



Compartmental epidemiological model (sir) to simulate the spread of sarcoptic mange in wild Peruvian vicuñas

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Abstract

Sarcoptic mange is a parasitic disease affecting various wildlife populations, including the vicuña (**Vicugna vicugna**), a species native to the Peruvian Andes that holds high ecological and economic value. Despite its importance, few predictive tools exist to anticipate the spread of this disease. The objective of this study was to design a compartmental epidemiological model (SIR) to simulate the spread of sarcoptic mange in wild Peruvian vicuñas. Methodologically, a quantitative approach was adopted, and the research is of a projective nature. Among the results, it was found that the model enabled the estimation of the disease's progression and the identification of epidemic peaks. It is concluded that the developed tool is useful for planning control and conservation measures for vicuñas.

Keywords: Model, Epidemiological, Simulation, Vicuña, Mange

Introduction

Historically, the vicuña (*Vicugna vicugna*) has been a distinctive economic and cultural resource of the high Andean regions of Peru, whose extreme spatial and climatic conditions result in limited job opportunities. Vicuñas are wild South American camelids representative of the Andes and are distinguished by producing the world's finest fiber, with a diameter ranging from 12 to 14 microns (Pacheco et al., 2019). This natural resource is highly valued in the region because it constitutes a fundamental pillar for the development of the communities that manage them under wild and semi-captive systems. To commercialize the fiber, according to (Quispe et al., 2022), the chaku must first be carried out. This process involves controlled capture and shearing to ensure the sustainable use of the fiber and the conservation of populations in Peru.

According to the Center for Research on Economics and Global Business – ADEX (2025), in 2024, Peruvian exports of vicuña fiber and its derivatives reached US\$ 5.2 million, registering a growth of 35.2% compared to 2023. This evidences the growing economic importance of this resource in international trade. This makes it an important economic activity for the population of Peru,

especially (Gomez et al., 2024) for those living in mountainous areas at altitudes above 3000 meters above sea level, regions typical of the Vicuñas. According to (Young & León, 2007), the high Andean ecosystems of Peru are characterized by low temperatures, high solar radiation, strong daily thermal variations, and seasonal rainfall, in addition to poorly developed soils with low organic matter content, adapted mainly to natural puna grasslands.

It is worth noting that in these mountainous areas, vicuñas face various threats to their conservation, including mange as a disease (Camero & Serrano, 2023), which has displaced poaching. Sarcoptic mange, the ectoparasite that causes severe skin lesions, compromises the animal's welfare. Furthermore, as explained by (St Clair et al., 2024), mange infestation causes intense pruritus, alopecia, skin thickening, crust formation, and loss of body condition, potentially leading to death in severe cases. As a result, fiber production is affected, since hair loss, crust formation, and the deterioration of the animal's body condition reduce the commercial value of the fiber, threatening the economic income of high Andean communities.

That is, this disease not only represents a health problem for vicuña populations but also affects the

economy of the local population. Regarding the spread of mange in vicuña populations, according to (Ferreira et al., 2022), it can be explained by multiple factors, including high population density, the gregarious behavior of camelids that facilitates direct contact between individuals, and contact with infected domestic camelids. This is because there are both free-ranging and captive vicuñas; therefore, if some of these populations intermingle and are infected, they transmit the disease from one population to another. From another perspective (Pence & Ueckermann, 2002), the prevalence of sarcoptic mange in wild camelids can vary between populations, depending on environmental factors, population density, and habitat conditions, suggesting that local ecological characteristics may limit or favor the transmission of the parasite. Within this perspective, the following study aims to design a compartmental epidemiological model to simulate the spread of sarcoptic mange in Peruvian wild vicuñas.

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Mange was specifically selected for this study as the cause of disease in vicuñas because it affects the skin of the herds, causing economic losses in fiber production and the population decline of vicuñas

associated with the spread of mange. Defined by (Ferreira et al., 2022), it is a highly contagious parasitic disease that invades the superficial layer of the host's skin, producing inflammation, intense pruritus, and progressive skin lesions. According to (Acebes et al., 2022), the transmission of mange in vicuña populations can occur both through direct contact between individuals and through indirect mechanisms associated with the social behavior of the species, particularly communal bathing areas or wallowing pits.

This transmission can also be increased by activities that concentrate animals, as explained by (Beltran et al., 2025): management activities involving the temporary concentration of vicuñas, such as the chaku or capture for shearing, can increase the risk of infectious disease transmission, as close contact between individuals facilitates the spread of pathogens. This activity heightens the risk of contagion for the wild population because, when captured for shearing, they may come into contact with untreated domestic vicuñas. Upon release, these individuals return to their free-ranging populations and infect healthy animals. According to (Vilá et al., 2022), this disease has been recorded in vicuña populations throughout South America, including Peru, Bolivia, Argentina, and Chile. Reported prevalence in different studies varies, ranging from less than 1% to 60% in some populations.

In this context, given the limited availability of models studying the spread of mange in vicuñas, this study aims to design a mathematical model using simulated data to demonstrate how population density in semi-captivity accelerates the contagion curve compared to those in the wild. Now, according to (Greenhalgh & Rozins, 2021, p. 1073) "for decades, mathematical models of disease transmission have provided researchers and public health officials with critical insights into the progression, control, and prevention of disease spread. Of these models, one of the most fundamental is the SIR differential equation model."

Compartmental epidemiological models (SIR) describe the spread of infectious diseases by dividing the population into different groups representing epidemiological states, such as susceptible, infected, and recovered. They model the transitions between

these groups using differential equations that represent the disease transmission processes (Brauer, 2008). Therefore, based on this mathematical model, it is pertinent to ask: What will be the characteristics of the compartmental epidemiological model designed to simulate the spread of sarcoptic mange in Peruvian wild vicuñas? This study aims to propose a tool that enables government entities and communities to make timely decisions to halt the spread of the disease through early intervention, reducing contagion via treatments and thus preventing the infection from reaching the entire vicuña population. This approach is recommended by (Zaravia et al., 2025), who state that health surveillance in animal populations is essential for early disease detection, monitoring its spread, and supporting the implementation of control measures to protect animal health and livestock production.

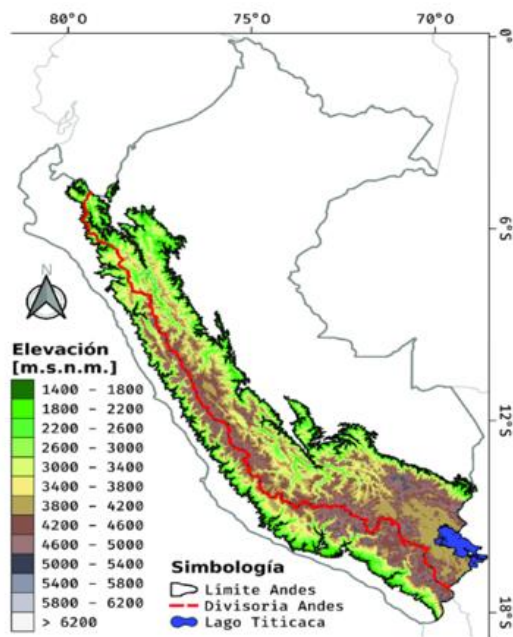


Figure 1. Altitudinal map of the Peruvian Andes

Source: The study area corresponds to the Peruvian Andean region, between 1500 and 4000 meters above sea level (Fig. 1). The predominant vegetation cover is grasslands (from 2500 to over 4800 meters above sea level), which are commonly used for grazing. Map extracted from Characterization of vegetation in the andes during the 2017 coastal el niño, by (Zubieta et al., 2017).

Methods

This study has a quantitative approach with a type of projective research defined by (Hurtado, 2000) as research that consists of developing a proposal, plan, program, or model as a solution to a problem or need, whether for a social group, institution, or geographic region, in a particular area of knowledge. Regarding the research design, it is documentary and non-experimental. The following phases were established for the algorithm design:

Library import phase to be executed in python

The model algorithm was designed with the Python programming language and the following libraries were used: Num Py (Harris, 2020) is the fundamental package for scientific computing in Python. It is a library that provides a multidimensional array object, various derived objects (such as masked arrays and matrices), and an assortment of routines for fast operations on arrays, including mathematical. Sci Py (Virtanen et al., 2020) provides algorithms for optimization, integration, interpolation, eigenvalue problems, algebraic equations, differential equations, statistics and many other classes of problems. And Matplotlib (Hunter, 2007) is a Python library specialized in creating two-dimensional graphs.

Model (SIR) definition phase

```
def modelo_sarna (y, t, beta, gamma (Abelló et al., 2020):
```

```
S, I, R = y
```

```
N = S(t) + I(t) + R(t)
```

This function defines the mathematical model.

Variables:

S = number of susceptible vicuñas

I = number of infected vicuñas

R = number of recovered vicuñas

N = total population

The vector y contains the three variables [S, I, R].

Model differential equations phase

$$D S dt = -\beta * S * I / N$$

$$D I dt = \beta * S * I / N - \gamma * I$$

$$D R dt = \gamma * I$$

These are the differential equations of the SIR model (Tolani, 2022):

Susceptibles

$$dS(t) = -\beta \frac{S(t) I(t)}{N}$$

dt

N

Interpretation

When susceptible individuals come into contact with infected individuals, some become infected; consequently, S decreases (García, 2014).

Infected

$$\frac{dI(t)}{dt} = -\beta \frac{S(t)I(t)}{N} - \gamma(I(t))$$

There are two processes (García, 2014).

a) New infections increase I

$$\beta \frac{S(t)I(t)}{N}$$

b) Recovery or removal reduces I

$$\frac{dR(t)}{dt} = \gamma(I(t))$$

Finally, the function returns [d Sdt, d Idt, dRdt].

Phase: Initial conditions

The initial state of the population is defined: total population = 1,000 vicuñas; initial infected = 10; initial recovered = 0; initial susceptible = 990.

Mathematically: $N = S(t) + I(t) + R(t)$.

Phase: s=Selection of epidemiological parameters

Transmission rate: wild = 0.25, captive = 0.45; recovery rate: 0.1; the average duration of infection is $1/\gamma = 10$ days.

Phase: simulation time-from 0 to 150 days, with 1,000 calculation points.

Phase: Solving differential equations

The odeint function is provided by the SciPy library and is required to solve the differential equations. Regarding the sample, wild and semi-captive vicuñas were selected for the simulation.

Results

Python algorithm to simulate the spread of mange in wild and semi-captive vicuñas.

```
import numpy as np
from scipy.integrate import odeint
import matplotlib.pyplot as plt
# SIR MODEL
```

```
def modelo_sarna (y, t, beta, gamma):
    S, I, R = y
    N = S + I + R
    D Sdt = -beta * S * I / N
    d Idt = beta * S * I / N - gamma * I
    d Rdt = gamma * I
    return [d Sdt, d Idt, d Rdt]
# INITIAL CONDITIONS
N = 1000
I0 = 10
R0 = 0
S0 = N - I0 - R0
y0 = [S0, I0, R0]
# PARAMETERS
beta wild = 0.25
beta captive = 0.45
gamma = 0.1
# TIME
t = np.linspace (0,150,1000)
# SIMULATION
res_wild = odeint (modelo_sarna, y0, t, args= (beta
wild, gamma))
res_captive = odeint (modelo_sarna, y0, t, args= (beta
captive, gamma))
# PLOTS
plt.figure (fig size= (12,6))
# Wild population
plt.subplot (1,2,1)
plt.plot (t, res_wild [:0], label="Susceptible")
plt.plot (t, res_wild [:1], label="Infected")
plt.plot (t, res_wild [:2], label="Recovered")
plt.title ("Disease Spread in Wild Population")
plt.xlabel ("Time (days)")
plt.ylabel ("Number of Vicuñas")
plt.legend ()
plt.grid (True)
# Semi-captive population
plt.subplot (1,2,2)
plt.plot (t, res_captive [:0], label="Susceptible")
plt.plot (t, res_captive [:1], label="Infected")
plt.plot (t, res_captive [:2], label="Recovered")
plt.title ("Disease Spread in Semi-Captive
Population")
plt.xlabel ("Time (days)")
plt.ylabel ("Number of Vicuñas")
plt.legend ()
plt.grid(True)
plt.tight layout ()
# SAVE FIGURE (300 dpi)
plt.savefig ("sarcoptic_mange_simulation.jpg",
```

dpi=300, b box_inches="tight")

plt. show ()

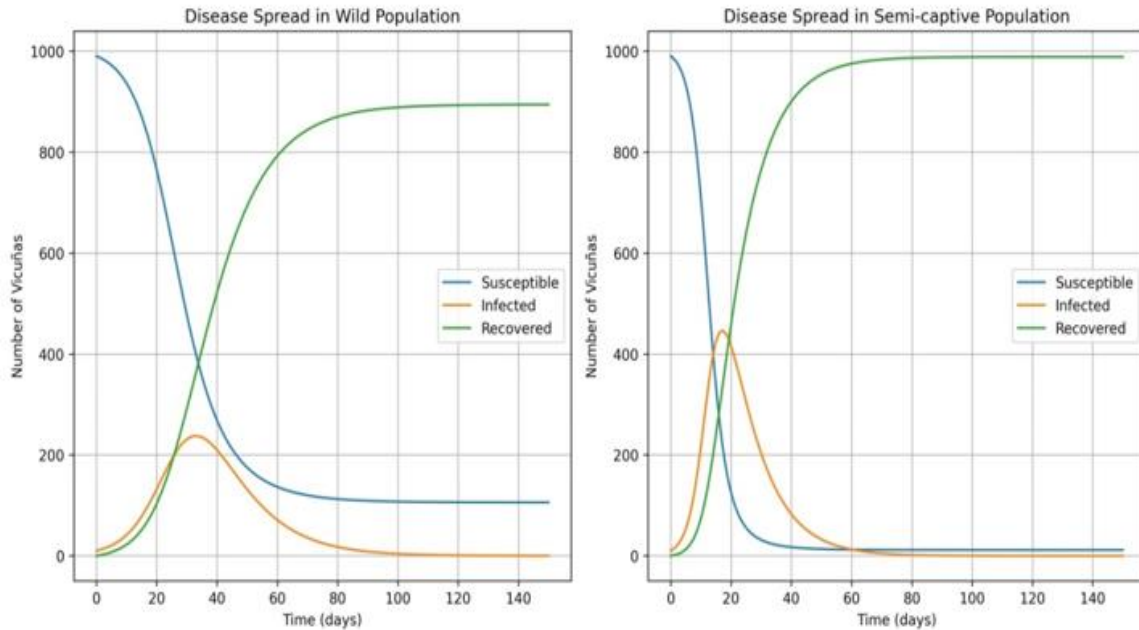


Figure 2. Compartmental epidemiological model to simulate the spread of sarcoptic mange in vicuñas

Source: Graphs generated by the Python algorithm for the wild population and the semi-captive vicuña population

The blue line represents the susceptible vicuñas, the red line represents the infected, and the green line represents the recovered. The model allows analysis of how the epidemic changes according to the contact rate, where $\beta_{\text{semi-captive}} > \beta_{\text{wild}}$, meaning the basic reproductive number is higher ($R_0 = \beta / \gamma$).

In both graphs, the horizontal axis represents time in days, and the vertical axis represents the number of individuals.

Blue Curve (Susceptible): Represents healthy vicuñas that can contract the disease. At the beginning, almost the entire population is in this category. As the epidemic progresses, the number falls because individuals become infected.

Orange Curve (Infected): Shows how many animals are sick and can transmit the mite at any given time. The peak of this curve indicates the moment of greatest epidemiological pressure.

Green Curve (Recovered): Represents individuals who have overcome the disease (or in mathematical models, those who cease to be infectious due to treatment or death). You will notice that this curve

always rises until it stabilizes when the outbreak ends.

Initial phase (day 0-20): It begins with a completely susceptible population of 1000 individuals. The introduction of a small number of infected individuals (2 on day 10, 20 on day 20) starts the spread. The exponential growth phase of infected individuals is evident between days 20 and 40.

Epidemic peak (around day 40-50): The infected peak is observed to be reached between days 40 and 50, with a maximum of 250 infected individuals on day 40. This figure is slightly higher than the visual estimate from the graph (230-250) and places the peak more precisely on day 40.

Decline phase (day 50-100): After the peak, the number of infected individuals decreases rapidly as individuals recover and the susceptible group is depleted. By day 100, the outbreak is practically controlled, with only 60 infected and 840 recovered.

Final state (day 100): at the end of the simulated period, the model predicts that 100 susceptible individuals never became infected. This is a key finding: in a wild population with low density and

limited contact, the disease fails to reach the entire population, leaving a group of animals that, being susceptible, could fuel a future outbreak if the pathogen is reintroduced.

Discussion

The SIR compartmental model has proven to be a useful tool for simulating the spread of mange in vicuña populations, allowing comparison of the impact of human management on disease dynamics.

Influence of management (Wild vs. Semi-captivity)

The comparison between both forms of management shows that semi-captivity management significantly increases the risk of epidemic outbreaks of greater magnitude and speed.

Contact rate (β) and basic reproductive number (R_0): The fundamental difference lies in the contact rate. In wild conditions (β_{wild}), vicuñas are distributed over extensive areas, which reduces interactions and therefore the probability of mange transmission. In contrast, in semi-captivity ($\beta_{\text{semi-captive}}$), confinement in enclosures and higher population density dramatically increase interactions. This results in a higher R_0 .

Implication: In both cases, it is confirmed that mange is a disease with epidemic potential in vicuñas. However, the higher R_0 in semi-captivity explains why the infected peak is more than double (450 vs 250) and is reached in almost half the time (day 18 vs day 40). The disease not only spreads more, but does so in a much more explosive manner.

Herd immunity threshold: In the wild population, the epidemic stops before infecting everyone, leaving 10% of the population susceptible (100/1000). This suggests that, in this scenario, an equilibrium was reached where the density of susceptibles fell below the threshold necessary to sustain transmission.

Implication: In wild populations, the spatial structure and lower density themselves act as a natural barrier that limits the outbreak size.

Epidemiological pressure and conservation: The massive infected peak in semi-captivity (450

individuals) represents great pressure on the ecosystem and the population. Such a high number of simultaneously sick animals could saturate the habitat's carrying capacity, increase competition for resources (food, water), and, in real cases, lead to higher mortality due to malnutrition or secondary infections something this SIR model does not capture but which is crucial for conservation.

Model limitations

Closed population: The model assumes no births, natural deaths (other than from the disease), or migration. In reality, wild vicuñas move, and there are population dynamics that could alter the course of the epidemic.

Absence of mortality from mange: The SIR model does not include death from the disease. In severe cases of mange, mortality can be significant. A future extension of the model (an SIR model with death) would provide a more realistic picture of the population impact.

Conclusion

The results obtained have direct implications for the management and conservation of vicuñas in Peru:

Surveillance in semi-captivity: Populations in enclosures or under intensive management (e.g., for shearing) require much stricter epidemiological surveillance. High density makes them hotspots highly vulnerable to explosive mange outbreaks.

Enclosure design and management: It is necessary to design management strategies that minimize contact density. This could include larger enclosures, pasture rotation, or the implementation of quarantine and observation periods before introducing animals to a captive group.

Control in wild populations: Although spread is slower in wild populations, the persistence of a susceptible group indicates that the pathogen could remain endemic at low levels or be easily reintroduced, so passive monitoring remains necessary. In conclusion, the model confirms that the transition from a wild state to a semi-captive one, common in many sustainable use initiatives, can dramatically increase the transmission dynamics of

mange. Conservation strategies must incorporate this epidemiological risk to ensure the long-term health and sustainability of vicuña populations.

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