# Dual Approach to Complex Ecological System Analysis and Modeling

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**Abstract** - In this paper we present new, dual approach to analysis and simulation of a complex nonlinear ecological system of preys and predators, using classic nonlinear dynamic Lotka-Volterra mathematical model (LVM) in parallel with an Agent Based model (ABM), using model attributes description of the system. We propose to implement this dual approach using "mathematical" approach together with an "agent based" approach using appropriate modeling environments, such as Matlab and NetLogo. As the system models become more complex we aim at using both LVM and AMB to reinforce each other and check each other findings. This way the validity of the model and its usefulness would be greatly increased, and some long standing ecological paradoxes may be explained and qualified.

*Keywords:  Mathematical Modeling; Agent Based Modeling; Lotka-Volterra Equation; Predator and  Prey; Complexity and Stability; Structure*

## 1. INTRODUCTION

In analysis and simulation of complex ecological systems, a researcher often starts with a nonlinear Lotka Volterra model (LVM) of predator prey dynamic system [1]. The problem with this approach is that the LVM is very simplified model and apart from a detailed stability analysis [1], there are no real life complex ecological dynamic system models which are flexible and useful enough. Some of the reasons are (i) Lack of any general model build up methodology, (ii) Lack of any structural analysis of complex dynamical ecological models, and (iii) Very few results explaining some well know ecological paradoxes. We aim to address some of these important issues. In this paper, examples of various Single Prey Single Predator (SPSP) as well as Multiple Prey Multiple Predator (MPMP) models are introduced in a gradual way, from simple to more complex ones. Our goal is to gain insight into (i) Predator-prey population, (ii) Structural properties of the models, (iii) Understanding of stability in multispecies communities, and (iv) Improve usability, robustness and adaptivity of LVM ecological models. With this approach we aim to go towards analytical description of the key classic problems in ecology, such as (i) Paradox of the Plankton,  (ii) Paradox of the Enrichment, (iii) Oksanen's description and tropic level numbers, and other general Complex Systems paradigms such as (iv) Adaptivity and (v) Emergence. We also compare LVM analytical stability results with simulated ABM results. We propose to take advantage of flexibility that ABM offers, and in doing so acquire key feedback to reinforce and improve nonlinear mathematics of the LVM as well.  This way we can build very complex but usable predator-prey ecological models which are also mathematically tractable.

## 2. NONLINEAR  MODEL LINEARIZATION

As a starting point, we can assume the most general non linear ecological model described as:

$$S:\ dX/dt = f[X(t),t] \qquad (1)$$

Any well-behaved non liner system can be linearized around equilibrium  points $X^*$ of the function $f[X(t)]$. This approach works well close to equilibrium points. The other advantage is that there are well known theoretical stability results for linear complex systems [1,4,6,7].

Unfortunately, linearization may be very restrictive and limited in its usefulness, hence analysis of real nonlinear ecological predator-prey systems will produce more realistic results. But, nonlinear problems are not easy to deal with. We propose here a step-by-step build-up of nonlinear models which will allow us to better understand effects of nonlinearities and interconnections in multi species environments.

## 3. GENERAL ECOLOGICAL NONLINEAR MODEL

General ecological nonlinear model in the context of our interest in this paper is described by [1]:

$$S:\ dX/dt = A(t,X)\ X \qquad (2)$$

where X is vector of (for example aquatic) species. The model in (2) is obviously a nonlinear one, but has an appearance of a linear system. The vector X may be as simple as a two dimensional vector (one pray, one predator), or it could consist of 10s and 100s of species arranged in some logical conglomerate of prey and predator species, all collected into the species vector X. Matrix $A(t,X)$ is a "community" matrix with its elements as nonlinear time-dependent functions $a_{ij}=a_{ij}(t,X)$, where "ij" indicates position in the matrix, i for the rows, j for the columns. In the case of X of dimension 2,  matrix  A is 2 by 2, and its elements are   $a_{11}$, $a_{12}$, $a_{21}$, and $a_{22}$, and they describe self and cross interactions among the two species.

One of our goals is to find a practical way how to model elements of community matrix for a specific ecological system of some aquatic species (small and big fish).

## 4. SINGLE PREY SINGLE PREDATOR MODELS

Next level of simplification of the ecological model is embodied in the well known nonlinear Lotka-Volterra Model (LVM), which is just a special case of the model (2).  Consult [1] for more details.  For our purposes in this paper, we will illustrate LVM at first using second order model, with Single Prey Single Predator (SPSP) model. Following that, more complex models will be also given.

*A.  LVM Solution*

Let us assume $X = [X_1, X_2]^T$, $X_1$ is prey species, $X_2$ is predator species. The classic LVM [1] is:

$$dX_1/dt = X_1 ( A_1 + A_{12} X_2) = A_1X_1 + A_{12}X_2X_1$$
$$dX_2/dt = X_2 ( A_2 + A_{21} X_1) = A_2X_2 + A_{21}X_1X_2 \tag{3}$$

which can also be written in a compact form as:

$$dX_i/dt = X_i ( A_i + A_{ij} X_j) \tag{4}$$

where i=1,2 and j is different than i, with j=1,2. Here $A_1$ is the growth rate of the prey. Note that with $A_{12} = 0$ the prey population $X_1$ continues to increase exponentially, which is equivalent to the absence of any predator $X_2$. With $A_{12} < 0$, predator $X_2$ will control prey population from growing exponentially. For the predator population, growth is dependent on $A_2 < 0$, the rate of predator removal from the system (either by death or migration), and $A_{21}$, the positive growth rate for predators. The solution to Equations 3 and 4 is periodic, with the predator population always following the prey. Fig. 1 gives an example from a typical SPSP LVM. We assumed constant values of positive $A_1$ and $A_{21}$, and negative growth rates $A_{12}$ and $A_2$. The other SPS models can be defined, such as positive $A_2$ and negative $A_{21}$ for the predator, depending on the predator model. The key is to keep the basic model stable.
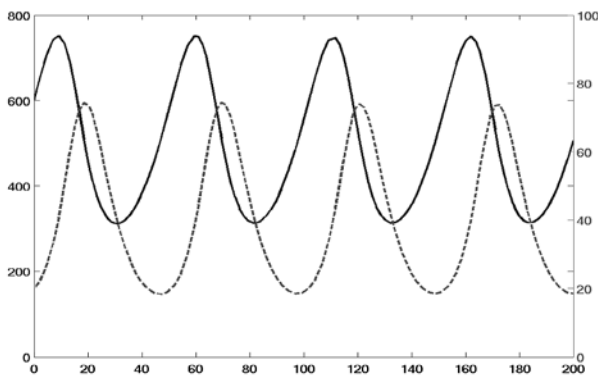


Figure 1. SPSP LVM Population Levels
(Prey Solid, Predator Dashed)

In terms of the general nonlinear model given in (2), and with no time dependency, the community matrix A is:

$$A(t,X) = A = \tag{5}$$

| $a_{11}(t,X)$ | $a_{12}(t,X)$ |
|---|---|
| $a_{21}(t,X)$ | $a_{22}(t,X)$ |

with:

$$
\begin{aligned}
a_{11} &= A_1 \\
a_{12} &= A_{12} X_1 \\
a_{21} &= A_{21} X_2 \\
a_{22} &= A_2
\end{aligned} \tag{6}
$$

General LVM stability results are given in [1].

### B. ABM Solution

The original LVM Equations 3 and 4 are very simple ecological model. They assume, for example, unlimited food available to the prey, and so the prey (and predator) growth rates are limited by corresponding "growth"

coefficients. In these equations, the growth coefficient is $A_1$ for the prey and $A_{21}$ for the predators. As a comparison, in ABM model, the growth rate for both populations can be determined by how successful they are at finding food. This can be modeled as a stochastic process which averages out to a stable rate across each population, hence corresponding to large extent to LVM approach, in the limit. Other effects can be incorporated as well, per modeling flexibility of ABM approach. Fig. 2 gives a typical agent based snapshot of simulation control window. Various model attributes are easily defined. For example, the predators are not consumed, but they disappear from the simulation at a constant rate by reaching the end of their programmed lifetime. This is represented by negative $A_2$. Their population increases linearly based on the prey consumption. This is proportional to the number of both populations, and thus represented by $A_{21}X_1X_2$.

In the ABM, when the food is increased initially, both growth values, $A_1$ and $A_{21}$, temporarily go out of equilibrium and they both increase initially. In the steady state, the prey growth rate remains constant, because their population growth is offset by increased predation, due to an increase in the predator population. The predator population, however, stays elevated, and so increased competition means that their growth rate returns to the original value, for initial food availability. Note that the coefficient $A_2$, the rate of predator removal (death or migration) from the system model, is determined by the predator attribute *age* and a limited lifetime for each individual. The prey also has an attribute for age, but in practice, very few fish die of old age. This is particularly true at higher levels of resources, because their average age drops as a consequence of fish being born faster while their population remains stable. It is this last fact that seems to cause the system to eventually become unstable, at very high levels of resources. We will compare this with general stability results in [1], in our future paper.

There is a limit to how quickly fish can be consumed after being spawned. As the limit is reached, endogenous spatial heterogeneities appear in time with increased volatility in both populations. Per Fig. 2, ABM gives lots of flexibility to model the system, but essentially gives no analytical insight and the solution such as the case with LVM. That is the essence of our dual approach here, i.e.

    (i)   Use ABM for its flexibility, and
    (ii)  LVM for its mathematical elegance

This way we can learn about using ABM to improve or change LVM. One obvious idea is to make the LVM model in Equations 3 and 4 times varying to some extent (Section D). The next model illustrates adding a "crowding" term in LVM which corresponds to species dynamic when disconnected from the other specie(s).

### C. Crowding Effect In LVM

The extended LVM with crowding effect is as follows:

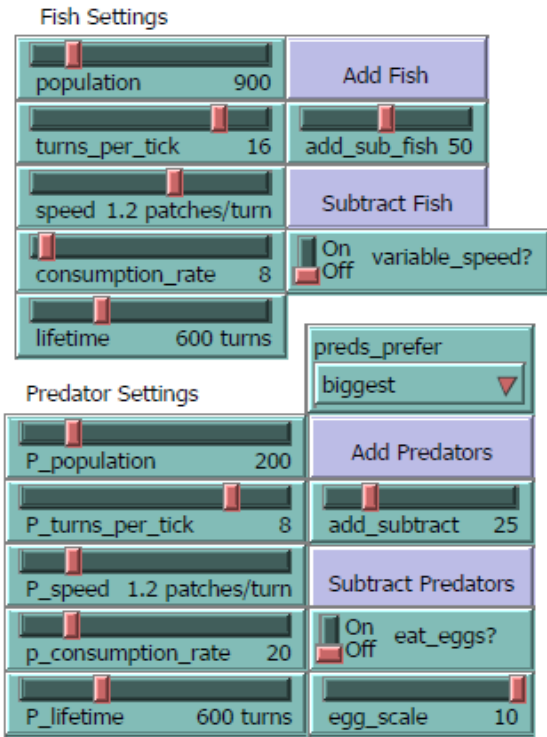$$dX_i/dt = X_i ( A_i + \sum A_{ij} X_j) \tag{7}$$

Figure 2. SPSP ABM simulation control window

where $i = 1,2$ and sum $\sum$ is over $j = 1,2$. This would be equivalent to prey self multiplication without predator in $dX_1/dt$. In this case community matrix (Equation 5) elements are:

$$a_{11} = A_1 + A_{11}X_1$$
$$a_{12} = A_{12} X_1$$
$$a_{21} = A_{21} X_2 \qquad (8)$$
$$a_{22} = A_2 + A_{22}X_2$$

In this model, $A_{12}$ and $A_{21}$ are negative, with newly introduced $A_{11}$ and $A_{22}$ positive. Another option is to go back to our original ABM in Equations 3 and 4 and simulation of Section B. In that case the last two equations in (8) change to:

$$a_{21} = A_{21} + A_{22} X_2 \qquad (9)$$
$$a_{22} = A_2$$

with $A_{21}$ and $A_{22}$ positive and $A_2$ negative. The key is not to allow either model to let the predator grow out of control (become unstable). When using ABM simulation, the "crowding" effects can be implemented according to options in Fig. 2, or by adding new options and additional model attributes.

Next step is to accommodate time varying community matrix. Again, the ABM model of Fig. 2 can accommodate this by simple addition of proper agent model attribute which translates easily in to LVM equation for A=A(t). We can also add dependency on populations themselves, i.e. A=A(t,X). That is discussed next.

*D. Time Varying LVM Community Matrix*

The time varying LVM in general is:

$$dX_i/dt = X_i [ A_i(t,X) + \sum A_{ij}(t,X) X_j] \qquad (10)$$

where $i=1,2$ and sum $\sum$ is over $j=1,2$. The Equation 10 is an extension of Equation 7, where we added time varying and population dependencies in the model. This can be presented in the compact form as:

$$dX/dt = A(t,X) X \qquad (11)$$

with:

$$A = A(t,X) = \qquad (12)$$

| $a_{11}(t,X)$ | $a_{12}(t,X)$ |
|---|---|
| $a_{21}(t,X)$ | $a_{22}(t,X)$ |

and for example:

$$a_{11}(t,X) = A_1(t,X) + A_{11}(t,X) X_1 \qquad (13)$$

similarly for the rest of the coefficients in (8). Note that community matrix elements are functions of both $X_1$ and $X_2$. This will give us lots of freedom in modeling dynamic of two interconnected species. The modeling should be done in individual steps (coefficient by coefficient) so we have full understanding of making even the simplest change. Both ABM and LVM approaches to compare and simulate accordingly, follow.

*Example 1*. Coefficients only functions of time, not of X, i.e. in (13), we have:

$$a_{ij}(t,X) = a_{ij}(t), i,j=1,2 \qquad (14)$$

*Example 2*. Coefficients only functions of X, not of time, i.e. from (8,13), we have:

$$a_{ij}(t,X) = a_{ij}(X), i,j=1,2 \qquad (15)$$

*Example 3*. Coefficients functions of local populations $X_1$ or $X_2$ only, but not of time, i.e.

$$a_{ij}(t,X) = a_{ij}(X_j), i,j=1,2 \qquad (16)$$

where we assumed local dependencies only, for example $a_{11}(X_1)$ is function of $X_1$ and not of $X_2$, etc. Obviously we can have more complicated case such as:

*Example 4*. Coefficients only functions of $X_1$ and/or $X_2$ but not of time, i.e.

$$a_{ij}(t,X) = a_{ij}(X_j), i\neq j, a_{ii}(t,X) = a_{ii}(X_j,X_j), i,j=1,2 \qquad (17)$$

where we left the "crowding" coefficients functions of only their corresponding specie population.

Finally, we introduce time and have the following time varying version of Example 4.

*Example 5*. Coefficients functions of time as well as of $X_1$ and/or $X_2$, i.e.

$$a_{ij}(t,X) = a_{ij}(t,X_j), i\neq j, a_{ii}(t,X) = a_{ii}(t,X_j,X_j), i,j=1,2 \qquad (18)$$

As we develop complex LVM and ABM, our approach here is to follow the above formulas in implementing LVM and ABM to model corresponding features into both models. This way we will be able to precisely interpret

every step of the two models. For example, in Example 5 earlier, we would agree on what does $A_{12}(t,X_2)$ mean in terms of t and $X_2$, similarly for other coefficients. That is then modeled in ABM via appropriate attributes of Fig. 2. As indicated bellow, Reference [1] has an extensive analysis of stability of LVM, which would be corroborated with carefully designed experiments in ABM simulations.

## 5. ABM SPSP SIMULATION

In this Section we summarize and discuss various details of ABM SPSP simulation, based on setup of Fig. 2, which can address and attempt to simulate various models and Examples of Section 4.

Simulation [9] was run for 1000 time step chunks which generate 'counts' for all the variables at each step, i.e. (i) New prey or predators introduced, (ii) Food consumed by prey or prey consumed by predators, (iii) Predator deaths (due to end of lifetime), and (iv) Population sizes. Without any changes during the 1000 time steps, the simulation (under certain settings) is stable, and each variable is averaged across the recorded time. Each food level had plenty of time to stabilize. The data from 1001 thru 2000 were used only for 0.20 food (20% chance of food growth per patch, per step); then changed to 0.30, ignored the next 1000 steps and used 3001 thru 4000 for 0.30, etc., for 0.40.

In the simulation the predators are assumed of the same size, but the prey grows larger as they eat, starting at 0. Hence, the measurement below of "biomass" for the prey as indicated in Table 1.

TABLE 1. ABM SIMULATION SUMMARY

| Food Rate | Fish Average | Fish St. Deviation | Predator Population | Fish Consumption |
|---|---|---|---|---|
| 0.20 | 1154.73 | 33.56 | 158.97 | 4562 |
| 0.30 | 1140.39 | 39.66 | 329.09 | 6841 |
| 0.40 | 1140.45 | 36.27 | 462.10 | 9120 |

| Food Rate | Predator Consumpt. | New Fish | New Predators | Predator Death |
|---|---|---|---|---|
| 0.20 | 61.41 | 74.19 | 2.124 | 2.117 |
| 0.30 | 125.88 | 144.2 | 4.392 | 4.391 |
| 0.40 | 177.87 | 225.7 | 6.158 | 6.179 |

We can use the simpler fish model where, like the predators, each fish can be exactly the same size and would not change. The effects of fish size can be easily removed from the model. So, for example, to calculate $A_{12}$ we don't really need the size of the fish, only the population size. Various options such as "big fish are easier to catch" can be also implemented in ABM. This can be programmed into the model, for example under the option labeled "Predator Preferences" which can be added to Fig. 2.

In the ABM simulation, we get the following behaviors:

    a) Completely stable
    b) Oscillating-but-stable, and
    c) Oscillating-but-unstable.

In the stable settings neither the fish nor the predator population changes. Since $dX_1/dt = 0$, we can (presumably) say that in terms of LVM, Equations 3 and 4:

$$A_1X_1 = A_{12}X_2X_1 \qquad (19)$$

which corresponds to prey growth rate equal to predator consumption rate of the prey. Similarly $dX_2/dt = 0$, hence:

$$A_2X_2 = A_{21}X_1X_2 \qquad (20)$$

which simply means that the predator growth rate equals the predator death rate. Per Equation (19), $A_1$, the growth rate of prey, irrespective of the number of prey, is equal to the consumption rate of predators times the number of predators. The death rate for the predators, in terms of the number of prey, irrespective of the number of predators, is equal to the consumption rate of preys times the number of preys, as in (20) above. In addition to that, in Table 1, we see that the last two columns, new predators and predator deaths ($A_2X_2$), are approximately equal, corresponding to the stable state, irrespective of the food rate.

Calculating the above during out-of-equilibrium periods (transients) is trickier, such as right after prey food is increased from 0.20 to 0.30. It becomes trickier when other nonlinear effects emerge. For example, increasing the food produces spatial inhomogeneities, i.e. there are areas where food or prey becomes scarce for a time, and the consumption rates vary across the simulation space. This emerges from the ABM simulation itself. However, these can be modeled by a random "jump" to predator and prey movement. Hence each turn, fish in the simulation jumps to new, random spatial coordinates. This particularly affects the predator numbers, as they consume prey faster only while the system is out of equilibrium. Once the system stabilizes (steady state) with a higher predator population, then each particular predator consumes roughly the same amount of fish as before the change.

This is the key dynamic of the ABM: the predators are more in number but have harder time finding prey, and the prey (more food) are more in number, making it easier for the predators to find prey. These two dynamics balance out, so that the equilibrium consumption rate per predator is the same. These numbers would grow in a kind of an S-curve, right after the food for the prey is increased, so that the number of predators would start to grow, then grow faster, then grow slower, and then stabilize at a new, higher level. The way to measure this would be to divide the total predator consumption rate by the total number of new predators. Per the assumptions of LVM, the fish growth is proportional to the amount of fish-food consumed, and the predator growth is proportional to the amount of fish (prey) consumed. See Table 2 bellow.

TABLE 2. PREDATOR CONSUMPTION / NEW PREDATORS

| Food Rate | Predator Consumption (Fish Biomass) | New Predators | Quotient |
|---|---|---|---|
| 0.20 | 61.41 | 2.124 | 28.91 |
| 0.30 | 125.88 | 4.392 | 28.66 |
| 0.40 | 177.87 | 6.158 | 28.88 |

Here, $A_{21}$, the predator growth rate, is a constant, even when the food available to the fish increases. So each predator eats same amount before and after the prey food is

increased. The prey growth rate, $A_1$, increases with more food, but the prey population size does not, because prey is consumed faster by the predators. As expected, these are all about the same size. The predator consumption rate is not the number of *fish* consumed, but the total *biomass*, which controls predator numbers. Hence the predators eat more, but there are more predators, so one eats about the same, after the new equilibrium. The consumption growth is stable initially, Fig. 3,4. In Fig. 5 we see an S-curve which flattens out, when the new equilibrium is reached.

## 6. MULTIPLE PREY MULTIPLE PREDATOR MODEL

We now extend the SPSP LVM (Section 3) to a general nonlinear model to include multiple species (MPMP):

$$dX_i/dt = X_i [ A_i(t,X) + \sum A_{ij}(t,X) X_j ] \qquad (20)$$

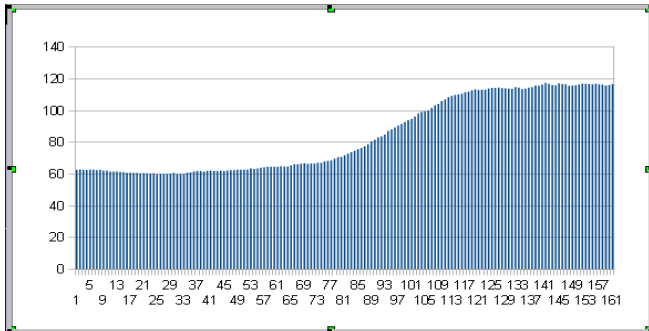where $i = 1, 2, ... , n$, and sum $\sum$ is over all $j = 1, 2, ... , n$.



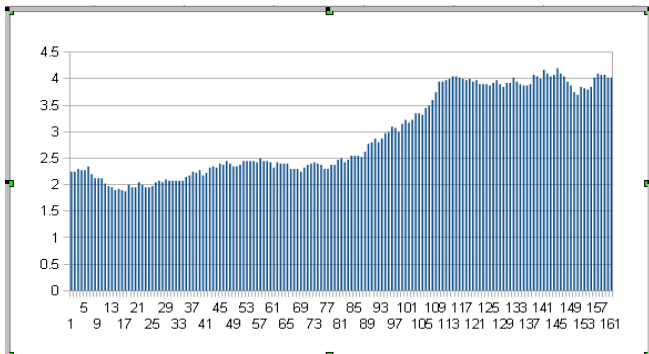Figure 3. Total Predator Consumption Rates
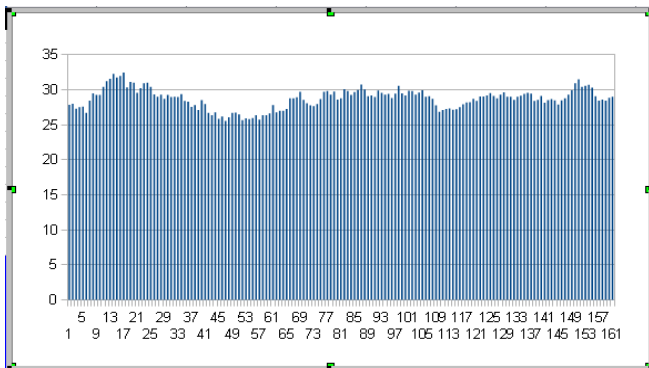


Figure 4. Total New Predator Growth



Figure 5. Predator Consumption / New Predator Growth

We can model 2 preys 1 predator, 4 preys 2 predators, 10 preys 3 predators, etc., hence building up complexity of the

LVM's. Here are some specific examples, where we continued from Example 5 (Section 4D) and increased the number of species. This may be influenced by a specific multispecies situation, such as an aquatic fish environment with a variety of preys and predators involved.

*Example 6*. Two preys one predator, coefficients time and functions of $X_1$, $X_2$, and $X_3$ or the total vector X, i.e.:

$$a_{ii}(t,X) = A_i(t,X) + A_{ii}(t,X_i) X_i$$
$$a_{ij}(t,X_j) = A_{ij}(t,X_j) X_i \qquad (21)$$

where $i,j = 1,2,3$, $i \neq j$, and $X_3$ is a predator. In compact form, community matrix $A(t,X)$ is now represented as 3x3 array:

$$A(t,X) = \qquad (22)$$

| $a_{11}(t,X)$ | $a_{12}(t,X_2)$ | $a_{13}(t,X_3)$ |
|---|---|---|
| $a_{21}(t,X_1)$ | $a_{22}(t,X)$ | $a_{23}(t,X_3)$ |
| $a_{31}(t,X_1)$ | $a_{32}(t,X_2)$ | $a_{33}(t,X)$ |

*Example 7*. Four preys (species 1,2,4,5) and two predators (3,6), for simplicity, and coefficients functions of time as well as of $X_i$, or the total vector X:

$$a_{ii}(t,X) = A_i(t,X) + A_{ii}(t,X_i) X_i, i=1,2,3,4,5,6$$
$$a_{ij}(t,X_j) = A_{ij}(t,X_j) X_i , i,j=1,2,3,4,5,6; i \neq j$$
$$a_{ij}(t,X_4) = 0, i=1,2,3; j=4,5,6$$
$$a_{ij}(t,X_4) = 0, j=1,2,3; i=4,5,6 \qquad (23)$$

The community matrix $A(t,X)$ is now 6x6 array:

$$A(t,X) = \qquad (24)$$

| $a_{11}$ | $a_{12}$ | $a_{13}$ | 0 | 0 | 0 |
|---|---|---|---|---|---|
| $a_{21}$ | $a_{22}$ | $a_{23}$ | 0 | 0 | 0 |
| $a_{31}$ | $a_{32}$ | $a_{33}$ | 0 | 0 | 0 |
| 0 | 0 | 0 | $a_{44}$ | $a_{45}$ | $a_{46}$ |
| 0 | 0 | 0 | $a_{54}$ | $a_{55}$ | $a_{56}$ |
| 0 | 0 | 0 | $a_{64}$ | $a_{65}$ | $a_{66}$ |

and it consists of two decoupled predator prey systems. Any of the zero coefficients $a_{ij}$ indicates lack of influence of j-th specie to i-th specie. Assuming that predators can prey on all of the species, but not on each other, we have:

*Example 8*. Community matrix $A(t,X)$ is still 6x6, with less 0 elements ("*" are also 0 for this Example):

$$A(t,X) = \qquad (26)$$

| $a_{11}$ | $a_{12}$ | $a_{13}$ | 0 | 0 | $a_{16}$ |
|---|---|---|---|---|---|
| $a_{21}$ | $a_{22}$ | $a_{23}$ | 0 | 0 | $a_{26}$ |
| $a_{31}$ | $a_{32}$ | $a_{33}$ | 0 | 0 | * |
| 0 | 0 | $a_{43}$ | $a_{44}$ | $a_{45}$ | $a_{46}$ |
| 0 | 0 | $a_{53}$ | $a_{54}$ | $a_{55}$ | $a_{56}$ |
| 0 | 0 | * | $a_{64}$ | $a_{65}$ | $a_{66}$ |

If predators prey on each other, then we have Example 9:

*Example 9*. Community matrix $A(t,X)$ is still 6x6, with even less 0 elements, "*" are $a_{36}$ and $a_{63}$ respectively.

*Example 10*. Here we have an overlapping model, where two almost decoupled specie communities share a common four (**boldfaced**) elements:

$$A(t,X) = \qquad (27)$$

| $a_{11}$ | $a_{12}$ | $a_{13}$ | 0 | 0 | 0 |
|---|---|---|---|---|---|
| $a_{21}$ | $a_{22}$ | $a_{23}$ | 0 | 0 | 0 |
| $a_{31}$ | $a_{32}$ | $\mathbf{a_{33}}$ | $\mathbf{a_{34}}$ | 0 | 0 |
| 0 | 0 | $\mathbf{a_{43}}$ | $\mathbf{a_{44}}$ | $a_{45}$ | $a_{46}$ |
| 0 | 0 | 0 | $a_{54}$ | $a_{55}$ | $a_{56}$ |
| 0 | 0 | 0 | $a_{64}$ | $a_{65}$ | $a_{66}$ |

This model can be handled by an approach in [5] where the model is "expanded" to decouple it effectively. Finally we add environmental effects [1] into LVM by:

$$S: \quad dX/dt = A(t,X) \, X + B(t,X) \qquad (28)$$

where B(t,X) models external effects of the environment (food, space, temperature). Let us look at Example 6, and add environmental vector B(t,X). We obtain community matrix A(t,X) in (22), with species vector $X=[X_1,X_2,X_3]^T$ and the corresponding environmental vector is:

$$B(t,X) = [B_1(t,X), \; B_2(t,X), \; B_3(t,X)]^T \qquad (29)$$

Or even simpler case, where each environmental component depends only on individual specie, i.e.

$$B(t,X) = [B_1(t,X_1), B_2(t,X_2), B_3(t,X_3)]^T \qquad (30)$$

As it was discussed in Section 4B and 5, ABM introduced food supply into the model and the above environment vector is the right place to introduce the food supply, as a **control** input into the LVM (future work research subject).

As the community matrices become larger and more complex, we note that there are certain structural properties in the way "0" elements are placed. This is calling for approaches described in [2,4,5,6] which take advantage of special structures to simplify calculations and expose key structural properties of the models. There are elements of "overlapping" components in community matrices, which can be "expanded and contracted" [5] in building effective controls in multispecies communities. As the number of species grow, smart shuffling of the position of species in the vector X may produce hierarchical structure of community matrix A(t,X) [4], producing much simpler controls and simpler stability analysis, as the overall community matrix is split into subsystems (agents) hierarchically interconnected.

## 7. STABILITY AND COMPLEXITY

There are some key existing mathematical results related to LVM which can be used and which can accommodate multi-species modeling and stability in particular [1]. They give regions of stability estimates and point to specific reasons for instability and balance between stability and complexity. These regions can be tested using both LVM and ABM approaches which will add a measure of confidence and practicality to the stability results. As several ecology researchers (not mathematicians) pointed out in literature, there seems to be a balance in competing multi-species environments between numbers of inter connections among the species versus interconnection strengths. Our (obvious) mathematical conjecture is:

*If we denote by N number of interconnections for a given species (in a multi species environment) and by I their intensity, then:*

$$N \; times \; I \; = \; Constant \qquad (31)$$

where equality sign is just a measure of closeness of two sides of the expression. We could rephrase this intuitive notion and add stochastic measure by using Expected Value E( ) as:

$$E(N \; times \; I) \; = \; Constant \qquad (32)$$

where intensity *I* may be represented by some norm. In this context the LVM would need to be expressed in a stochastic form by adding certain stochastic processes either in random parameters in the community matrix elements, or as an additive colored or white noise process to the model itself. We will consider this in future work.

## 8. CONCLUSION

In this paper we set the scene for a robust and effective, dual model based approach (LVM, AMB) to build simple-to-complex predator-prey ecological models and examples of Single Prey Single Predator (SPSP) as well as Multiple Prey Multiple Predator (MPMP) models. This approach aims to produce practical results which can be used in real life ecological problems, and to better understand classic notions in multi-species models, as (i) Paradox of the Plankton, (ii) Paradox of the Enrichment, (iii) Oksanen's description and tropic level numbers, and other general Complex Systems paradigms such as (iv) Adaptivity and (v) Emergence. Our dual approach relies on methodology of step-by-step model build-up and reinforcement using two very different approaches, i.e. "mathematical" LVM and "ad-hoc" ABM. Proposed approach adds to the overall rigorousness of the obtained results and their validation and interpretations, by meticulously checking and comparing results of ABM and LVM as more and more complex models are built. In the research which follows, we will (i) Explore specific examples from this paper using appropriate computing environments such as Matlab, Mathematica, NetLogo, and (ii) Compare theoretical LVM stability results [1] with ABM modeling.

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