Predator-Prey competition modelling

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Abstract

In nature predator-prey dynamics are cyclic, which limits both populations from growing beyond environmental constraints, thus ensuring the survival of both populations. In this paper, we aim to investigate different methods of simulating such dynamics and measuring their properties, to find out how model stability and simulation run-length are influenced. A basic Lotka-Volterra-inspired setup, along with modifications, such as introducing a limited food source for the prey, chasing and fleeing dynamics and genetic inheritance were implemented in our aims to achieve more stable cyclic collective behaviour, given the stochasticity of the problem. As means of comparison between the different setups, we introduce two new metrics - the stability score and the cycle ratio score. They quantify our findings that nature-like mechanisms, such as chasing and fleeing, achieve more stable simulations and enabling evolution of genotypes for individuals results in longer species lifetimes.

Keywords— swarm-dynamics, collective-intelligence, Lotka-Volterra models, predator-prey dynamics

1 Introduction

Collective dynamics and organisation are inspired by various phenomena in nature that occur for species like fish, birds and even mold. Without centralized control, each organism individually follows a set of communal rules from which collective behavior emerges.[1] Both the individual as well as the population benefit from this; [2] the sharing of the same goal leading to collective dynamics is beneficial for exploration, colonisation, predator avoidance, and food gathering, and therefore is very important to understand to model agents that exhibit similar behaviour.[3] This paper will examine various ways of agent-based modeling that simulate competitive behaviours observable in nature. The observations will be compared to the Lokta-Volterra Model, a mathematical way of modeling dynamic population sizes for predators and prey.[4] The Lotka-Volterra model consists of two ordinary differential equations with periodic solutions, hence the identical repeating cycles in the number of individuals for predator and prey populations:

$$\frac{dx}{dt} = \alpha x - \beta xy \text{ and } \frac{dy}{dt} = \delta xy - \gamma y$$

where x, y are the number of individuals of the prey and predator populations respectively. In this model, it is assumed that prey does not need food. Its only source of death is predation, represented by the factors αx and $-\beta xy$, respectively. The δxy term in the predator population signifies the natural growth rate, also dependent on the number of prey x. The $-\gamma y$ term represents the natural rate of decay of this population, which is proportional to the number of predators.[4]

There are two main experiments conducted, investigating the impact of different features of population dynamics in the simulation. In the first experiment, a simple implementation with just as many rules as necessary for exhibiting Lotka-Volterra-like dynamics will be compared to other simulations where intelligent movement behavior and in another case a limited food source is introduced. The second experiment will introduce the representation of certain traits of agents in the form of inheritable genes to the predator population, thereby introducing evolutionary-strategies-like gene encoding to the simulation.
Evolutionary strategies is an evolutionary algorithm, used for evolving real-valued genotypes. It uses intermediary recombination, i.e. the genotype vector of the children lie on the interpolation between the two parent genotype vectors. The mutation operator is a Gaussian perturbation.[5]
This work uses most of the concepts of evolutionary strategies and applies it to our problem, where no fitness evaluation is needed. Our methodology is explained more in depth in section 2.3.

EXPERIMENT 1:

BASE CASE. The base case models the environment and agents in a way that allows for Lokta-Volterra-like dynamics to show in the simulations. The prey is assumed to be immortal unless subject to predation and reproduces indefinitely while the predators need to consume prey to survive and reproduce asexually.
LIMITED FOOD. The same behavior of the base case with the addition of introducing a limited food source for the prey, thereby limiting the reproduction rate in the case of exponential over-population.
SHARKNADO. Building on the base case, introducing advanced conditional movement behaviour to both the prey and the predator population instead of purely random wandering.

EXPERIMENT 2:

SHARKNADO. The most advanced case of EXPERIMENT 1 as a base line behavior for asexual and pseudo-sexual reproduction.
ASEXUAL INHERITANCE. SHARKNADO-case behavior with the addition of asexually (i.e. one parent producing offspring by itself) inherited genes in the predator population.
PSEUDO-SEXUAL INHERITANCE. SHARKNADO-case movement behavior with pseudo-sexual recombination of traits in the predator population since the evolution of attributes in asexually reproducing populations otherwise relies purely on the mutation of genes and survivor selection. Since the genes are encoded as single real values instead of a categorical double-encoding with alleles as in nature, it is henceforth referred to as *Pseudo*-sexual reproduction.

From these two experiments, two distinct research questions will be investigated in the following:

RQ1. How does adding a limited food supply or chasing and fleeing mechanisms affect the predator-prey simulation?

RQ2. How does introducing asexual and pseudo-sexual genetic inheritance mechanisms affect the predator-prey simulation?

Multiple metrics and graphs will be used to answer the research questions, as described in section 2. The cases will be assessed by the combination of visualisations and numerical metrics to investigate the research questions. Furthermore, the different cases will be compared, to reveal the longevity of certain methods in modeling. The simulation run-length and the agents per frame give great insight into the overall success of an experiment, since longer simulations and more balanced dynamics between two populations indicate a stable simulation. This will provide an insight into how viable populations survive, given the respective design choice in the theoretical representation of agents.

2 Methodology

To answer the research questions, multiple modeling decisions are made in order to accommodate all variations in the experiments. To investigate population dynamics in an environment, two classes of agents are defined; for the LIMITED FOOD case, an additional idle agent named "Grass" is introduced. The following section expounds agent behavior in the respective cases.

2.1 Types of agent's movements

As C. Reynolds discussed in his paper, agents can be modeled using multiple states to influence their movement. Those proposed steering forces are used in our implementations. A visual representation of those can be seen in the appendix. [6] (B)

Separation: Agents change their movement direction to keep distance to local agents. Separation is evaluated based on the agents position, and its neighbors positions. (13)

Alignment: Agents adjust their position to move towards the average direction of neighboring agents. Alignment is calculated based on the average velocities of the agents within a visual radius. (14)

Cohesion: Agents steer towards the average position of their neighbors. Cohesion is computed based on the average position of the agents in the visual range. (15)

Random Movement: Agents wanders randomly.

2.2 Agent Behaviour

2.2.1 Predator

A predator agent randomly wanders and dies if no energy is left. Otherwise, it loses energy and looks for prey to eat. When prey is within the visual radius, the agent eats it, gains energy and consequently can reproduce with a *probability P*.
In the case of SHARKNADO the predator agent implements a new mechanic, making it chase prey using cohesion 15. It also flocks with neighboring predators for more efficient hunting.B The predator in the asexual extension of SHARKNADO essentially follows the same behavior as before, with the addition of a variable energy expense, visual radius, speed and max energy encoded by its genes. When reproducing, it will inherit its genes, mutated given a likelihood, to its offspring.2.3
For PSEUDO-SEXUAL gene inheritance, the agents are initialized with a random max age, which is used in combination with energy to determine whether an agent dies or not. It is also used to ascertain whether an agent is of mating age. If an agent is able to mate and sees a partner that is also able to mate, one of them will enter a pregnancy phase, where no other mating behavior is allowed. When this timer ends, offspring is generated and consequently inherits the genes from both parents as described in 2.3. The corresponding flowcharts can be viewed in the appendix. (C.0.1), (C.0.5),(C.0.6).

2.2.2 Prey

Contrary to the predator, the prey is modeled in a simple way. It starts out in the wandering state and can reproduce with a *probability P*. In the case of LIMITED FOOD, prey has the additional necessity to consume food for survival. An energy level is introduced with a certain consumption, like in the case of the predator. The prey roams the field, looking for food, reproducing with *probability P* if it ate. In the SHARKNADO case prey also receives more complex movement abilities, namely cohesion, separation and alignment. If predators are around, the prey will flee using separation.13 The prey also will flock with neighboring prey.B (C.0.2),(C.0.3).

2.2.3 Food

In the case of LIMITED FOOD, a third agent was introduced to serve as food for the prey. The food agent starts in an idle state. If it is eaten by another agent, it loses volume. If the food-agent is fully eaten, the agent regrows its volume over time. When it is fully regrown, the position of the agent changes randomly and the agent returns to its idle state. (C.0.4).

2.3 Inheritance of Attributes

For RQ2 based on the SHARKNADO case, ways to encode different values for predators' attributes are introduced. For the experiment, the focus lies on two genes: mass and vision. The mass influences the agents maximum energy positively and decreases its speed. The vision attribute lets the agent see further, however, it increases its energy consumption. In order to modify those values, two approaches were implemented: one with an asexually reproducing population and one with a population using evolutionary strategies, that do not rely on a fitness score, but on the individual's ability to survive for an extended time.[5] The asexual method uses a simple mutation operator allowing the offspring's gene to vary uniformly by α from its parent.

$$G_{\text{offspring}} = \mathcal{U}_{[G_{\text{parent}} \pm \alpha]} \tag{1}$$

Contrary to the previous approach, the PSEUDO-SEXUAL case uses two parents to produce the attributes of the offspring. Those parents are not selected by a fitness-score, but randomly meet each other within their visual radius. The crossover operator is combined in the same equation with a mutation operator, using normal noise:

$$G_{\text{offspring}} = \mathcal{U}_{[0,\alpha]}(G_{\text{parent}_2} - G_{\text{parent}_1}) + G_{\text{parent}_1} + \mathcal{N}_{[0,0.2\alpha]} \tag{2}$$

Note that this type of attribute inheritance heavily relies on the first parent. However, due to the agents having the same probability of being the primary parent, this design choice will not direct the evolutionary development in a certain direction. Additionally, being a primary parent will leave the agent with a timer, that prohibits new reproduction for a set period of time. This makes agents that were not primary parents before have a higher chance to becoming ones, in their next attempt of reproduction.

2.4 Metrics

2.4.1 Stability Score

We introduce a stability score metric, which aims to measure how stable predator and prey populations evolve over time by analyzing peak and valley data of the cycles, by gathering an array of points of the peaks and valleys of both populations H: predators and P: prey. They are denoted as H_p, H_v, P_p, P_v, with p and v as subscripts indexing peaks and valleys respectively.

For each of the aforementioned arrays of points, a normalized standard deviation value is calculated.(6) The normalization factor of the standard deviation of the array of points is the difference between the two means (of peaks and valleys), because it is invariant to the mean number of individuals in the whole population, but only varies based on the mean amplitude of the oscillations. The υ values are used in the formula for the stability score.(7)

$$\upsilon = \frac{\sigma}{\mu_p - \mu_v} \tag{6}$$

$$S = \max\{\upsilon_{P_p}, \upsilon_{P_v}\} + \max\{\upsilon_{H_p}, \upsilon_{H_v}\} \tag{7}$$

$$\lim_{\upsilon_{P_p}, \upsilon_{P_v}, \upsilon_{H_p}, \upsilon_{H_v} \to 0^+} S^* = 0 \tag{8}$$

Each $\max\{\}$ expression calculates an upper bound on the normalized variance within the peaks and valleys of a population. As they are summed, an upper bound is set on the combined stability of the two populations. Therefore, the more stable the simulation, the closer to 0 the score will be, as in Equation (8). The stability score is specifically tailored custom metric applicable to our problem, as it is based upon a simulation with a large stochastic factor, instead of mathematical equations. This setup calls for a measure, which uses the data yielded by the experiment and complements this stochasticity.

2.4.2 Cycle Ratio Score

The cycle ratio score is a measure of the difference between cycle lengths (periods) of the predator and prey populations. c_P and c_H are the mean cycle lengths for the prey and predator populations respectively. It is useful because an inference of the dependency of the population numbers on one another could be made. If this metric is optimal, i.e. close to 0, then the populations of predators and prey have the same cycle lengths on average, even though one of the curves might have an offset in time from the other.

$$C = \frac{\max\{c_P, c_H\}}{\min\{c_P, c_H\}} - 1 \tag{11}$$

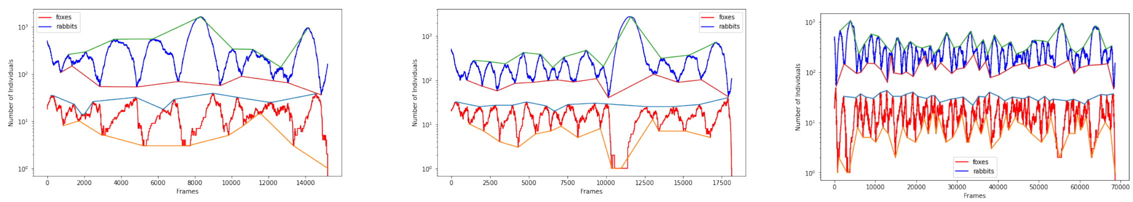
$$\lim_{c_H \to c_P} C^* = 0\,, \tag{12}$$

3 Experiments

Executing the experiments for this paper was done in a structured way to show a pattern that would answer the research questions. For the experimental setup, the chosen independent variables are the version of models for the agents, totalling to five, which are organised in two main experiments 1. The BASE CASE forms the basis for all other versions, and SHARKNADO consequently forms the basis for the ASEXUAL and SEXUAL cases. The controlling variables are the size of the environment and the number of agents in it. For all 5 setups, it was 500 prey agents and 20 predators while the size of the environment was 500 by 500 pixels. Having the same number of starting agents and the same environment size for each experiment is crucial since population‘s density greatly affects its stability and ability to survive. Therefore, the dependent variables are the population numbers per frame and the total length of the experiments. In the following text, the methods of analysing the results are further described.

3.1 Experiment 1

The experiment for RQ1 was set up as a qualitative and quantitative comparison between the three cases in 1. For this purpose, out of a sample size of 20 for each setup, the median number of time steps per run are picked and compared. The stability and difference between cycle lengths was assessed for the three setups. The BASE CASE achieved a stability score of 1.88, the LIMITED FOOD one - 1.59 and the SHARKNADO case achieved a stability score of 1.25, which was by far the most stable of the three. BASE CASE had a cycle ratio score of 0.12, while the LIMITED FOOD case got a 0.11 score and the SHARKNADO got a score of 0.05. These numbers could be seen in Table 1. This shows that the BASE CASE has the least dependence between the two population numbers, while SHARKNADO has the biggest dependence between the two populations, followed by the LIMITED FOOD case. The stability scores are in line with the cycle ratio scores for the three setups, which shows evidence supporting the claim that adding more complex dynamics, such as a limited food source for the prey and chasing and fleeing mechanics, makes for better mutual regulation of the populations, resulting in more stable simulations.

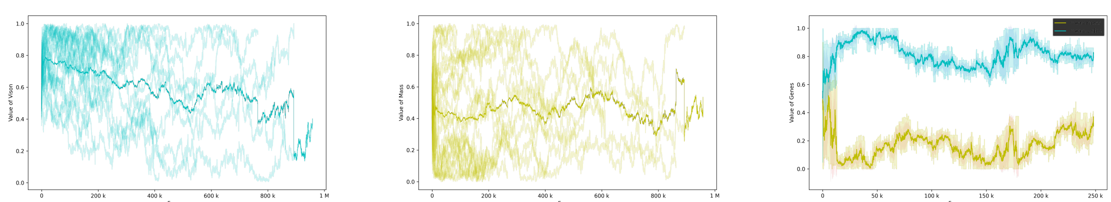


(a) Base case (b) Limited food case (c) Sharknado case

Figure 1: Stability plots

3.2 Experiment 2

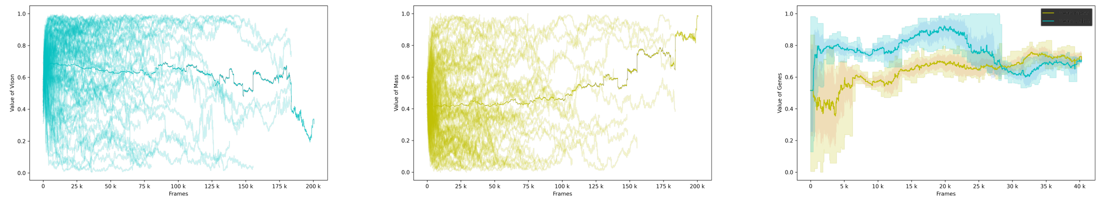
To answer RQ2, regarding asexual and pseudo-sexual inheritance of genes, the SHARKNADO case was extended to accommodate those additions. SHARKNADO was used as base case, since it produced the most promising stability score in the first rounds of experiments. The simpler addition was the agents asexual gene inheritance as described in 2.3. The asexual mechanic produces significantly more stable simulations that in the median case are able to last for over 380,000 frames. Depicted below, the general trend of the two genes for all simulations with the asexual methodology can be seen. The plots suggest due to their wide spread of gene values, that there is not one dominating gene that always produces surviving individuals, but that there is an interaction between two genes 2(a,b). This interaction can be seen in great detail in figure 2(c), where the two genes seem to traverse in opposing directions throughout the simulation.



(a) Vision Genes for all Simulations (b) Mass Genes for all Simulations (c) Gene Convergence

Figure 2: Gene Plots Asexual Case

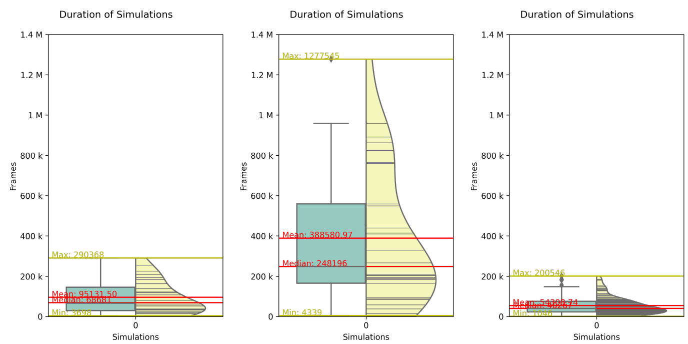
Regarding the PSEUDO-SEXUAL case, an α value of 0.05 was chosen for (6). In this case the predator population dies out faster, which is expected since introducing mating behavior limits the number of times offspring can be produced due to the requirement of having two parents. Since genes are transmitted through interaction of agents, the visualisation of gene behavior should show different behaviour from the ASEXUAL case. As seen in the graphics 3(a,b), no pattern is visible, suggesting that no single gene determines the possibility for survival, similar to the previous case. However, the gene convergence plot 3(c) shows altered behavior, that observes a more drastic convergence in the traditional sense. Genes seem to be more random at start, however, have a decreasing standard deviation over time. Due to noise, the actual standard deviation will always change and an outbreak is possible as seen in 3(c).



(a) Vision Genes for all Simulations (b) Mass Genes for all Simulations (c) Gene Convergence

Figure 3: Gene Plots Pseudo-Sexual Case

The direct comparison between the numeric metrics of both cases can be seen in the following table 1. Additionally, the distribution of simulation run-length for all comparable simulations in these experiments show how likely populations are to survive. As seen in the boxplots, the ASEXUAL case dwarfs the performance of the others. Also, the numeric metrics suggest that the ASEXUAL case has a higher ability to survive, however the stability metrics show no significant differences 1. To look at the SHARKNADO and PSEUDO-SEXUAL boxplot in larger scale, refer to the appendix at D.1.1, D.1.2.



(a) Sharknado (b) Asexual (c) Pseudo-Sexual

Figure 4: Simulation Length Boxplots

	Base Case	Limited Food	Sharknado	Asexual	Pseudo-Sexual
Stability Score S	1.88	1.59	1.25	1.27	1.48
Cycle Score C	0.12	0.11	0.05	0.09	0.04
Number of Cycles	23	24	104	345	80

Table 1: Metrics for the Cases

4 Conclusion

Concluding the research, the metrics and findings suggest that introducing "intelligent" movement behavior, like chasing and fleeing, enables a better mutual regulation of the predator and prey populations towards stability. Additionally, genes seem to make the simulations more stable and regulate agents attributes to maximize simulation run-length. As of the limitations of this study, having numerous parameters to tune made the models harder to fully balance. Additionally, due to limited computing capacities, we were not yet able to optimize the PSEUDO-SEXUAL case to its full potential. However, it is reasonable to assume that further tuning of the parameters would make it exceed or at least be on par with the ASEXUAL case. During the experimentation phase, we found sexual reproduction for a population hard to realize, due to low likelihood of few surviving predators meeting within the environment. Looking forward, multiple interesting additions are possible. Experimenting with adding genetic inheritance functionality to the prey population would show if co-evolution-like dynamics would be exhibited. Additionally, a more nature-like representation and the addition of more genes would extend this research. Introducing genders and recessive and dominant alleles is a way of investigating the effects of natural evolution on population stability and longevity.

References

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Appendices

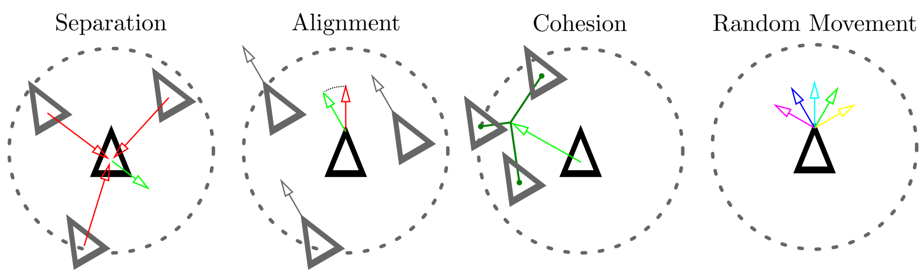
A Consumption Requirement Table

Table 2 shows whether an agent of a specific class needs to actively eat for survival for each case.

	Base Case	Limited Food	Sharknado	Asexual	Pseudo-Sexual
Prey		X			
Predator	X	X	X	X	X
Grass	—		—	—	—

Table 2: Food necessities of species

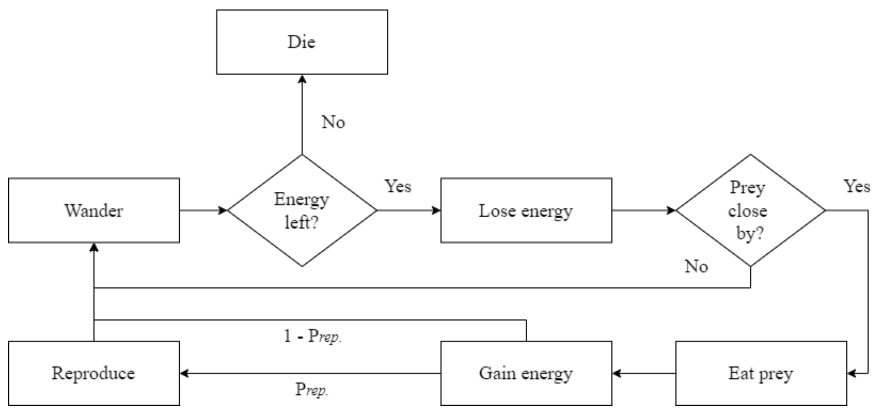
B Types of agent's movements



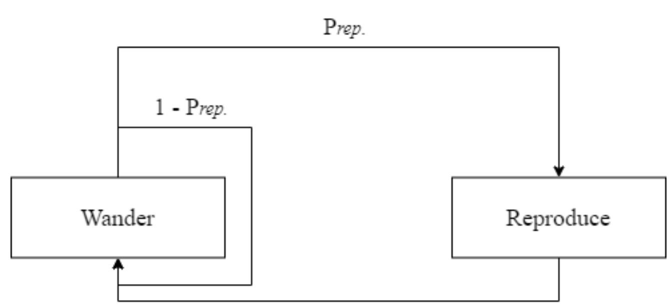
Formulae		
Separation	Alignment	Cohesion
$$s = \frac{1}{\lvert N\rvert}\sum_{i\in N}(X_{agent} - X_i) \quad (13)$$	$$V_N = \frac{1}{\lvert N\rvert}\sum_{i\in N} V_i \quad (14)$$ $$a = V_N - V_{agent} \quad (16)$$	$$\overline{X}_N = \frac{1}{\lvert N\rvert}\sum_{i\in N} X_i \quad (15)$$ $$f(c) = \overline{X}_N - X_{agent} \quad (17)$$ $$c = f_c - V_{agent} \quad (18)$$

C Agent behaviour

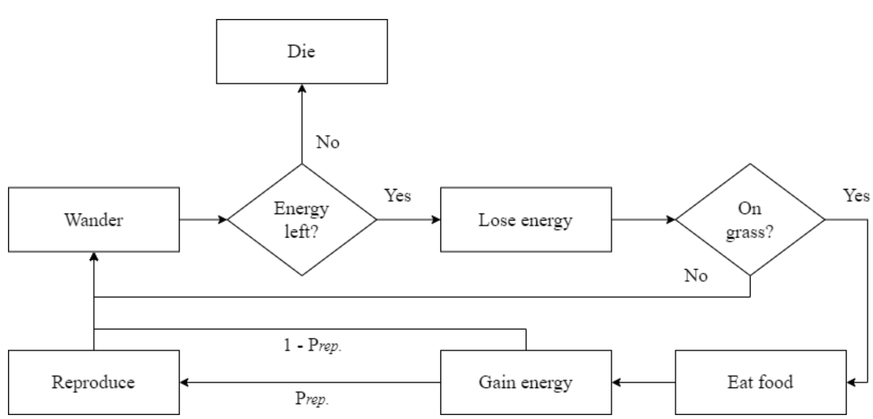
C.0.1 Base case: hunter and Sharknado: hunter



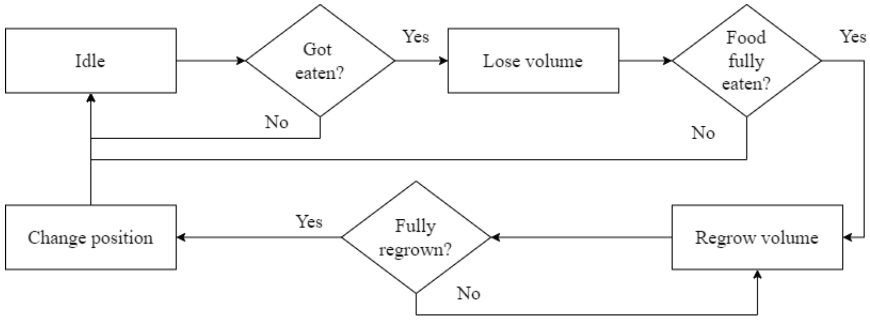
C.0.2 Base case: prey and Sharknado: prey



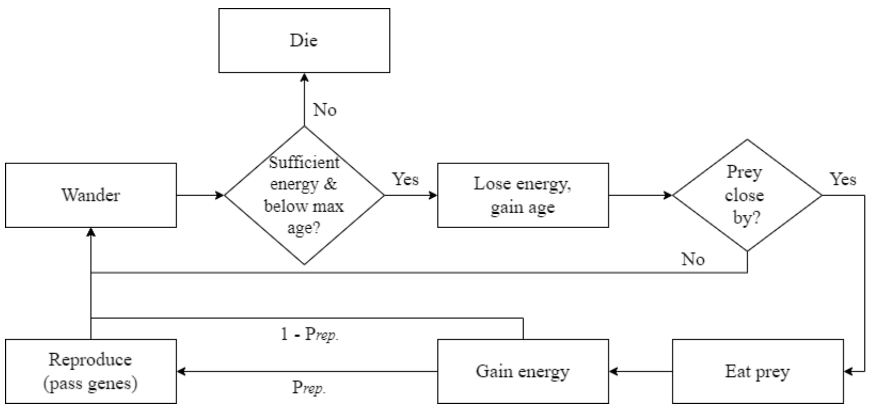
C.0.3 Limited food: prey



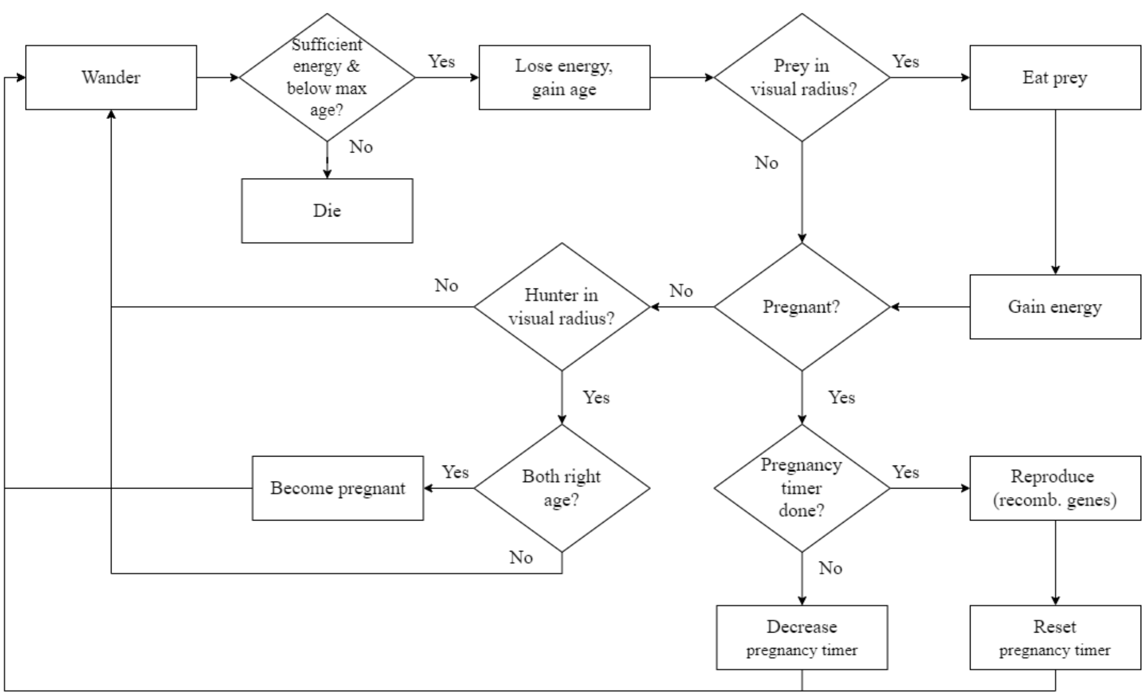
C.0.4 Limited food: food



C.0.5 Asexual: hunter



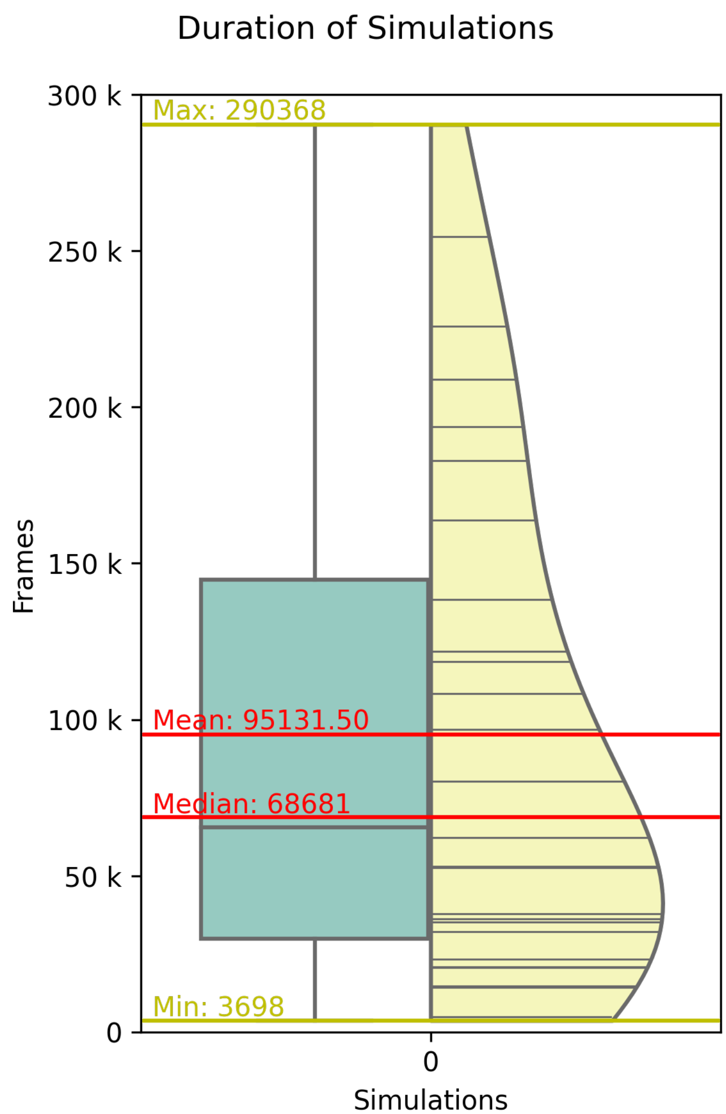
C.0.6 Sexual: hunter



D Experiments

D.1 Exp 2

D.1.1 Sharknado Boxplot



D.1.2 Pseudo-Sexual Boxplot