Introduction to Evolutionary Games - 2
Escuela de Bioestocástica

Kerlyns Martínez - Nicolás Rivera

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Here we have

$$\begin{aligned} \dot{x} &= ax \\ \dot{y} &= by \end{aligned} \quad \Longrightarrow \quad \begin{aligned} x(t) &= x_0 e^{at} \\ y(t) &= y_0 e^{bt} \end{aligned}$$

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Therefore,

$$\frac{x(t)}{y(t)} = \frac{x_0}{y_0} e^{(a-b)t}$$

- if $a = b$ then the quotient is constant: the size of the population are in the same proportion
- if $a > b$ then $\lim_{t\to\infty} \frac{x(t)}{y(t)} \to \infty$: Population A outcompete population B
- if $a < b$ then $\lim_{t\to\infty} \frac{x(t)}{y(t)} \to 0$: Population B outcompete population A

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A much more interesting case is when the total abundance is constant, i.e. we set $x(t) + y(t) = 1$. In this setting the simplest model is

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$$(a - \phi(t))x(t) + (b - \phi(t))y(t) = 0 \rightarrow ax + by = \phi(x + y) \rightarrow \phi = (ax + by)$$

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$$\dot{x} = x(1 - x)(a - b) \Rightarrow \begin{cases} x(t) = 0 & \text{if } x(0) = 0 \\ x(t) = 1 & \text{if } x(0) = 1 \\ x(t) = \frac{x_0 e^{(a-b)t}}{1 - x_0 + x_0 e^{(a-b)t}} & \text{if } x(0) \in (0, 1) \end{cases}$$

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Exercise

If $x(0) \in (0, 1)$, show that $\lim_{t\to\infty} x(t) \rightarrow 1$ if $a > b$, and $\lim_{t\to\infty} x(t) \rightarrow 0$ if $b < a$

Selection

We can have more than two species, e.g. A, B, and C

$$\dot{x}(t) = (a - \phi(t))x(t)$$
$$\dot{y}(t) = (b - \phi(t))y(t)$$
$$\dot{z}(t) = (c - \phi(t))z(t)$$

with $x(t) + y(t) + z(t) = 1$. In this case $\phi(t) = ax(t) + by(t) + cy(t)$ which is, again, the average fitness. However, solving this equation is much harder.

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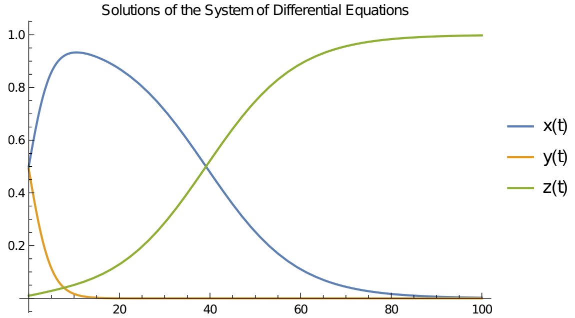
But.... Computers!

Mathematica is my to-go software for solving stuff. Other alternatives like Mathlab or several libraries in python (scypy, numpy, etc)

```
a = 1.9; b = 1.5; c = 2; (*fitness value*)
phi[t_] := a*x[t] + b*y[t] + c*z[t]; (*average fitness*)
eq1 = (x'[t] == (a - phi[t])*x[t]); (*the three equations and initial conditions*)
eq2 = (y'[t] == (b - phi[t])*y[t]);
eq3 = (z'[t] == (c - phi[t])*z[t]);
initialConditions = {x[0] == 50/100, y[0] == 49/100, z[0] == 1/100};
solution =  NDSolve[{eq1, eq2, eq3, initialConditions},
{x[t], y[t], z[t]}, {t, 0, 100}]; (*solver for ODE*)
{xSol, ySol, zSol} = {x[t], y[t], z[t]} /.
   solution[[1]]; (*extract the solutions*)
Plot[{xSol, ySol, zSol}, {t, 0, 100}, PlotLegends-> {"x(t)", "y(t)", "z(t)"},
 FrameLabel -> {"t", "Values"},  PlotLabel-> "Solutions of the System of Differential
```

Example with $a = 1.9$, $b = 1.5$, $c = 2$, $x(0) = 50/100$, $y(0) = 49/100$, $z(0) = 1/100$



DETOUR: Simplex and Equilibrium Points

Dynamics on the Simplex

In the previous examples, we had that the total abundance was constant.

The collection of points $(x_1, \ldots, x_n)$ such that $x_i \geq 0$ and $\sum_{i=1}^{n} x_i = 1$ are called the simplex S_n.

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The collection of points $(x_1, \ldots, x_n)$ such that $x_i \geq 0$ and $\sum_{i=1}^{n} x_i = 1$ are called the simplex S_n.

- Each point of the simplex represents the abundance of the population.
- If we keep the total abundance fixed at 1, then any evolutionary dynamics will be a dynamic on the simplex.

A bit on equilibrium Points

When we have a system of diferential equations

$$\dot{x} = f(x, y, z)$$
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Solutions to such a system are important because they are points of "0" velocity. Those points are called **equilibria points**

A bit on equilibrium Points

No all equilibria are the same

1. **Stable Equilibrium**: the system tends to return to that point after a perturbation
2. **Unstable Equilibrium**: the system moves away after a perturbation
3. **Saddle Point**: the system returns and moves away in different directions after a perturbation
4. **Center**: the system moves around the equilibrium
5. **Others**

END OF DETOUR

Mutation

An important operator is **mutation**: this means that one species transform into others by different means (pure mutation, but also like eating).

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Let's consider again two species A and B.

- Let x and y be the abundances of A and B respectively, and assume the dynamic is on the simplex
- Suppose that A has fitness a, and mutates into B at rate m_{AB}. Similarly
- Suppose that B has fitness b and mutates into A at rate m_{BA}.
- We will assume that both $m_{AB} > 0$ and $m_{BA} > 0$

Then, the system of equations is given by

$$\dot{x} = ax - m_{AB}x + m_{BA}y - \phi x$$
$$\dot{y} = by - m_{BA}y + m_{AB}x - \phi y$$

since $x + y = 1$ and $\dot{x} + \dot{y} = 0$, we have $\phi(t) = ax + by$.

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Equilibrium Point? We shall solve $\dot{x} = 0$, $\dot{y} = 0$. Let's solve for x:

$$0 = \dot{x} = ax - m_{AB}x + m_{BA}y - (ax + by)x$$

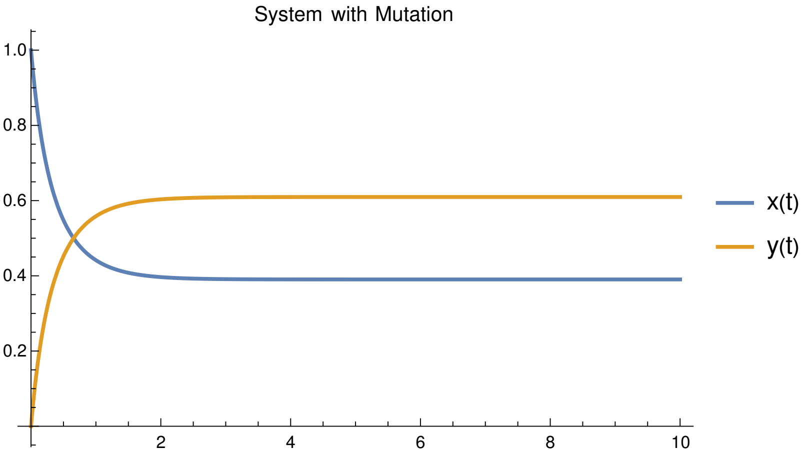
replacing $y = 1 - x$ yields

$$(b - a)x^2 + (a - b - (m_{AB} + m_{BA}))x + m_{BA}$$

- if $a = b$, then $(m_{AB} + m_{BA}))x + m_{BA}$
- if $a \neq b$, then we have a quadratic equation. The analysis of equilibrium points is harder here.

$$x \to \frac{b - a + m_{AB} + m_{BA} \pm \sqrt{(b - a + m_{AB} + m_{BA})^2 - 4(b - a)m_{BA}}}{2(b - a)}$$

A system with $a = 5$, $b = 3$, $m_AB = 2$, $m_{BA} = 0.5$



Mutation Matrix

Let's have a look again at our system of differential equations:

$$\dot{x} = ax - m_{AB}x + m_{BA}y - \phi x$$
$$\dot{y} = by - m_{BA}y + m_{AB}x - \phi y$$

Now consider another species, C, then we would have a system like

$$\dot{x} = ax - (m_{AB} + m_{AC})x + (m_{BA}y + m_{CA}z) - \phi x$$
$$\dot{y} = by - (m_{BA} + m_{BC})y + (m_{AB}x + m_{CA}z) - \phi y$$
$$\dot{z} = cz - (m_{CA} + m_{CB})z + (m_{AC}x + m_{BC}y) - \phi z$$

Then, we can write

$$Q = \begin{pmatrix} -(m_{AB} + m_{AC}) & m_{AB} & m_{AC} \\ m_{BA} & -(m_{BA} + m_{BC}) & m_{BC} \\ m_{CA} & m_{CB} & -(m_{CA} + m_{CB}) \end{pmatrix}$$

then, by using the notation $\overrightarrow{x} = (x, y, z)$, the mutation part can be written as

$$Q^{\intercal}\overrightarrow{x}$$

Mutation Matrix

In general, any mutation matrix Q is such that

1. For diagonal entries: $Q_{ii} \leq 0$
2. For odd-diagonal entries $Q_{ij} \geq 0$
3. The sum of the entries of each column is 0.

Summary

Reproduction:

- Reproduction can be model as ax with $a > 0$ being the reproduction rate, meaning that each indidivual reproduces at rate a
- Dead can be model as $-dx$ meaning that each individual dies at rate d
- the simplest model is then $\dot{x} = (a - d)x$. We can allow $a \in \mathbb{R}$ and encode reproduction and dead in the variable a

Selection and Competition:

- We allow more than one species, we can model the abundance of two species with two variables x and y
- If we fix the total abundance $x + y = 1$, then we introduce competence
- Average fitness *balance* the equations

$$\dot{x} = ax - \phi x$$
$$\dot{y} = by - \phi y$$

with $\phi(t) = ax(t) + by(t)$.

Mutation

- models the rate that one species transform into another one via a mutation

$$\dot{x} = ax - m_{AB}x + m_{BA}y - \phi x$$
$$\dot{y} = by - m_{BA}y + m_{AB}x - \phi y$$

- it can be encoded in a mutation matrix Q

Extra: Modelling Infections - SIR model

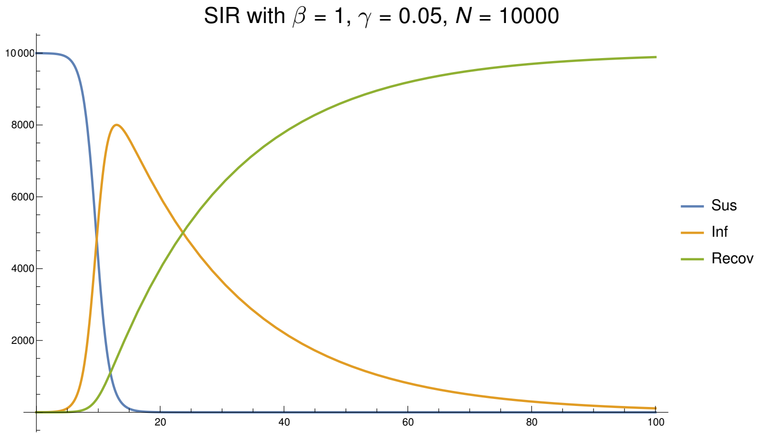
Suppose we have an infection in a population of size N.

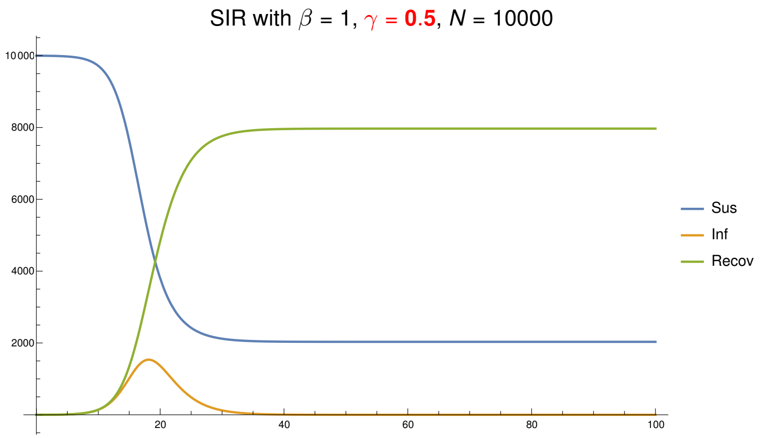
1. There are three type of subjects: infected, susceptible, and recovered
2. Susceptible agents can be infected
3. Infected can infect susceptible
4. Recovered cannot infect nor be infected (they are inmune or dead)

We have the following dynamics

1. An infected agent meets a random agent at rate β and infects her
2. Infected agents recover at rate γ

Can we write the model?


SIR with β = 1, γ = 0.05, N = 10000
10 000
8000
6000
4000
2000
20
40
60
80
100
Sus
Inf
Recov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