ONTARIO TECH UNIVERSITY
FACULTY OF SCIENCE, COMPUTER SCIENCE

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Simulation and Modelling Course Project: Food Web Simulation

by

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Abstract:

Ecosystem simulation designed around food web interactions representing biological interactions in a local ecosystem.

Repository:

https://github.com/JamesMeta/Simulation-of-Ecosystem-Food-Chains

Run Simulation.py while inside the parent directory using a python (3.5+) capable terminal.

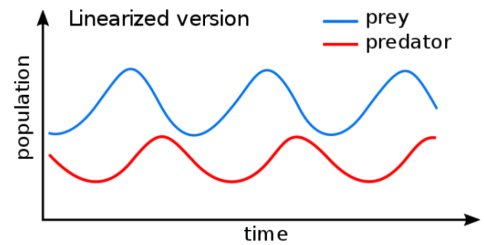
Demonstration:

https://youtu.be/1EuounfYO8k

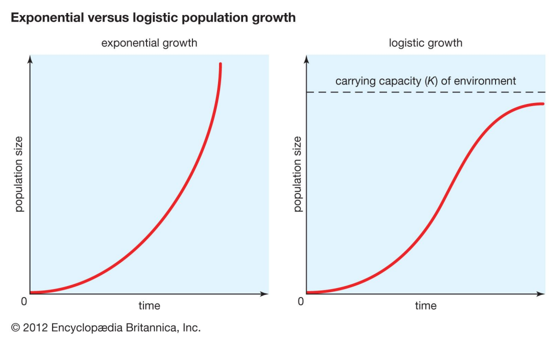
1 Introduction

The goal of the project was to simulate an ecosystem with multiple intertwined food webs, and see if said ecosystem was able to reach sustainable levels that mimic natural ecological processes. Among the considered outcomes was:

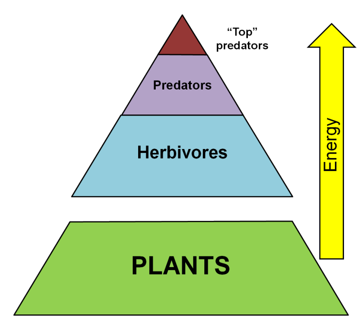
1. Population graphs of carnivores and herbivores relating to predation, primarily the resulting wave forms and how they compare to observed phase synchronizations.



2. Reproductive survival numbers that are regulated by the carrying capacity of the environment.



3. Population analysis of food chains / trophic levels. In the terms of environmental science this would be biomass distributions.



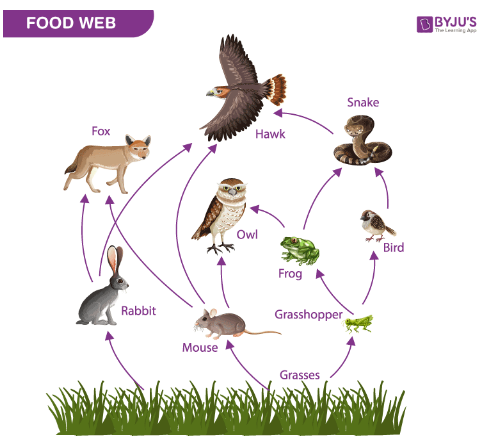
2 Inspirations and Related Work

This project was inspired by our groups appreciation of nature, and ecosystem simulation interactive media like Equilinox. The logic for the interactions of animals is based on BYJU's food web topic explanation example. Due to the nature of this simulation and our goals there was no single academic paper our report was based on, as the goal was to represent well known natural observations.

A Equilinox

"Equilinox is a relaxing nature simulation game in which you can create and nurture your own ecosystems."

B BYJU Food Web



This food web was chosen because it includes all four trophic levels, with one producer (grass), and multiple primary (rabbit, mouse, grasshopper), secondary (small bird, frog, snake), and tertiary (hawk, fox, owl) consumers.

3 Methodology

Implementation of this simulation, on a logic level relies on the decision trees shown in our repository's design folder. The higher level functioning of interactions in the ecosystem are sorted into organisms types and each organism types logic. The design class for organism types sorts animals (previously included grass, the term "organism" is a hold over of an earlier build) into carnivores or herbivores. The logic of each of these two animal and one plant types is outlined in the AI decision trees provided in the GitHub repository's assets folder. The logic animals follow are yes/no diagrams that progress in order of importance (sleep, water, food, reproduction) and assert logical processes that animals have when they realize their values of these are low, such that if an organism is thirsty, it will head towards where it knows water exists and drink from it, this cascades in order of importance to an organism.

For example if food is a more important resource than water at a given time, however sleep will always be prioritized when an animal is too tired. Beyond the natural order of resource importance, each animal type has thresholds for each of these statistics. Thresholds work such that animals will only consider consuming a resource once they have passed a minimum threshold for that statistic and will start to prioritize that action the higher its current value is, this continues until it reachers the maximum value of that statistic, at which point the animal dies. For example, a fox who is only slightly thirsty will still prioritized extreme starvation despite water being a more prioritized resource. It is important to note that sleep will always take priority in this threshold system however.

This project was originally intended to work with random map seeds but after getting through a rudimentary development, the idea was scrapped in favour of a constant environment. This idea would also in theory, allow us to better define the animals biological factors while still understanding the scope of the ecosystems interactions, we then used multiple sufficiently different but unchanging test ecosystems to determine if simulation errors were systemic, or organism dependant.

Our simulation used many methodologies provided in class. The progression of the ecosystem is dependent on the ordinary differential equation of time.

$$\frac{dT}{dt} = f(T) \tag{1}$$

The reasoning behind this was that our simulation is concerned with monitoring real time event systems of an environment rather than using them to make decisions to progress the simulation.

The second important differential equation set for our simulation are the Lotka-Volterra-predator-prey models equations.

$$\frac{dx}{dt} = \alpha x - \beta xy, \frac{dy}{dt} = \delta xy - \gamma y, \tag{2}$$

These equations represent the demographic changes of the predation relationship outlined in 1.1. Because this equation relies on knowledge of the environments carrying capacity, which in our case was an unknown variable. The methodolgy behind these equations was used to identify and recreate the biological process of predation.

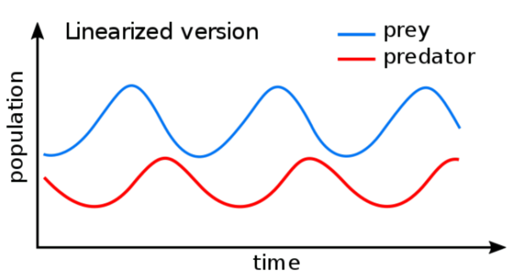
Due to the nature of our simulation, each animal knows the location of the resource areas it can consume from at birth. While this is covered later in our scope and limitations section, we mitigated this issue by having animals wander using random walks when there was no demand for them to consume a resource. This system uses the threshold values mentioned earlier to accommodate and represent natural animal movements in code.

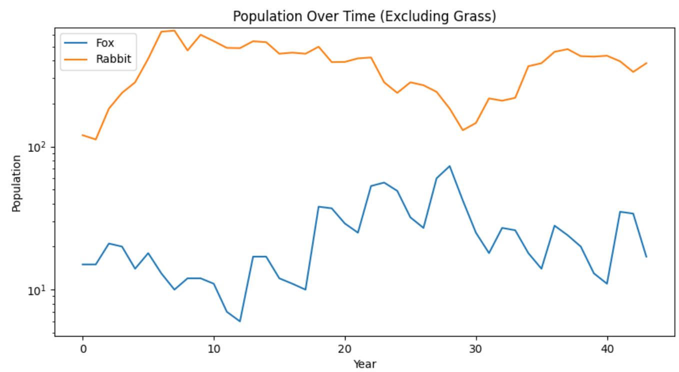
The last important differential equation we used was position which is got by the velocity of an animal. This is used when animals go to hunt or wander and follows form below.

$$\frac{dx}{dt} = v(t) \tag{3}$$

4 Results

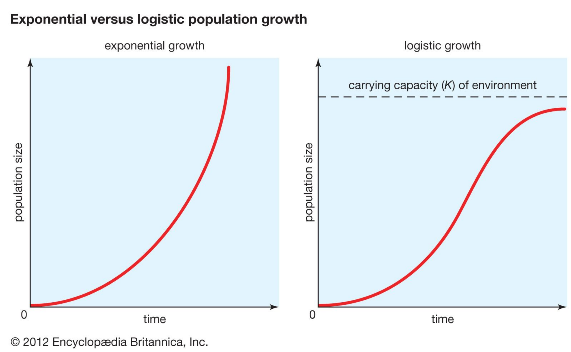
In this reports introduction we outline three ecosystem processes we wanted to achieve with our simulation. First among these was predation graphs. As shown in our test that contained just rabbits and foxes, the relationship between the two species populations was directly proportional, where a gain in one coincided with a loss in the other.

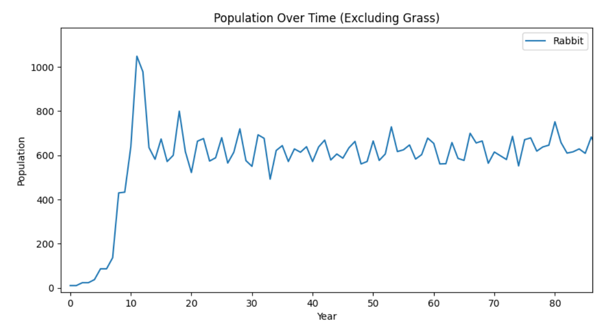




Testing individual food chains within the food web allowed us to verify if the ecological relationships of our simulation were working as intended, and gave us the level of confidence for tests of an ecosystems entire food web.

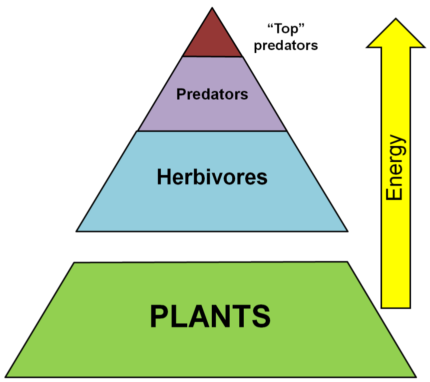
The second test of validity for our simulation was carrying capacity. Ecosystems in nature are limited to the amount of life they can support for a given organism or larger still, their group. Because most ecosystems are inherently greedy environments, rampant consumption of available resources should lead to an initial burst in population, followed by a short dying out, then a stabilization once the population has adjusted to the carrying capacity of the ecosystem.

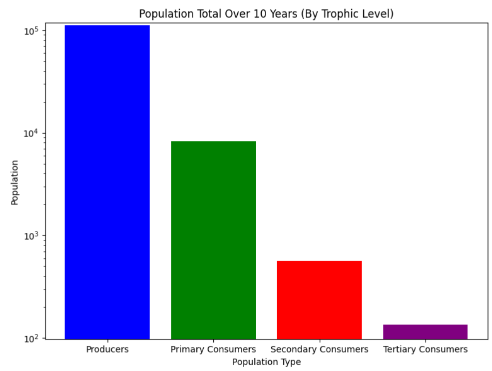




In the graph provided above, there is a clear demonstration of this phenomena in action where rabbits were spawned into an environment with only grass. This allowed them to consume all available grass and because there was no predation, the carrying capacity of the environment was limited only by the amount of grass the ecosystem produced. The importance of no predation in this example is that, we can see that a rabbit populations ideal scenario follows this biological reality, the system could detect when animals were over grazing consumable resources. Upon the introduction of the primary consumer the ecosystem reacted dramatically to reach a new total ecosystem balance, and once the ecosystem had reestablished a constant level, it can be clearly seen that the ecosystem being tested had the carrying capacity of 600 rabbits over the last 75 years of simulation time. To draw from this, implementation of ecosystem interactions mimic most natural processes of ecosystem decay.

Lastly, we wanted to focus on interactions between trophic levels, specifically matters of scale throughout the ecosystem. The difference between knowing if ecosystems could be simulated beyond basic food chains is closely related to energy flow though the simulation, commonly known as biomass distribution and organisms trophic levels in a given ecosystem.





This graph above, scaled on the y-axis in order of magnitudes represents precisely the correct flow of energy in ecosystems and proves that this simulated ecosystem functions with realistic values.

5 Scope and Limitations

The largest assumption made by our program is that all animals will know where each resource area is. This design choice drastically effected the scope of the simulation and made us prioritize small environments as we assume the animals time to become accustomed too that area would be negligible, however this introduces large problems with scalability.

By design, AI variables would always have to be monitored and updated throughout development. This resulted in most problems revealed by the simulation being fixed as they appeared. Examples of code errors included gender assertion at time of reproduction and animals being able to drink, eat, and sleep after death. Logical problems were also fixed when we realized simulations wouldn't behave like nature. For example, predator carnivores engage in cannibalism if they would otherwise die out before prey populations could support them. Running the code on our GitHub repository allows the user to view these content tests from all phases of the project.

A limitation of our program is that ecosystems can never become extinct. This was the large biological reality we couldn't successfully program within the time and scope of the project. This limitation expresses itself in code as grass being infinitely respawnable on grasslands. The natural logic behind this is such, grasslands can not move or form after world instantiation. Mimicking the real world development of ecosystems would have been unnecessary in our example as the test map size would not allow that much variety. But furthermore, implementation of this feature would be grossly out of scope and incredibly computationally expensive.

6 Conclusion

In conclusion, we feel confident in our groups deliverables of interactions between animals in a diverse ecosystem. We contribute this progress to our ability to fragment the building of the simulation into self-contained tests. Using this process, we were able to systematically design efficient food chains, and ecosystem logic surrounding trophic levels and biomass ability, and then understand how that logic interacts with its environment when there is more than a single food, drink, or rest area, or more than a single food chain.

We are happy that the goals we set out to accomplish around fundamentals of ecosystems and simulations through code.

7 References

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