

The Cycle Of Life: A microbial culture simulation

“In the beginning was simplicity.”

– Richard Dawkins, *The Selfish Gene*

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The Problem :

The package is a microorganism culture simulation program .It simulates a culture of microorganism with various attributes like speed, metabolic rate (rate of food consumption) , minimum requirement of age and food for reproduction. All microorganisms have “genes” which simulate some special features like being a plant or animal, having resistance to antibiotics, being able to eat fellow animals, etc.

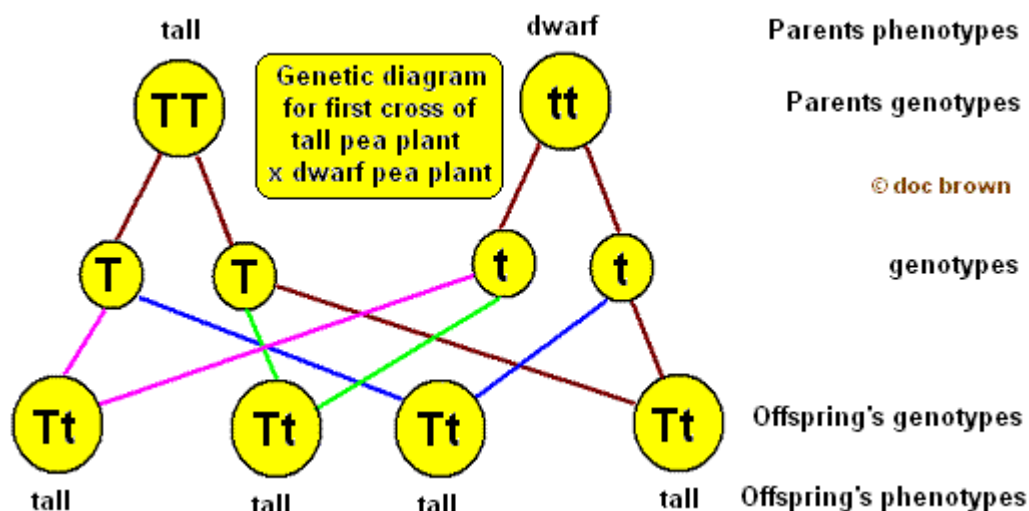
As understood by Mendel’s Theory of Inheritance and genetics all characteristics are passed on by genes. For each characteristic a pair of genes are present. Here a special type of “sexual intercourse” called conjugation is present as in there is no male and female microbes which produce a new organism instead two organism come together and “mix” there genetic material and the net result are 2 organisms with a new set of genes.

Each gene can be of 2 types dominant or recessive. If any of the 2 genes present in a micro-organism is dominant then the dominant trait is shown otherwise the recessive trait is shown. The special characteristics are may give a new trait or change an attribute with some reasonable cost. Depending on the “environment” the genes may increase or reduce the chances of survival and those who survive will reproduce and pass on their traits (theory of natural selection!).

Also an idea of maintaining of population of plants and animals through a food chain can be seen. For example: If there are too many plants the number of plants will reduce and the number of animals will increase because of lack of competition for food.

Some statistical data is generated and stored in a file for a later analysis though a rough graphical simulation is also present to keep a track of the simulation.

This can be used as an interactive tool to show school kids an idea of “inheritance” and “natural selection”. Also it is a first step (albeit a very small one) toward what can be called a complete ecological simulation.



Design of the code:

We all know that micro-organism will have genetic information stored in some way or the other. Though all micro-organisms don't have nuclei we have a nuclei class which stores all the "hereditary information" about the organism and all of its behaviours which are induced or modified by genes. There is an organism class which has the information changing over its lifetime (age and energy) and it has a nucleus from which it gets its attributes and related behaviours.

The genes are represented by structs having a symbol (for identification) , a pair (for each characteristic a pair of gene is present) and a lambda which contains is a representation of the effects of the gene. Plants and animals are not a class but are decided by the presence of the plant and animal gene respectively.

Each organism belongs to an environment (pun intended). There is an environment class which is basically the space in which it lives. It has a list of all plants, animals and antibodies (kill all unless resistance is present) present in the environment.

There is a database class which stores various numerical data and can write that and various messages in a file.

There is an object of database in the environment for storing the various numerical data and later writing that into a file.

The environment has a process function that finds the next state of the system and updates the screen.

Various buttons are made to allow some user control during the simulation.

The screen is representative of a toroid that is the organisms which go to the bottom wrap back to the top, similarly for right and left.

The colour coding is as follows:

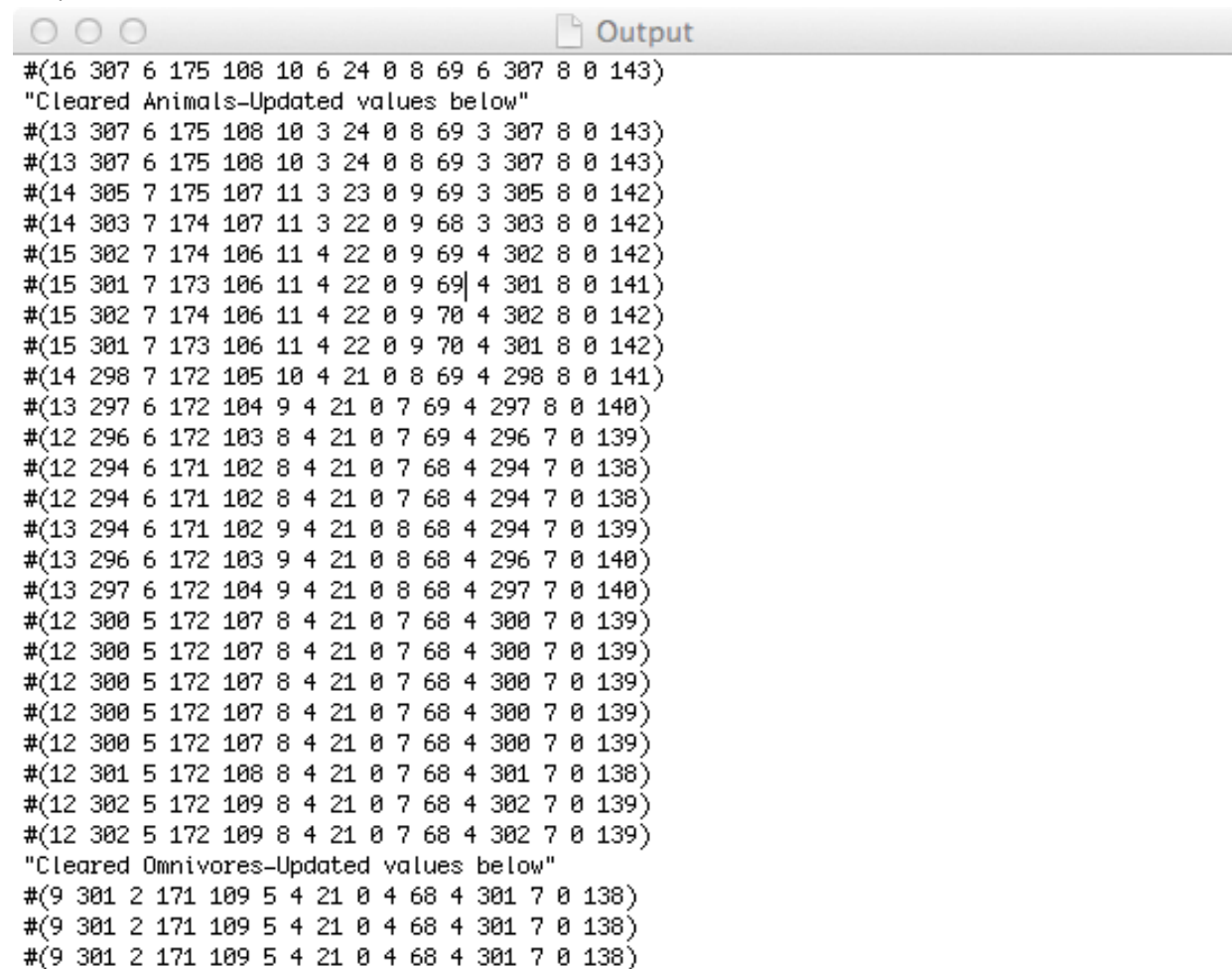
- 1) Non-toxic plants - Bright green.
- 2) Toxic plants – Olive green.
- 3) Animals without an omnivore gene – Yellow.
- 4) Type 1 animals with active omnivore trait – Red.
- 5) Type 1 animals with inactive omnivore trait – Brown.
- 6) Non-type 1 animals with active omnivore trait – Light purple.
- 7) Non-type 1 animals with inactive omnivore trait – Blue.
- 8) Antibodies – Black.
- 9) All marked organisms do not have a border; others have a black border.

Note: The routine used to display the objects has been adapted from the drawing routine code of assignment 3.

Sample Output:

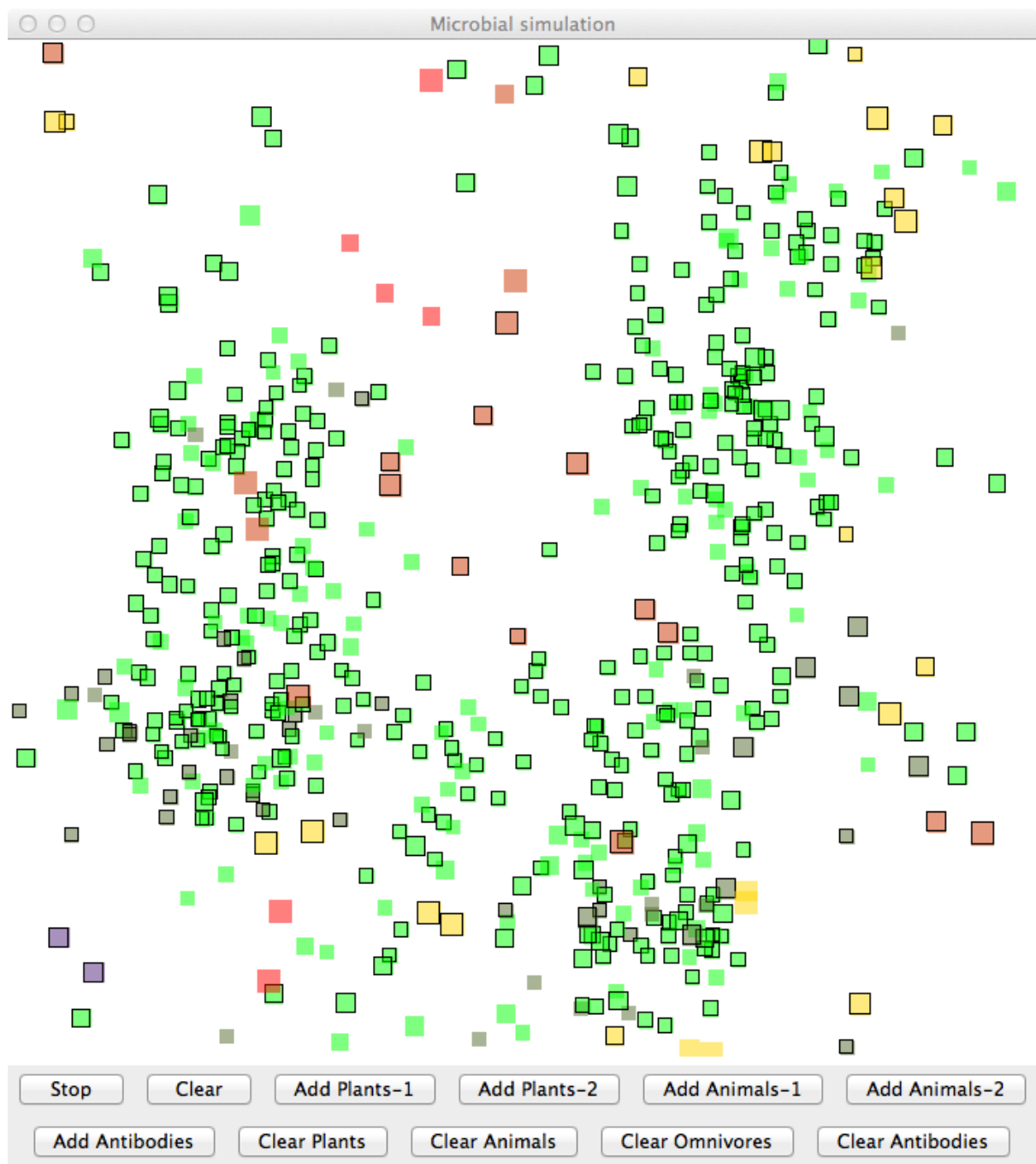
Input: Initial number of plants ,animals and antibodies from the drracket terminal.A name for the output file is also asked.

Output File Screenshot



```
#(16 307 6 175 108 10 6 24 0 8 69 6 307 8 0 143)
"Cleared Animals-Updated values below"
#(13 307 6 175 108 10 3 24 0 8 69 3 307 8 0 143)
#(13 307 6 175 108 10 3 24 0 8 69 3 307 8 0 143)
#(14 305 7 175 107 11 3 23 0 9 69 3 305 8 0 142)
#(14 303 7 174 107 11 3 22 0 9 68 3 303 8 0 142)
#(15 302 7 174 106 11 4 22 0 9 69 4 302 8 0 142)
#(15 301 7 173 106 11 4 22 0 9 69 4 301 8 0 141)
#(15 302 7 174 106 11 4 22 0 9 70 4 302 8 0 142)
#(15 301 7 173 106 11 4 22 0 9 70 4 301 8 0 142)
#(14 298 7 172 105 10 4 21 0 8 69 4 298 8 0 141)
#(13 297 6 172 104 9 4 21 0 7 69 4 297 8 0 140)
#(12 296 6 172 103 8 4 21 0 7 69 4 296 7 0 139)
#(12 294 6 171 102 8 4 21 0 7 68 4 294 7 0 138)
#(12 294 6 171 102 8 4 21 0 7 68 4 294 7 0 138)
#(13 294 6 171 102 9 4 21 0 8 68 4 294 7 0 139)
#(13 296 6 172 103 9 4 21 0 8 68 4 296 7 0 140)
#(13 297 6 172 104 9 4 21 0 8 68 4 297 7 0 140)
#(12 300 5 172 107 8 4 21 0 7 68 4 300 7 0 139)
#(12 300 5 172 107 8 4 21 0 7 68 4 300 7 0 139)
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#(12 300 5 172 107 8 4 21 0 7 68 4 300 7 0 139)
#(12 301 5 172 108 8 4 21 0 7 68 4 301 7 0 138)
#(12 302 5 172 109 8 4 21 0 7 68 4 302 7 0 139)
#(12 302 5 172 109 8 4 21 0 7 68 4 302 7 0 139)
"Cleared Omnivores-Updated values below"
#(9 301 2 171 109 5 4 21 0 4 68 4 301 7 0 138)
#(9 301 2 171 109 5 4 21 0 4 68 4 301 7 0 138)
#(9 301 2 171 109 5 4 21 0 4 68 4 301 7 0 138)
```

Graphic Window Screenshot:



Limitations:

The following are mostly extra features which are not an essential part of the simulation and were not implemented due to lack of time. These can be independently developed and integrated with the simulation without much modifications.

- 1) Real time analysis of generated data not done and graphs not displayed.
- 2) Organisms at the edge with their centres before the edge will not have their remaining parts appearing at the opposite edge.
- 3) There are only a few traits which are transmitted sexually (5 in both plants and animals ,not counting the plant and animal gene).More can be developed and added.(Though to make them interesting some work will be required)Eg:Attributes modifying traits don't have a very visual effect but are very important.Genes with more visual and highly apparent effect (Eg: A gene which gives it maybe an "adrenaline rush" in dangerous situations can be made).
- 4) If number of micro-organisms become very large the program slows down and the buttons take time to respond.

Points of Interest:

- 1) Many actions take place with some probability.Hence the simulation is not deterministic and the same initial state could lead to very different results.
- 2) The organisms are represented and even used as axis-aligned squares which makes finding intersections faster and easier.
- 3) The program tries to mimic an actual culture of microbes.There is a organism and nucleus class but no plant and animal class because at the level of microbes ,plants and animals vary just because of prescnce and absence of some genes.
- 4) There is a day-night cycle which affects the photosynthesis of the plants.They don't sleep because they are microbes.
- 5) The environment has a nutrition value which is inversely related to the number of plants.If the number is above a critical point the nutrition value becomes 0 making plant survival difficult.