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Block random models in biological sciences

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Abstract:

A block random model, studied earlier in economics is introduced for biological sciences. Two approaches which handle participants as species and participants as individuals give pictures on processes from different points of view. In ecology it can provide an opportunity for some intervention to avoid development of dangerous conditions. For epidemiological applications a sample problem is presented to illustrate that epidemics spread curve is usually U-shaped or even multiple U-shaped. This is not because of human indiscipline but it is rather a consequence of randomness appearing in the processes.

Keywords: Random matrices, Eigenvalues, Lyapunov stability, Biology, Ecology, Epidemiology.

1. Introduction

System of random linear differential equations in ecology was first studied by May [4]. Following his famous work, it became widely accepted that ecological systems are most often unstable.

In paper [1], a block random matrix was proposed for studying complex systems. In [2] and [3], the block random model was introduced in economics. First steps in these investigations were much simpler in economics than in biological sciences, since participants are well defined in economics, their behavior can be easily followed by monetary tools. In biology, we are faced to individuals or species which are obeyed to natural laws, mutual interactions between them are much more difficult to characterize, further one has to take into consideration their lifespan, too. Though a one year cycle can be observed in economy, the role of this cycle has significantly greater importance in biology.

Another interesting remark is that in biological sciences it is possible to introduce the model in two levels, a model for species as participants which gives for us a remote image and a model for individuals as participants which gives us a close-up picture.

2. Block random model in biology

Though phenomena in biological sciences are quite complicated and even are non-linear one cannot give up hope to approximate them by linear or at least piecewise linear models. Another important aspect of the model is that it has to deal with any randomnesses that arise. Both assumptions are fulfilled by the block random model proposed by the paper.

2.1 Theoretical background

The theoretical backgrounds belonging to the theory of random matrices dates back to the 80s and 90s. The following is a summary of the main concepts and statements that play important role in the behavior of the model.

Definition: Let $A_n = (a_{ij})$ be an $n \times n$ matrix whose entries are independent random variables. Let $D = (d_{ij})$ be an $m \times m$ matrix. We suppose that $S = S(n) = \{S_1, \dots, S_m\}$ is a disjoint partition of the index set. We assume that for $i \in S_k$ and $j \in S_l$ we have $Ea_{ij} = d_{kl}$. Then the matrix $A_n = A_n(m, D, S)$ is said to be a non-symmetric **block random matrix** and $D = (d_{kl})$ is called its **density matrix**.

In applications we think that m is fixed while n tends to infinity but is at least arbitrarily large.

Theorem: Let $A_n = (a_{ij}) = A_n(m, D, S)$ be a non-symmetric block random matrix. Assume that $a_{ij} - E(a_{ij})$ are independent and identically distributed random variables. Suppose that the 4th moments of the entries exist, σ^2 stands for variance. Then A_n has m structural eigenvalues of order n while the rest of the eigenvalues are much more smaller, they are of order $n^{\frac{1}{2}}$.

In practice special type of block random matrices that is slightly unstable block random matrices have remarkable importance.

Definition: Block random system is **slightly unstable** if all of the m structural eigenvalues of the $n \times n$ system matrix A_n have negative real parts.

Block random matrices in general have some large in absolute value eigenvalues and a lot of small eigenvalues around zero. Systems which have some large eigenvalues of positive real parts cannot exist for a long time because they carry out self-destruction, they describe roughly the phenomenon of explosion. In reality only slight unstable systems can stay for a longer time.

2.2 Block random model for species as participants

Denote space X , called Size space, the n -dimensional space of sizes of species and denote space Y , called Birth space, the n -dimensional space of births per unit of time of species taking part in the investigations. Size in this context means number of individuals, births per unit of time means the alteration in the number of individuals in a period of time of investigation. Coordinates of $x \in X$ and $y \in Y$ are in a one-to-one correspondence with species as participants. Exactly, x_i means the number of individuals belonging to the i^{th} species while y_i denotes an increase in the number of individuals in a given period of time of the species in question. The roles of Size space and Birth space are analogue with the roles in papers [2] and [3] where X is Capital space and Y is Profit space. We briefly repeat the derivation in paper [2] to obtain the equation of the block random model.

We suppose that the function $F : X \rightarrow Y : R^n \rightarrow R^n$ is known. Let us linearize the function $y(t) = F(x(t))$ at $t=0$

$$y(t) \approx F(x(0)) + L(x(t) - x(0))$$

If we differentiate by t and take into account that the alteration of the size is birth rate we get

$$\dot{y}(t) = Ly(t) = \frac{1}{n}Ay(t)$$

where the form of Jacobian $L = \frac{1}{n}A$ shows that the structure of the system is somewhat independent from the number of its participants.

Elementary equation of index (i,j) $\dot{y}_i = a_{ij}y_j$ can be written as $P_i\dot{y} = P_iAP_jy$, where for the projection matrix $P_k = (p_{ij})$ all of the entries are zero except $p_{kk} = 1$.

Let A_{ij} be the matrix whose entries are zero except the entry a_{ij} . Then A_{ij} can be expressed by means of projectors $A_{ij} = P_iAP_j$. Since

$$A = \sum_{i=1}^n \sum_{j=1}^n A_{ij} = \sum_{i=1}^n \sum_{j=1}^n P_iAP_j = \left(\sum_{i=1}^n P_i \right) A \left(\sum_{j=1}^n P_j \right)$$

then for the sum of n^2 elementary equations

$$n \left(\sum_{i=1}^n P_i \right) \dot{y} = \left(\sum_{i=1}^n P_i \right) A \left(\sum_{j=1}^n P_j \right) y$$

which means

$$n\dot{y} = Ay$$

Thus the original equation

$$\dot{y} = \frac{1}{n}Ay$$

is the sum of all n^2 elementary equations.

In order to see clearly in this complex situation, one can handle similar participants together. Participants can be classified into groups by several aspects. The most relevant criteria that allow grouping are in connection with the behavior of items, that is the way how they influence each other's life. Strengths of actions with which one participant acts to the other can be collected into the system matrix A_n of order n . It is reasonable to assume that actions between participants belonging to corresponding groups are similar, they vary around a certain value, with a certain amount of alteration. Thus we can think that system matrix is a random matrix which - taking into account the groups of participants - consists of blocks, that is system matrix forms a block random matrix. Expected values of actions are collected into

the density matrix whose entries can be called general strengths of actions. The amount of alteration is represented by the dispersion of the entries of the block random matrix in question.

Block random system consists of variable number of participants. Crisis means a significant change in the number of participants. Analysis of crisis has shown that a smaller system is more stable than a larger one with the same parameters [2]. In paper [3] the effect of two parameters - density matrix and dispersion - of block random systems is studied. It is pointed out that in some circumstances so called structural cycles can characterize the behavior of systems. It is reasonable to think that these results can be transferred also to biological systems with few restrictions.

2.3 Block random model for individuals as participants

To have a closer picture of the phenomena, we can assume that the participants of the system are individuals while species form the groups. This cast requires introduction of auxiliary variables that characterize participants. They can be called Vitality as X and Activity as Y whose roles are analogue with the spaces Capital and Profit in economics. Like alteration of capital is profit, we think that alteration of vitality is activity. In other words if an individual exhibits activity then - contrary to the recommendations of fitness - it manifests in decrease its vitality.

Thus denote X the n -dimensional space of vitalities and Y the n -dimensional space of activities of the participants. Establishing the model is analogue with the above one which concerns species as participants, therefore we think that skipping its description would not cause any problem. If there are some doubts with space Vitality we can think that space X will be omitted during establishing the model.

If set of participants consists of individuals then participants change frequently which is difficult to take into consideration in analyzing behavior of the model.

3. Natural selection

Crises in block random models are realized in such a manner that a large amount of participants are leaving the system. In biology it is realized by extinction of individuals or even species.

It is widely accepted that aptitude plays important role but is not the only factor in natural selection. This is just the case for block random model since extinction of participants depends not only on their suitability but it is primarily influenced by their role in the community.

4. Applications in Ecology

The aims of application of block random models in ecology could be to explore the basic parameters in ecological systems to approach equilibrium state and thus to prevent the extinction of endangered species.

In paper [3] it was investigated that how the two parameters, that is, density matrix and dispersion influence the speed of processes. Speed of changes plays a crucial role in ecology, too. Obviously, control of the system can be accomplished primarily by changing the density matrix, whereas achieving a change in dispersion generally requires a stronger effort.

5. Dynamics of infectious diseases

The dynamics of epidemics plays crucial role in planning measures which can stop the spread of infections. The ways in which pathogens spread from one person to another are different. However it is widely accepted that the behavior of infectious diseases is similar. Usually the number of infections is starting to decrease thanks to effective measures and even the epidemic seems to be disappearing. But after a while infections often appear again and begins a second increase in the number of cases. Thus the course of epidemic curve is usually U-shaped, double or even multiple U-shaped.

The block random model with individuals as participants allows the understanding of epidemic curves, if not their exact development, but their main characteristics. These waves in the number of infections are the so called structural cycles in the terminology of block random systems [3].

Many believe that the increase in the number of infections can be attributed to human improvidence, that is, after a while people do not follow the rules strictly. In contrast, the model tells us that things don't go badly because of people's behavior, but because of the eigenvalues of the system that have positive real parts. This recognition may be important in planning future measures to address the epidemic.

5.1 Example

The model consists of 2 groups, $n_1=8$ elements form the group of people and $n_2=13$ elements are contained in the group of pathogens. Index 1 is connected to people while index 2 refers to pathogens. Thus d_{11} describes the general strength of actions between people, d_{12} means the general strength of actions by which pathogens act on people, d_{21} stands for people's actions on pathogens and d_{22} represents the pathogens' general strength of actions between each others.

$$D = \begin{pmatrix} d_{11} & d_{12} \\ d_{21} & d_{22} \end{pmatrix} = \begin{pmatrix} 0.1 & -0.4 \\ 0.1 & -0.1 \end{pmatrix}$$

Dispersion of the strengths of actions is $\sigma=0.02$.

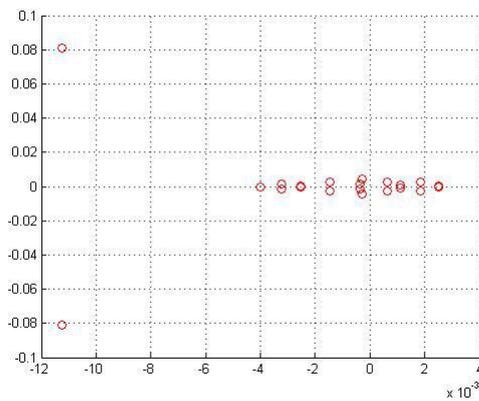


Figure 1. Eigenvalues of a 21 participants system of 2x2 blocks

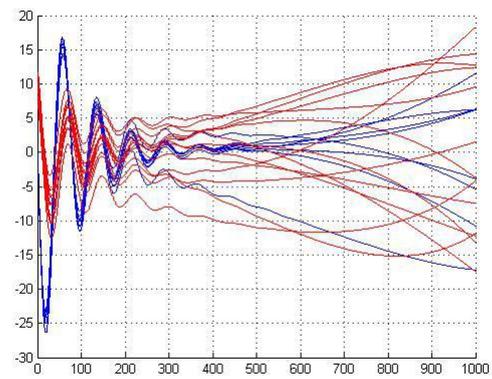


Figure 2. Activities in the first structural cycle. 13 red curves for pathogens and 8 blue curves for the people

Due to appropriate measures, the shape of envelope of trajectories may be similar to Figure 9 in [3] with the difference that at best it shows a decreasing trend. Human and pathogen activity, that is, envelope of trajectories will show repetitive peaks that are not a result of human indiscipline but of randomness at the system level.

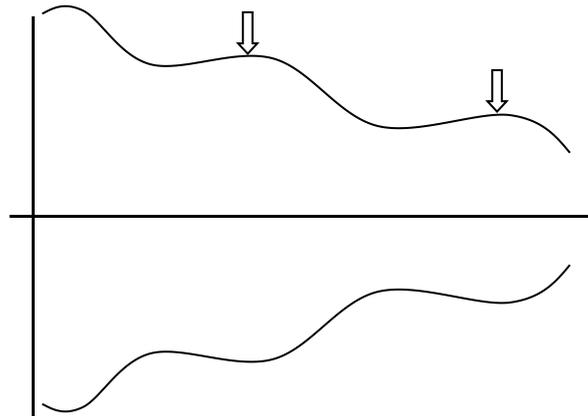


Figure 3. Envelope of trajectories. The arrows indicate the interactions required to flatten the epidemic curve

The sample model presented above is far from reality, as it does not take into account, among other things, the variable number of participants. The purpose of its introduction is to provide a general description of the behavior of such biological systems.

Calculations were made in MatLab 2012b under Windows 10.

6. Appendix

```
%-----
% eigenvalues and solutions of a 21x21 system of 2x2 blocks
%-----

E=[0.1,-0.4;0.1,-0.1];

disp('E');disp(E);

d=0.02;

disp('dispersion');disp(d);

n1=8;n2=13;

n=n1+n2;

nn=[n1,n2];
```

```

disp('sizes of blocks');

disp(nn);

%-----

% assembling system matrix

%-----

randn('seed',400);

A1=random('normal',E(1,1),d,n1,n1);
A2=random('normal',E(1,2),d,n1,n2);
A3=random('normal',E(2,1),d,n2,n1);
A4=random('normal',E(2,2),d,n2,n2);

A=[A1,A2;A3,A4];

A=A/n;

disp('system matrix');disp(A);

%-----

% eigenvalues of system matrix

%-----

sa=eig(A);

disp('eigenvalues of system');disp(sa);

s1=real(sa);
s2=imag(sa);

hold on;

%-----

% plotting of eigenvalues for figure 1

%-----

plot(s1,s2,'ro');grid;pause;

hold off;

```

```

close

%-----

% initial values

%-----

uind=[2,2,2,2,2,2,2,2,10,10,10,10,10,10,10,10,10,10,10,10];
rand('seed',600);
x0=zeros(n,1);
for i=1:n
    s=0.5*(rand(1)-0.5);
    x0(i)=uind(i)*s;
end;
y0=uind+x0;
disp('y0'); disp(y0);

%-----

% solution of system of differential equations

%-----

t=0:0.1:1000;% time interval for solution

k=length(t);
B=-A*uind;
z=zeros(k,1);
sys=ss(A,B,eye(n),zeros(n,1));
[y,t,x]=initial(sys,y0,t);% the solution

%-----

% plotting for figure 2

%-----

hold on;

```

```

for i=1:n1
    z=z+x(:,i);
    plot(t,x(:,i));% blue curves
end;

for i=n1+1:n
    z=z+x(:,i);
    plot(t,x(:,i),'r','LineWidth',1);% red curves
end;

grid;

pause;

close;

```

References

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