```
> #Jeton Hida
  #Final Math 336 Answers & Explanations
  read "/Users/jeton/Desktop/Math 336/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);

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(1)

```
> #Question 1
```

```
> a:=proc(n) option remember:
  if n=0 then
  1:
  elif n=1 then
  1:
  elif n=2 then
  2:
  else 2*a(n-1)-a(n-3)
  fi:
```

```
end:

seq(a(i),i=0..1000)[-1]; #Number of rabbits at day 1000
```

703303677114228158218352548771835497701812698363587327426049050871545371181 96\
93357974224949456261173348775044924176599108818636326545022364710601205337\
41212738673391111981393731255987676900919022452453234035 01 (2)

```
> seq(a(i),i=0..1000)[-2]; #Number of rabbits at day 999
```

434665576869374564356885276750406258025646605173717804024817290895365554179 49\
05189040387984007925516929592259308032263477520968962323987332247116164299\
64409065331879382989696499285160037044761377951668492288 75 (3)

```
> evalf(seq(a(i),i=0..1000)[-1]/(seq(a(i),i=0..1000)[-2]))
```

1.618033989 (4)

```
> #1.618033989 is the number of rabbits at day 1000 divided by the
  number of rabbits at day 999

> #Question 2

> #Rate of change! Differential equation! Continous time!
> #x'(t)=5/2*x(t)*(1-x(t))*(1-(1/2)*x(t))

> #a. Underlying function is f(x) = 5/2*x*(1-x)*(1-(x/2), to find
  equilibrium points equate this to 0 and solve for values of x that
  satisfy the equation. Equate to 0 because a rate of change of 0
  means we do not move from this point if we start or end up at it.

> EquP([5/2*x*(1-x)*(1-(x/2))],[x])
```

{[0], [1], [2]} (5)

```
> solve(5/2*x*(1-x)*(1-(x/2))=0,x) #This method also works, shows
  that this is basically all that the EquP function is doing, so our
  set of equilibrium points is {0,1,2}
```

0, 1, 2 (6)

```
> #b. To find stable equilibrium points we take our equilibrium
  points we just found, these will be our candidate equilibrium
  points, and now we take the derivative of our underlying function
  and substitute our equilibrium points in for x and see what that
  value is. If it is <0 it is a stable equilibrium point, if it is >0
  then it is unstable. If =0 then it is a borderline case called
  semistable.

> F:=(5/2)*x*(1-x)*(1-(x/2))
```

$$F := \frac{5\,x\,(1-x)\left(1-\frac{x}{2}\right)}{2} \quad (7)$$

```
> A:=diff(F,x)
```

$$A := \frac{5\,(1-x)\left(1-\frac{x}{2}\right)}{2} - \frac{5\,x\left(1-\frac{x}{2}\right)}{2} - \frac{5\,x\,(1-x)}{4} \quad (8)$$

```
> subs(x=0,A)
```

(9)

$$\frac{5}{2} \tag{9}$$

```
> subs(x=1,A)
```

$$-\frac{5}{4} \tag{10}$$

```
> subs(x=2,A)
```

$$\frac{5}{2} \tag{11}$$

```
> #With this we see 0 and 2 are unstable since 5/2 > 0. 1 is a stable
  equilibrium point since -5/4 < 0, so the set of all stable
  equilibrium points is {1}.
```

```
> #c. dsolve will be used for this. Need to find the solution to the
  differential equation, otherwords the equation of x(t). With
  initial condition x(0)=.1 we'll find x(100). Since we know 1 is a
  stable equilibrium point we can imagine that the value will be
  somewhere near it.
```

```
> A:=dsolve({diff(x(t),t)=5/2*x(t)*(1-x(t))*(1-(x(t)/2)),x(0)=.1},x
  (t))
```

$$A := x(t) = \frac{\sqrt{19\,e^{\frac{5t}{2}} + 81} - 9}{\sqrt{19\,e^{\frac{5t}{2}} + 81}} \tag{12}$$

```
> evalf(subs(t=100,A))
```

$$x(100) = 1.000000000 \tag{13}$$

```
> #Answer makes sense, as 1 is a stable equilibrium point. Could
  probably show this in the function TimeSeries as well with a
  horizontal asymptote at x=1.
```

```
> Help(TimeSeries)
```

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

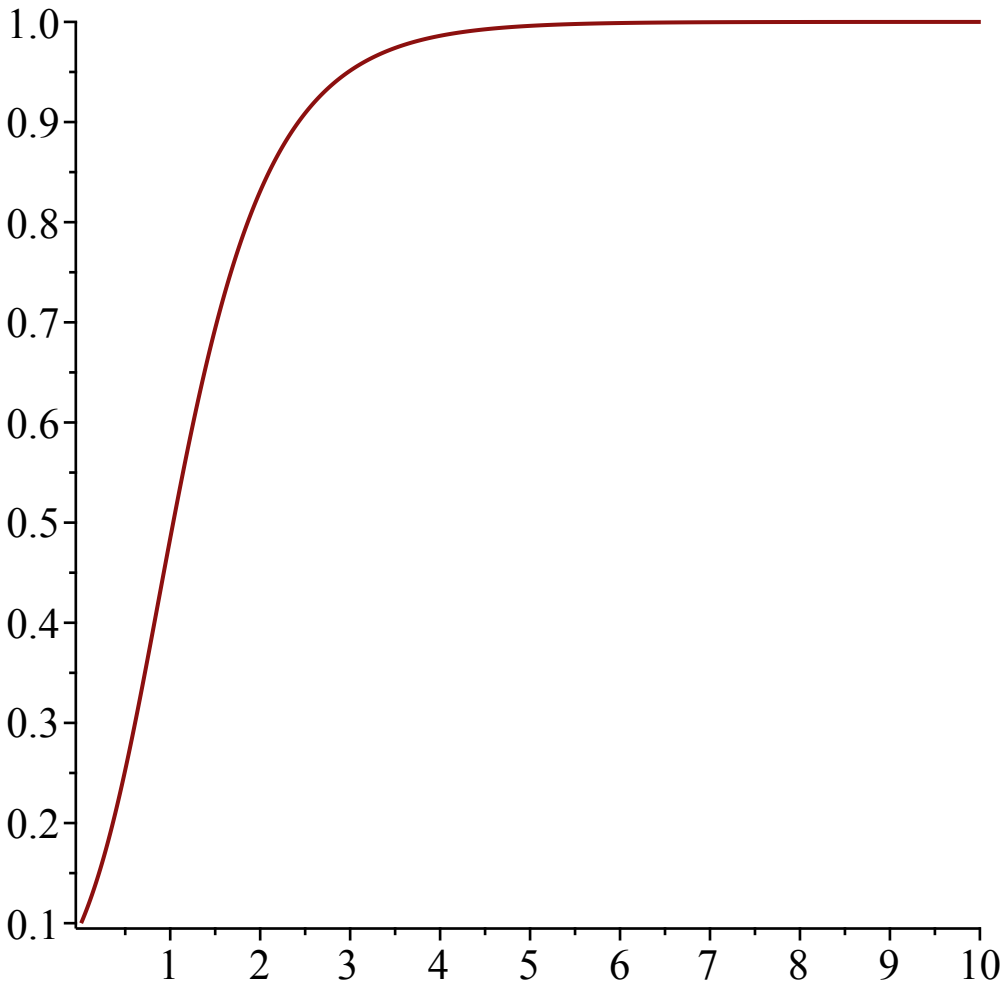
The time-series of x[i] vs. time of the Dynamical system approximating the the autonomous continuous dynamical process

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);* (14)

```
> TimeSeries([5/2*x*(1-x)*(1-(x/2))],[x],[.1],.01,10,1)
```




```
> #Question 3

> #Talking about a quantity today, so discrete time difference
  equation.
> #x(n)=5/2*x(n-1)*(1-x(n-1))*(1-(x(n-2)/2))

> #a. For equilibrium solutions of a difference equation, we'll need
  to use the underlying function f(x) and equate it to x. An
  equilibrium point for such an equation means that if we are at this
  value then we will continue to stay at this value tomorrow, the day
  after, and even 1000 days into the future. The function FP will
  calculate it for us, but I will also show how to find a solution
  with Maple solve command. Underlying function is f(x) = 5/2*x*(1-x)
  *(1-(x/2))

> FP([5/2*x*(1-x)*(1-(x/2))],[x]);
  evalf(FP([5/2*x*(1-x)*(1-(x/2))],[x]));
```

$$\left\{[0], \left[\frac{3}{2} - \frac{\sqrt{105}}{10}\right], \left[\frac{3}{2} + \frac{\sqrt{105}}{10}\right]\right\}$$

$$\{[0.], [0.475304923], [2.524695077]\} \quad (15)$$

```
> solve(5/2*x*(1-x)*(1-(x/2))=x,x)
```

(16)

$$0,\ \frac{3}{2}+\frac{\sqrt{105}}{10},\ \frac{3}{2}-\frac{\sqrt{105}}{10} \tag{16}$$

```
> #These are our set of equilibrium solutions.
```

```
> #b. Finding stable equilibrium solutions for difference equations
  is similar to how we did it for the differential equation, except
  that when plugging our candidates into the derivative of the
  underlying function we are comparing the absolute value of our
  answer to the 1 instead of 0. If the absolute value is < 1 then we
  have a stable equilibrium,if > 1 then it is unstable. If = 1 this
  is our borderline case where we could say it is semistable.
```

```
> F:=diff(5/2*x*(1-x)*(1-(x/2)),x)
```

$$F := \frac{5\,(1-x)\left(1-\frac{x}{2}\right)}{2}-\frac{5\,x\left(1-\frac{x}{2}\right)}{2}-\frac{5\,x\,(1-x)}{4} \tag{17}$$

```
> A:=solve(5/2*x*(1-x)*(1-(x/2))=x,x)[1]
```

$$A := 0 \tag{18}$$

```
> B:=solve(5/2*x*(1-x)*(1-(x/2))=x,x)[2]
```

$$B := \frac{3}{2}+\frac{\sqrt{105}}{10} \tag{19}$$

```
> C:=solve(5/2*x*(1-x)*(1-(x/2))=x,x)[3]
```

$$C := \frac{3}{2}-\frac{\sqrt{105}}{10} \tag{20}$$

```
> evalf(subs(x=A,F))
```

$$2.500000000 \tag{21}$$

```
> evalf(subs(x=B,F))
```

$$7.467606542 \tag{22}$$

```
> evalf(subs(x=C,F))
```

$$-0.2176065357 \tag{23}$$

```
> #With this info we can say that 0 and 3/2 + sqrt(105)/10 are
  unstable equilibrium points, while 3/2 - sqrt(105)/10 is our only
  stable equilibrium point. The function SFP will give us the same
  answer.
```

```
> SFP([5/2*x*(1-x)*(1-(x/2))],[x])
```

$$\{[0.475304923]\} \tag{24}$$

```
> #This decimal value is equivalent to 3/2 - sqrt(105)/10, so our
  answer is correct.
```

```
> #c. Use Orb function for this question.
```

```
> Orb([5/2*x*(1-x)*(1-(x/2))],[x],[.1],1000,1000)[1]
```

$$[0.4753049232] \tag{25}$$

```
> #This is our value at x(1000) with 10 decimal accuracy. Makes sense
  as we would expect to get near the stable equilibrium point as time
  goes on.
```

```
> #Question 4
```

```
> #Equal proportions of AA, Aa, and aa in first generation so u=v=w.
  u+v+w=1 u,v,w=1/3. Need to calculate u, v, and w for next
  generation. To do that we need to calculate the genotype
  frequencies for offspring based on every combination of random
  mating between parents of all genotypes. 6 combinations of
  different matings between genotypes possible. They are AA x AA,AA x
  Aa,AA x aa,Aa x Aa,Aa x aa,aa x aa. We see that from this that the
  offspring genotype frequencies can be summed into the following
  equations
  #u(n+1)=u(n)^2+u(n)*v(n)+1/4*v(n)^2
  #v(n+1)=u(n)*v(n)+2*u(n)*w(n)+1/2*v(n)^2+v(n)*w(n)
  #w(n+1)=1/4*v(n)^2+v(n)*w(n)+w(n)^2

> #a.

> #The genotype of AA for the next generation (gen 2) is based on the
  equation for u(n+1) so with u(n)=v(n)=w(n)=1/3 we have:


> evalf((1/3)^2+(1/3*1/3)+(1/4)*(1/3)^2)
                                  0.2500000000                    (26)

> #The genotype of Aa for the next generation (gen 2) is based on the
  equation for v(n+1) so with u(n)=v(n)=w(n)=1/3 we have:

> evalf((1/3*1/3)+(2*1/3*1/3)+(1/2*(1/3^2))+(1/3*1/3))
                                  0.5000000000                    (27)

> #The genotype of aa for the next generation (gen 2) is based on the
  equation for w(n+1) so with u(n)=v(n)=w(n)=1/3 we have.

> evalf((1/4*(1/3)^2)+(1/3*1/3)+(1/3)^2)
                                  0.2500000000                    (28)

> #This obviously still satisfies the equation that u+v+w=1. The
  proportion of the population that will have genotype Aa is .5 or
  1/2. Also will use HWg function from DMB.txt to prove our answers
  are correct, our matrix M will consist of entries all equal to 1.
  HWg(1/3,1/3,[[1,1,1],[1,1,1],[1,1,1]])

                                  [1/4, 1/2]                      (29)

> #b.

> #Hardy Weinberg Law states that the frequencies of genotypes will
  stabilize after one generation, UNDER VERY SPECIFIC ASSUMPTIONS, so
  we'd expect that the proportion of Aa genotype in the 1000th
  generation will be the same as it is in generation 2.

> #Let's show that we have achieved stability, going to show genotype
  frequencies for generation 3.

> evalf((1/4)^2+(1/4*1/2)+(1/4*(1/2)^2)) #This is u (AA genotype
  freq.) for generation 3
                                  0.2500000000                    (30)

> evalf((1/4*1/2)+(2*1/4*1/4)+(1/2*(1/2)^2)+(1/2*1/4)) #This is v (Aa
  genotype freq.) for generation 3
                                  0.5000000000                    (31)
```

```
> evalf((1/4*(1/2)^2)+(1/2*1/4)+(1/4)^2) #This is w (aa genotype
  freq.) for generation 3
```

$$0.2500000000 \tag{32}$$

```
> #We see that frequencies stayed the same for generation 3, so they
  remain stable for forever into the future. Therefore the proportion
  of Aa individuals in the 1000th generation will also be .5 or 1/2.

> #Question 5

> #Twice as likely now for a female AA to mate with a male Aa. Equal
  proportions again to start out with so u=v=w=1/3

> NR:=HWg(1/3,1/3,[[.5,1,.5],[.5,.5,.5],[.5,.5,.5]])
```

$$NR := [0.2750000000, 0.4999999998] \tag{33}$$

```
> Orb(NR,[u,v],[.3,.4],1000,1010)
```

$$[[0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998], [0.2750000000, 0.4999999998]] \tag{34}$$

```
> #Used the HWg function, and even though the M matrix was pertaining
  to survivability, it works the same if we decide to use it as a non
  random mating matrix, showing which combination is more likely to
  occur. The female AA x male Aa mating was considered 2x more likely
  to occur than all other pairings so gave that a value of 1 and
  every other pairing is half as likely so gave those values of .5 in
  the matrix.

> #a. So the proportion of individuals of genotype Aa in generation 2
  is .4999999998.

> #b. The proportion of individuals in generation 1000 with genotype
  Aa is the same as it was in generation 2 as it seems that the
  frequency stabilizes so it is also 0.4999999998.

> #Question 6

> #x(n)=(1+x(n-1)+y(n-1))/(2+x(n-1)+3*y(n-1)) y(n)=(1+x(n-1)+3*y(n-1)
  )/(3+x(n-1)+2*y(n-1))

> #Underyling transformation is (x,y) -> ((1+x+y)/(2+x+3*y), (1+x+3*
  y)/(3+x+2*y))

> F:=[(1+x+y)/(2+x+3*y), (1+x+3*y)/(3+x+2*y)]
```

$$F := \left[\frac{1+x+y}{2+x+3\,y}, \frac{1+x+3\,y}{3+x+2\,y}\right] \tag{35}$$

```
> evalf(FP(F,[x,y]))
```

$$\{[0.4705902280, 0.7478789082]\} \tag{36}$$

```
> evalf(SFP(F,[x,y]))
```

$$\{[0.4705902280, 0.7478789082]\} \tag{37}$$

```
> #From what we know about stable fixed points, we could imagine that
  if we start at values near enough to the SFP, we will tend towards
```

```
the SFP. 'Near enough' is a general term that we cannot really
calculate fully, so even if we start at numbers very 'far' (in
relation to each other on a number line) from our stable fixed
point we could still very well end up at the stable fixed point.
Will use Orb function to estimate where we end up in the first 1010
timesteps. From there if we have stability, then we can assume that
for the timestep you ask for we will still remain at that same
value of y.
```

```
> Orb(F,[x,y],[100.,1000.],1000,1010)
```

$$[[0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080], [0.4705902280, 0.7478789080]] \quad (38)$$

```
> #We see that our value of y at timestep 1010 so y(1010)=
  .7478789080, we'd imagine this stays true even to the value you ask
  for in the exam.

> #Question 7

> Help(SIRS)
```

SIRS(s,i,beta,gamma,nu,N): The SIRS dynamical model with parameters beta,gamma, nu,N (see section 6.6 of Edelstein-Keshet), s is the number of Susceptibles, i is the number of infected, (the number of removed is given by N-s-i). N is the total population. Try:

SIRS(s,i,beta,gamma,nu,N); (39)

```
> #N=1000, gamma=.5, nu=100, s=300, i=300

> SIRS(s,i,beta,gamma,nu,N)
```

$$[-\beta\, s\, i + \gamma\,(N - s - i), \beta\, s\, i - \nu\, i] \quad (40)$$

```
> #a. beta = .05

> F:=SIRS(s,i,.05,.5,100,1000)
```

$$F := [-0.05\, s\, i + 500.0 - 0.5\, s - 0.5\, i, 0.05\, s\, i - 100\, i] \quad (41)$$

```
> SEquP(F,[s,i])
```

$$\{[1000., 0.]\} \quad (42)$$

```
> #Since this is our stable equilibrium point we can assume that in
  the long run we do reach these values of S and I. With that said we
  can calculate R because R=N-S-I, so R=0 in the long run. We can
  also tell because we have an R0 value of less than 1 so the disease
  will die out in the population.

> #b. beta = 1.4

> F:=SIRS(s,i,1.4,.5,100,1000)
```

$$F := [-1.4\, s\, i + 500.0 - 0.5\, s - 0.5\, i, 1.4\, s\, i - 100\, i] \quad (43)$$

```
> SEquP(F,[s,i])
```

$$\{[71.42857143, 4.619758351]\} \quad (44)$$

```
> #R=N-S-I so:

> 1000-71.42857143-4.619758351
```

$$923.9516702 \tag{45}$$

```
> #Around 924 members of the population will be in the removed group
  in the long run.

> #c. For this we will look strictly at the R0 value, R0 = (N*beta)
  /nu, we compare this to 1, if >1 then the disease will really
  spread throughtout the population, if <1 the disease will die out.
  Let's see where it is equal to 1


> 100/1000
```

$$\frac{1}{10} \tag{46}$$

```
> #beta=1/10 is our threshold value.
> F:=SIRS(s,i,.11,.5,100,1000)
```

$$F := [-0.11\,s\,i + 500.0 - 0.5\,s - 0.5\,i,\ 0.11\,s\,i - 100\,i] \tag{47}$$

```
> SEquP(F,[s,i])
```

$$\varnothing \tag{48}$$

```
> F:=SIRS(s,i,.11,.5,100,1000)
```

$$F := [-0.11\,s\,i + 500.0 - 0.5\,s - 0.5\,i,\ 0.11\,s\,i - 100\,i] \tag{49}$$

```
> SEquP(F,[s,i])
```

$$\{[909.0909091,\ 0.4522840344]\} \tag{50}$$

```
> F:=SIRS(s,i,.09,.5,100,1000)
```

$$F := [-0.09\,s\,i + 500.0 - 0.5\,s - 0.5\,i,\ 0.09\,s\,i - 100\,i] \tag{51}$$

```
> SEquP(F,[s,i])
```

$$\{[1000.,\ 0.]\} \tag{52}$$

```
> #Anything greater than a beta value of 1/10, there will start to be
  a nonzero number of infected individuals in the long run. This is
  our cut-off value for beta.

> #Question 8

> 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); (53)

```
> #a.
  F:=GeneNet(0,1,.2,2,m1,m2,m3,p1,p2,p3)
```

$$F := \left[-m1 + \frac{1}{p3^2 + 1},\ -m2 + \frac{1}{p1^2 + 1},\ -m3 + \frac{1}{p2^2 + 1},\ -0.2\,p1 + 0.2\,m1,\ -0.2\,p2 + 0.2\,m2,\ -0.2\,p3 + 0.2\,m3\right] \tag{54}$$

```
> SEquP(F,[m1,m2,m3,p1,p2,p3])
```

$$\{[0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038, 0.6823278038]\} \quad (55)$$

```
> Dis(F,[m1,m2,m3,p1,p2,p3],[.2,.1,.3,.1,.4,.5],.01,150)[-1]
```

$$[150.01, [0.6823278250, 0.6823277949, 0.6823277851, 0.6823278250, 0.6823278250, 0.6823277750]] \quad (56)$$

```
> #The height of the horizontal asymptote is .6823278038, this is the
  stable equilibrium point for all variables, also confirmed with the
  use of Dis as our values get closer and closer to that stable
  equilibrium point.

> #b.

> F:=GeneNet(0,3,.2,2,m1,m2,m3,p1,p2,p3)
```

$$F := \left[-m1 + \frac{3}{p3^2 + 1}, -m2 + \frac{3}{p1^2 + 1}, -m3 + \frac{3}{p2^2 + 1}, -0.2\,p1 + 0.2\,m1, -0.2\,p2 + 0.2\,m2, -0.2\,p3 + 0.2\,m3\right] \quad (57)$$

```
> SEquP(F,[m1,m2,m3,p1,p2,p3])
```

$$\{[1.213411663, 1.213411663, 1.213411663, 1.213411663, 1.213411663, 1.213411663]\} \quad (58)$$

```
> #There is also a horizontal asymptote for these and it is shown by
  the stable equilbrium, the height of the horizontal asymptote is at
  1.213411663.

> Dis(F,[m1,m2,m3,p1,p2,p3],[.2,.1,.3,.1,.4,.5],.01,150)[-1]
```

$$[150.01, [1.214165713, 1.213061389, 1.213008023, 1.213797356, 1.213638232, 1.212799623]] \quad (59)$$

```
> #Also supported by the results of the Dis function.

> #c.

> F:=GeneNet(0,50,.2,2,m1,m2,m3,p1,p2,p3)
```

$$F := \left[-m1 + \frac{50}{p3^2 + 1}, -m2 + \frac{50}{p1^2 + 1}, -m3 + \frac{50}{p2^2 + 1}, -0.2\,p1 + 0.2\,m1, -0.2\,p2 + 0.2\,m2, -0.2\,p3 + 0.2\,m3\right] \quad (60)$$

```
> SEquP(F,[m1,m2,m3,p1,p2,p3])
```

$$\varnothing \quad (61)$$

```
> F:=GeneNet(0,45,.2,2,m1,m2,m3,p1,p2,p3)
```

$$F := \left[-m1 + \frac{45}{p3^2 + 1}, -m2 + \frac{45}{p1^2 + 1}, -m3 + \frac{45}{p2^2 + 1}, -0.2\,p1 + 0.2\,m1, -0.2\,p2 + 0.2\,m2, -0.2\,p3 + 0.2\,m3\right] \quad (62)$$

```
> SEquP(F,[m1,m2,m3,p1,p2,p3])
```

$$\varnothing \quad (63)$$

```
> F:=GeneNet(0,40,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (64)$$

```
> F:=GeneNet(0,30,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (65)$$

```
> F:=GeneNet(0,20,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (66)$$

```
> F:=GeneNet(0,10,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (67)$$

```
> F:=GeneNet(0,5,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.515980228, 1.515980228, 1.515980228, 1.515980228, 1.515980228, 1.515980228]\} \quad (68)$$

```
> F:=GeneNet(0,5.1,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.528555777, 1.528555777, 1.528555777, 1.528555777, 1.528555777, 1.528555777]\} \quad (69)$$

```
> F:=GeneNet(0,6,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.634365293, 1.634365293, 1.634365293, 1.634365293, 1.634365293, 1.634365293]\} \quad (70)$$

```
> F:=GeneNet(0,7,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.739203861, 1.739203861, 1.739203861, 1.739203861, 1.739203861, 1.739203861]\} \quad (71)$$

```
> F:=GeneNet(0,8,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (72)$$

```
> F:=GeneNet(0,7.5,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (73)$$

```
> F:=GeneNet(0,7.2,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.758855227, 1.758855227, 1.758855227, 1.758855227, 1.758855227, 1.758855227]\} \quad (74)$$

```
> F:=GeneNet(0,7.3,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\{[1.768534008, 1.768534008, 1.768534008, 1.768534008, 1.768534008, 1.768534008]\} \quad (75)$$

```
> F:=GeneNet(0,7.4,.2,2,m1,m2,m3,p1,p2,p3):
  SEquP(F,[m1,m2,m3,p1,p2,p3]);
```
$$\varnothing \quad (76)$$

```
> #Through rigorous testing we see that the the value of alpha which
  still holds a stable equilibrium, but loses it once you add .1, is
  7.3.

> #Question 9

> 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); **(77)**

```
> F:=ChemoStat(N,C,2.5,2.7)
```

$$F := \left[\frac{2.5\,C\,N}{C+1} - N, -\frac{C\,N}{C+1} - C + 2.7 \right] \quad \textbf{(78)}$$

```
> #a.
```

```
> SEquP(F,[N,C])
```

$$[5.083333333, 0.6666666667] \quad \textbf{(79)}$$

```
> Dis(F,[N,C],[100,200],.01,150)[-1]
```

$$[150.01, [5.083333450, 0.6666666474]] \quad \textbf{(80)}$$

```
> #In the long run the value of the Bacterial population density will
  be around 5.083333333.
```

```
> #b.
```

```
> SEquP(F,[N,C])
```

$$\{[5.083333333, 0.6666666667]\} \quad \textbf{(81)}$$

```
> Dis(F,[N,C],[100,200],.01,150)[-1]
```

$$[150.01, [5.083333450, 0.6666666474]] \quad \textbf{(82)}$$

```
> #In the long run, the value of the nutrient concentration will be
  .6666666667.
```

```
> #Question 10
```

```
> with(LinearAlgebra)
```

[*&x*, *Add*, *Adjoint*, *BackwardSubstitute*, *BandMatrix*, *Basis*, *BezoutMatrix*, *BidiagonalForm*, **(83)**
BilinearForm, *CARE*, *CharacteristicMatrix*, *CharacteristicPolynomial*, *Column*,
ColumnDimension, *ColumnOperation*, *ColumnSpace*, *CompanionMatrix*,
CompressedSparseForm, *ConditionNumber*, *ConstantMatrix*, *ConstantVector*, *Copy*,
CreatePermutation, *CrossProduct*, *DARE*, *DeleteColumn*, *DeleteRow*, *Determinant*,
Diagonal, *DiagonalMatrix*, *Dimension*, *Dimensions*, *DotProduct*, *EigenConditionNumbers*,
Eigenvalues, *Eigenvectors*, *Equal*, *ForwardSubstitute*, *FrobeniusForm*,
FromCompressedSparseForm, *FromSplitForm*, *GaussianElimination*, *GenerateEquations*,
GenerateMatrix, *Generic*, *GetResultDataType*, *GetResultShape*, *GivensRotationMatrix*,
GramSchmidt, *HankelMatrix*, *HermiteForm*, *HermitianTranspose*, *HessenbergForm*,
HilbertMatrix, *HouseholderMatrix*, *IdentityMatrix*, *IntersectionBasis*, *IsDefinite*,
IsOrthogonal, *IsSimilar*, *IsUnitary*, *JordanBlockMatrix*, *JordanForm*, *KroneckerProduct*,
LA_Main, *LUDecomposition*, *LeastSquares*, *LinearSolve*, *LyapunovSolve*, *Map*, *Map2*,
MatrixAdd, *MatrixExponential*, *MatrixFunction*, *MatrixInverse*, *MatrixMatrixMultiply*,
MatrixNorm, *MatrixPower*, *MatrixScalarMultiply*, *MatrixVectorMultiply*,
MinimalPolynomial, *Minor*, *Modular*, *Multiply*, *NoUserValue*, *Norm*, *Normalize*, *NullSpace*,
OuterProductMatrix, *Permanent*, *Pivot*, *PopovForm*, *ProjectionMatrix*, *QRDecomposition*,

RandomMatrix, *RandomVector*, *Rank*, *RationalCanonicalForm*, *ReducedRowEchelonForm*, *Row*, *RowDimension*, *RowOperation*, *RowSpace*, *ScalarMatrix*, *ScalarMultiply*, *ScalarVector*, *SchurForm*, *SingularValues*, *SmithForm*, *SplitForm*, *StronglyConnectedBlocks*, *SubMatrix*, *SubVector*, *SumBasis*, *SylvesterMatrix*, *SylvesterSolve*, *ToeplitzMatrix*, *Trace*, *Transpose*, *TridiagonalForm*, *UnitVector*, *VandermondeMatrix*, *VectorAdd*, *VectorAngle*, *VectorMatrixMultiply*, *VectorNorm*, *VectorScalarMultiply*, *ZeroMatrix*, *ZeroVector*, *Zip*]

```
> #9x9 Matrix will be needed. Random surfer who is on webpages 1,2,3
  stays there with prob .2, webpages 4,5,6 stays on them with prob
  .4, webpages 7,8,9 stays on them with prob .6. Equally likely to go
  to any of the other 8 pages depending on where they start.
```

```
> T:=Matrix([[.2,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8],[.8/8,
  .2,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8],
  [.8/8,.8/8,.2,.8/8,.8/8,.8/8,.8/8,.8/8,.8/8],[.6/8,.6/8,.6/8,
  .4,.6/8,.6/8,.6/8,.6/8,.6/8],[.6/8,.6/8,.6/8,.6/8,.6/8,
  .4,.6/8,.6/8,.6/8,.6/8],[.6/8,.6/8,.6/8,.6/8,.6/8,
  .4,.6/8,.6/8,.6/8],[.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.6,.4/8,.4/8],
  [.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.6,.4/8],
  [.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.4/8,.6]])
```

$$T := \begin{bmatrix} [0.2, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000] \\ [0.1000000000, 0.2, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000] \\ [0.1000000000, 0.1000000000, 0.2, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000, 0.1000000000] \\ [0.07500000000, 0.07500000000, 0.07500000000, 0.4, 0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000] \\ [0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000, 0.4, 0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000] \\ [0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000, 0.07500000000, 0.4, 0.07500000000, 0.07500000000, 0.07500000000] \\ [0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.6, 0.05000000000, 0.05000000000] \\ [0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.6, 0.05000000000] \\ [0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.05000000000, 0.6] \end{bmatrix} \quad \textbf{(84)}$$

```
> #a.
```

```
> #To find the page ranks, in the long run, we need to take this
  transition matrix to a high power. Make it 1000
```

```
> T^1000
```

$$\begin{bmatrix} [0.0769230769230796, 0.0769230769230796, 0.0769230769230796, 0.102564102564106, \end{bmatrix} \quad \textbf{(85)}$$

```
  0.102564102564106, 0.102564102564106, 0.153846153846159, 0.153846153846159,
  0.153846153846159 ],
 [ 0.0769230769230796, 0.0769230769230796, 0.0769230769230796,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230796, 0.0769230769230796, 0.0769230769230796,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230795, 0.0769230769230795, 0.0769230769230795,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230795, 0.0769230769230796, 0.0769230769230796,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230795, 0.0769230769230795, 0.0769230769230795,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230796, 0.0769230769230796, 0.0769230769230796,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230796, 0.0769230769230796, 0.0769230769230796,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ],
 [ 0.0769230769230795, 0.0769230769230795, 0.0769230769230795,
  0.102564102564106, 0.102564102564106, 0.102564102564106, 0.153846153846159,
  0.153846153846159, 0.153846153846159 ]]
> #A random surfer will be at web page 1, with probability of
  .0769230769230796.

> #b.

> #Using the information from the T^1000, a random surfer will be at
  web page 9, with probability of 0.153846153846159.
```