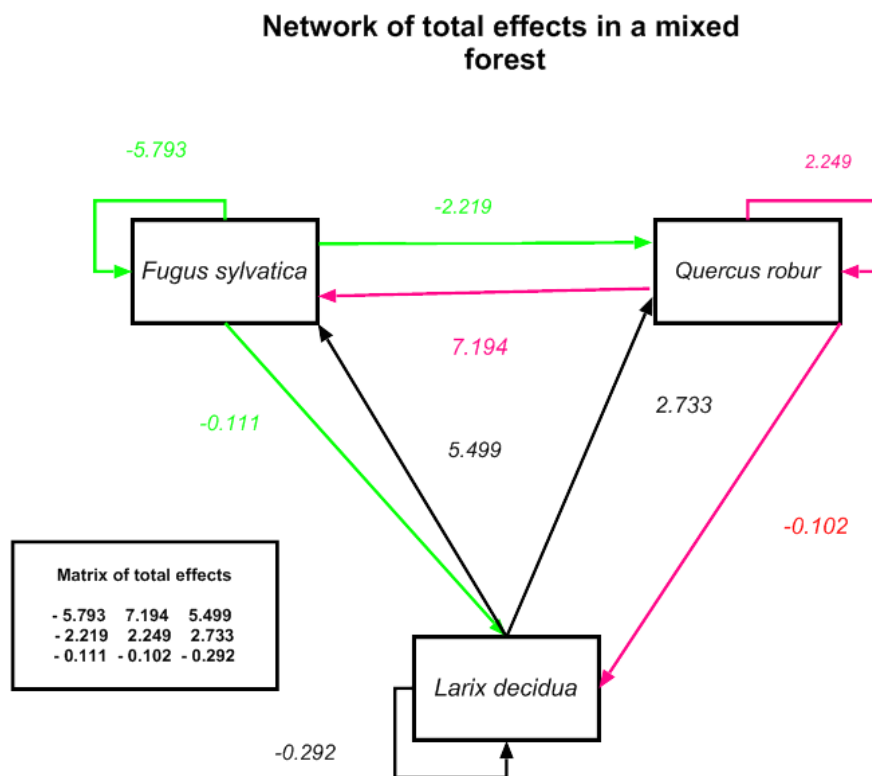


The Simulative Identification of Overyielding, and Total Effects in Mixed Forests

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Costa da Caparica
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A table with all my texts available in the library of the Instituto Superior de Agronomia, is located in the following URL:

[https://www.repository.utl.pt/handle/10400.5/196/simplesearch?
filterquery=Barreto%2C+Lu%C3%ADs+Soares&filtername=author&filtertype>equals](https://www.repository.utl.pt/handle/10400.5/196/simplesearch?filterquery=Barreto%2C+Lu%C3%ADs+Soares&filtername=author&filtertype>equals)

Seventeen papers I published in *Silva Lusitana*, from 2001 to 2013, are available in thhe following URL:

<http://www.scielo.mec.pt/cgi-bin/wxis.exe/iah/>

With compliments

The Simulative Identification of Overyielding, and Total Effects in Mixed Forests

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Abstract. The author uses his theory for mixed stands, and his model BACO2 for tree competition to present two simulators for overyielding in forests with two, and three species. A simulator that generates the matrix of total effects for mixed forests with three species is also displayed. The language used is Scilab.

Key words: mixed forests; overyielding; Scilab simulators; total effects

Sumário. O autor recorre à sua teoria para os povoamentos mistos e ao seu modelo BACO2 para apresentar simuladores para a deteção de sobre produção em florestas mistas com duas e três espécies. Disponibiliza também um simulador para estabelecer a matriz de efeitos totais em florestas com três espécies. A linguagem utilizada é o Scilab.

Palavras-chave: efeitos totais; florestas mistas; simuladores em Scilab; sobreprodução;

1. Introduction

This text is a follow-up of Barreto (2020a,b). To avoid excessive repetitions I suggest its reading and also the familiarization with my theory for tree competition, and related models, displayed in Barreto (2011: chapters 9, 14-18).

In Barreto (2020a,b), I approached overyielding (**OY**) in mixed forests with two, and more species, and I showed that simulations underpinned by my theory for forests, and associated models (Barreto, 2011), are capable to reproduce empirical data about the emergence of OY in real forests. Now, after I had established the validation and corroboration of my theory in this particular issue, the aim of this text is twofold:

- To make available the listing of simulators, written in Scilab, for the emergence of OY for several combinations of the relative size of the dominant species and its initial proportions in the total number of trees. The main output are graphics similar to the figure 2, in Barreto (2020a).
- To analyse, and simulate the emergence of total effects in mixed forest , and provide the script of a simulator for this purpose.

2. Characterizing some species

As previously, I characterize the competitive ability of a species using the ratio of *initial density/final density* in the Gompertz equation of a cohort of trees R_2 . The competitive coefficient in the Gompertz equation is c , see equation (4.45) in Barreto (2011). The characterization of the bionomic strategies of the tree species is approached in Barreto (2011: chapter 9). The greater is the value of R_2 of a species, the greater is its competitive ability.

As model BACO2 is the core of the simulators, for the sake of completeness, and to open a easier possibility to extend the simulators to more than three species, I display model BACO2 for competition.

Let us consider a mixed forest with n species, being the density of species i at age t in a mixed forest represented by y_{i-21t} .

Under the perspective of the competitive pressure the trees of species i are suffering, the total density of the stand for this species is measured as:

$$y_{i-21t} = y_{i-21t} + \sum_{j=1}^n \frac{rmr_{jt}}{rmr_{it}} y_{j-21t} \quad j \neq i \quad (1)$$

where $rmr_{it} (= -c_i \ln(R_{i-2}) \exp(-c_i(t-t_0)))$ is the relative mortality of species i , at age t , in a pure stand.

The relative mortality of species i , at age t , ${}^mrmr_{it}$, is defined as:

$${}^mrmr_{it} = rmr_{it} (1 + \sum_{j=1}^n f_{jt} \ln(\frac{rmr_{jt}}{rmr_{it}})) \quad j \neq i \quad (2)$$

Where f_j is the fraction of trees of species j , at age t , in the mixed forest:

$$f_{jt} = \frac{y_{j-21t}}{\sum_{i=1}^n y_{i-21t}} \quad (3)$$

I can write my model BACO2 for tree competition as:

$$\frac{dy_{i-21t}}{dt} = y_{i-21t} {}^mrmr_{it} \quad (4)$$

Model BACO2 is a general model fort biological competition (Barreto, 2017). This unity or sistemicity is a relevant attribute of my theories for ecology, and forests.

Table 1. Characteristics of some tree species. The age of the initial density in R_2 is 10 years

Species	c	R_2	LHS	Acronym
<i>Abies alba</i>	0.0310	167.4859	K-2	Aal
<i>Abies grandis</i>	0.0550	371.2490	K-3	Agr
<i>Abies procera</i>	0.0490	542.0928	K-3	Apr
<i>Acer pseudoplatanus</i>	0.0450	45.4938	$r \leftrightarrow K$	Aps
<i>Alnus glutinosa</i>	0.0290	01-11-51	r-3	Agl
<i>Alnus rubra</i>	0.0490	119.7037	r-1	Aru
<i>Betula pendula</i>	0.0350	20.0478	r-3	Bpe
<i>Cedrus atlantica</i>	0.0360	67.2634	-	Cat
<i>Cryptomeria japonica</i>	0.0710	74.1245	-	Cja
<i>Eucalyptus grandis</i>	0.0620	103.6363	-	Egr
<i>Fagus sylvatica</i>	0.0430	946.7456	K-3	Fsy
<i>Fraxinus excelsior</i>	0.0380	87.7699	$r \leftrightarrow K$	Fex
<i>Larix decidua</i>	0.0430	40.0983	K-1	Lde
<i>Larix kaempferi</i>	0.0350	26.9133	-	Lka
<i>Picea abies</i>	0.0420	210.0399	K-2	Pab
<i>Picea mariana</i>	0.0350	96,3245	r-1	Pma
<i>Picea sitchensis</i>	0.0480	72.3078	K-1	Psi
<i>Pinus contorta</i>	0.0380	60.0460	r-2	Pco
<i>Pinus elliotii</i>	0.0830	52.2975	-	Pel
<i>Pinus halepensis</i>	0.0820	5,4260	r-3	Pha
<i>Pinus nigra ssp. laricio</i>	0.0510	81.4408	K-2	Pni
<i>Pinus pinaster</i>	0.0500	01-06-91	r-3	Ppa
<i>Pinus pinea</i>	0.1050	01-11-52	K-2	Ppe
<i>Pinus resinosa</i>	0.0260	51,8765	r-2	Pre
<i>Pinus strobus</i>	0.0300	22.4103	r-3	Pst
<i>Pinus sylvestris</i>	0.0300	34.2586	K-1	Psy
<i>Pinus taeda</i>	0.0600	22.5832	r-2	Pta
<i>Pseudotsuga menziesii</i>	0.0460	82.1957	K-1	Pme
<i>Quercus robur/petraea</i>	0.0410	125.9635	K-2	Qro/Qpe
<i>Tsuga heterophylla</i>	0.0390	81.02	K-1	The

3. Simulating Overyielding in Forests with Two Species: BACOVER2

Generalizing the convention adopted in Barreto (2020), a mixture of n species is referred as **species 1 + species 2 + + species n** . The ordering of the species mirror the decreasing order of their values of R_{-2} . This is, it is verified $R_{-21} > R_{-22} > \dots > R_{-2n}$. A mixture with European beech, Norway spruce, and sessile oak is named as **Fsy + Pab + Qpe**, because it happens $946.7 > 210.0 > 125.9$. The order of the species reflects their decreasing competitive abilities.

In a mixture with n species, initially with a total number of T trees, and an initial fraction of the dominant species equal to P_i , the initial numbers of the trees of each other species are equal to $(T - P_i * T) / (n - 1)$. We use $T = 10000$.

Only species 1 has variable relative size of the final dimension of the tree. The relative dimension of the final size of the trees of the other $n - 1$ species are equal to 1.

I had described the **standard mixture** here simulated. In the Scilab listings these options can be easily modified.

Simulator BACOVER2, and BACOVER3 is an application of the system of ODE (model BACO2) included in the simulator **ry2plot**, and **ry3plot** presented in Barreto (2020b). The systems of ODE are inserted in two nested loops, one for the relative size of the tree (R_t), and the other for the initial proportions of the number of trees of the dominant species (P_i).

The input of the simulators are the same as for **ry2plot**, and **ry3plot**. See page 23, in Barreto (2020b).

Now, let see the outputs of what the simulators.

The simulators create a graphic with relative variations rates as in simulators **ry2plot**, and **ry3plot**.

The simulators for values of R_t from 0.5, 1.0, 1.5, ... 10, and for values of P_i from 0.1, 0.2, ... 0.9, calculates 180 values of relative yield (RY).

To the values of relative yield, using as independent variables R_t , P_i , their squares and their product, an equation is fitted, using a function of Scilab for this purpose. The simulated values of RY, and the fitted values are compared graphically. A surface of the residuals is also presented. The mean relative error of the fitted values is also displayed.

The fitted equation is used to create a function to estimate values of R_y , for pairs of values of R_t , and P_i .

Now, we introduce the listing of the simulator, and an example of its use. The simulated forest has *Picea abies*, and *Quercus robur* (Pab+Qro).

```

//*****
//*      Simulator BACOVER      *
//* © Luís Soares Barreto, 2010, 2020 *
//*      *
//*****

c1=input('Meter valor de c1= ')
r1=input('Meter valor de r1= ')
c2=input('Meter valor de c2= ')
r2=input('Meter valor de r2= ')
g=input('Meter valor de g= ')

a=-1.3333333;
rv1=r1^a;
rv2=r2^a;
p1=[1000 2000 3000 4000 5000 6000 7000 8000 9000];
p2=[9000 8000 7000 6000 5000 4000 3000 2000 1000];
Z=[];H=[];anal=[];
scf(0)
clf
t0=0:g-10
x=10:g;

//Relative mortality rates, and
//Relative growth rates of the total biomass of a tree
rmr1=-c1*log(r1)*exp(-c1*t0);
rmr2=-c2*log(r2)*exp(-c2*t0);
rgr1=-c1*log(rv1)*exp(-c1*t0);
rgr2=-c2*log(rv2)*exp(-c2*t0);
M=[rmr1;rmr2;rgr1;rgr2]';
scf(0)
plot2d(x,[M])
xtitle("Relative variation rates","years","rvr")

```

```

b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
xgrid()

hl=legend(['rmr1','rmr2','rgr1','rgr2'],a=4)
b.children // list the children of the axes.
poly1= b.children.children;
poly1.thickness = [2,2,2,2];

//Loops to obtain the relative yields
//Loop for the relative size of the trees of the dominant species
for m=0.5:0.5:10
    CO=[];V=[];
    //Loop for the initial densities of the twoo species
    for n=1:1:9
        //Model BACO2 for tree competition
        deff("yprim=f(t,y)",[

            'f1=y(1)/(y(1)+y(2))';
            'f2=y(2)/(y(1)+y(2))';
            'rmr1=-c1*log(r1)*exp(-c1*t)';
            'rmr2=-c2*log(r2)*exp(-c2*t)';

            "yprim1=y(1)*rmr1*(1+f2*log(rmr2/rmr1))";..
            "yprim2=y(2)*rmr2*(1+f1*log(rmr1/rmr2))";..
            "yprim=[yprim1;yprim2]"
        ])
        y0=[p1(n),p2(n)];
        t0=0;
        t=0:g-10;
        [M]=(matrix(ode(y0,t0,t,f),2,g-9))';

        //tree biomasses

```

```

vf1=1;vf2=m*vf1;
ac=[vf2*rv1^exp(-c1*t)];
ap=[vf1*rv2^exp(-c2*t)];

//Standing biomasses of pure stands at age g
vpc=ac(1,g-9)*p1(n)*r1^(exp(-c1*(g-10))-1);
vpp=ap(1,g-9)*p2(n)*r2^(exp(-c2*(g-10))-1);
Tp=vpc+vpp;

//Standing biomass of the mixed stand at age g
vmc=M(g-9,1)*ac(1,g-9);
vmp=M(g-9,2)*ap(1,g-9);

//ratio (mixed biomass)/(sum of the biomasses of the pure stands)
R=(vmc+vmp)/Tp;
V=[V R];

end

H=abs([H;V]);

end

K=H;

//Graphic
X=[0.1:0.1:0.9];
Y=[0.5:0.5:10];
scf(1)
clf(1)

surf(X,Y,H,'facecol','cyan','edgecol','blu')
h=ones(20,9);
surf(X,Y,h)
xlabel("Relative Yield","Pi","Rt","Ry")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;

```

```

b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children;
poly1.thickness = [2,2,2,2];

//Analysis of the data of relative yields
anal=[min(H), median(H), mean(H), max(H),stdev(H)];
pi=[0.1:0.1:0.9];
H=[pi;H];
m=[0,0.5:0.5:10]';
H=[m,H];
format(6)
disp(H)
tit=['min', 'median', 'mean', 'max','st dev'];
disp(tit)
disp(anal)

z=ones(1,9);
b=matrix([0.5:0.5:10],1,20);
x1=[ b(1)*z; b(2)*z;b(3)*z;;b(4)*z;b(5)*z;b(6)*z;b(7)*z;
b(8)*z;b(9)*z;;b(10)*z;b(11)*z;b(12)*z;b(13)*z;
b(14)*z;b(15)*z;;b(16)*z;b(17)*z;b(18)*z;b(10)*z; b(20)*z]';
x1=matrix(x1,180,1);
a=0.1:0.1:0.9;
x2=[a a a a a a a a a a a a a a a a a a a]';
b=[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1];
x0=[b b b b b b b b b]';
x11=x1.^2;
x22=x2.^2;
x12=x1.*x2;

y=matrix(K',180,1)';
XX=[x1 x2 x11 x22 x12 y]';

```

```

X=XX';

deff(' [e]=G(a,z) ', 'e=a(1)+a(2)*z(1)+a(3)*z(2)+a(4)*z(3)+a(5)*z(4)+a(6)*z(5)-
z(6) ')

a0 = [1;1;1;1;1;1];
[aa,SSE]=datafit(G,X,a0)

disp('Output of the regression')

disp(aa)

disp(SSE)


yf=aa(1)+aa(2)*x1+aa(3)*x2+aa(4)*x11+aa(5)*x22+aa(6)*x12;


err=(y'-yf)./y';

disp('Mean relative error of the fitted values')

disp(mean(err))


scf(2)
clf(2)
plot2d([y',yf])

xtitle("Comparison of the simulated, and fitted relative yields","Pair Pi-
Rt", "RY")

legend(["Fitted","Simulated"],2)

b=get("current_axes");

    b.title.font_size=5;
    b.x_label.font_size=3;
    b.y_label.font_size=3;
    b.z_label.font_size=3;


    poly1= b.children.children;
    poly1.thickness = [2,2];


scf(3)
clf(3)
x=[0.1:0.1:0.9];
y=[0.5:0.5:10];

```

```

surf(X,Y,K,'facecol','cyan','edgecol','blu')
xlabel("Surface of relative yield simulated, and fitted","Pi","Rt","RY")
b=get("current_axes");
    b.title.font_size=5;
    b.x_label.font_size=3;
    b.y_label.font_size=3;
    b.z_label.font_size=3;

H2=matrix(yf,9,20)';
surf(X,Y,H2,'facecol','blu','edgecol','red')

scf(4)
clf(4)
D=(K-H2);
surf(X,Y,D,'facecol','green','edgecol','red')
z=zeros(20,9);
    surf(X,Y,z)
    xlabel("Residuals","Pi","Rt","RY")
b=get("current_axes");
    b.title.font_size=5;
    b.x_label.font_size=3;
    b.y_label.font_size=3;
    b.z_label.font_size=3;

deff('z=g(a,b) ','z=aa(1)+aa(2)*a+aa(3)*b+aa(4)*a^2+aa(5)*b^2+aa(6)*a*b')

```

column 1 to 6

0.	0.1	0.2	0.3	0.4	0.5
0.5	0.974	0.951	0.932	0.916	0.906
1.	0.994	0.989	0.985	0.983	0.981

1.5	1.013	1.023	1.029	1.033	1.033
2.	1.031	1.053	1.066	1.071	1.071
2.5	1.048	1.079	1.096	1.102	1.099
3.	1.064	1.103	1.122	1.128	1.122
3.5	1.079	1.124	1.145	1.149	1.14
4.	1.094	1.144	1.165	1.167	1.155
4.5	1.107	1.161	1.182	1.182	1.168
5.	1.12	1.177	1.198	1.195	1.178
5.5	1.132	1.192	1.212	1.207	1.187
6.	1.144	1.206	1.224	1.217	1.195
6.5	1.155	1.218	1.235	1.226	1.202
7.	1.166	1.23	1.246	1.234	1.208
7.5	1.176	1.241	1.255	1.242	1.214
8.	1.186	1.251	1.263	1.248	1.219
8.5	1.195	1.261	1.271	1.255	1.223
9.	1.204	1.269	1.278	1.26	1.227
9.5	1.212	1.278	1.285	1.265	1.231
10.	1.221	1.286	1.291	1.27	1.234

column 7 to 10

0.6	0.7	0.8	0.9
0.901	0.904	0.917	0.945
0.981	0.983	0.987	0.992
1.031	1.027	1.02	1.011
1.065	1.054	1.04	1.021
1.089	1.073	1.052	1.028
1.108	1.087	1.062	1.032
1.122	1.098	1.068	1.035
1.134	1.106	1.074	1.038
1.143	1.113	1.078	1.04
1.151	1.118	1.081	1.041
1.158	1.123	1.084	1.043

1.164	1.127	1.086	1.044
1.169	1.13	1.088	1.045
1.173	1.133	1.09	1.045
1.177	1.136	1.092	1.046
1.181	1.138	1.093	1.047
1.184	1.14	1.094	1.047
1.187	1.142	1.095	1.048
1.189	1.144	1.096	1.048
1.192	1.145	1.097	1.049

```
!min median mean max st dev !
```

0.901	1.123	1.121	1.291	0.091
-------	-------	-------	-------	-------

Output of the regression

```
0.833
0.078
0.491
- 0.004
- 0.476
- 0.030

0.126
```

Mean relative error of the fitted values

```
- 0.001
```

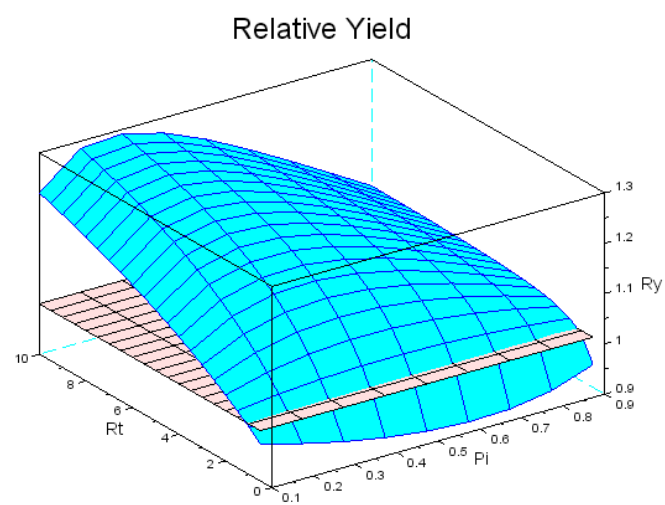
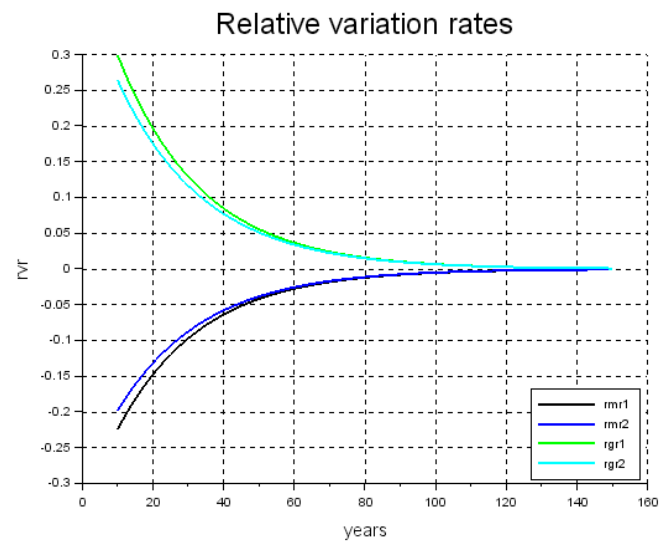
Now we use the regression to obtain the value of overyielding for $R_t=4.8$, and $P_i=0.06$:

```
g(4.8,0.6)
```

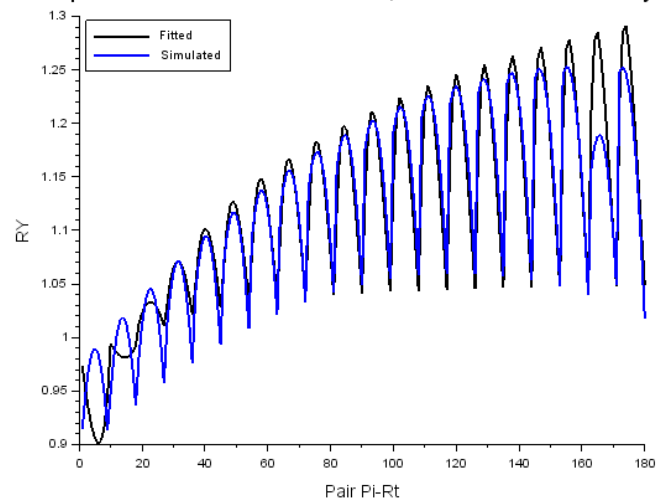
```
ans =
```

```
1.157
```

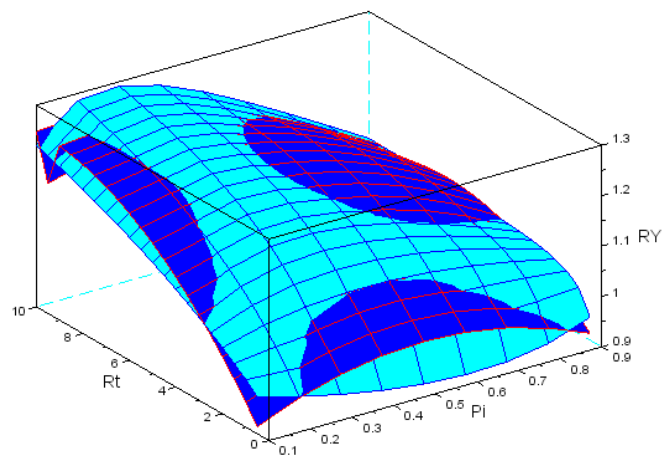
The simulator presents also five self-explanatory graphics:

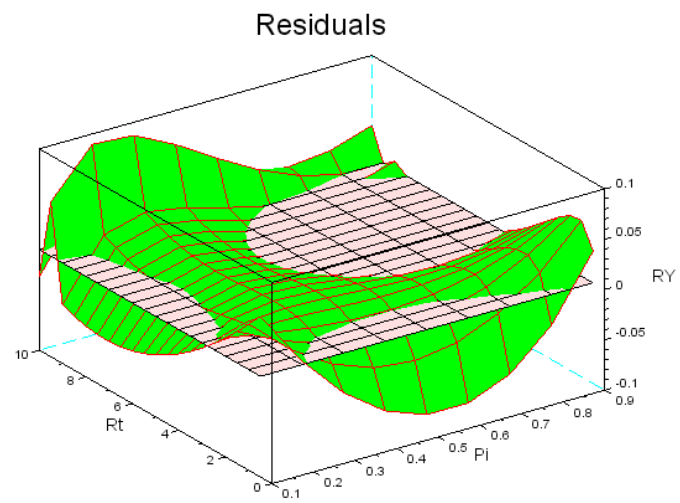


Comparison of the simulated, and fitted relative yields



Surface of relative yield simulated, and fitted





4. Simulating Overyielding in Forests with Three Species: BACOVER3

As both simulators BACOVER2, and BACOVER3 were simultaneously introduced in the previous section, in this section I only display the listing of the late simulator, and an illustration of its application. The forest simulated is Qro+Fex+Lde.

```
//*****
//*      Simulator BACOVER3      *
//* © Luís Soares Barreto, 2010, 2020 *
//*                                *
//*****

c1=input('Meter valor de c1= ')
r1=input('Meter valor de r1= ')

c2=input('Meter valor de c2= ')
r2=input('Meter valor de r2= ')

c3=input('Meter valor de c3= ')
r3=input('Meter valor de r3= ')

g=input('Meter valor de g= ')

a=-1.3333333;
rv1=r1^a;
rv2=r2^a;
rv3=r3^a;

p1=[1000 2000 3000 4000 5000 6000 7000 8000 9000];
p2=[4500 4000 3500 3000 2500 2000 1500 1000 500];
p3=[4500 4000 3500 3000 2500 2000 1500 1000 500];
```

```

Z=[];H=[];V=[];

scf(0)

clf

Z=[];H=[];anal=[];

xset("window",0)

clf

t0=0:g-10;

x=10:g;

//Relative mortality rates, and
//Relative growth rates of the total biomass of a tree
rmr1=-c1*log(r1)*exp(-c1*t0);
rmr2=-c2*log(r2)*exp(-c2*t0);
rmr3=-c3*log(r3)*exp(-c3*t0);
rgr1=-c1*log(rv1)*exp(-c1*t0);
rgr2=-c2*log(rv2)*exp(-c2*t0);
rgr3=-c3*log(rv3)*exp(-c3*t0);
M=[rmr1;rmr2;rmr3;rgr1;rgr2;rgr3]';
plot2d(x,[M])
legend(["rmr 1","rmr 2","rmr 3","rgr 1","rgr 2","rgr 3"], a=1)
xlabel("Relative variation rates","Years","rvr")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children;
poly1.thickness = [2,2,2,2,2,2];
xgrid()

for m=0.5:0.5:10

```

```

CO=[];V=[];

for n=1:1:9

    deff("yprim=f(t,y)",[
        'f1=y(1)/(y(1)+y(2)+y(3))';
        'f2=y(2)/(y(1)+y(2)+y(3))';
        'f3=y(3)/(y(1)+y(2)+y(3))';

        'rmr1=-c1*log(r1)*exp(-c1*t)';
        'rmr2=-c2*log(r2)*exp(-c2*t)';
        'rmr3=-c3*log(r3)*exp(-c3*t)';

        "yprim1=y(1)*rmr1*(1+f2*log(rmr2/rmr1)+f3*log(rmr3/rmr1))";..
        "yprim2=y(2)*rmr2*(1+f1*log(rmr1/rmr2)+f3*log(rmr3/rmr2))";..
        "yprim3=y(3)*rmr3*(1+f1*log(rmr1/rmr3)+f2*log(rmr2/rmr3))";..
        "yprim=[yprim1;yprim2;yprim3]" ])
    y0=[p1(n),p2(n),p3(n)];
    t0=0;
    t=0:g;

    [M]=(matrix(ode(y0,t0,t,f),3,g+1));

    //biomasses of the trees

    vf2=1;vf3=1;vf1=m*vf2;
    a1=[vf1*rv1^exp(-c1*t)];
    a2=[vf2*rv2^exp(-c2*t)];
    a3=[vf3*rv3^exp(-c3*t)];
    //volume em pé puro aos 90 anos
    vp1=a1(1,g+1)*p1(n)*r1^(exp(-c1*g)-1);
    vp2=a2(1,g+1)*p2(n)*r2^(exp(-c2*g)-1);

```

```

vp3=a3(1,g+1)*p3(n)*r3^(exp(-c3*g)-1);
Tp=vp1+vp2+vp3;

//Biomasses of the mixed stand
vm1=M(g+1,1)*a1(1,g+1);
vm2=M(g+1,2)*a2(1,g+1);
vm3=M(g+1,3)*a3(1,g+1);
//mixed/(sum of pure stands)
R=(vm1+vm2+vm3)/Tp;
V=[V R];
end

H=abs([H;V]);
end
K=H;
//Graphic
X=[0.1:0.1:0.9];
Y=[0.5:0.5:10];
scf(1)
clf(1)
surf(X,Y,H,'facecol','cyan','edgecol','blu')
h=ones(20,9);
surf(X,Y,h)
xlabel("Relative Yield","Pi","Rt","Ry")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children;
poly1.thickness = [2,2,2,2];

```

```

//Analysis of the data of relative yields
anal=[min(H), median(H), mean(H), max(H),stdev(H)];

pi=[0.1:0.1:0.9];
H=[pi;H];
m=[0,0.5:0.5:10]';
H=[m,H];
format(6)
disp(H)
tit=['min', 'median', 'mean', 'max','st dev'];
disp(tit)
disp(anal)

z=ones(1,9);

b=matrix([0.5:0.5:10],1,20);
x1=[ b(1)*z; b(2)*z;b(3)*z;;b(4)*z;b(5)*z;b(6)*z;b(7)*z;
b(8)*z;b(9)*z;;b(10)*z;b(11)*z;b(12)*z;b(13)*z;
b(14)*z;b(15)*z;;b(16)*z;b(17)*z;b(18)*z;b(10)*z; b(20)*z]';

x1=matrix(x1,180,1);

a=0.1:0.1:0.9;
x2=[a a a a a a a a a a a a a a a a a a a]';

b=[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1];
x0=[b b b b b b b b b]';
x11=x1.^2;
x22=x2.^2;
x12=x1.*x2;

y=matrix(K',180,1)';
XX=[x1 x2 x11 x22 x12 y]';
X=XX';

```

```

deff(' [e]=G(a,z) ', 'e=a(1)+a(2)*z(1)+a(3)*z(2)+a(4)*z(3)+a(5)*z(4)+a(6)*z(5)-
z(6) ')

a0 = [1;1;1;1;1;1];
[aa,SSE]=datafit(G,X,a0)

disp('Output of the regression')

disp(aa)

disp(SSE)


yf=aa(1)+aa(2)*x1+aa(3)*x2+aa(4)*x11+aa(5)*x22+aa(6)*x12;


err=(y'-yf)./y';

disp('Mean relative error of the fitted values')

disp(mean(err))


scf(2)
clf(2)
plot2d([y',yf])

xtitle("Comparison of the simulated, and fitted relative yields","Pair Pi-
Rt","RY")

legend(["Fitted","Simulated"], 2)

b=get("current_axes");

    b.title.font_size=5;

    b.x_label.font_size=3;

    b.y_label.font_size=3;

    b.z_label.font_size=3;


    poly1= b.children.children;

    poly1.thickness = [2,2];


scf(3)
clf(3)
X=[0.1:0.1:0.9];
Y=[0.5:0.5:10];

```

```

surf(X,Y,K,'facecol','cyan','edgecol','blu')

xlabel("Surface of relative yield simulated, and fitted","Pi","Rt","RY")

b=get("current_axes");

    b.title.font_size=5;

    b.x_label.font_size=3;

    b.y_label.font_size=3;

    b.z_label.font_size=3;


H2=matrix(yf,9,20)';

surf(X,Y,H2,'facecol','blu','edgecol','red')


scf(4)

clf(4)

D=(K-H2);

surf(X,Y,D,'facecol','green','edgecol','red')

z=zeros(20,9);

    surf(X,Y,z)

    xlabel("Residuals","Pi","Rt","RY")

b=get("current_axes");

    b.title.font_size=5;

    b.x_label.font_size=3;

    b.y_label.font_size=3;

    b.z_label.font_size=3;


    deff('z=g(a,b)','z=aa(1)+aa(2)*a+aa(3)*b+aa(4)*a^2+aa(5)*b^2+aa(6)*a*b')


Meter valor de c1= 0.041

Meter valor de r1= 126

Meter valor de c2= 0.038

Meter valor de r2= 88

Meter valor de c3= 0.043

Meter valor de r3= 40

```

Meter valor de $g = 150$

column 1 to 6

0.	0.1	0.2	0.3	0.4	0.5
0.5	0.937	0.904	0.876	0.853	0.837
1.	0.965	0.956	0.950	0.945	0.944
1.5	0.992	1.004	1.013	1.019	1.022
2.	1.017	1.047	1.068	1.079	1.082
2.5	1.042	1.087	1.115	1.128	1.129
3.	1.065	1.124	1.157	1.17	1.168
3.5	1.087	1.157	1.194	1.206	1.199
4.	1.109	1.188	1.227	1.238	1.226
4.5	1.13	1.217	1.257	1.265	1.249
5.	1.149	1.244	1.284	1.289	1.269
5.5	1.169	1.268	1.309	1.31	1.286
6.	1.187	1.292	1.331	1.329	1.301
6.5	1.205	1.313	1.351	1.346	1.314
7.	1.222	1.334	1.37	1.362	1.326
7.5	1.238	1.353	1.388	1.376	1.337
8.	1.254	1.371	1.404	1.389	1.347
8.5	1.269	1.388	1.418	1.401	1.356
9.	1.284	1.404	1.432	1.411	1.364
9.5	1.299	1.419	1.445	1.421	1.371
10.	1.312	1.434	1.457	1.431	1.378

column 7 to 10

0.6	0.7	0.8	0.9
0.829	0.832	0.851	0.898
0.945	0.950	0.960	0.976
1.022	1.02	1.016	1.009

1.078	1.067	1.05	1.028
1.119	1.1	1.073	1.04
1.152	1.125	1.09	1.048
1.178	1.144	1.102	1.054
1.199	1.16	1.112	1.058
1.217	1.173	1.12	1.062
1.232	1.183	1.127	1.065
1.245	1.192	1.132	1.067
1.256	1.2	1.137	1.069
1.266	1.206	1.141	1.071
1.274	1.212	1.144	1.073
1.282	1.217	1.147	1.074
1.289	1.222	1.15	1.075
1.295	1.226	1.152	1.076
1.301	1.229	1.154	1.077
1.306	1.233	1.156	1.078
1.31	1.236	1.158	1.079

!min median mean max st dev !

0.829	1.172	1.176	1.457	0.146
-------	-------	-------	-------	-------

Output of the regression

0.688
0.123
0.854
- 0.006
- 0.801
- 0.045
0.353

Mean relative error of the fitted values

- 0.001

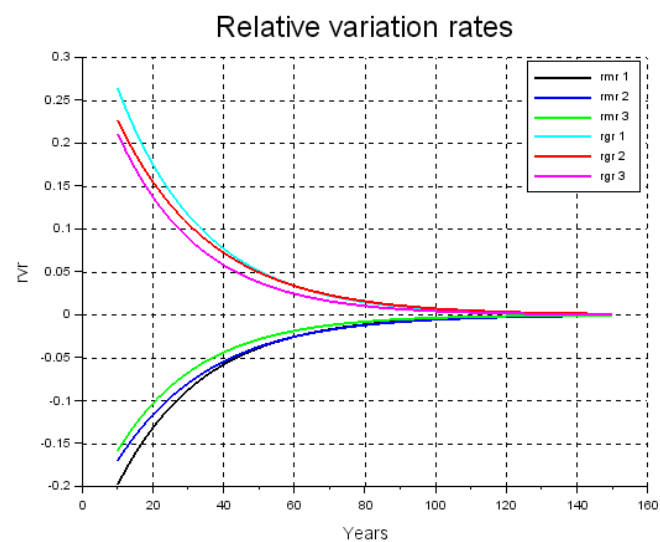
Now we use the regression to obtain the value of overyielding for $R_t=4.8$, and $P_i=0.06$:

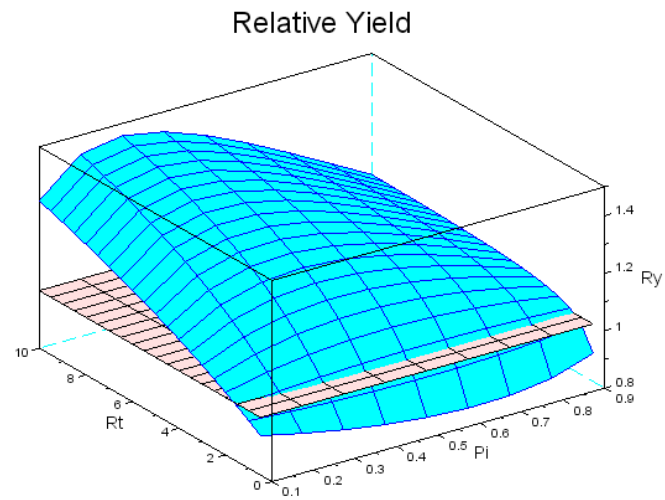
$g(4.8, 0.6)$

ans =

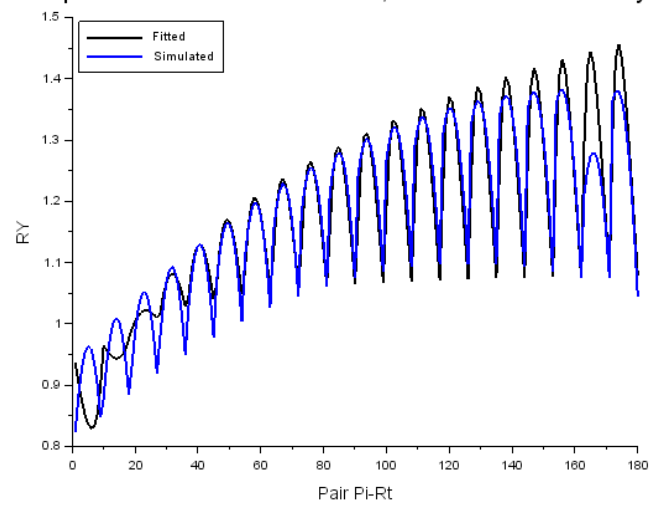
1.239

The fives graphic we obtain are the following:

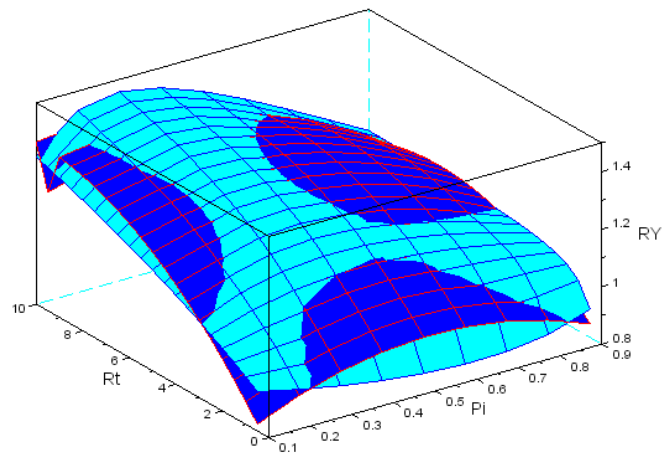




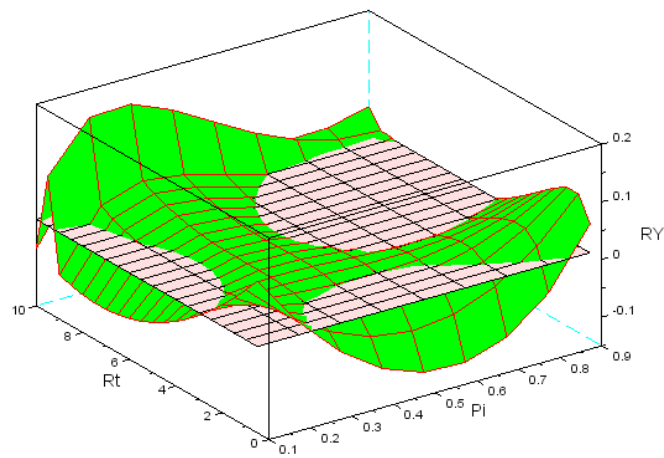
Comparison of the simulated, and fitted relative yields



Surface of relative yield simulated, and fitted



Residuals



5. Direct, Indirect, and Total Effects: An Illustration

5.1 Direct, Indirect, and Total Effects

This section is an adaptation of chapter 2 of Barreto (2019).

In the social, and financial sphere, we are all familiar with chain effects triggered by a single event or measure adopted by a government. To face the present pandemic of covid-19, the European states decided not diminish the income of the European citizens. This decision, among other more elaborated justifications, can be sustained by the following causal chain:

decreased income of citizens → diminished consumption → smaller investment in production of goods for the consumers → more unemployment

This example is a very simple causal chain. Real systems are much more complex and the task of economists are much more difficult and plagued with disagreement. What makes the understanding of the behaviour of complex systems (as ecosystems, and national economies) intricate, and their dynamics almost unpredictable beyond a short period of time, are the rich network of direct, and **indirect effects (those mediated by a third component)**.

Let us introduce an example that will be numerically illustrated ahead. Consider the following chain of omnivory:

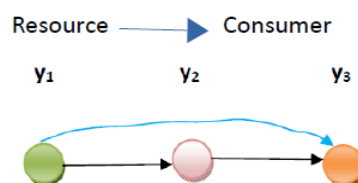


Figure 1. Diagrammatic representation of omnivory. Populations as: y_1 is the plant; y_2 is the herbivore; y_3 is the omnivore

The omnivore y_3 has a negative direct effect on plant y_1 , and a positive indirect effect because it diminishes the number of herbivores y_2 that also consume the plant.

The total effect (TE) of y_3 on y_1 is the sum of the direct, and indirect effects:

Total or net effect of y_3 on y_1 = Direct effect of y_3 on y_1 + indirect effect of y_3 on y_1

If y_3 has a very small consumption of y_1 , y_2 grazes y_1 intensively, and y_3 consumes intensively y_2 , the total effect of y_3 on y_1 may be **positive**.

On the other side, If y_3 has a heavy consumption of y_1 , y_2 grazes y_1 lightly, and y_3 consumes lightly y_2 , the total effect of y_3 on y_1 may be **negative**.

At the community level of any ecosystem, e.g., a forest, we can conjecture the following chain:

Populations → direct effects (interactions) → indirect effects → total effects → community behaviour

Tentatively, let me introduce an ontological interpretation (figure 2).

The direct effects are controlled by the properties of the components, and they are constrained by laws (e.g., physical, chemical) actuating in each given situation. Indirect, and total effects emerge from the dynamical interactions of the components.

It is the network of TE that controls the community. We can add the effects of the environmental factors on the community, and arrive to a similar conclusion: the network of TE controls the ecosystem, **a complex adaptive system (CAS)**.

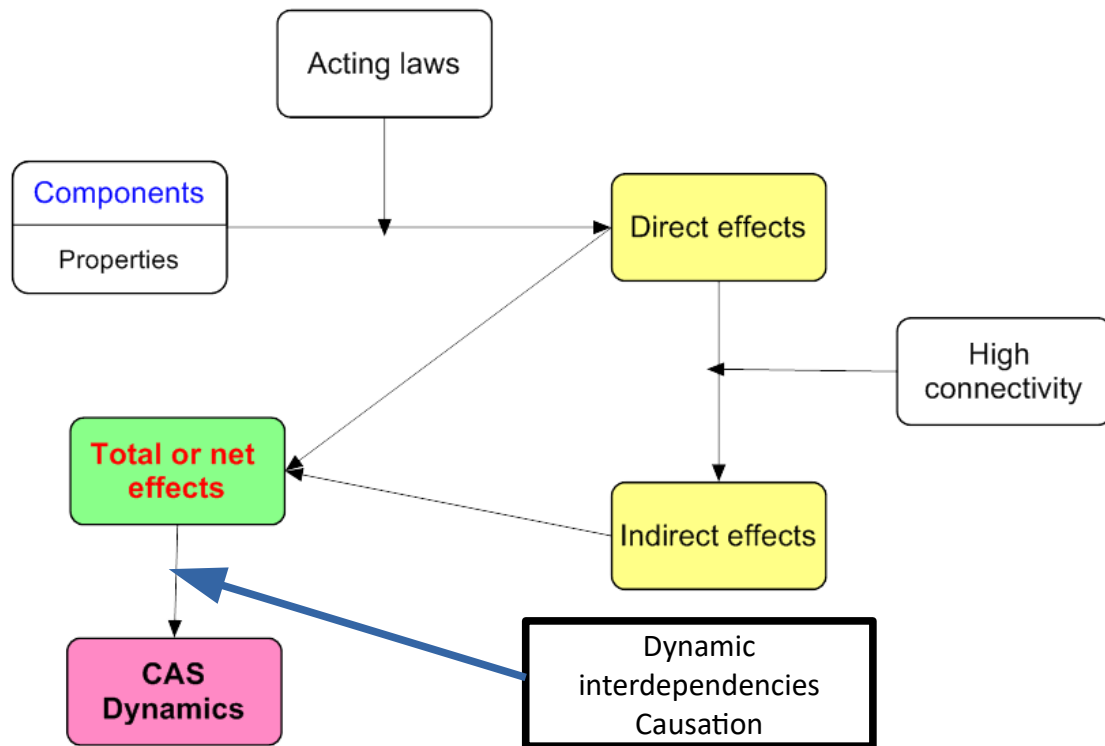


Figure 2. Simplified conjecture about the dynamics of CAS

Thus, if we want to understand ecosystems (CAS) we must find a procedure to measure TE. It is at this point that MAR(1) or VAR(1) models reveal their utility.

If we construct a matrix with the **coefficients of the multivariate autoregressive linear models**, we have the **community matrix A** . To obtain the **matrix of TE** (Barreto, 2019: section 2.2):

- We calculate the inverse of matrix **A** ;
- The inverse matrix is multiplied by -1 to obtain the matrix of total effects **E** .

Let e_{ij} be the element of line i , and column j of **E** . The element e_{ij} is the total effect of species j (column) on species i (row). The matrix **E** is a Jacobean matrix.

Now we apply these concepts to a system of omnivory.

5.2 A Model for Omnivory

The model for omnivory is an extension of model SBPRED for predation (Barreto, 2016: section 18.4). This model exhibits two ODE that are modified forms of the ODE of the Gompertz equation. The equation for the resource is:

$$y_1' = c_1 y_1 (\ln K - \ln y_1) - \frac{a y_1 y_2}{1 + a h y_1} \quad (5)$$



K is the carrying capacity, asymptotic or final value of y_1 . The speed of growth is determined by the parameter c_1 .

The expression for the consumption is called the hyperbolic or Holling type 2 functional response, and it is multiplied by the number of consumers y_2 . *The greater is a , the area of discovery, the greater is the consumption.* The handling time of the resource, h , is the time required to dominate, eat, and digest the prey, before the consumer start searching another prey. *The greater is h , the smaller is the consumption per time unit.*

The ODE for the consumer, y_2 , is:

$$y_2' = c_2 y_2 (\ln(b y_1) - \ln y_2) \quad (6)$$

The carrying capacity of the predator is equal to the number of prey multiplied by the parameter b , that mirrors the contribution of each prey to the carrying capacity of the predator ($K_2 = b y_1$). The parameter b depends on the parameters of the functional response, and the efficiency of the predator on transforming the preys in its own growth

Now we can introduce the model to omnivory.

5.2.1 Assumptions

Let us approach the interaction of omnivory represented in figures 1.

We assume the following:

- The basal species (y_1) is a plant that only plays the role of resource;
- The middle species (y_2) is a herbivore that plays both the role of consumer, and resource;
- The top species (y_3) is an omnivore that consumes the previous two species

5.2.2 The Model

The model is written as:

$$y_1' = c_1 y_1 (\ln K - \ln y_1) - \frac{a_1 y_1 y_2}{1 + a_1 h_1 y_1} - \frac{a_2 y_1 y_3}{1 + a_2 h_2 y_1 + a_3 h_3 y_2} \quad (7)$$

$$y_2' = c_2 y_2 (\ln(b_1 y_1) - \ln y_2) - \frac{a_3 y_2 y_3}{1 + a_2 h_2 y_1 + a_3 h_3 y_2} \quad (8)$$

$$y_3' = c_3 y_3 (\ln(b_2 y_1 + b_3 y_2) - \ln y_3) \quad (9)$$

For easier reference I call this model **PANT3**.

5.2.3 Model Analysis

PANT3 has not an explicit solution, thus we will use a numerical approach.

This model evinces stable fixed points, and periodic solutions. Now let us illustrate the concepts of the previous section, using Scilab:

```
// omnivory
g=200; //Number of time periods of the simulation

//***** Parameters *****
c1=0.05; k=80; a1=0.1; h1=1; a2=.8; h2=1; c2=0.1;
b1=.4; a3=0.6; h3=0.7; c3=0.15; b2=.3; b3=.2;
//*****

//Model of the system of omnivory
deff("yprim=f(t,y)",["yprim1=c1*y(1)*(log(k)-log(y(1)))-a1*y(1)*y(2)/
(1+a1*h1*y(1))-a2*y(1)*y(3)/(1+a2*h2*y(1)+a3*h3*y(2))";
"yprim2=c2*y(2)*(log(b1*y(1))-log(y(2)))-a3*y(2)*y(3)/
(1+a2*h2*y(1)+a3*h3*y(2))";
"yprim3=c3*y(3)*(log(b2*y(1)+b3*y(2))-log(y(3)))";
"yprim=[yprim1;yprim2;yprim3]"]);

y0=[5,2,1];
t0=0;
t=0:g;
[M]=(matrix(ode(y0,t0,t,f),3,g+1))';

size(M)
x=1:201;

scf(0)
clf(0)
plot2d(x,M)

xtitle("Simulation of omnivory","Time","N°");

legend(["Plant","Herbivore","Omnivore"])
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
b.z_label.font_size=3;
```

```

poly1= b.children.children;
poly1.thickness = [2,2,2];

xgrid();

// Fitting the MAR model
y=M(2:201,:)';
x=M(1:200,:)';
[a,b,sig]=reglin(x,y);
E=-inv(a);
disp("Community matrix")
disp(a)
disp("Matrix of total effects")
disp(E)
disp("Eigenvalues of the community matrix")
disp(spec(a))
disp("Eigenvalues of the matrix of total effects")
disp(spec(E))
disp('Total effects receive by each species')
disp([sum(E(1,:)),sum(E(2,:)),sum(E(3,:))])

```

We obtain the following output:

```
-->exec('G:\OY_TE\SCILAB\omni1TOT.sce', -1)
```

Community matrix

```

1.0168897 - 0.3024921 - 0.2932348
0.0321182 0.8337981 - 0.1001373
0.0514407 0.0012654 0.8434838

```

Matrix of total effects

```

- 0.9536362 - 0.3454026 - 0.3725347 <-----
0.0437113 - 1.183283 - 0.1252818
0.0580929 0.0228400 - 1.1626519

```

Eigenvalues of the community matrix

```

0.8824100 + 0.1226647i
0.8824100 - 0.1226647i
0.9293517

```

Eigenvalues of the matrix of total effects

```

- 1.1117761 + 0.1545491i
- 1.1117761 - 0.1545491i
- 1.0760189

```

Total effects receive by each species

```
- 1.6715735 - 1.2648535 - 1.081719
```

The omnivore has a negative total effect on the plant ($e_{13}=-0.3725347$).

The dominant eigenvalue of matrix **A** close to 1 (0.876) mirror the stationarity of the fixed point of the system. The negative real part of the eigenvalues of the matrix of TE (**E**) reflects the stability of the solution.

Figure 3 is created.

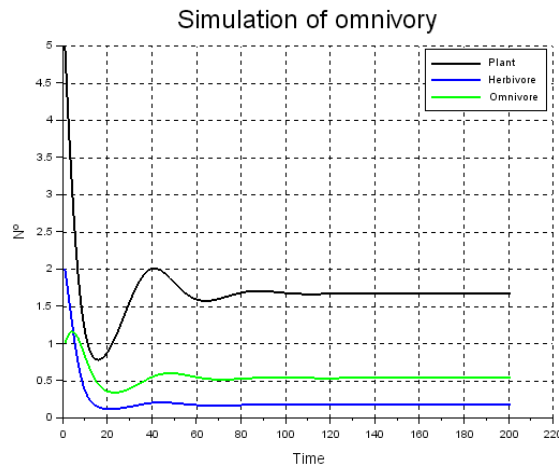


Figure 3. Simulation of the dynamics of model PANT3, with $a_1=0.1$

Now we assume that the area of discovery of the herbivore is not 0.1 but 1 ($a_1=1$). Let us see what happens to the system. Now, we obtain the following output:

```
-->exec('G:\OY_TE\SCILAB\omni1TOT.sce', -1)
```

Community matrix

```
0.9585725  - 0.7917061    0.1453014
0.0566667   0.7661254  - 0.1216097
0.0611952  - 0.0148310   0.8224840
```

Matrix of total effects

```
- 0.9846006  - 1.0170198   0.0235680  <-----
  0.0846971  - 1.2215303  - 0.1955741
  0.0747844   0.0536427  - 1.2211092
```

Eigenvalues of the community matrix

```
0.7841114 + 0.1924436i
0.7841114 - 0.1924436i
0.9789591
```

Eigenvalues of the matrix of total effects

```
- 1.2028735 + 0.2952199i
```

- 1.2028735 - 0.2952199i
 - 1.0214931

Total effects receive by each species

- 1.9780524 - 1.3324073 - 1.0926821

Now the total effect of the omnivore on the plant is positive and equal to $e_{13} = 0.0235680$.
 The dynamics of the system is evinced in figure 4.

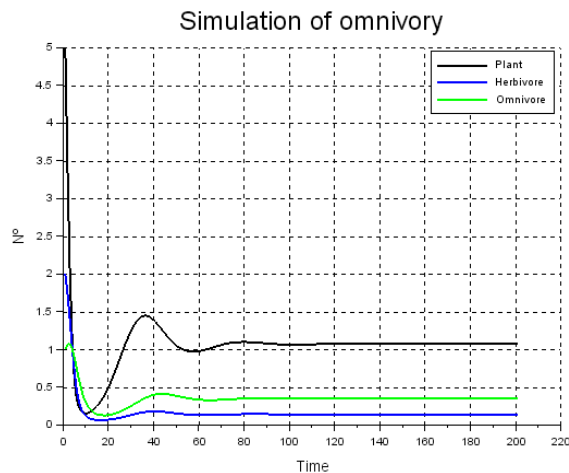


Figure 4. Simulation of the dynamics of model PANT3, with $a_1=1$

Model PANT3, and the used analytical procedure evinced satisfactory sensitivity, and coherence.

The problem of obtaining matrix **E** is solved with a trustful solution.

In figure 5 the flowchart of the analytical process is exhibited.

From here on, the matrix of the coefficients of the MAR model will be called **community matrix**, and will be represented by **A**. The **matrix of total effects** is represented by **E**.

Matrix **E** is relevant for the analysis of complex adaptive systems, such as the community, and the ecosystem (Barreto, 2019).

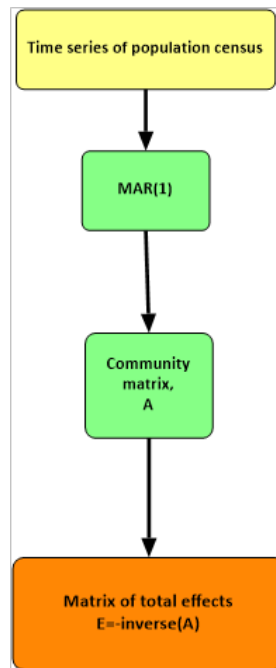


Figure 5. A flowchart of the method to obtain the matrix of total effects

6. Simulating the Emergence of Total Effects in a Forest with Three Species

Simulator **ry3tot** is an extension of simulator **ry3plot** (Barreto, 2020b). To this previous simulator we added the calculations for the community, and total effects matrices. Thus, it is a Scilab functions whose inputs are:

c_i ($i=1,2,3$) The values of the coefficient of competition in the equation of Gompertz. For some species they are exhibited in table 1;

r_i ($i=1,2,3$) The values of **R_{-2}** . For some species they are exhibited in table 1;

p_i ($i=1,2,3$) . They are the initial number of trees of species i ;

f_i ($i=1,2,3$) . They are the final stem volume of the average tree of species i ;

g is the age of the trees in the last year of simulation minus 10.

For easier interpretations of the output of the simulations, we suggest that the species in the input to be introduced in decreasing order of **R_{-2}** . This order is in agreement with the competitive hierarchy.

Let us consider a forest with Fsy+Qro+Lde, an hypothetical input in simulator **ry3plot** is:

ry3($c_1, r_1, c_2, r_2, c_3, r_3, p_1, p_2, p_3, f_1, f_2, f_3, g$)

ry3(0.043, 946.7, 0.041, 126.0, 0.043, 40.0, 2000,2000,2000, 7, 6,3,120)

If instead of stem volume of the mean tree we enter total biomass of the mean tree, in the listings of the functions the value of **a** must be changed from -1.5 to -1.333333. The functions mention indistinctively volume and biomass.

The written output of the functions are:

- For each species, and last year of simulation, the ratios of 'standing volume in mixed forest/standing volume in pure forest';
- The value of the relative yield, **Ry**. As already known $Ry > 1$ implies overyielding;
- Matrices **A**, and **E**;
- The eigenvalues of matrices **A**, and **E**;
- The sums of the total effects received by each species (the sums of the rows of matrix **E**).

The ranking of the species identified by the magnitudes of the ratios 'standing volume in mixed forest/standing volume in pure forest', and the 'sums of the total effects received by each species' can be or not be coincident. At the present moment I did not establish any relationship between them, if it exists.

The listing of function **ry3TE** is the following ;

```

//*****
//*      Simulator ry3TE      *
//* © Luís Soares Barreto, 2010, 2020 *
//*      *
//*****
disp('ry3te(c1,r1,c2,r2,c3,r3,p1,p2,p3,f1,f2,f3,g)')
function [R]=ry3te(c1,r1,c2,r2,c3,r3,p1,p2,p3,f1,f2,f3,g)

//c1=0.043;r1=946;c2=0.041;r2=126;c3=0.043;r3=40;
//p1=6000;p2=3000;p3=1000;f1=4;f2=2;f3=1;g=90;
//It assumes the size of the tree is the stem volume
//If the size of the tree is total biomass make a=-1.333333

a=-1.5;
b=-0.5;
rv1=r1^a;
rv2=r2^a;
rv3=r3^a;
rv1t=r1^b;rv2t=r2^b;rv3t=r3^b;

scf(0)
clf(0)
t0=0:g-10;
x=10:g;

//Relative mortality rates, and
//Relative growth rates of the total biomass of a tree
rmr1=-c1*log(r1)*exp(-c1*t0);
rmr2=-c2*log(r2)*exp(-c2*t0);
rmr3=-c3*log(r3)*exp(-c3*t0);
rgr1=-c1*log(rv1)*exp(-c1*t0);
rgr2=-c2*log(rv2)*exp(-c2*t0);
rgr3=-c3*log(rv3)*exp(-c3*t0);
M=[rmr1;rmr2;rmr3;rgr1;rgr2;rgr3]';

plot2d(x,[M])
legend(["rmr 1","rmr 2","rmr 3","rgr 1","rgr 2","rgr 3"], a=1)
xlabel("Relative variation rates","Years","rvr")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children;
poly1.thickness = [2,2,2,2,2,2];
xgrid()

//pure stands biomasses
k=0:g;
vf1=f1;vf2=f2;vf3=f3;
p1f=p1/r1;p2f=p2/r2;p3f=p3/r3;
b1f=p1f*vf1;b2f=p2f*vf2;b3f=p3f*vf3;
bpt1=b1f*rv1t^exp(-c1*k);
bpt2=b2f*rv2t^exp(-c2*k);
bpt3=b3f*rv3t^exp(-c3*k);

//BACO2

```

```

deff("yprim=f(t,y)",[

"f1=y(1)/(y(1)+y(2)+y(3))";
"f2=y(2)/(y(1)+y(2)+y(3))";
"f3=y(3)/(y(1)+y(2)+y(3))";

"rmr1=-c1*log(r1)*exp(-c1*t)";
"rmr2=-c2*log(r2)*exp(-c2*t)";
"rmr3=-c3*log(r3)*exp(-c3*t)";

"yprim1=y(1)*(rmr1)*(1+(f2)*log((rmr2)/(rmr1))+(f3)*log((rmr3)/(
(rmr1))))";..
"yprim2=y(2)*(rmr2)*(1+(f1)*log((rmr1)/(rmr2))+(f3)*log((rmr3)/(
(rmr2))))";..
"yprim3=y(3)*(rmr3)*(1+(f1)*log((rmr1)/(rmr3))+(f2)*log((rmr2)/(
(rmr3))))";..
"yprim=[yprim1;yprim2;yprim3]");
y0=[p1,p2,p3];
t0=0;
t=0:g;

[M]=(matrix(ode(y0,t0,t,f),3,g+1))';

//biomasses of the trees
a1=[vf1*rv1^exp(-c1*t)];
a2=[vf2*rv2^exp(-c2*t)];
a3=[vf3*rv3^exp(-c3*t)];
//Standing volume or biomass of pure forests at age g
vp1=bpt1(1,g);
vp2=bpt2(1,g);
vp3=bpt3(1,g);
Tp=vp1+vp2+vp3;

//Biomasses of the mixed stand
vm1=M(g+1,1)*a1(1,g+1);
vm2=M(g+1,2)*a2(1,g+1);
vm3=M(g+1,3)*a3(1,g+1);

//Standing biomasses all time
vm1t=M(:,1).*a1(1,:);
vm2t=M(:,2).*a2(1,:);
vm3t=M(:,3).*a3(1,:);

tot=vm1t'+vm2t'+vm3t';
proji=matrix([vm1t vm2t vm3t tot'],g+1,4);
scf(1)
clf(1)
t=10:g+10;
plot2d(t,proji)
xlabel("Mixed stand. Total biomasses","Years","Units of biomass")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
//b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children; //store polyline handle into poly1

```

```

//poly1.foreground = [1,2,4,5]; // another way to change the style...
poly1.thickness = [4, 2,2,2];

legend(["Species 1","Species 2","Species 3","Total"], a=2)

//mixed/(sum of pure stands)
R=(vm1+vm2+vm3)/Tp;

a=matrix([a1 a2 a3],g+1,3);

tit=['Over or underyielding'];
disp(tit)
format(6)

TP=bpt1+bpt2+bpt3;
G=[tot' TP'];
scf(2)
clf(2)
plot(t,G)
    xtitle("Total biomasses pure and mixed","Years","Units of biomass")
b=get("current_axes");
b.title.font_size=5;
b.x_label.font_size=3;
b.y_label.font_size=3;
//b.z_label.font_size=3;
b.children // list the children of the axes.
poly1= b.children.children; //store polyline handle into poly1
//poly1.foreground = [1,2,4,5]; // another way to change the style...
poly1.thickness = [2,2];

legend(["Total mixed","Total pure"], a=2)

y=M(2:81,:)';
x=M(1:80,:)';
[a,b,sig]=reglin(x,y);
E=-inv(a);
disp("Community matrix")
disp(a)
disp("Matrix of total effects")
disp(E)
disp("Eigenvalues of the community matrix")
disp(spec(a))
disp("Eigenvalues of the matrix of total effects")
disp(spec(E))
disp('Ratio mixed/pure for the species')
rati=([vm1/vp1 vm2/vp2 vm3/vp3])
disp(rati)
disp('Sum of the effects received by each species')
rec=([sum(E(1,:)),sum(E(2,:)),sum(E(3,:))])
disp(rec)
disp("Over- or underyielding")

endfunction

```

Now, let us introduce an application of the simulator, for a forest with *Fagus sylvatica*, *Quercus robur*, and *Pinus sylvestris* (Fsy+Qro+Psy):

```
-->exec('G:\4OY_TE\SCILAB\ry3plot3VFTOT.sci', -1)
```

```
ry3te(c1,r1,c2,r2,c3,r3,p1,p2,p3,f1,f2,f3,g)
```

```
-->ry3te(0.043, 946.7,0.041,126,0.03,34.3,3000,3000,3000,4,4,4,120)
```

AVERTISSEMENT : Transposition du vecteur ligne X pour obtenir des dimensions compatibles

Community matrix

```
- 8.437 - 4.622    13.91
- 2.073 - 0.433     3.34
- 7.005 - 3.567    11.42
```

Matrix of total effects

```
- 11.51 - 5.214    15.55
- 0.459 - 1.845     1.098
- 7.203 - 3.774     9.793
```

Eigenvalues of the community matrix

```
0.944
0.860
0.746
```

Eigenvalues of the matrix of total effects

```
- 1.059
- 1.163
- 1.34
```

Ratio mixed/pure for the species

10.91 0.984 0.333

Sum of the effects received by each species

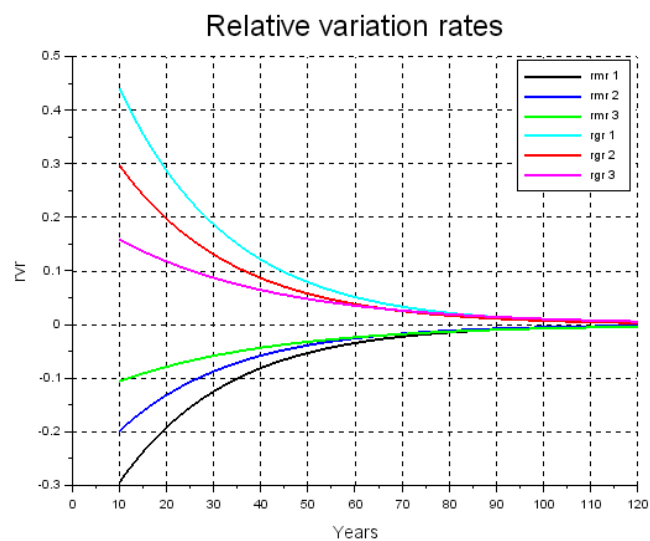
- 1.175 - 1.206 - 1.185

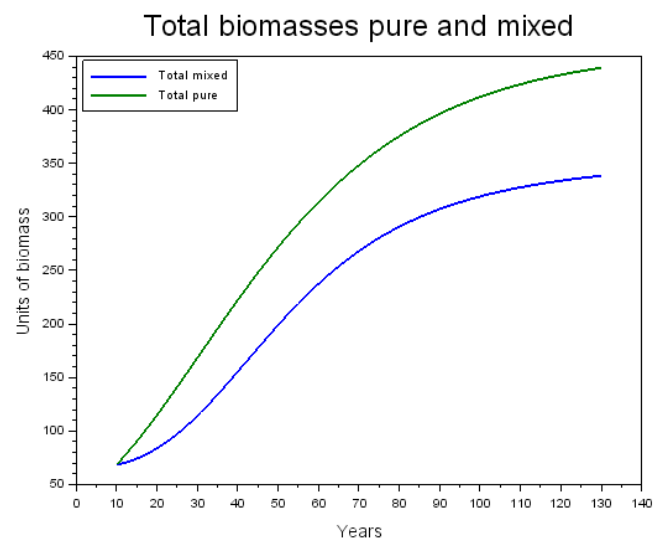
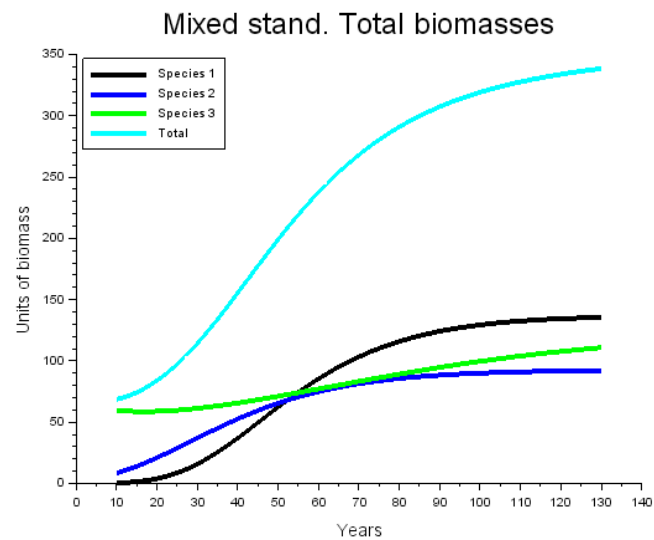
Over- or underyielding

ans =

0.771

The simulator displays the same graphics as simulator ry3plot, as shown in the next three figures.





As the initial conditions of the simulations are the same for all three species, matrix **E** is coherent with the competitive hierarchy. The two more strong competitors have negative impacts on the three tree populations (the elements of the first, and second column are all negatives). Only *Psy* has positive impacts in all three populations (all elements of the third column are positive). Unequal starting conditions for the species give origin to less predictive elements of matrix **E**.

The eigenvalue close to one of matrix **A** (0.944) let us predict that the sizes of the tree populations converge to stable asymptotic values, as matrix **E** has eigenvalues with negative real part.

For a more conspicuous representation of the interactions among the species, we can create a network of total effects, as exhibited in the cover of this text.

7. Getting Parameters for the Use of the Simulators

Almost all tree species characterized in table 1 are European, and North-American. To allow a more ample utilisation of the simulators we present a brief procedure to get similar data for other species.

The simulators are underpinned by a theory that assumes a Gompertzean pattern of dynamics for the forest variables. For the case of the number of trees in a cohort (only intraspecific competition) in an area unit (y_{-2}) Gompertz equation can be written as:

$$y_{-2} = y_{-2f} R_{-2}^{\exp(-c(t-t_0))} \quad (10)$$

where y_{-2f} is the final or asymptotic value of the variable; R_{-2} is the ratio 'number of trees at age t_0 / y_{-2f} '; c is the coefficient of competition of the species; t_0 is the age at which the variable enter in a Gompertzean trajectory.

An simple procedure to fit a Gompertz equation to a time series is now described. Let us create a cohort of trees of Qro:

```
clear
scf(0)
clf
t=10:1:120;
g=[400*125^exp(-0.041*(t-10))];
plot(g, 'r')
```

Now, we fit an autoregressive linear model to the logarithms of the values of the time series:

```
x=log(g(1:110));
y=log(g(2:111));
[a,b,sig]=reglin(x,y);
```

From the parameters of the regression we extract the parameters of the species:

```

c=-(a-1);
k=exp(b/c);
R=g(1)/k
R =

125.

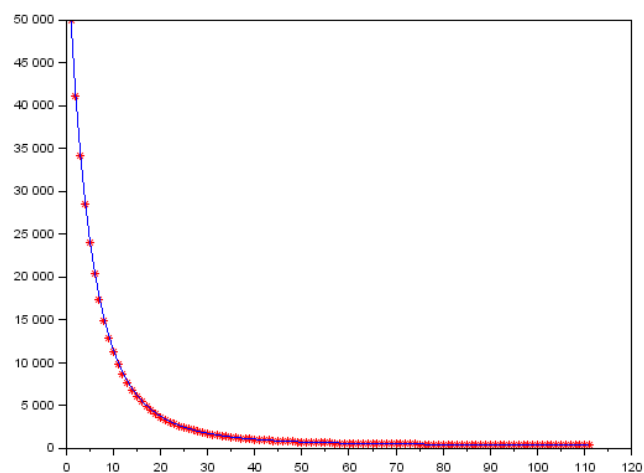
disp(['c=',+string(c), '    yf=',+string(k), '    R=',+string(R)])

!c=  0.0401709    yf=  400    R=  125  !

z=k*R^exp(-c*(t-10));
plot(z)

```

The values of y_{-2f} , and R_{-2} are estimated with exactitude. The estimation of c has a very small deviation. We obtain also a graphic with the data and the simulated values (black line).



8. Conclusive Remarks

As far as I can foresee, this text is my last contribution to overyielding, and the emergence of total effects in mixed forests. I admit that I developed an approach rational, coherent, and clear. It is my understanding that my treatment of this issue contributed for the solution of some problems in this area.

This successful achievement was possible because my inquiry was underpinned by a coherent theory for the structure, yield, and dynamics of forests (Barreto, 2011), that is a particular case of my mathematical, and unified theory for ecology (Barreto, 2017).

As I already emphasized (Barreto, 202b): a) I explained facts by means of systems of hypotheses entailing the propositions that express the facts concerned; b) I increased knowledge by deriving new propositions (e.g., predictions) from the premises in conjunction with relevant information. Briefly, I used a sound methodological, and epistemological approach.

Two embracing books dedicated to mixed forests are Pretzsch, Forrester, Bauhus (2017), and Bravo-Oviedo, Pretzsch, del Río (2018).

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