

Feline Leukemia Virus transmission in Iberian Lynx population

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Abstract: We combined two models -the SIR model for disease dynamics modified to take into account inter-species transmission, and the Rosenzweig-MacArthur for population dynamics, modified to look at prey-mesopredator-predator relations- to study the case of a Feline Leukemia Virus (FeLV) outbreak within the rabbits-cats-lynx system in the Doñana Park in Spain. We performed sensitivity analysis of the parameters in order to determine the cause of infection in the lynx population, looked into different possible scenarios and performed stability analysis of equilibrium to study the system's behaviour. Finally, we described and compared different conservation measures to prevent the lynxes from extinction. The results suggest that the transmission of FeLV from cats to lynxes leads to an outbreak in the lynx population. Moreover, the most effective measure to prevent an outbreak is to vaccinate the lynxes against FeLV. The paper highlights that mesopredators play an important role in disease dynamics of apex predators and not only in the predator - prey dynamics.

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1 Introduction

The Iberian lynx, *Lynx pardinus*, is the most endangered feline species in the world. It is found in Spain and Portugal and 20 years ago, its population was as small as 100 adult individuals in total. This was partly due to the main prey of the Iberian lynx, the European rabbit, *Oryctolagus cuniculus*. During the second half of the 20th century, the European rabbit suffered from diseases like rabbit haemorrhagic disease which contributed to its decline. Since then, the remaining lynx populations have been protected and some individuals were reintroduced, leading to a total of 475 Iberian lynxes in 2017[1].

The Iberian lynx is known to compete with cats (*Felis sp.*) for preys and cats killed by lynxes are frequently reported. In 2007, an epidemic of Feline Leukemia Virus (FeLV) struck one of the populations of Iberian lynxes in Doñana, Spain. Out of approximately 50 lynxes, 12 got infected and 7 died within a year[2]. The virus was contracted by contact with infected cats, and then likely spread inside the lynx population.

The Feline Leukemia Virus is a retrovirus affecting the Felidae family, commonly called felids. It is mostly transmitted by exchange of blood and saliva, which happens a lot for felids during grooming or fights involving biting. The virus is highly infectious, but a fraction of infected carry the matching antibodies and thus develop immunity. These immune individuals cannot spread the virus to susceptibles. For individuals who become persistently infected, FeLV provokes a generalized infection of the blood and immune system cells, which causes the cats to be more susceptible to other infections. As there is no known cure yet, the infected felids eventually die of overwhelming infections.

Finally, in 2017, conservation researchers monitoring the Iberian lynx population came across the first case of a lynx consuming a cat[3]. Since cats also consume European rabbits, our 3 animals are linked by a trophic web of the shape Predator (lynx) – Mesopredator (cat) – Prey (rabbit).

Since the Iberian lynx population is already at risk of extinction, an epidemic of FeLV could be a big concern for conservation specialists. Therefore in this project, we plan to investigate two major questions:

- **How does the FeLV spread to lynxes: does it spread more through lynx-cat interactions or lynx-lynx interactions?**
- **How to protect the lynx population: which conservation measures could be implemented and how efficient would they be?**

2 Model

Similar models already exist but not for this particular situation. Moreover, most models are either of the form Prey-Mesopredator-Predator without disease or Prey-Predator with disease. So we basically combined these two into one. There are two main dynamics to model: population and disease dynamics. For population dynamics, we used the Rosenzweig-MacArthur model, and for the disease the SIR model.

In this section we describe the model we implemented. From now on, we denote the populations by L (Lynxes), C (Cats) and R (Rabbits).

2.1 Assumptions

Several assumptions have been made, either because of a lack of information or for simplicity:

1. Rabbit population is mostly constant and large. This is a big assumption because in reality, the population of the European rabbit is reduced due to the important epidemics it has faced in the past. We assumed this for simplicity and also to account for the other potential preys that are not included in our model. [4]
2. Infection doesn't change hunting efficiency. That is, if an animal (lynx or cat) is infected, it is neither more or less efficient in hunting or in being hunted. This is assumed for simplicity, because FeLV infection has a variety of consequences and can also open the door to other infections, which makes it hard to blame specific symptoms on the virus.
3. Lynxes cannot become naturally immune to the disease. While this is theoretically possible, there is a limited amount of information on FeLV epidemics in lynxes. We assume that they can recover without immunity, but otherwise they eventually die. [2]
4. Cats do not attack lynxes. If a lynx attacks a cat, it results in the cat's death, thus there is no transmission of the virus from lynxes to cats.
5. Finally, some assumptions have been made while estimating parameters. These will be detailed in the next sections.

2.2 Population Dynamics

At first, we wanted to use the prey-predator dynamics seen in class involving Lotka-Volterra equations and then extend it to take into account the mesopredator. But in the end we decided to use another version of this model: the Rosenzweig-MacArthur model. This choice has been made mainly for two reasons. Firstly, this is an extended and more accurate version of the Lotka-Volterra model. Secondly, some parameters for the population dynamics have been found in a paper that used this kind of model. [4] We also added a slight modification to this model.

2.2.1 The Rosenzweig-MacArthur Model

In this part we explain the idea behind this model. Here is an example for a simple prey-predator dynamics with prey x and predator y (and parameters a , b , p , q):

$$\begin{aligned}\frac{dx}{dt} &= ax\left(1 - \frac{x}{\gamma}\right) - p\frac{xy}{1+x} \\ \frac{dy}{dt} &= q\frac{xy}{1+x} - by\end{aligned}$$

Two things are different from the usual model. First, the parameter γ which is the carrying capacity of the environment for the prey. In the absence of predators, the prey population will grow, but not up to infinity. It stops at a certain threshold γ , which makes more sense biologically. Second, the interaction between x and y is no longer simply multiplicative, but divided by a term $x + 1$. This is so that the predation rates saturate when x becomes very large.

For these reasons, we used this model and adapted it to study the Prey-Mesopredator-Predator interactions.

2.2.2 Modification

We also added a slight modification to this model so that it takes into account the carrying capacity of predators. As before, this makes more sense biologically (cats cannot grow up to infinity). The parameters for this are shown in the next subsection.

2.2.3 Parameters

Most parameters come from estimations. This is mainly the case for cats parameters (e_{CR} , e_{LC} , q_L , p_C etc.). We could not find a good source with parameters so we inferred them from lynx parameters, following the fact that cats need less food to grow more (because they are smaller, they will be a more efficient predator [5]), and that lynxes eat cats very rarely.

For initial population values, we estimated C_0 to be around 500. Note that this is the sum of feral and domestic cat populations. While there are not many feral cats left (around 30 [6]), the disease comes from domestic cats from neighbouring towns, and these cats are very numerous.

Concerning carrying capacities, we inferred them from initial population values. The values for K_L and K_R are equal.

Parameter	Definition	Estimate	Units	Source
e_{LR}	Growth rate of lynxes thanks to rabbits consumed	0.127	Per day	[4]
e_{CR}	Growth rate of cats thanks to rabbits consumed	0.24	Per day	[7], Estimation
e_{LC}	Growth rate of lynxes thanks to cats consumed	0.0001	Per day	Estimation
q_L	Death rate of cats because of lynxes	0.1	Cat per lynx per day	Estimation
p_C	Death rate of rabbits because of cats	0.5	Rabbit per cat per day	[7], Estimation
p_L	Death rate of rabbits because of lynxes	0.5	Rabbit per lynx per day	[4]
x_L	Death rate of lynxes without prey	0.12	Per day	[4]
x_C	Death rate of cats without prey	0.08	Per day	Estimation
y_R	Growth rate of rabbits	6.1	Per day	[4]
K_L	Carrying capacity of environment for lynxes	800	Lynx	Estimation
K_C	Carrying capacity of environment for cats	800	Cat	Estimation
K_R	Carrying capacity of environment for rabbits	1500	Rabbit	Estimation
L_0	Initial lynx population	30	Lynx	[2]
C_0	Initial cat population	500	Cat	Estimation
R_0	Initial rabbit population	800	Rabbit	Estimation

2.2.4 Equations

Using these parameters, we get the following equations for population dynamics:

- $\frac{dL}{dt} = e_{LC} \frac{CL}{C+60} (1 - \frac{L}{K_L}) + e_{LR} \frac{RL}{R+48} (1 - \frac{L}{K_L}) - x_L L$
- $\frac{dC}{dt} = e_{CR} \frac{CR}{R+48} (1 - \frac{C}{K_C}) - q_L \frac{CL}{C+60} - x_C C$

- $\frac{dR}{dt} = y_R R(1 - \frac{R}{K_R}) - p_C \frac{CR}{R+48} - p_L \frac{RL}{R+48}$

Note that what changes is the values 48 and 60 that appear in the prey-predator interactions. They represent the extent to which the environment provides protection to the prey [4].

2.3 Disease Dynamics

To model the disease dynamics, we chose to use the SIR model seen in class. We modified it to match the dynamics of FeLV observed independently in cats [8] and lynxes [2], and then connected the 2 systems. In this subsection, there will be no mention of the rabbits because they only take part in the population dynamics part of our model.

2.3.1 The SIR Model

The SIR model is a compartmental model for disease dynamics where we separate the population in 3 compartments: Susceptibles, Infected and Recovered. The basic equations are as follows:

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}$$

β represents the infection rate of the disease, which is the probability that a susceptible meets an infected, multiplied by the probability of transmitting the disease when a contact occurs. γ is the recovery rate of infected individuals.

2.3.2 Modification

We added several modifications to the basic SIR model to match our situation. First, since there is no recovery from FeLV for cats but there can be immunity, we used the Recovered compartment for the immune cats. That is, when a cat gets infected, it will move on to the Recovered compartment if it is immune to FeLV. If it is not, the cat stays in the Infected compartment.[8] Then, since we assume there is no immunity for lynxes, we used a SIS model instead. Thus when a lynx recovers, it goes back to the Susceptible compartment. Finally, to account for the fact that the disease spreads from cats to lynxes, we added an infection term in the lynx model. Infected lynx are not only created by interactions between a susceptible and an infected lynx, but also by interactions between an infected cat and a susceptible lynx.

2.3.3 Parameters

Parameter	Definition	Estimate	Units	Source
β_L	Number of interactions infected lynx-lynx leading to infection	0.0027	Lynx per day	Estimation
β_C	Number of interactions infected cat-cat leading to infection	0.015	Cat per day	Estimation
β_{CL}	Number of interactions infected cat-lynx leading to infection	0.002	Lynx per day	Estimation
γ_L	Recovery rate for lynxes	0.00011	Per day	[2]
ρ_C	Recovery rate for cats	0.00046	Per day	[8]
δ_L	Death rate of lynxes because of disease	0.0032	Per day	[2]
δ_C	Death rate of cats because of disease	0.0007	Per day	[8]
init_infected	Fraction of initially infected cats	0.03	\emptyset	Estimation

Note that the parameters β 's are not exactly the same as in the usual SIR model. This is because they are supposed to depend on the population size. In the SIR model, the population is constant so that they are constant too. But in our model, since we consider population dynamics as well, the population is not constant. In general, infection rates are computed this way:

$$\text{infection rate} = \frac{\text{number of interactions with individuals} * \text{fraction of infections}}{\text{population}}.$$

In our case, consider the infection rate between infected cats and lynxes:

$$\text{infection rate} = \frac{\text{number of lynxes encountered} * \text{fraction of infections}}{\text{Lynx population}} = \frac{\beta_{CL}}{L}$$

Now as for their values, they once again mainly come from estimations, information on this matter being really scarce. Here we show our reasoning and assumptions used to compute β_{CL} :

- The lynx population is estimated to be around 30 individuals in a 250 000 km^2 area. Therefore the lynx density is $\frac{30}{250000}$.
- A cat moves in a 5*5 km square everyday, so it would be in the same 1*1 km square as $25 * \frac{30}{250000}$ lynxes.
- If a cat and a lynx are in the same 1*1 km square, they meet with probability 0.7 (the cat can escape or the lynx can not kill it), which gives us a total of $0.7 * 25 * \frac{30}{250000}$ interactions between an infected cat and the lynx population.
- If the lynx kills the cat, it has a 0.95 probability of becoming infected (infection by blood/saliva). So in the end our value for β_{CL} is $0.95 * 0.7 * 25 * \frac{30}{250000} = 0.002$

This clearly has some flaws in it but we could not find any data for it.

2.3.4 Equations

Using these parameters, we get the following equations for disease dynamics:

- $\frac{dS_L}{dt} = \gamma_L I_L - \beta_L I_L \frac{S_L}{L} - \beta_{CL} I_C \frac{S_L}{L}$
- $\frac{dI_L}{dt} = \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L} - \gamma_L I_L - \delta_L I_L$
- $\frac{dS_C}{dt} = -\beta_C I_C \frac{S_C}{C}$
- $\frac{dI_C}{dt} = \beta_C I_C \frac{S_C}{C} - \rho_C I_C - \delta_C I_C$
- $\frac{dR_C}{dt} = \rho_C I_C$

Note that each β term is divided by the total population size of the relevant animal to account for the fact that the usual β parameters in SIR models depend on population size.

2.4 Final Model

Figure 1 shows a diagram summarizing the model. We have 6 compartments, so 6 equations, with 23 parameters.

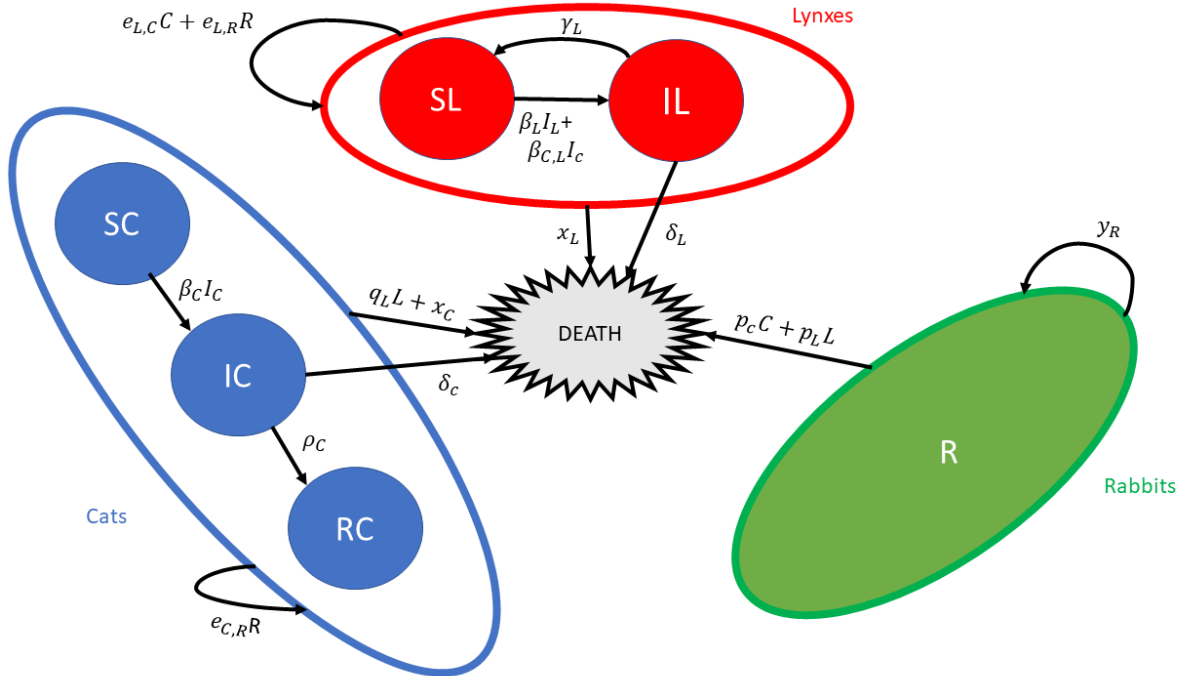


Figure 1: The coupled population and disease dynamics of the Lynx- Cat - Rabbit system.

Combining the equations for the population and disease dynamics, we get the final equations:

- $\frac{dS_L}{dt} = [e_{LC} \frac{CS_L}{C+60} (1 - \frac{L}{K_L}) + e_{LR} \frac{RS_L}{R+48} (1 - \frac{L}{K_L}) + \gamma_L I_L] - [x_L S_L + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L}]$
- $\frac{dI_L}{dt} = [e_{LC} \frac{CI_L}{C+60} (1 - \frac{L}{K_L}) + e_{LR} \frac{RI_L}{R+48} (1 - \frac{L}{K_L}) + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L}] - [x_L I_L + \gamma_L I_L + \delta_L I_L]$
- $\frac{dS_C}{dt} = [e_{CR} \frac{RS_C}{R+48} (1 - \frac{C}{K_C})] - [q_L \frac{S_C L}{C+60} + x_C S_C + \beta_C I_C \frac{S_C}{C}]$
- $\frac{dI_C}{dt} = [e_{CR} \frac{RI_C}{R+48} (1 - \frac{C}{K_C}) + \beta_C I_C \frac{S_C}{C}] - [q_L \frac{I_C L}{C+60} + x_C C + \rho_C I_C + \delta_C I_C]$
- $\frac{dR_C}{dt} = [e_{CR} \frac{RR_C}{R+48} (1 - \frac{C}{K_C}) + \rho_C I_C] - [x_C R_C + q_L \frac{R_C L}{C+60}]$
- $\frac{dR}{dt} = [y_R R (1 - \frac{R}{K_R})] - [p_C \frac{CR}{R+48} + p_L \frac{RL}{R+48}]$

Where $L = S_L + I_L$, $C = S_C + I_C + R_C$.

2.5 Conservation Models

We chose to look at 3 different conservation models: isolation of infected lynxes, control of the cat population and vaccination of susceptible lynxes. For each one, we used our final model and added a few modifications to express the effect of the conservation measure.

2.5.1 Lynx Isolation

To model the isolation of infected lynx from the rest of the population, we added a compartment for isolated lynxes. Infected lynxes are transferred to this compartment at a rate $isol_L$. Isolated lynxes die of FeLV at the same rate as the rest of the infected population, but have a higher chance of recovering and going back to susceptibles, denoted $cure_L$. We added to this model the fact that quarantined lynxes can be treated by the conservation specialists, which increases their chance of recovering. Therefore for this conservation measure, the equations are as follows (using Q_L to denote quarantined lynxes).

- $\frac{dS_L}{dt} = [e_{LC} \frac{CS_L}{C+60} (1 - \frac{L}{K_L}) + e_{LR} \frac{RS_L}{R+48} (1 - \frac{L}{K_L}) + \gamma_L I_L + cure_L Q_L] - [x_L S_L + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L}]$
- $\frac{dI_L}{dt} = [e_{LC} \frac{CI_L}{C+60} (1 - \frac{L}{K_L}) + e_{LR} \frac{RI_L}{R+48} (1 - \frac{L}{K_L}) + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L}] - [x_L I_L + \gamma_L I_L + isol_L I_L + \delta_L I_L]$
- $\frac{dQ_L}{dt} = isol_L I_L - [cure_L Q_L + \delta_L Q_L]$
- $\frac{dS_C}{dt} = [e_{CR} \frac{RS_C}{R+48} (1 - \frac{C}{K_C})] - [q_L \frac{S_C L}{C+60} + x_C S_C + \beta_C I_C \frac{S_C}{C}]$
- $\frac{dI_C}{dt} = [e_{CR} \frac{RI_C}{R+48} (1 - \frac{C}{K_C}) + \beta_C I_C \frac{S_C}{C}] - [q_L \frac{I_C L}{C+60} + x_C C + \rho_C I_C + \delta_C I_C]$

- $\frac{dR_C}{dt} = [e_{CR}\frac{RR_C}{R+48}(1 - \frac{C}{K_C}) + \rho_C I_C] - [x_C R_C + q_L \frac{R_C L}{C+60}]$
- $\frac{dR}{dt} = [y_R R(1 - \frac{R}{K_R})] - [p_C \frac{CR}{R+48} + p_L \frac{RL}{R+48}]$

For our simulation, we chose $isol_L = 0.01$ which represents 1 lynx quarantined every 100 days or approximately 3 months.

2.5.2 Cats Control

To model a control of the cat population, we simply changed the initial population size and carrying capacity of the environment for cats. In reality, this could be achieved with a reduction of the feral cat population of the area, and a total isolation of infected domestic cats. That way, less cats are actually present in our area of study.

For our simulations, we chose to place the initial population size and the carrying capacity at 50 cats.

2.5.3 Lynx Vaccination

Finally to implement the vaccination of susceptible lynxes, we added a compartment to the model for vaccinated lynxes. They answer to the same population dynamics as the susceptible lynxes but cannot get infected. This adds one new parameter, vac_L , which is the percentage of the susceptible lynxes that are vaccinated in one day. The equations for the cat and rabbit populations stay the same. Thus the equations for this conservation measure are:

- $\frac{dS_L}{dt} = [e_{LC}\frac{CS_L}{C+60}(1 - \frac{L}{K_L}) + e_{LR}\frac{RS_L}{R+48}(1 - \frac{L}{K_L}) + \gamma_L I_L] - [x_L S_L + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L} + vac_L S_L]$
- $\frac{dI_L}{dt} = [e_{LC}\frac{CI_L}{C+60}(1 - \frac{L}{K_L}) + e_{LR}\frac{RI_L}{R+48}(1 - \frac{L}{K_L}) + \beta_L I_L \frac{S_L}{L} + \beta_{CL} I_C \frac{S_L}{L}] - [x_L I_L + \gamma_L I_L + \delta_L I_L]$
- $\frac{dS_C}{dt} = [e_{CR}\frac{RS_C}{R+48}(1 - \frac{C}{K_C})] - [q_L \frac{S_C L}{C+60} + x_C S_C + \beta_C I_C \frac{S_C}{C}]$
- $\frac{dV_L}{dt} = e_{LC}\frac{CV_L}{C+60}(1 - \frac{L}{K_L}) + e_{LR}\frac{RV_L}{R+48}(1 - \frac{L}{K_L}) + vac_L S_L - x_L V_L$
- $\frac{dI_C}{dt} = [e_{CR}\frac{RI_C}{R+48}(1 - \frac{C}{K_C}) + \beta_C I_C \frac{S_C}{C}] - [q_L \frac{I_C L}{C+60} + x_C C + \rho_C I_C + \delta_C I_C]$
- $\frac{dR_C}{dt} = [e_{CR}\frac{RR_C}{R+48}(1 - \frac{C}{K_C}) + \rho_C I_C] - [x_C R_C + q_L \frac{R_C L}{C+60}]$
- $\frac{dR}{dt} = [y_R R(1 - \frac{R}{K_R})] - [p_C \frac{CR}{R+48} + p_L \frac{RL}{R+48}]$

We ran our model with $vac_L = 0.01$, which represents 1 lynx vaccinated every 100 days. We chose this low value to account for the fact that to vaccinate a lynx, conservators first need to catch it, test it to see if it is infected with FeLV and then vaccinate it, so the process might take a while.

3 Results

3.1 Main Model Output

The outputs of our main model can be seen in Figure 2. First, we note that the populations of cats and rabbits are large and stable. In the cat population, there was a outbreak of FeLV with the peak of infection happening after about 2 years. Then the infection dies down. Throughout the simulation, the number of immune cats goes up steadily until they make up almost the whole population.

Then regarding the lynx population, we calculated the basic reproductive number for the infection in lynxes using the two transmission rates: (1) between the cats and the lynxes and (2) within the lynx population. The basic reproductive number for FeLV for lynxes was 1.47. Since $R_0 > 1$, we would expect the infection to lead to an epidemic, and we see in Figure 2 that it is the case. The lynxes get rapidly infected before 500 days of the beginning of the outbreak. By then, we note a rapid exponential decline in the lynx population. The population goes extinct within 4000 days of the outbreak.

3.2 Stability Analysis

Disease and population dynamics usually have very different equilibria (stable $I=0$ for SIR and unstable periodic for Lotka-Volterra). The Rosenzweig Mac-Arthur model has a bit of a mix: the points in the phase plane spiral towards an equilibrium point. Since we combined these two approaches, we thought it would be interesting to perform an analysis of the ODEs to find and classify equilibria.

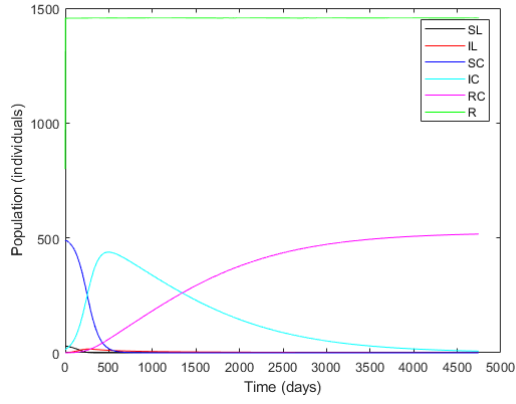
Since the system is non-linear, we had to use linearization around an equilibrium point: $X^* = [0 \ 0 \ 524.6 \ 0 \ 0 \ 1457.2]$.

This point has been computed with Matlab's *fsolve* starting from a guess $X_0 = [0 \ 0 \ 0.5 \ 525 \ 0 \ 0 \ 1458]$. It corresponds to an equilibrium situation between cats and rabbits after the disease is gone, without lynxes.

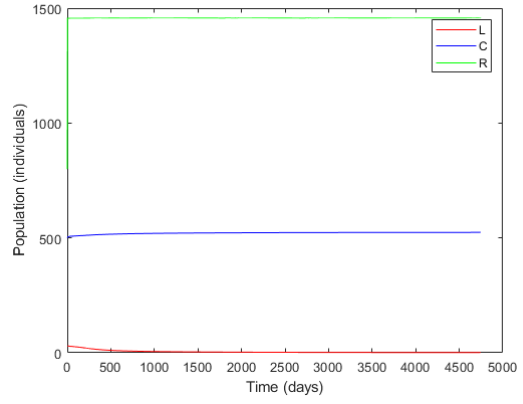
Then, using Matlab's *jacobian*, we computed the Jacobian of the system and evaluated it at X^* , then computed its eigenvalues. These are shown in this vector:

$$\begin{bmatrix} -0.000052 \\ 0.00056 \\ 0.0021 \\ 0.014 \\ -0.15 \\ -5.75 \end{bmatrix}$$

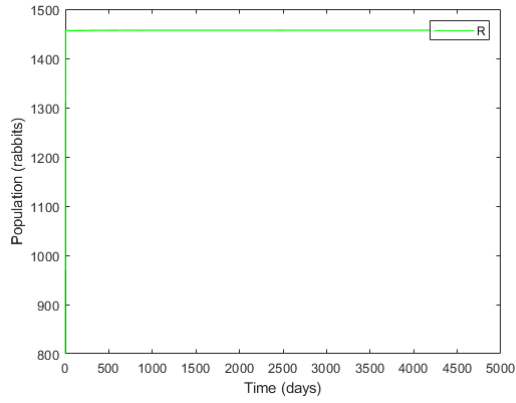
As we can see, no eigenvalues has real part 0, and some are positive, therefore this equilibrium is unstable. This comes from the population dynamics. The main explanation is that this equilibrium doesn't have any infected animal ($X^*(2) = X^*(4) = 0$). So what happens if we add for example 0.1 susceptible lynx? They will thrive (as any superpredator), not killed by the disease and grow exponentially away from equilibrium. Below is a graph



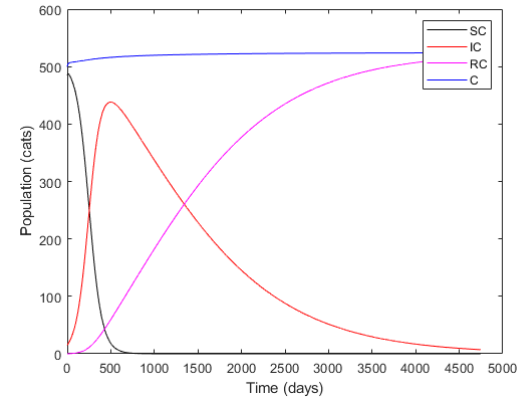
(a) All compartments



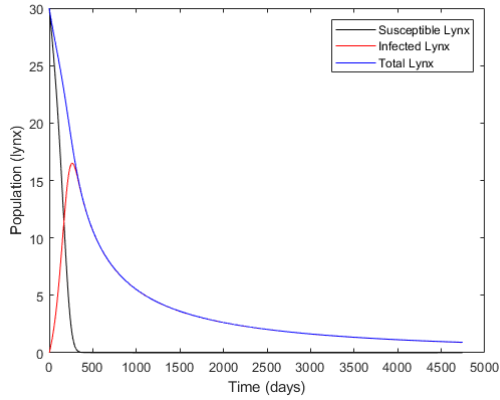
(b) Total population of each animal



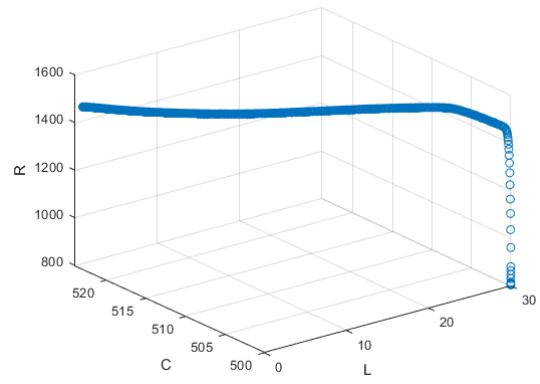
(c) Rabbit population



(d) Cat population



(e) Lynx population



(f) Phase diagram

Figure 2: Outputs of the main model

of 10 simulations of the lynx population, each being a 5 years run from the equilibrium plus a little perturbation ranging from 0 to 1 susceptible lynx added. We can see that it clearly moves far from X^* , confirming its instability.

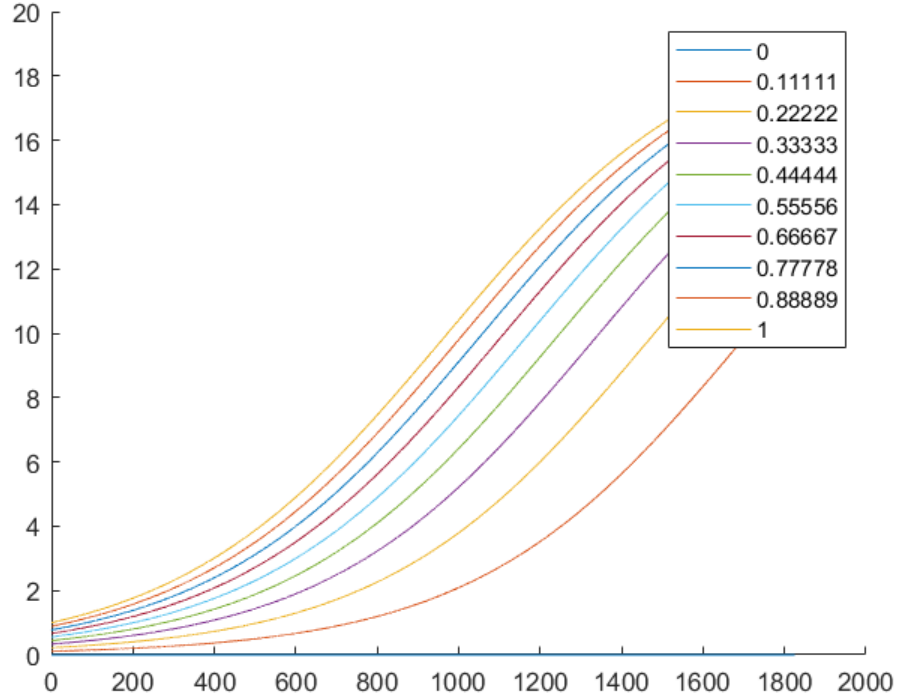


Figure 3: Lynx population during 5 years after perturbation from the equilibrium

Note that this is a very interesting result in terms of conservation: if an epidemic of FeLV is detected in the park, it could be a good idea to transfer healthy individuals into a non-infected environment until the epidemic is completely stopped in the park (at this point we would be at equilibrium). Then, reintroducing these individuals will allow them to grow and expand the lynx population without fear of the disease.

3.3 Sensitivity Analysis

To estimate the impact of each of the transmission rates on the transmission of FeLV in lynxes, we compared the sensitivity of the model to the transmission parameters for (1) between cats and lynx β_{CL} and (2) within the lynx population β_L . The model sensitivity of transmission of FeLV from cats to lynx was -0.0713, while the sensitivity of transmission of FeLV within the lynx population was -0.0084. The model was not highly sensitive to both the transmission parameters as the sensitivity values were low. However, the sensitivity value for the transmission from cats to lynx was ten times higher than the transmission between the lynx population.

3.4 Conservation Measures

To explore the efforts to control disease spread, we considered three conservation measures (1) quarantining individual lynx who are infected, (2) controlling the population of feral cats, and (3) vaccinating the susceptible lynx.

3.4.1 Lynx Isolation

When we isolate lynxes at a rate of 1 infected lynx every 100 days, we get the population dynamics for the lynx population shown in Figure 4.

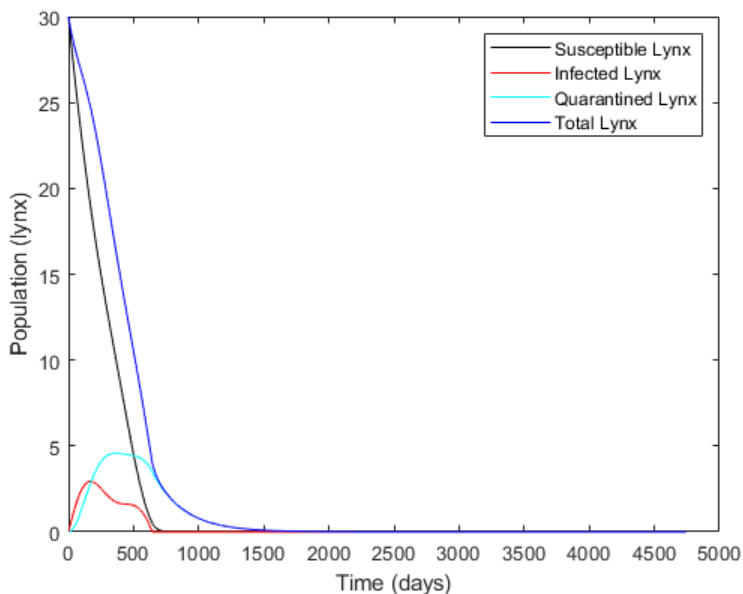


Figure 4: Population dynamics of lynxes with 1 lynx quarantined/100 days

When the infected lynx are quarantined individually, the model suggests that lynx population declines rapidly. Although the lynxes do not get severely infected, the population goes extinct within 1500 days of the outbreak. This is likely because the way we constructed the model implies that quarantined lynxes do not reproduce. Therefore as long as they are in isolation, they cannot sustain the population; and we see on our graph that after approximately 2 years, the remaining lynx population is entirely made up of quarantined individuals.

3.4.2 Cats Control

When we limit the number of cats in the protected area to 50, we get the population dynamics for the lynx population shown in Figure 5.

We see that the total lynx population drops down to approximately 10 individuals and then seems to grow again. We ran the stimulation for a longer time (8000 days, i.e. 20 years)

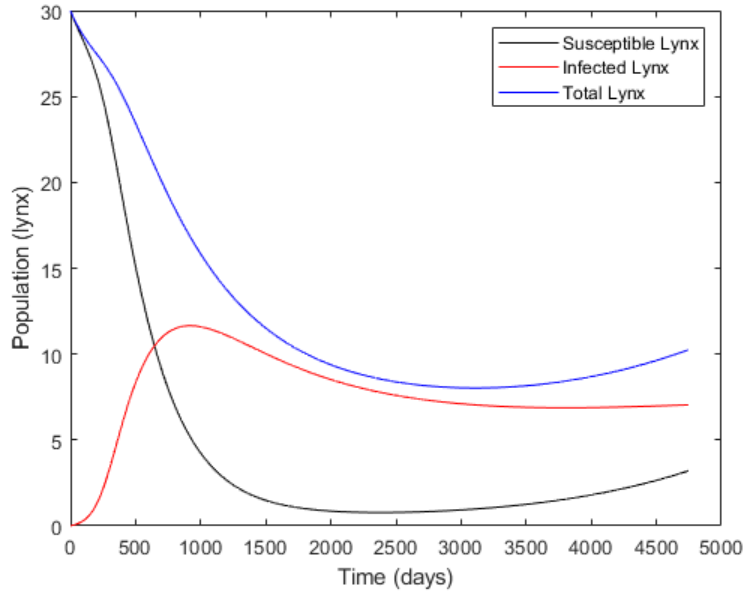


Figure 5: Population dynamics of lynxes with at most 50 cats in the area

and the population keeps growing, with a decrease of infected individuals. Therefore this seems to be a good outcome, but on the other hand, the cat population starts to decrease because of the large number of lynxes. This could become a problem since in this situation, the cat population of the area is already limited to only 50 individuals.

3.4.3 Lynx Vaccination

With a vaccination rate of one lynx every 100 days, we get the results for the dynamics of the lynx population as shown in Figure 6.

When the susceptible lynxes are vaccinated once every 100 days, the infection can be controlled and the virus can be eradicated in 2000 days (5 years). The population recovers from the infection and stabilizes to around 20 individuals who are vaccinated against the virus. This is good because it means that as long as the virus doesn't mutate and renders the vaccine ineffective, the lynx population will not suffer from a new FeLV epidemic.

4 Discussion

Our model provides the population dynamics of the lynx population under an outbreak of FeLV originating from the cat population in the same region. The model along with our parameter estimations suggest that the infection of FeLV into the lynx population will lead to a deadly epidemic. Exploring disease control measures for the lynx population, vaccination is the most effective way of saving the lynx population out of the three conservation measures implemented during the 2007 outbreak.[9]

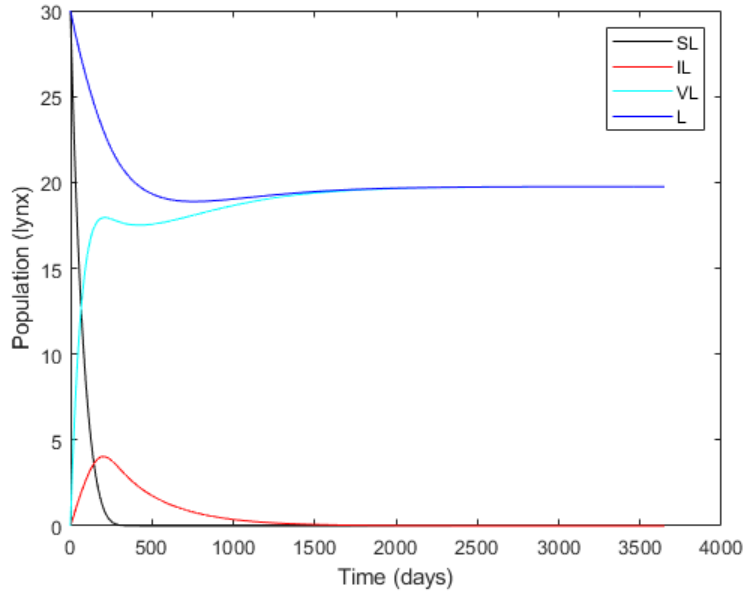


Figure 6: Population dynamics of lynxes with 1 lynx vaccinated every 100 days

The lynx population is affected by transmission from both cats and other lynxes. The model suggests that there is more transmission of FeLV from cats to lynxes rather than transmission within the lynx population. The greater effect of transmission from cats to lynxes indicates that, with respect to the transmission of FeLV in lynx, the cats act as a reservoir of the virus and interactions between lynxes and cats can lead to outbreaks in the lynx population. However, the model overall was not highly sensitive to both the transmissions. This insensitivity of the model may have led us to consider a longer time frame for the outbreak. The lynx population may actually go extinct sooner than the model predicts.

We considered three conservation measures (1) quarantining infected lynx, (2) controlling the population of cats within the protected area, and (3) vaccinating susceptible lynxes. Between the first two conservation measures, controlling cat population was a more effective manner of saving the lynx population which was also highlighted by the relatively larger sensitivity of the model to the transmission of FeLV from cats to lynx. Moreover, when the lynxes are isolated, their reproductive possibilities reduce which drives the population extinct sooner than the infection itself.

The model suggests that the best method to save lynxes is vaccinating them. Vaccinating helps the population recover in number and helps stabilize the population which has also been strongly argued for in past studies [2][9]. Even with a modest capture and vaccination rate of just 1 lynx every 100 days, the measure is the most effective. However, the model assumes that a vaccination gives lifelong immunity. In reality, the vaccinations used for the lynx are the same as the cats and require booster shots to provide strong immunity [9]. Keeping track of vaccination booster shots in a wild population may be difficult. However,

higher rates of captures and vaccinations have been shown to be possible during the 2007 outbreak [9]. A higher vaccination rate may not only prevent infection once, but regular vaccination may prevent future outbreaks.

Our model highlights the need to take preventative conservation actions such as vaccination against FeLV and controlling cat populations within protected areas. However, the model is based on mostly estimated parameters. Further studies need to be performed to collect empirical data so as to enhance the understanding of disease dynamics of FeLV in the lynx and improvement in model predictions. Such enhancements may improve precision of the outbreak timelines. The model also needs to account for animal behaviour and natural history of the lynx. For instance, male lynx are more prone to fighting during breeding season over access to mates[10] which may lead to a higher spread of disease through males of the population. Moreover, the lynx population and the rabbit population have both been decimated due to habitat destruction and a disease in the rabbits.[4] Therefore, future studies need to account for the fragility of the small size of the population and the functional extinction of the population to enhance the understanding of the implications of the disease dynamics of such outbreaks.

5 Response to Questions From Presentation

In this section, we answer questions that have been asked during and after the presentation.

- Are the cats wild or domestic and does it matter?
When we estimated the total population size for the cats, we accounted for feral cats and domestic cats in the area. However, there is little information on disease dynamics of FeLV in feral cats since they are much more complicated to obtain than for domestic cats. Thus the disease dynamics are based on studies conducted on domestic cats. We don't think this is a problem because the domestic cat population is more than 10 times bigger than the feral cats' in our simulation.
- Considering the small number of lynxes, is a continuous model appropriate?
We thought about this question when designing the model but for simplicity we decided to still use a continuous model. Moreover, the numbers of cats and rabbits are large so for these populations the continuous model makes sense. But we acknowledge the fact that our predictions on the population size of lynxes would be more precise with a discrete model.
- Are 1000s of days the correct timescale for an FeLV epidemic?
We decided to use this timescale because the natural life expectancy of a lynx is 13 years (5000 days). This way we can see if with the disease our lynx population dies off faster than it would with no disease. Concerning the timescale of the actual disease, we only had one main source describing the FeLV epidemic in the Doñana population, so we used the information of this paper to infer our parameters. In our results, we

see on the graphs that most of the disease dynamics occur in the first 2 years, which seems to match the observations of our source.

- Based on our model, which conservation measure would we recommend?
According to our model, the most efficient conservation measure would be vaccinating the lynxes. We see that it is the measure that allows the lynx population to stabilize at the highest value. For an even better efficiency, we could also advise conservation specialist to combine the vaccination method with the cats control, which also seemed to have a good effect on the lynx population survival.

6 Contributions of Each Group Member

We all contributed equally to the power point presentation.

6.1 Agathe Yvinec Tolmer

- Provided the necessary background and biological knowledge
- Parameter research
- Introduction, response to questions and contributed to section 2.1, 2.3, 2.5, and 3 of the report
- Bibliography

6.2 Thomas Rimbot

- Parameter research and estimations
- Implemented the code for basic model and conservation measures
- Ran simulations to debug the model
- Stability analysis of the equilibrium
- Abstract and contributed to section 2 and 3.2 of the report

6.3 Pranav Sadana

- Modelling background: developing the disease dynamic models (SIS, SISV)
- Sensitivity analyses and biological implications of the model and its parameters
- Discussion, conclusion and contributed to section 3 of the report

7 Conclusion

This paper combines a predator-prey dynamics model, the Rosenzweig-MacArthur Model, with a disease dynamics model, SIR model. The coupling of the two models was then applied to a Predator - Mesopredator - Prey situation. The model was used to explore the transmission of the Feline Leukemia Virus (FeLV) in the lynx population of a protected area of Doñana, Spain, through the mesopredators, cats. Our results suggest that the transmission of FeLV from cats to lynx would lead to an epidemic outbreak. We also highlight the effectiveness of preventative measures of vaccination, as well as the role of mesopredators in disease dynamics of endangered apex predators which may be applied to other similar systems.

References

- [1] (). Iberian lynx — WWF, [Online]. Available: https://wwf.panda.org/our_work/wildlife/profiles/mammals/iberian_lynx/ (visited on 03/17/2020).
- [2] M. L. Meli, V. Cattori, F. Martínez, G. López, A. Vargas, F. Palomares, J. V. López-Bao, R. Hofmann-Lehmann, and H. Lutz, “Feline leukemia virus infection: A threat for the survival of the critically endangered iberian lynx (*lynx pardinus*),” *Veterinary Immunology and Immunopathology*, Special Issue: 9th International Feline Retrovirus Research Symposium 2008, vol. 134, no. 1, pp. 61–67, Mar. 15, 2010, ISSN: 0165-2427. DOI: 10.1016/j.vetimm.2009.10.010. [Online]. Available: <http://www.sciencedirect.com/science/article/pii/S0165242709003365> (visited on 03/17/2020).
- [3] F. Nájera, S. Sánchez-Cuerda, G. López, T. Rey-Wamba, C. Rueda, N. Vallverdú-Coll, J. Panadero, M. Palacios, J. V. López-Bao, and J. Jimenez, “Lynx eats cat: Disease risk assessment during an iberian lynx intraguild predation,” *European Journal of Wildlife Research*, vol. 65, Jun. 1, 2019. DOI: 10.1007/s10344-019-1275-5.
- [4] R. Upadhyay, P. Roy, C. Venkataraman, and A. Madzvamuse, “Wave of chaos in a spatial eco-epidemiological system: Generating realistic patterns of patchiness in rabbit-lynx dynamics,” *Mathematical Biosciences*, vol. 281, Sep. 2016. DOI: 10.1016/j.mbs.2016.08.014.
- [5] R. D. Holt and G. R. Huxel, “Alternative prey and the dynamics of intraguild predation: Theoretical perspectives,” *Ecology*, vol. 88, no. 11, pp. 2706–2712, Nov. 2007, ISSN: 0012-9658. DOI: 10.1890/06-1525.1.
- [6] C. Soto Navarro and F. Palomares, “Surprising low abundance of european wildcats in a mediterranean protected area of southwestern spain,” *Mammalia*, Aug. 15, 2013. DOI: 10.1515/mammalia-2013-0054.
- [7] J.-P. Soucy, “Cats, rabbits, birds, and viruses, oh my! modelling the conservative implications of a complex virus release in a predator-prey system,” 2017. DOI: 10.1137/16S015553.
- [8] E. Fromont, M. Artois, M. Langlais, F. Courchamp, and D. Pontier, “Modelling the feline leukemia virus (FeLV) in natural populations of cats (*felis catus*),” *Theoretical Population Biology*, vol. 52, no. 1, pp. 60–70, Aug. 1, 1997, ISSN: 0040-5809. DOI: 10.1006/tpbi.1997.1320. [Online]. Available: <http://www.sciencedirect.com/science/article/pii/S0040580997913204> (visited on 03/15/2020).
- [9] G. López, M. López-Parra, L. Fernández, C. Martínez-Granados, F. Martínez, M. L. Meli, J. M. Gil-Sánchez, N. Viqueira, M. A. Díaz-Portero, R. Cadenas, H. Lutz, A. Vargas, and M. A. Simón, “Management measures to control a feline leukemia virus outbreak in the endangered iberian lynx,” *Animal Conservation*, vol. 12, no. 3, pp. 173–182, 2009, eprint: <https://zslpublications.onlinelibrary.wiley.com/doi/pdf/10.1111/j.1469-1795.2009.00241.x>, ISSN: 1469-1795. DOI: 10.1111/j.1469-1795.2009.00241.x. [On-

line]. Available: <https://zslpublications.onlinelibrary.wiley.com/doi/abs/10.1111/j.1469-1795.2009.00241.x> (visited on 04/10/2020).

- [10] J. Mattisson, P. Segerström, J. Persson, M. Aronsson, and G. R. Rauset, “Lethal male–male interactions in eurasian lynx,” *Mammalian Biology*, vol. 78, no. 4, pp. 304–308, 2013. DOI: 10.1016/j.mambio.2012.11.006. [Online]. Available: https://journals-scholarsportal-info.myaccess.library.utoronto.ca/details/16165047/v78i0004/304_lmiiel.xml (visited on 04/10/2020).