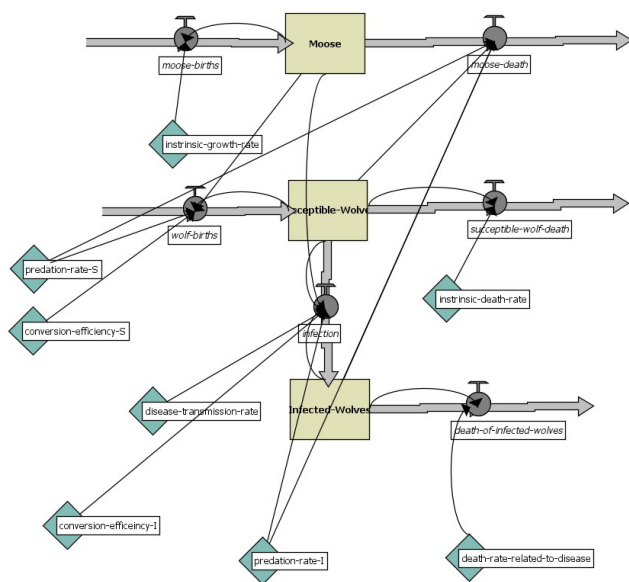


<sup>†</sup>These authors contributed equally to this work

This study investigates the impact of disease on the predator-prey dynamics between wolves (*Canis lupus*) and moose (*Alces alces*) on Isle Royale, utilizing Agent-Based Modeling (ABM) to simulate disease transmission scenarios. The introduction of canine parvovirus (CPV) was found to significantly reduce wolf populations, leading to decreased predation pressure on moose and a subsequent increase in their numbers. These findings enhance our understanding of how disease outbreaks can disrupt ecological balance, particularly in isolated ecosystems. While the research provides valuable insights into the long-term consequences of disease on predator-prey relationships, limitations such as reliance on historical data and simplified ecological interactions must be acknowledged. Overall, this study underscores the importance of integrating disease dynamics into ecological models and highlights the need for further research to inform conservation strategies in similar ecosystems.

1-4



**Figure 2.** Code diagram illustrating the interactions between moose and wolves, with focus on birth rates, predation rates, and disease dynamics.

- **Processes:** Moose move randomly across the environment, reproduce based on their intrinsic growth rate, and die due to natural causes or predation by wolves. The code diagram shows the flow from “moose-births” to the “Moose” population and the outflow to “moose-death,” indicating the balance between birth and death rates.

#### Wolves:

- **Attributes:** Wolves are divided into two categories: susceptible (healthy) and infected (diseased).
- **Processes:**
  - **Birth:** Wolf reproduction is shown in the diagram as “wolf-births,” contributing to the “Susceptible-Wolves” population.
  - **Predation:** Wolves hunt moose, with the “predation-rate-S” affecting susceptible wolves and “predation-rate-I” affecting infected wolves. These rates determine the flow of energy to the wolves and the reduction in the moose population.
  - **Infection:** Susceptible wolves can become infected through a disease transmission process, represented by the “infection” flow between “Susceptible-Wolves” and “Infected-Wolves.”
  - **Mortality:** Both susceptible and infected wolves have distinct death rates. The diagram indicates “susceptible-wolf-death” and “death-of-infected-wolves,” with an additional death rate specific to the disease (“death-rate-related-to-disease”).

#### 2.2.2. Initialization

**Population Initialization:** The initial populations for both wolves and moose are set based on historical data, for example, 50 wolves and 800 moose. The agents are placed randomly within the simulated environment.

**Parameter Initialization:** Global parameters such as predation rates, birth rates, and disease transmission rates are initialized based on ecological studies. These parameters govern the flow rates and transitions shown in the diagram.

#### 2.2.3. Process Implementation

**Movement:** Both wolves and moose move randomly across the environment, searching for food or prey.

**Reproduction:** Both species reproduce based on their intrinsic rates, which are influenced by age and energy levels. The diagram shows “intrinsic-growth-rate” and “moose-births” for moose, and “wolf-births” for wolves.

**Predation:** Wolves hunt moose according to their health status, with successful hunts increasing the wolves’ energy levels. Predation rates differ for susceptible and infected wolves, as shown in the “predation-rate-S” and “predation-rate-I” in the diagram.

**Disease Transmission:** The disease spreads among wolves through contact, reducing their energy levels and lifespan. The “disease-transmission-rate” in the diagram connects “Susceptible-Wolves” to “Infected-Wolves,” indicating the flow from healthy to diseased individuals.

### 2.3. Visualization Techniques and Sensitivity Analysis

#### 2.3.1. Visualization

**Population Dynamics:** The model outputs time series graphs displaying the populations of wolves and moose over time, with separate lines for susceptible and infected wolves. This allows visualization of how disease impacts wolf population and predation rates.

#### 2.3.2. Sensitivity Analysis

**Parameter Variation:** A sensitivity analysis is conducted by varying key parameters like predation rates, birth rates, and disease transmission rates. The results are analyzed to determine the robustness of the model outcomes.

**Outcome Analysis:** Different scenarios are tested to observe how changes in disease transmission or predation rates affect overall population dynamics, as depicted in the flows and interactions in the diagram.

### 2.4. Model Assumptions

The model focuses exclusively on the interactions between moose and wolves, specifically examining the dynamics between these two species. It simplifies the ecological context by assuming that the population of balsam fir, the primary food source for moose, remains constant throughout the study period. This assumption allows the model to concentrate on the predator-prey dynamics without the added complexity of fluctuating food resources. Additionally, the model presumes that the effects of climate change are negligible, thereby excluding any potential impact on the habitat or the populations of moose and wolves. These assumptions streamline the model, enabling a clearer analysis of the direct interactions between the predator (wolves) and prey (moose) populations.

## 3. Results and Discussion

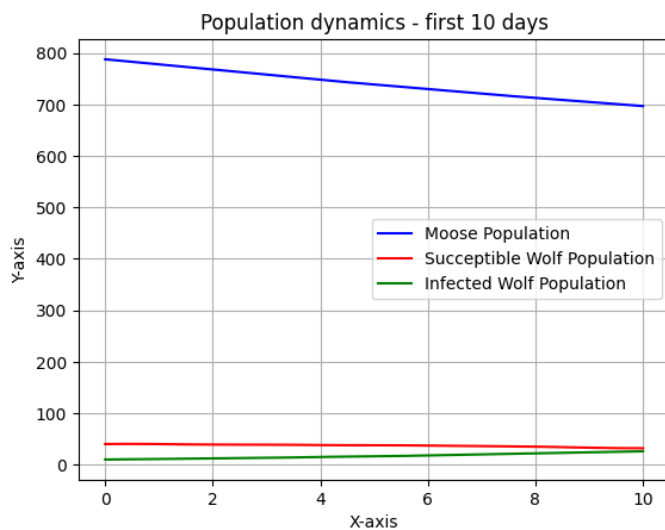
In this section, we present the results derived from our comprehensive simulation models, which were meticulously constructed based on empirical studies of predator-prey dynamics and disease ecology. Our approach began with the careful collection and analysis of relevant empirical data to establish accurate initial conditions and parameter values for our models. With these data, we simulated the population dynamics of wolves and moose over a specified period, focusing on tracking changes in the numbers of susceptible and infected individuals within each species.

Our simulation efforts aimed to capture the complexities of real-world ecosystems, specifically examining how diseases such as Canine Parvovirus influence predator-prey interactions and overall population stability. To provide a thorough understanding of these dynamics, we implemented a range of sensitivity analyses. These analyses involved systematically varying key parameters, including disease transmission rates and the mortality rate due to disease, to observe how these changes impact the model’s outcomes. By exploring different scenarios, we assessed the robustness of our model and its sensitivity to variations in disease dynamics.

It is important to note that due to the inherent limitations in the available data, our predictions cannot be exact. The lack of comprehensive data on certain aspects of the disease dynamics and ecological interactions means that while our model provides valuable insights and approximate predictions, it may not capture all nuances of real-world behavior. Nonetheless, the results offer a reasonable approximation and contribute meaningfully to our understanding of disease impacts on predator-prey systems. This detailed examination enhances our grasp of the specific case study of wolves and moose and underscores the importance of integrating disease dynamics into predator-prey models, despite the limitations of data constraints.

Parameter	Value
Intrinsic growth rate	0.048
Predation rate (Susceptible)	0.12
Conversion efficiency (Susceptible)	0.09
Disease transmission rate	0.99
Intrinsic death rate	0.45
Death rate related to disease	0.89
Predation rate (Infected)	0.000048
Conversion efficiency (Infected)	0.045
Infected Wolves	10
Moose	788
Susceptible Wolves	40

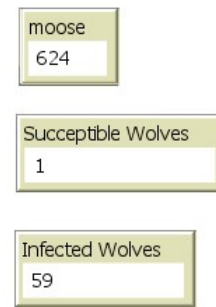
**Table 1.** Initial Model parameters and their values.



**Figure 3.** Simulation of first 10 days

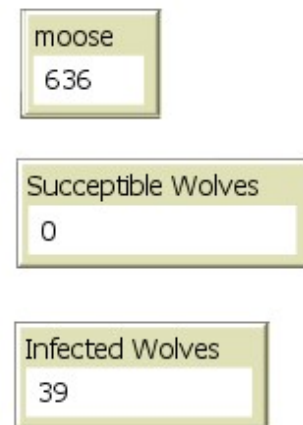
The graph illustrates the population dynamics over the first 10 days for three groups: moose, susceptible wolves, and infected wolves. The moose population, represented by a blue line, shows a clear decreasing trend, starting from around 800 and gradually declining throughout the period. In contrast, the susceptible wolf population, shown by the red line, remains stable, hovering around 50 without significant change. Similarly, the infected wolf population, depicted by the green line, stays nearly flat near zero, indicating very little variation or a consistently low number of infected wolves over the same time frame.

Figure 4 indicates the current population counts for moose and wolves, showing that the moose population has decreased to 624, reflecting a decline from an earlier value (likely 800 as previously noted). Meanwhile, the population of susceptible wolves is critically low, with only one individual remaining susceptible to infection. In contrast, there are 59 infected wolves, suggesting that the infection has spread widely among the wolf population. This disparity high-



**Figure 4.** Population after 40 days

lights the ongoing decline in the moose population and the significant impact of infection within the wolf population.



**Figure 5.** Population after 200 days

After 200 days (Figure 5), the population dynamics reveal that the moose population has increased slightly to 636. The number of susceptible wolves has dropped to zero, indicating that either all wolves have succumbed to the infection or the susceptible wolves have died out. The number of infected wolves has also decreased to 39, reflecting a significant decline from the 59 infected wolves observed at the 40-day mark. This suggests that the disease has caused deaths among the wolf population. As a result of the declining wolf population, the moose population appears to be growing, likely due to reduced predation pressure. The scenario reflects the detrimental impact of disease on the wolves, potentially leading to long-term ecological shifts in predator-prey dynamics.

The situation can be considered a disease outbreak within the wolf population. Initially, after 40 days, a significant portion of the wolves became infected, with 59 infected and only one susceptible wolf remaining. By 200 days, all susceptible wolves have either died or become infected, leaving the population with zero susceptible wolves and 39 infected individuals. This widespread and severe infection has caused a notable decline in the wolf population, indicating that the disease has spread rapidly and caused substantial mortality. As a result, the moose population has increased, likely due to reduced predation pressure, illustrating the outbreak's broader ecological consequences and its significant impact on predator-prey dynamics.

The sensitivity analysis table reveals how varying the disease transmission rates in a wolf population influences both the wolves and their prey, the moose. As the transmission rate decreases, a larger portion of the wolf population remains healthy, leading to more effective predation and a significant reduction in the moose population. Conversely, higher transmission rates result in a predominantly infected wolf population, which appears to reduce their predation efficiency,

Disease Transmission Rate	Susceptible Wolves	Infected Wolves	Moose
0.5	0	62	475
0.3	3	74	315
0.1	47	52	84

**Table 2.** Population dynamics under different disease transmission rates.

allowing the moose population to grow. This suggests that the disease transmission rate plays a critical role in the predator-prey dynamics, with lower rates maintaining a balanced ecosystem, while higher rates could lead to an imbalance, favoring the prey population due to the diminished hunting capability of the infected predators.

#### 4. Conclusion

The study explored the dynamics of disease impact on the predator-prey relationship between wolves and moose on Isle Royale, using Agent-Based Modeling (ABM) to simulate various disease transmission scenarios. The main findings indicate that the introduction of canine parvovirus (CPV) significantly affects wolf populations, leading to a decrease in predation pressure on moose and consequently an increase in their numbers.

These results are crucial for understanding the original questions posed in the introduction regarding the long-term consequences of disease outbreaks on predator-prey dynamics. The findings enhance our comprehension of how diseases can alter not only predator behavior and health but also the overall stability of ecosystems, particularly in isolated environments like Isle Royale. By validating empirical data and demonstrating the cascading effects of disease on population dynamics, this research provides valuable insights for conservation efforts aimed at maintaining ecological balance.

However, the study has limitations that must be acknowledged. The reliance on historical data for initial population parameters may introduce uncertainties, as ecological dynamics can vary significantly over time. Additionally, the model simplifies complex interactions by assuming constant food resources and negligible climate impacts, which may not accurately reflect real-world conditions. The inherent challenges in capturing the full range of ecological interactions and disease dynamics also pose potential sources of error, limiting the generalizability of the findings.

In conclusion, this study underscores the significant role that disease plays in shaping predator-prey relationships and highlights the need for further research in this area. Future studies should aim to incorporate more comprehensive data on ecological interactions and consider the impacts of environmental changes, such as climate variability, on disease dynamics. By expanding the scope of research to include these factors, we can better understand the complexities of predator-prey systems and develop more effective conservation strategies.

#### 5. References

- [1] [The Population Biology of Isle Royale Wolves and Moose: An Overview](#)
- [2] Martcheva, M. (2015). An introduction to mathematical epidemiology (Vol. 61, pp. 9-31). New York: Springer.
- [3] We have utilized ChatGPT (OpenAI, 2024) as a tool to assist with grammar and writing refinements.

#### 6. Member Contributions

1. Tharuka Anthony - Methodology section
  2. Danula perera - Results & Discussion section
  3. Nimna Suharshani - Introduction Section, References Section
  4. Sandali Hansika - Introduction Section, Conclusion Section
- All members are equally contributed to create the NetLogo code.