# Competition Model of Two Species in Population Biology Using pplane

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Muhammad Salah Elsadany
Computational Biology and Genomics, Biomedical Sciences Program
University of Science and Technology, Zewail City
Giza, Egypt
s-muhammadelsadany@zewailcity.edu.eg

## 1. Introduction

A population can be defined as a group of individuals from the same species that have very similar characteristics to each other and high probability of interacting with each other [1]. The population members do dwell in a particular geographic area with the capacity to interbreed. To interbreed, individuals in a population must be able to mate with other individuals in order to create fertile offspring. Not all individuals are able to survive and reproduce due to genetic variations in them [2]. Population biology is simply the study of these biological populations. The population biology field includes genetics and evolutionary questions and it's more broad than the population ecology field [1]. There are two types of populations: local populations and metapopulations. A local population may be limited to a smaller area or a wider area can be filled, making up for the whole species [2]. A metapopulation is where individuals of local populations disperse between other local populations [2]. Due to different physical factors existing in the environment that serve as restricting factors toward exponential population growth, most populations are not stable. Metapopulations are clusters of separated populations that interact at some degree with each other. There are a variety of distinct functional structures on which meta-populations can be constructed. The metapopulation structure is based on the degree of isolation/connectivity between meta-populations and the nature of the size of each subpopulation. As the subpopulation is a particular group of a metapopulation, the metapopulation is therefore composed of several sub-populations.

Population biology focuses mainly on understanding and predicting the dynamics of populations, Explaining, predicting, and understanding these biological populations dynamics will require models represented in the language of mathematics. These mathematical models are essential and represent a core point in making precise theoretical arguments about different factors that affect the change in population size over time. Different mathematical models have been developed and presented through the last era in the population biology field and they have shown their importance and high impact in the field. One of the most successful mathematical theories in population biology has been that of the dynamics of age-structured population growth. It can give detailed predictions about the long term changes in the population size based on given information about the age at which individuals have offspring and the probabilities of death at different ages [3]. This theory has played an important role in the field of conservation biology. It could be used in developing a plan to promote the long term survival of an endangered species. Moreover, different R programming codes have been developed tackling this theory and represent its results. [4] represents one of these codes that is used in one of the ecology courses in University of Georgia. Another successful theory in the population biology field is the theory of spatial spread. From this one, we can predict the future rate of spread of some populations from initial observations [5]. It is of great importance as it can help in the design of control measures to reduce the rate of spread of pests.

# 2. Motivation and Objectives

Understanding the complex ecological communities that have numerous different species interacting with each other and the environment requires understanding of the simpler ecological systems of one or two species first. That is why in this report I focused only on studying population biology for a single species. Focusing on the study of a single species will help me develop a model of 2 species interacting with each other because understanding the dynamics of a single species model will lead to answering the primary questions of population biology. Moreover, a single species model is the simplest model to be studied from a population approach at the beginning.

The planar autonomous systems have been applied to two-species populations like two species of trout, who compete for food from the same supply, and foxes and rabbits, who compete in a predator-prey situation. This report focuses only on the competition model between two species.

# 3. Competition Model Description

A competition model in the simplest form in population biology means the presence of 2 different species in the same environment competing on some constantly available food supply. For example, two kinds of insects feeding on a fallen type of fruit. To represent the interaction between two species, we need first to identify the model representing single species. A population growth rate model can be represented in different ways. Here we will focus on the logistic growth model, which is the simplest possible model. The intrinsic growth rate can be defined as shown in this formula:

$$\frac{x'(t)}{x(t)} = r, \qquad r \geq 0.$$

$$x'(t) - rx(t) = 0 \qquad (1)$$

Where r is the growth rate constant and it must have a value more than or equal to zero.
Another complex model to show the rate of growth for a population can be driven from this formula:

$$\mathbf{x`(t) = (a - bx(t))x(t)} \qquad (2)$$

Where x here represents the population x. Population x grows or decays according to the above logistic equation (2), in absence of population y. This model is called the Verhulst model [6]. The “a” constant represents the growth rate for the population x. “b” measures inhibition due to lack of food or space in the environment.
The same is applied for another species, y, living in the same environment. It grows or decays, in absence of population x, according to the logistic equation:

$$\mathbf{y`(t) = (c - dy(t))y(t)} \qquad (3)$$

To build a more complex mathematical model for each population, it must include the

chance encounters with other variables which is another population in this case. Population x decays at a rate **-pxy**, p > 0, due to chance encounters with population y [6]. The same is applied on population y as it decays at a rate **-qxy**, q > 0, due to chance encounters with population x [6].
Adding the Verhulst rates and the chance encounter rates gives the Volterra competition system:

**x`(t) = (a - bx(t) - py(t) ) x(t)** (4)
**y`(t) = (c - dy(t) - qx(t) ) y(t)** (5)

In this Volterra Competition system:

- The constants "a" and "c" are growth rate constants for populations
- The constants "b" and "d" measure inhibition due to lack of food or space
- The constants "p" and "q" measure competition with other species

The equations show that each population satisfies a time-varying first order differential equation. Population x has growth rate **r = a-bx-py** which decreases if population y grows, resulting in a reduction of population x. Likewise, population y has a growth rate **r = c-dy-qx**, which reduces population y as population x grows.

## 3.1. Equilibria

The equilibrium points **x** satisfy f(x) = **0** where f is defined by:

$$f(\mathbf{x}) = \begin{pmatrix} (a-bx-py)x \\ (c-dy-qx)y \end{pmatrix}, \quad \mathbf{x} = \begin{pmatrix} x \\ y \end{pmatrix}$$

(6)

To isolate the most important applications, the assumption will be made of exactly four roots in population quadrant I. This is equivalent to the condition bd − qp 6= 0 plus all equilibria have nonnegative coordinates. Three of the four equilibria are found to be (0, 0), (a/b, 0), (0, c/d). The last two represent the carrying capacities of the Verhulst models in the absence of the second population. The fourth equilibrium (x0, y0) is found as the unique root of the linear system:

$$\begin{pmatrix} b & p \\ q & d \end{pmatrix} \begin{pmatrix} x_0 \\ y_0 \end{pmatrix} = \begin{pmatrix} a \\ c \end{pmatrix}$$

(7)

which according to Cramer's rule is

$$x_0 = \frac{ad-pc}{bd-qp}, \quad y_0 = \frac{bc-qa}{bd-qp}.$$

(8)

## 3.2. Linearized Competition System

The Jacobian matrix J(x, y) is computed from the partial derivatives of system variables f, g, which are found as follows:

$$\begin{array}{lllll} f(x,y) & = & (a-bx-py)x, & = & ax-bx^2-pxy \\ g(x,y) & = & (c-dy-qx)y & = & cy-dy^2-qxy \\ f_x & = & \frac{\partial}{\partial x}(ax-bx^2-pxy) & = & a-2bx-py \\ f_y & = & \frac{\partial}{\partial y}(ax-bx^2-pxy) & = & -px \\ g_x & = & \frac{\partial}{\partial x}(cy-dy^2-qxy) & = & -qy \\ g_y & = & \frac{\partial}{\partial y}(cy-dy^2-qxy) & = & c-2dy-qx \end{array}$$

(9)

The Jacobian matrix is given explicitly by:

$$J(x,y) = \begin{pmatrix} f_x & f_y \\ g_x & g_y \end{pmatrix} = \begin{pmatrix} a-2bx-py & -px \\ -qy & c-2dy-qx \end{pmatrix}$$

(10)

The matrix J is evaluated at an equilibrium point (a root of F(u) = **0**) to obtain a 2×2 matrix A for the linearized system d v(t) = Av(t). The four linearized systems are:

| | |
|---|---|
| Equilibrium $(0,0)$ Nodal Repeller | $\frac{d}{dt}\vec{u}(t) = \begin{pmatrix} a & 0 \\ 0 & c \end{pmatrix} \vec{u}(t)$ |
| Equilibrium $(a/b, 0)$ Saddle or Nodal Attractor | $\frac{d}{dt}\vec{u}(t) = \begin{pmatrix} -a & -ap/b \\ 0 & c - qa/b \end{pmatrix} \vec{u}(t)$ |
| Equilibrium $(0, c/d)$ Saddle or Nodal Attractor | $\frac{d}{dt}\vec{u}(t) = \begin{pmatrix} a - cp/d & 0 \\ -qc/d & -c \end{pmatrix} \vec{u}(t)$ |
| Equilibrium $(x_0, y_0)$ Saddle or Nodal Attractor | $\frac{d}{dt}\vec{u}(t) = \begin{pmatrix} -bx_0 & -px_0 \\ -qy_0 & -dy_0 \end{pmatrix} \vec{u}(t)$ |

(11)

- If **bd−qp > 0**, then equilibria (a/b, 0), (0, c/d), (x0, y0) are respectively a **saddle, saddle, nodal attractor.**
- If bd−qp < 0, then equilibria (a/b, 0), (0, c/d), (x0, y0) are respectively a **nodal attractor, nodal attractor, saddle.**

## 3.3. Biological meaning of bd-qp

As mentioned above, the quantities bd and qp are measures of inhibition and competition.

| | |
|---|---|
| Survival-extinction | The inequality **bd-qp < 0** means that **competition qp** is **large** compared with **inhibition bd**. The equilibrium point (x0; y0) is **unstable** in this case, which biologically means that the **two species cannot coexist**: one species survives and the other becomes **extinct**. |
| Coexistence | The inequality **bd - qp > 0** means that **competition qp** is **small** compared with **inhibition bd**. The equilibrium point (x0; y0) is asymptotically **stable** in this case, which biologically means the **two species coexist**. |

# 4. Proposed Models

In this section, two models were studied using a MATLAB software and an R code developed by University of Utah.

The first model to be investigated represents a Survival-extinction one. It satisfies the following system:

$$\begin{aligned} x'(t) &= x(t)(24 - x(t) - 2y(t)), \\ y'(t) &= y(t)(30 - y(t) - 2x(t)). \end{aligned}$$

We apply the general competition theory with a = 24, b = 1, p = 2, c = 30, d = 1, q = 2.

The second model to be investigated represents a Coexistence model. It satisfies the following system:

$$\begin{aligned} x'(t) &= x(t)(24 - 2x(t) - y(t)), \\ y'(t) &= y(t)(30 - 2y(t) - x(t)). \end{aligned}$$

We apply the general competition theory with a = 24, b = 2, p = 1, c = 30, d = 2, q = 1.

Both models were investigated using phase diagrams to define the behavior of the system and interaction between the two species with time. Also, defining the equilibria points as a main feature of the phase diagrams.

## 4.1. Utah Model

University of Utah presented an R code to plot the phase diagrams for both models presented here. The code for these specific models can be found in [7]. It uses two main packages in R: DEtools and DEplot. Both packages deal with Differential Equations and their plots.

## 4.2. Pplane Model

Pplane is an interactive MATLAB software tool for studying planar autonomous systems of differential equations [8]. The user may enter the differential equation and specify a display window using the interactive controls in the Setup window. Up to 4 parameters may also be specified. In addition the user is given a choice of the type of field displayed and the number of field points [8]. For running a demo, it is recommended to follow steps mentioned in [9].

# 5. Results and Discussion

## 5.1. Utah Model

### 5.1.1. Survival-extinction Model

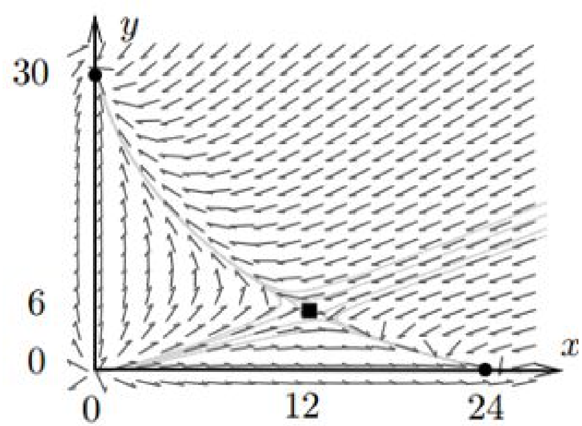


**Figure (1):** Utah Model, Survival-extinction Model [6]

### 5.1.2. Coexistence Model

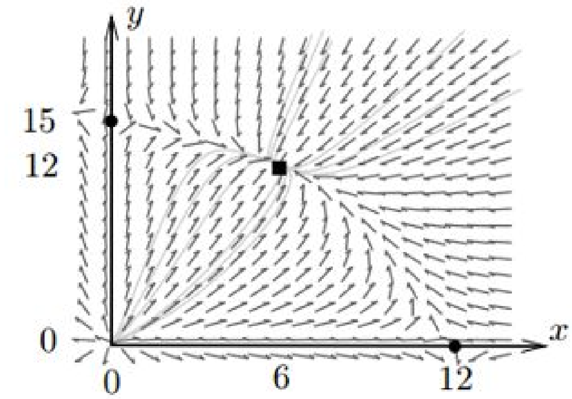


**Figure (2):** Utah Model, Coexistence Model [6]

## 5.2. Pplane Model

### 5.2.1. Survival-extinction Model

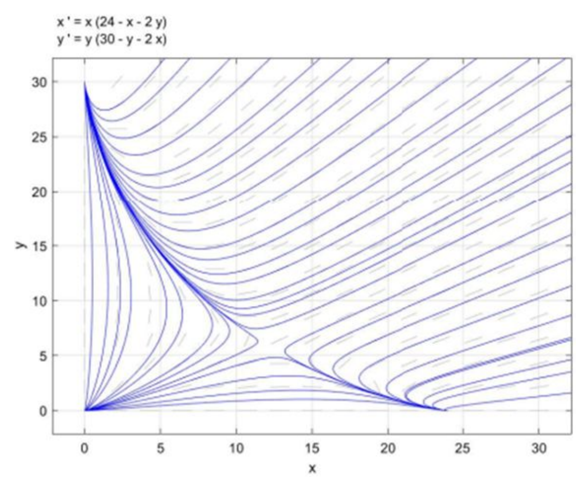


**Figure (3):** pplane Model, Survival-extinction Model

### 5.2.2. Coexistence Model

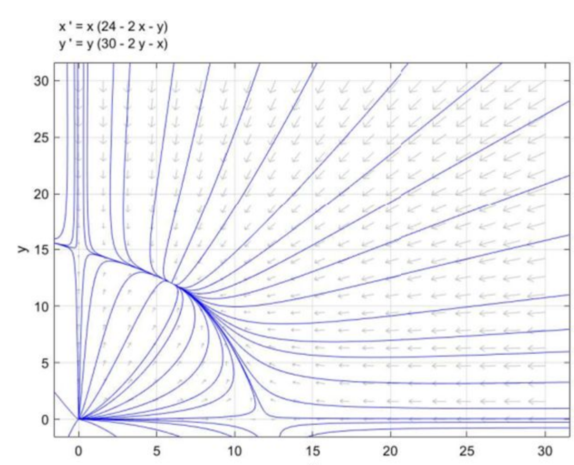


**Figure (4):** pplane Model, Coexistence Model

### 5.3. Discussion

For the Survival-extinction model, the equilibria are (0, 0), (0, 30), (24, 0) and (12, 6). They are classified as node, node, node, saddle, respectively. The population with initial advantage survives, while the other dies out.

For the Coexistence model, the equilibria are (0, 0), (0, 15), (12, 0) and (6, 12). They are classified as node, saddle, saddle, node, respectively. A solution with $x(0) > 0$, $y(0) > 0$ limits to (6, 12) at $t = \infty$.

Both models of Utah and pplane showed the same values and phase diagrams for Survival-extinction model and Coexistence model.

## 6. Conclusion

Interactions of populations in biology can be described in the language of mathematics and it showed how important it is in different applications. Before considering interacting populations, it is necessary to consider the growth of a single population. That is why in this report I focused on a single species growth model before tackling the competition model problem. The pplane showed the same results Utah gave using their code for both models: Survival-extinction model and Coexistence model.

## References

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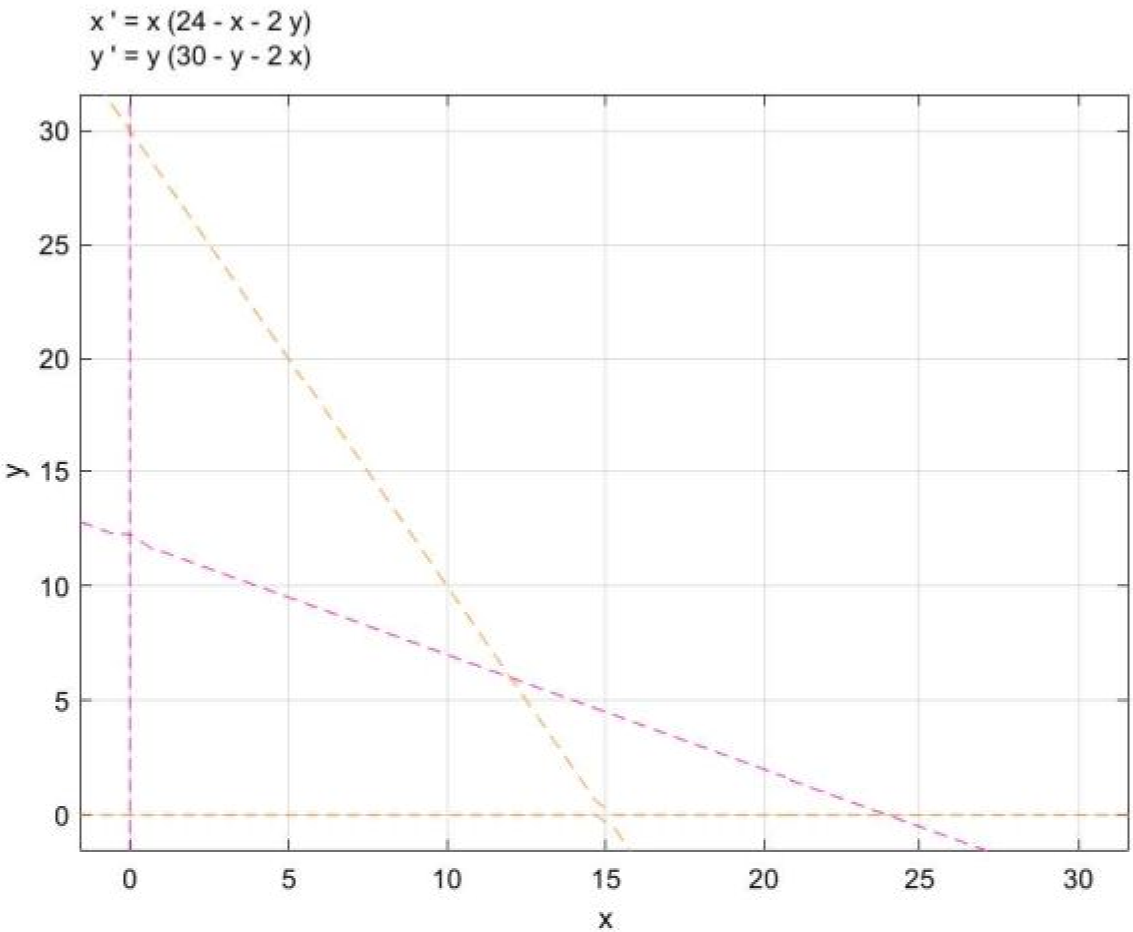
[9]Math.purdue.edu, 2021. [Online]. Available: https://www.math.purdue.edu/~park633/pplane.pdf.

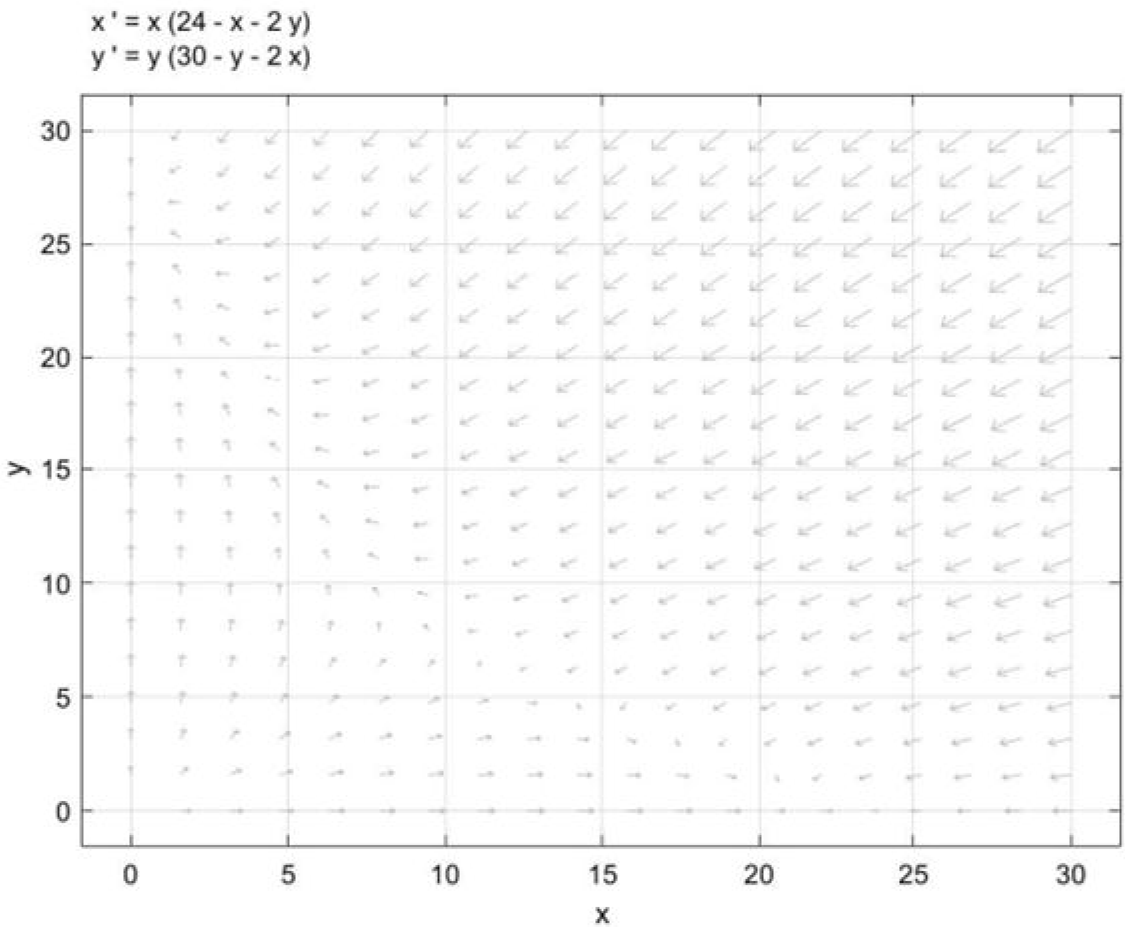
# Appendix A

## Pplane Results

### Survival-extinction Model

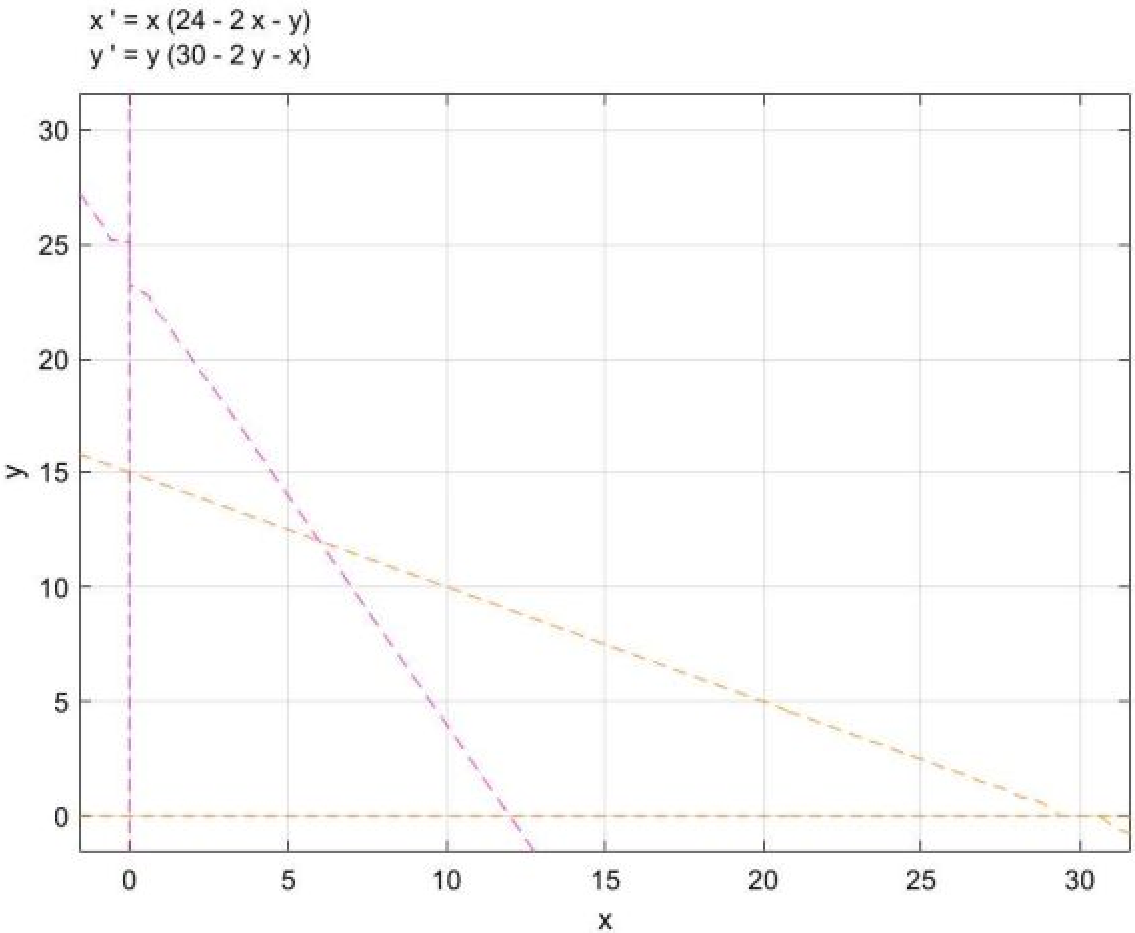



Nullclines plane for Survival-extinction model, pplane

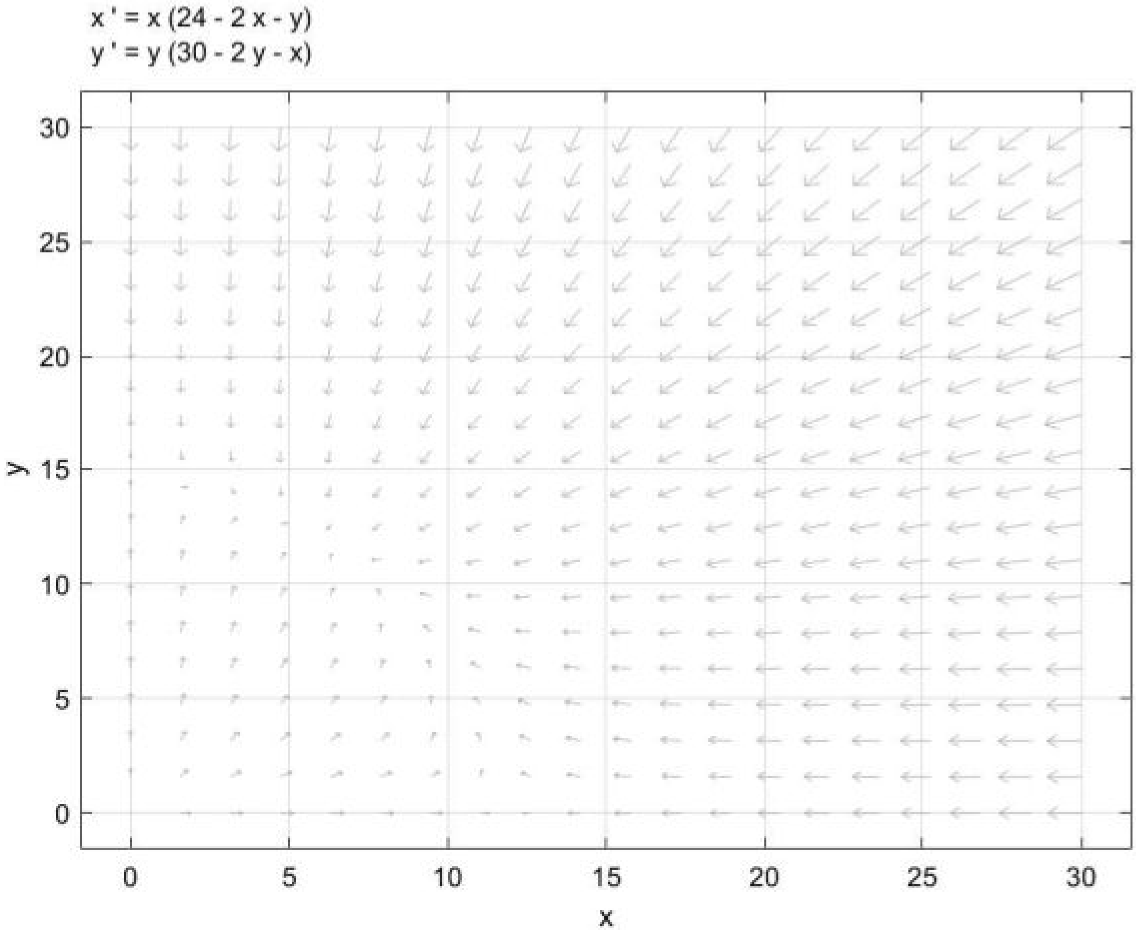



Arrows plane for Survival-extinction model, pplane

## Coexistence Model




Nullclines plane for Coexistence model, pplane




Arrows plane for Coexistence model, pplane