to become non-zero**

(after many time steps).

> $Dis(SIRS(s, i, 0.09, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

$$[100.01, [999.9999900, 1.129345003 \times 10^{-549}]] \quad (33)$$

> $Dis(SIRS(s, i, 0.1, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

$$[100.01, [999.9999900, 2.164137001 \times 10^{-94}]] \quad (34)$$

> $Dis(SIRS(s, i, 0.15, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

$$[100.01, [666.6666637, 1.658374827]] \quad (35)$$

> $Dis(SIRS(s, i, 0.12, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

$$[100.01, [833.3333302, 0.8291874107]] \quad (36)$$

> $Dis(SIRS(s, i, 0.11, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1]$

$$[100.01, [909.0909099, 0.4522841394]] \quad (37)$$

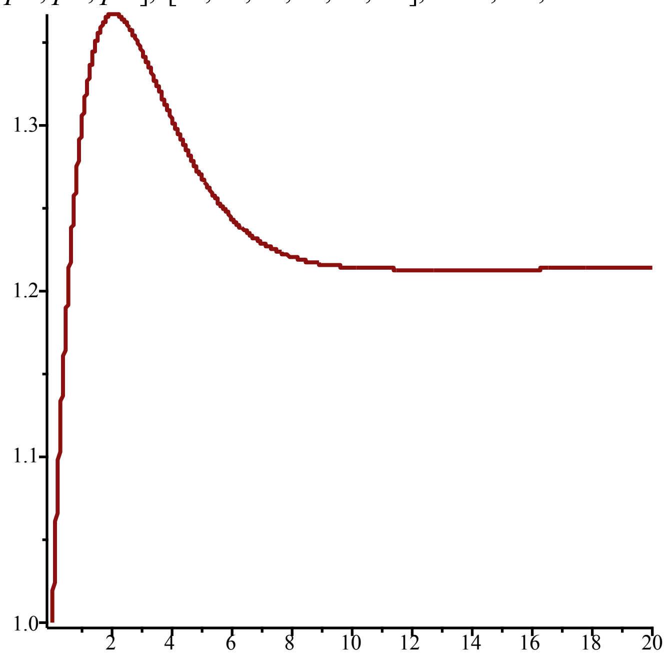
> **for** *count* **from** 1 **to** 20 **do** $print(Dis(SIRS(s, i, 0.09 + count \cdot 0.001, 0.5, 100, 1000), [s, i], [300.0, 300.0], 0.01, 100)[-1][2][2])$ **od**:

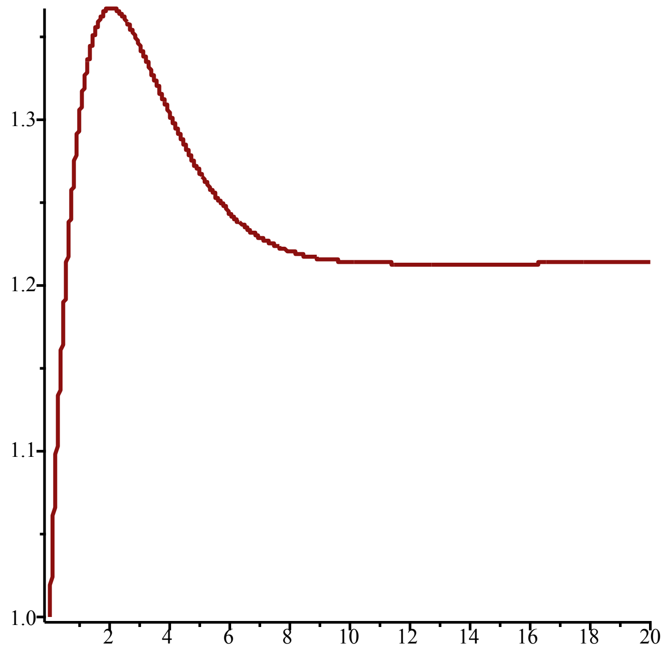
$$6.545409239 \times 10^{-502}$$
$$1.131768269 \times 10^{-454}$$
$$5.992934746 \times 10^{-408}$$
$$9.967107490 \times 10^{-362}$$
$$5.335617683 \times 10^{-316}$$
$$9.414360104 \times 10^{-271}$$
$$5.602373312 \times 10^{-226}$$
$$1.149757936 \times 10^{-181}$$
$$8.315278843 \times 10^{-138}$$
$$2.164137001 \times 10^{-94}$$
$$2.068528966 \times 10^{-51}$$
$$7.405843705 \times 10^{-9}$$
$$0.1452413925$$
$$0.1913496623$$
$$0.2369100749$$
$$0.2816108325$$
$$0.3254753469$$
$$0.3685278212$$
$$0.4107900444$$
$$0.4522841394 \quad (38)$$

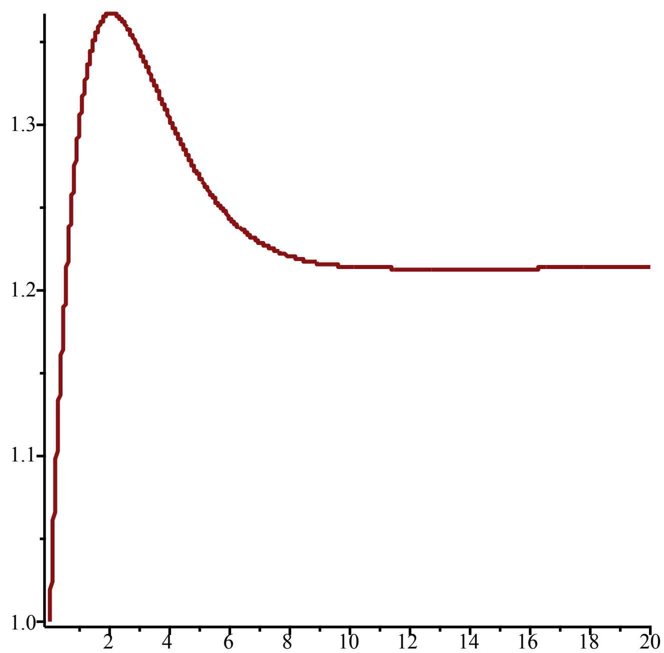
> **#The above shows numerically that a non-negative number of infected people starts when Beta is approximately 0.1. This is confirmed by the fact that it is known that if Beta > Nu/N than the disease becomes endemic (non-negative number of infected people) for this model. This is 100/1000=0.1.**

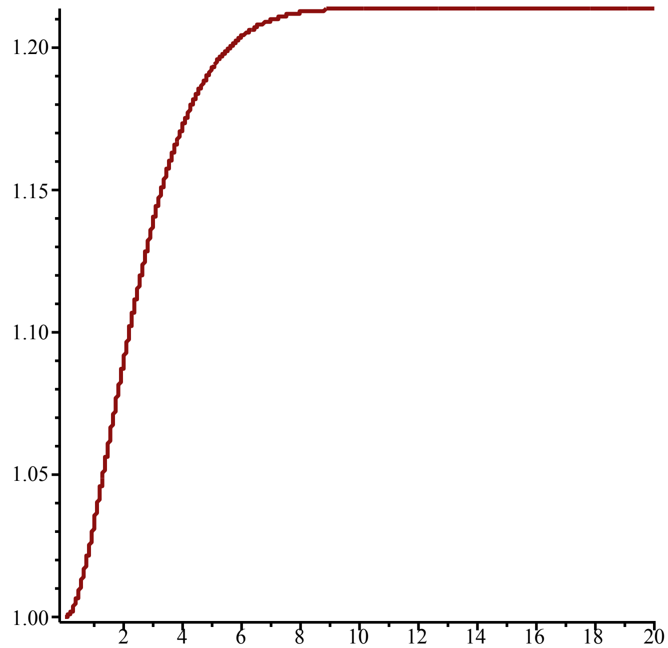
>

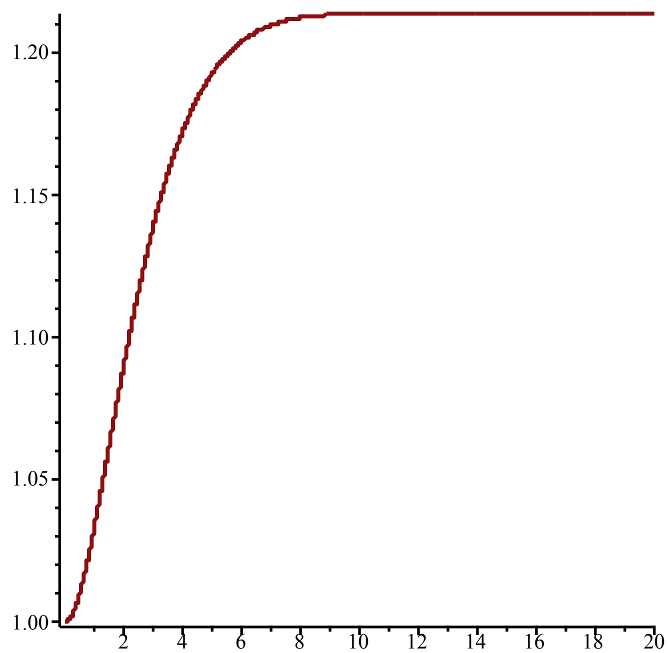
```
> #8)
> #a)
> SEquP(GeneNet(0.0, 1.0, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3])
  {[0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038]}   (39)
> #Not much explaining needed for this one: solved for the stable
  equilibrium solution of the underlying transformation of GeneNet()
  and found it to be 0.6823278038 for all 6 proteins
  (variables/quantities).
> #b)
> SEquP(GeneNet(0.0, 3.0, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3])
  {[1.213411663, 1.213411663, 1.213411663, 1.213411663, 1.213411663, 1.213411663]}   (40)
> for something from 1 to 6 do print(TimeSeries(GeneNet(0.0, 3.0, 0.2, 2.0, m1, m2, m3, p1, p2,
     p3), [m1, m2, m3, p1, p2, p3], [1., 1., 1., 1., 1., 1.], 0.01, 20, something)) od:
```

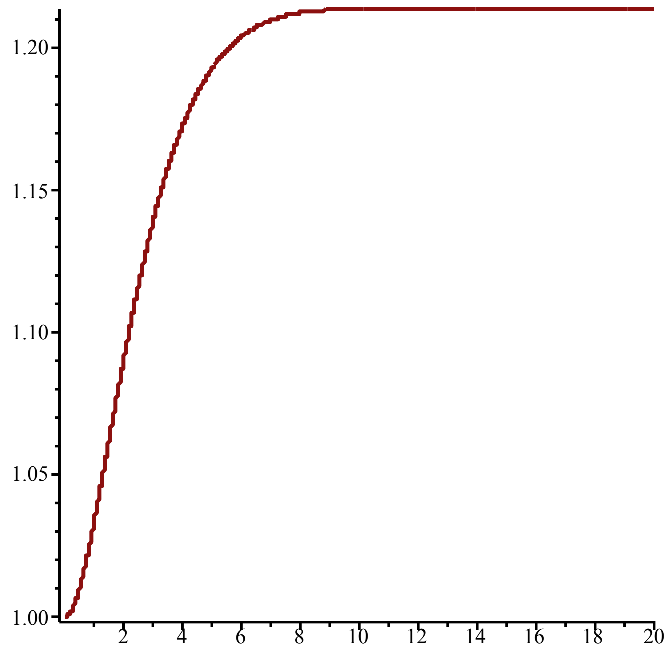



1.3
1.2
1.1
1.0
2 4 6 8 10 12 14 16 18 20


1.3
1.2
1.1
1.0
2 4 6 8 10 12 14 16 18 20


1.20
1.15
1.10
1.05
1.00
2 4 6 8 10 12 14 16 18 20


1.20
1.15
1.10
1.05
1.00
2 4 6 8 10 12 14 16 18 20




```
> #As apparent above, the horizontal asymptote is now at 1.213411663
  for all 6 proteins (variables/quantities).
> #c)
> SEquP(GeneNet(0.0, 4.0, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3])
```

{[1.378796700, 1.378796700, 1.378796700, 1.378796700, 1.378796700, 1.378796700]} **(41)**

```
> for tests from 1 to 10 do print(3.0 + tests, SEquP(GeneNet(0.0, 3.0 + tests, 0.2, 2.0, m1, m2,
    m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3]))od:
```

4.0, {[1.378796700, 1.378796700, 1.378796700, 1.378796700, 1.378796700, 1.378796700]}

5.0, {[1.515980228, 1.515980228, 1.515980228, 1.515980228, 1.515980228, 1.515980228]}

6.0, {[1.634365293, 1.634365293, 1.634365293, 1.634365293, 1.634365293, 1.634365293]}

7.0, {[1.739203861, 1.739203861, 1.739203861, 1.739203861, 1.739203861, 1.739203861]}

8.0, ∅

9.0, ∅

10.0, ∅

11.0, ∅

12.0, ∅

13.0, ∅ **(42)**

```
> #Somewhere between alpha=7 and alpha=8 the system loses stability.
  Lets look closer!
> for closertests from 1 to 10 do print(7.0 + closertests·0.1, SEquP(GeneNet(0.0, 7.0
    + closertests·0.1, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3]))od:
```

7.1, {[1.749079318, 1.749079318, 1.749079318, 1.749079318, 1.749079318, 1.749079318]}

7.2, {[1.758855227, 1.758855227, 1.758855227, 1.758855227, 1.758855227, 1.758855227]}

7.3, {[1.768534008, 1.768534008, 1.768534008, 1.768534008, 1.768534008, 1.768534008]}

7.4, ∅

$7.5, \varnothing$

$7.6, \varnothing$

$7.7, \varnothing$

$7.8, \varnothing$

$7.9, \varnothing$

$8.0, \varnothing$ **(43)**

```
> #Somewhere between alpha=7.3 and alpha=7.4 the system loses
  stability. Lets look closer!
```

> **for** *closerclosertests* **from** 1 **to** 10 **do** $print(7.3 + closerclosertests \cdot 0.01, SEquP(GeneNet(0.0, 7.3 + closerclosertests \cdot 0.01, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3]))$ **od**:

7.31, {[1.769496635, 1.769496635, 1.769496635, 1.769496635, 1.769496635, 1.769496635]}

7.32, {[1.770458315, 1.770458315, 1.770458315, 1.770458315, 1.770458315, 1.770458315]}

7.33, {[1.771419053, 1.771419053, 1.771419053, 1.771419053, 1.771419053, 1.771419053]}

7.34, {[1.772378849, 1.772378849, 1.772378849, 1.772378849, 1.772378849, 1.772378849]}

7.35, {[1.773337706, 1.773337706, 1.773337706, 1.773337706, 1.773337706, 1.773337706]}

7.36, {[1.774295627, 1.774295627, 1.774295627, 1.774295627, 1.774295627, 1.774295627]}

7.37, {[1.775252614, 1.775252614, 1.775252614, 1.775252614, 1.775252614, 1.775252614]}

7.38, {[1.776208668, 1.776208668, 1.776208668, 1.776208668, 1.776208668, 1.776208668]}

7.39, {[1.777163792, 1.777163792, 1.777163792, 1.777163792, 1.777163792, 1.777163792]}

$7.40, \varnothing$ **(44)**

```
> #Somewhere between alpha=7.39 and alpha=7.40 the system loses
  stability. Lets look closer!
```

> **for** *closesttests* **from** 1 **to** 10 **do** $print(7.39 + closesttests \cdot 0.001, SEquP(GeneNet(0.0, 7.39 + closesttests \cdot 0.001, 0.2, 2.0, m1, m2, m3, p1, p2, p3), [m1, m2, m3, p1, p2, p3]))$ **od**:

7.391, {[1.777259253, 1.777259253, 1.777259253, 1.777259253, 1.777259253, 1.777259253]}

7.392, {[1.777354705, 1.777354705, 1.777354705, 1.777354705, 1.777354705, 1.777354705]}

7.393, {[1.777450148, 1.777450148, 1.777450148, 1.777450148, 1.777450148, 1.777450148]}

$7.394, \varnothing$

$7.395, \varnothing$

$7.396, \varnothing$

$7.397, \varnothing$

$7.398, \varnothing$

$7.399, \varnothing$

$7.400, \varnothing$ **(45)**

```
> #Somewhere between alpha=7.393 and alpha=7.394 the system loses
  stability! But for this exam, alpha=7.39 is a good enough answer
  because for alpha=7.39 there is a stable equilibrium, but at alpha=
  7.39+0.01=7.40, there does NOT exist a stable equilibrium.
```

>

> **#9)**

> *#a)*

> $ChemoStat(N, C, 2.5, 2.7)$

$$\left[\frac{2.5\,C\,N}{C+1} - N,\ -\frac{C\,N}{C+1} - C + 2.7\right] \quad \textbf{(46)}$$

> $Dis(ChemoStat(N, C, 2.5, 2.7), [N, C], [0.5, 0.3], 0.01, 500)[-1]$

$$[500.01, [5.083333349, 0.6666666650]] \quad \textbf{(47)}$$

> $Dis(ChemoStat(N, C, 2.5, 2.7), [N, C], [11.5, 3.3], 0.01, 100)[-1]$

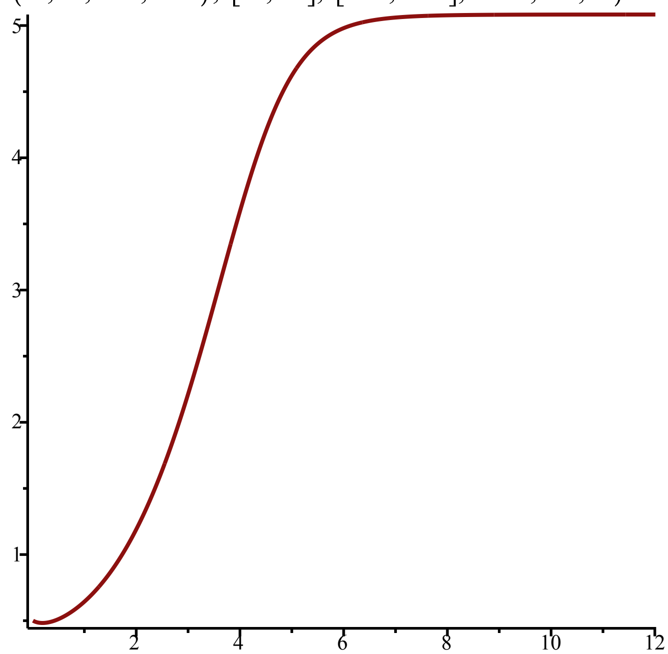
$$[100.01, [5.083333450, 0.6666666474]] \quad \textbf{(48)}$$

> $Dis(ChemoStat(N, C, 2.5, 2.7), [N, C], [1.5, 0.03], 0.01, 100)[-1]$

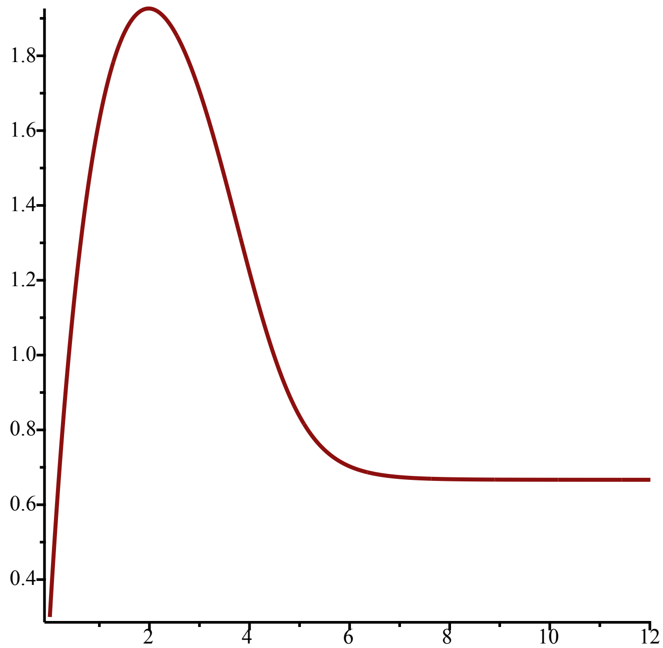
$$[100.01, [5.083333349, 0.6666666650]] \quad \textbf{(49)}$$

> **#Varying the initial conditions, and we still get the same long-term behavior!**

> $TimeSeries(ChemoStat(N, C, 2.5, 2.7), [N, C], [0.5, 0.3], 0.01, 12, 1)$



> $TimeSeries(ChemoStat(N, C, 2.5, 2.7), [N, C], [0.5, 0.3], 0.01, 12, 2)$



> #The bacterial population density, N, converges to 5.083333349

> #*b)*

> #The nutrient concentration, C, converges to 0.6666666650

> $SEquP(ChemoStat(N, C, 2.5, 2.7), [N, C])$

$$\{[5.083333333, 0.6666666667]\} \quad \textbf{(50)}$$

> #The values [N=5.083333349, C=0.6666666650] that the system converges to after many (A=500) time steps is ALMOST equivalent to the stable equilibrium shown above. Note, it will never truly reach exactly the stable equilibrium solution (unless initial conditions were exactly those values), but it gets very, very close as time goes to infinity! Even the SEquP() output of [5.083333333, 0.6666666667] is a decimal approximation!

>

> #10)

> $M := Matrix([[0.2, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1], [0.1, 0.2, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1], [0.1, 0.1, 0.2, 0.1, 0.1, 0.1, 0.1, 0.1, 0.1], [0.075, 0.075, 0.075, 0.4, 0.075, 0.075, 0.075, 0.075, 0.075], [0.075, 0.075, 0.075, 0.075, 0.4, 0.075, 0.075, 0.075, 0.075], [0.075, 0.075, 0.075, 0.075, 0.075, 0.4, 0.075, 0.075, 0.075], [0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.6, 0.05, 0.05], [0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.6, 0.05], [0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.05, 0.6]])$

(51)

$$M := \begin{bmatrix} 0.2 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 \\ 0.1 & 0.2 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 \\ 0.1 & 0.1 & 0.2 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 & 0.1 \\ 0.075 & 0.075 & 0.075 & 0.4 & 0.075 & 0.075 & 0.075 & 0.075 & 0.075 \\ 0.075 & 0.075 & 0.075 & 0.075 & 0.4 & 0.075 & 0.075 & 0.075 & 0.075 \\ 0.075 & 0.075 & 0.075 & 0.075 & 0.075 & 0.4 & 0.075 & 0.075 & 0.075 \\ 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.6 & 0.05 & 0.05 \\ 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.6 & 0.05 \\ 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.05 & 0.6 \end{bmatrix} \qquad \textbf{(51)}$$

> M^{1000}

(52)

[[0.0769230769230792, 0.0769230769230792, 0.0769230769230793, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230793, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230793, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,
0.153846153846158],
[0.0769230769230792, 0.0769230769230792, 0.0769230769230792, 0.102564102564106,
0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158,

0.153846153846158]]

```
> %[1]
```

[0.0769230769230792, 0.0769230769230792, 0.0769230769230793, 0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846158, 0.153846153846158, 0.153846153846158] **(53)**

```
> #The probability that a random surfer will be at web-page 1 is
  0.0769230769230792
> #b)
> #The probability that a random surfer will be at web-page 9 is
  0.153846153846158
>
> #OTHER APPROACH BELOW:
> H := Matrix([[0.2, 0.4, 0.4], [0.3, 0.4, 0.3], [0.2, 0.2, 0.6]])
```

$$H := \begin{bmatrix} 0.2 & 0.4 & 0.4 \\ 0.3 & 0.4 & 0.3 \\ 0.2 & 0.2 & 0.6 \end{bmatrix} \quad \textbf{(54)}$$

> H^{1000}

$$\begin{bmatrix} 0.230769230769238 & 0.307692307692317 & 0.461538461538476 \\ 0.230769230769238 & 0.307692307692317 & 0.461538461538476 \\ 0.230769230769238 & 0.307692307692317 & 0.461538461538476 \end{bmatrix} \quad \textbf{(55)}$$

```
> %[1]
```

$$\begin{bmatrix} 0.230769230769238 & 0.307692307692317 & 0.461538461538476 \end{bmatrix} \quad \textbf{(56)}$$

> $\frac{0.230769230769238}{3}$

$$0.07692307693 \quad \textbf{(57)}$$

> $\frac{0.307692307692317}{3}$

$$0.1025641026 \quad \textbf{(58)}$$

> $\frac{0.461538461538476}{3}$

$$0.1538461538 \quad \textbf{(59)}$$

```
> #By symmetry:
  #   prob(webpage 1,2,3)= 0.07692307693
  #   prob(webpage 4,5,6)= 0.1025641026
  #   prob(webpage 7,8,9)= 0.1538461538
```