

Increasing Complexity and Increased Stability in Daisyworld

Artificial Life Project

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1 Introduction

The purpose of this work is to show that increasing the complexity of a self-regulating ecosystem increases its overall stability. The model used is based on *Daisyworld*, a simple ecosystem where a single resource is affected both by individuals and by an external, perturbing force. The version described in this document adds the concept of “diversity” to the original model; several different species are defined through a genotype and contribute to the global effect the system has on the resource.

By increasing the number of species it will be shown how the system is more *resilient*, or can return faster to his normal shape after a perturbation has occurred.

2 Related Work

The Daisyworld model has been introduced by Lovelock in 1988 (as referenced in [1]) to describe how an ecosystem can affect its own environment to

maximize the conditions for life. Daisyworld describes an ideal planet orbiting around a star; the star's power is increasing over time (the *perturbation*) and this in turn affects the planet temperature (the *resource*), which without any external forces acting on it would normally increase. The planet's surface, however, is covered by black and white daisies; the global *albedo* of the daisies affects the global temperature of the surface. Black daisies would absorb more heat from the sunlight, thus increasing the overall temperature; white daisies would affect the resource in the opposite way.

Moreover, each type of daisy has a preferred temperature range at which it blooms. Outside of this range there are no daisies on the surface; as soon as the planet's temperature enters a specific range of acceptable values, the daisies start covering the entire surface.

As soon as the temperature of the planet (which has a neutral albedo) enters the acceptable range the black daisies start to appear; their presence results in an increase of the overall temperature due to their albedo. Once the blooming temperature of the white daisies is reached the situation diametrically changes; white daisies replace the black ones and the low albedo of the flowers creates a global effect of "reflection" of the star's light; less heat is absorbed and the global temperature becomes regulated by the mere presence of the daisies.

However, when the surface becomes entirely covered with white daisies, this homeostatic effect cannot be sustained any longer; the increasing power of the star becomes too strong for the white daisies to "counteract" it and the system exhibits *hysteria*. As soon as the temperature goes beyond the acceptable values for the life of the white daisies, they start dying - and the global temperature rises immediately to much higher values.

The *Daisyworld* model and its further implications have been widely

discussed and analyzed; see [1] for an analysis of some of its further implications, and the work of McKann for a review (as referenced by [4] and [5]). The model, even though it was originally envisioned to mathematically describe Gaia theory, has been applied to various fields; see [2] for an application in the field of robotics and active perception.

In “Investigating Gaia: A new mechanism for regulation” a slightly different daisyworld model is used and proven to behave as the original one [3]. In this new version each individual is defined by a two-loci genotype that specifies the resource’s value at which it adapts best (called the A trait) and its effect on the resource (the e trait). This model is demonstrated through a simulation, where for each timestep a tournament is performed between randomly-chosen individuals. The winner is allowed to “breed” by replacing another individual in the current population. Mutations also can alter the genotype of this new individual.

This implementation, too, exhibits the properties of self-regulation and adaptation: the resource is pushed towards a stable equilibrium even though the perturbation keeps increasing. The daisies are following the overall increase in temperature with their mean A trait. It is noteworthy to note that the presence of more species of “individuals” (interpreted as an increase in biodiversity) allows more regulating epochs to emerge: even though the ecosystem is less robust to external perturbation, it is more *resilient*.

The latest model is refined in the work of Dyke ([4]) and McDonald-Gibson ([5]); even though slightly different variations are implemented, they yield to the same conclusions.

Diversity in those models is calculated as the mean number of unique individuals (or individuals with the same A trait in their genotype) over a set of simulations where the mutation rate changes from 0.0 (no mutations

are added, thus no new individuals are seed into the population) to 1.0 (a chaotic, highly dynamical system). Data is collected also to show that systems with too much diversity (or high mutation rates) can regulate the resource for smaller intervals of time.

3 Algorithms Used

The algorithms used to obtain the data analyzed in this report are based on the two papers derived from the first work of McDonald-Gibson [3]. Both versions have been implemented and run with similar data sets. The results are described in section 5 and 6.

The common points for the two set of algorithms are:

- the resource is perturbed externally by a force that grows linearly over time;
- the resource is perturbed internally by all individuals according to the relation:

$$\frac{dR}{dt} = \alpha \sum_i \theta_i + \beta(P - R)$$

where θ_i is the *sum effect* of the individuals, i.e. the sum of their e trait; P is the current perturbation, R is the resource and α and β are fixed parameters that model respectively the internal and external effects on R ;

- each individual has a two-loci haploid genotype specifying the level at which the individual is best fit (the A allele), and how it affects the resource (the e allele);
- a fixed-sized population is randomly initialized;
- no individuals are best fit for the starting level of the resource;

- at each timestep a tournament is performed, where the winner replaces a random individual from the population;
- mutation can occur with probability μ on the newly “born” individual if there has been a replacement;
- if no individual has a higher fitness, no replacement occurs in the population;

The key differences are:

- the fitness function;
- a different approach for mutations that cause the individual to exhibit traits with values outside the permitted bounds;
- the sum effect on the resource;
- the approach taken to deal with two individuals with the same fitness;
- the initial value at which the e allele is initialized

Both simulations have been run with the following default parameters:

parameter	description	default value
μ	mutation rate	0.1
t	number of timesteps	100
P_0	perturbation start value	0
P_t	perturbation end value	100
A_{min}	resource value at which individuals best adapt (min)	15
A_{max}	resource value at which individuals best adapt (max)	85
ρ	mutation standard deviation	0.05
i	number of intervals used for time-regulation sampling	200

3.1 The First Set of Simulations

The first set of simulations, from now on called ECAL, is based on the work of Dyke ([4]) for the European Conference on Artificial Life:

- the fitness function of the i^{th} individual is defined as

$$F_i = \begin{cases} 1 - \lambda(A_i - R)^2 & \text{if } |A_i - R| < \lambda^{-\frac{1}{2}} \\ 0 & \text{otherwise} \end{cases}$$

- if an individual undergoes a mutation that brings his genotype outside the permitted bounds, the trait stays unchanged for that timestep. For example, let the e trait vary from -1.0 to 1.0 ; if an individual has an e trait of 1.0 , a mutation could bring it up to 1.05 ; in this case the e trait would be kept at 1.0 ;
- the sum effect is calculated as the algebraic sum of all e trait for the entire population;
- if two individuals have the same fitness function, no replacement occurs and the old individual is left untouched;
- the e allele is a real number between -1.0 and 1.0 ; if $e < 0$ the individual is said to negatively affect the resource, i.e. to decrease it; if $e > 0$ the individual positively affects the resource;

The remaining parameters used for this simulation are:

parameter	description	default value
P	population size	2000
γ	death rate	0.01
λ	width of fitness function	0.04
α	population effect on the resource	0.0025
β	perturbation effect on the resource	0.1
R_0	resource initial value	-50
R_t	resource final value	150

3.2 The Second Set of Simulations

The second set of simulations, from now on called JTB, is based on the work by McDonald-Gibson ([5]) and submitted to the Journal of Theoretical Biology:

- the fitness function of the i^{th} individual is defined as

$$F_i = \max \begin{cases} 1 - \frac{(A_i - R)^2}{\lambda^2} \\ 0 \end{cases}$$

- the principle of *reflexion* is used: if a mutation takes an allele's value outside the permitted boundaries, the amount overdue will be subtracted (or added to) from the upper or lower bounds respectively;
- the sum effect is calculated by increasing or decreasing the resource value by one unit, respectively, if $0 \leq e < 0.5$ or if $0.5 \leq e < 1$;
- if both individuals have zero fitness a random individual will be generated and used as replacement;
- the e allele is a real number between 0.0 and 1.0;

The parameters are initializes as follows:

parameter	description	default value
P	population size	1000
γ	death rate	0.005
λ	width of fitness function	5
α	population effect on the resource	0.0005
β	perturbation effect on the resource	0.01
R_0	resource initial value	-50
R_t	resource final value	150

It is noteworthy to mention that the value $(A_i - R)^2$, used in the fitness function, is multiplied by the same factor of 0.04 in both simulations. However, the JTB version squares the λ value, which could lead to different results in case of multiple simulations varying on this specific parameter.

4 Assumptions

While writing the code to run both simulations, some assumptions had to be made and were checked against the results provided in the papers.

The first assumption regarded the use of “reflexion” in the ECAL simulation. Although based on the original work by McDonald-Gibson (where reflexion is used), this paper does not address the issue. This simulation has been run with both variations and did not show any substantial difference in the results. The choice was then not to insert any reflexion in the mutation routine; alleles mutated to values too high (or too low) were re-set back to the maximum value permitted.

The second choice regarded the effect that a single individual has on the resource at a global level; whilst in the ECAL model the *sum effects* are calculated as the algebraic sum of the e allele, in the JTB model a unary sum/subtraction is performed. This, however, did not show to be an

issue as both papers clearly stated that the initialization process could use indifferently the values -1.0 and 1.0 or a range of real values between those and the final behaviour of the simulation would not be different. Therefore the source code has been implemented as literally stated in the articles and as described in the previous section of this document.

The third choice is primarily focused on the development of the program: to be able to run the program on a remote cluster each parameter was to be set by the command line and not by using any pre-processor definition. This explains the excessive length of the routines used for command-line parsing and set-up of the parameters.

Due also to ease of development, both simulations have been incorporated into the same source code. The choice of which version to run is done only once for each timestep; this has led to the repetition of part of the code that were mostly identical but for the differences listed in section 3.2 and 3.1. Rationale for this choice was not to have an if-then branch in every specific routine (such as the genetic algorithm, the resource evaluation and the mutation routine), which would only affect performance.

5 Results and Sample Runs

Simulations for both versions have been run, trying to replicate the results showed in [4] and [5]. In all graphs the resource is drawn as a solid black line; the perturbation is magenta; the average A trait at each timestep are plotted in red; the *sum effects* are blue and the number of unique A trait within the population is cyan. It must be noted here that the y axes does not contain only the resource level: only for the cyan line the y axes should be interpreted as the *number* of different individuals in the population at a certain time. This choice has been made for space constraints and to

show exactly how a sudden change in the (bio)diversity would result in an immediate response by the resource/ecosystem loop.

The graphs in figure 1 show a daisyworld with no population effect on the resource. In the ECAL graph the mean A trait does not follow the resource linearly as it is showed on the relative paper [4]. In the JTB graph, however, the mean A trait - albeit oscillating - is following the perturbation force.

Figure 2 shows a sample run of the ECAL version for each different mutation rate; all remaining parameters have been left to their default values. The graphs show how higher values for the mutation rate can lead to a longer - but more perturbed - regulation for of the resource.

Figure 3 shows a sample run of the JTB version for each different mutation rate; all remaining parameters have been left to their default values. Those graphs, on the other hand, show much better how regulatory epochs can be achieved by increasing the mutation rate.

The graphs in figure 4 show how the time is regulated over all mutation rates between 0.0 and 1.0; an average of the regulated time is taken, at samples of i timesteps, for 100 simulations for each mutation rate.

6 Analysis

Figure 1 shows a “degenerated” daisyworld where the environment-resource-individuals loop is no longer closed. Here the population does not exert any influence on the resource, which follows the perturbation very closely (the two lines overlap and only the perturbation is visible on the graph).

In figure 2 the graphs show how much different mutation rates can affect the resource. As low rates can “push back” the resource for a limited amount of time, slightly higher mutation rates (on the order of 0.3) can keep the

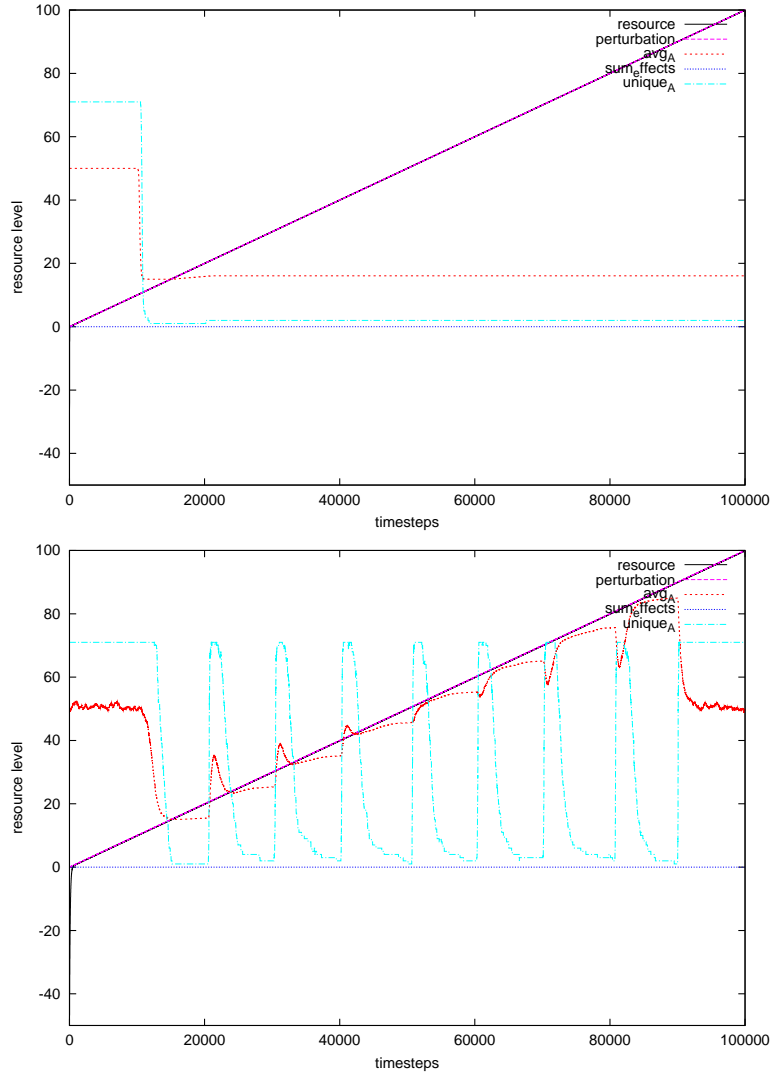


Figure 1: Sample runs of the ECAL and the JTB simulation, respectively, with no population effect on the resource

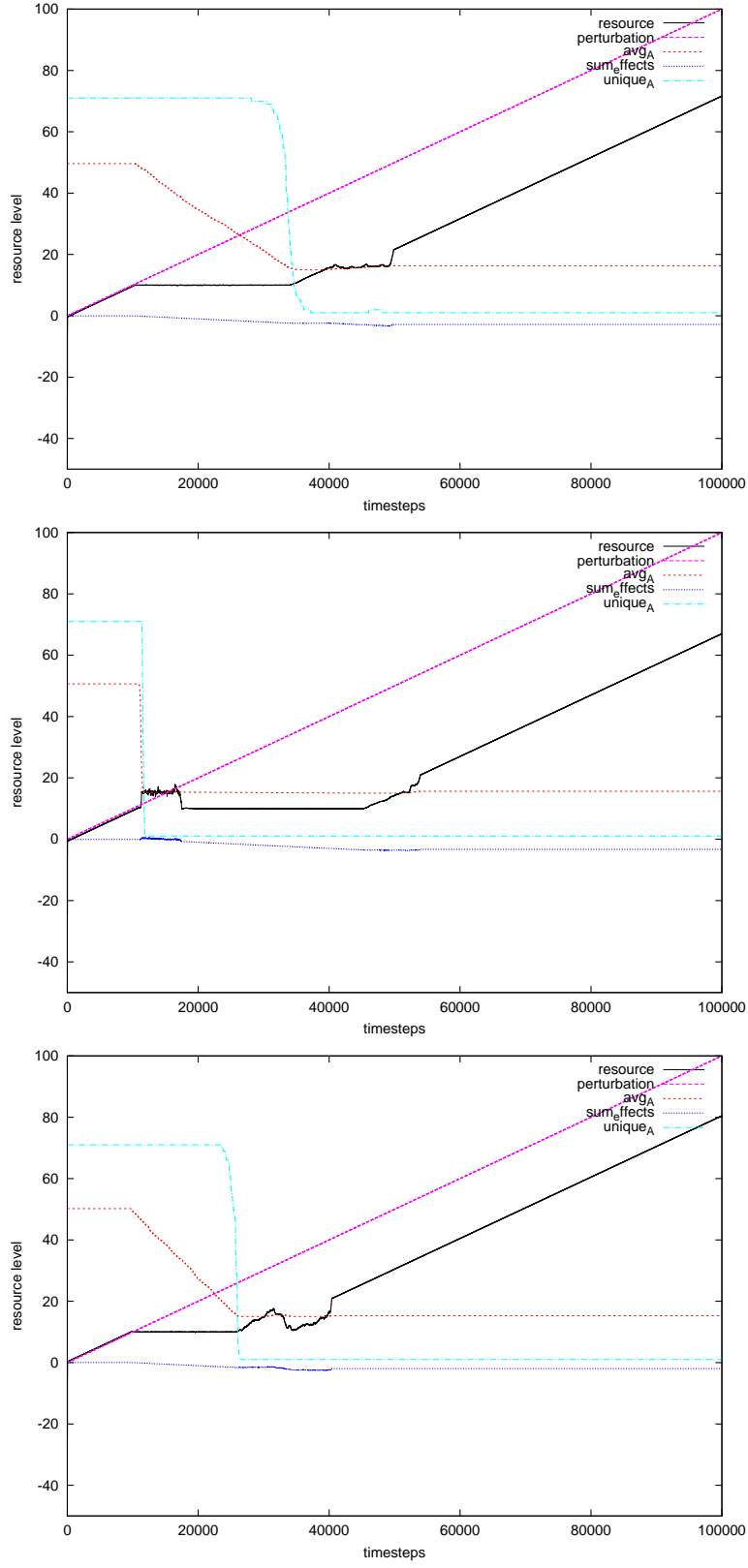


Figure 2: Sample runs of the ECAL version with the mutation rate set respectively to $\mu = 0.1$, $\mu = 0.3$ and $\mu = 0.8$

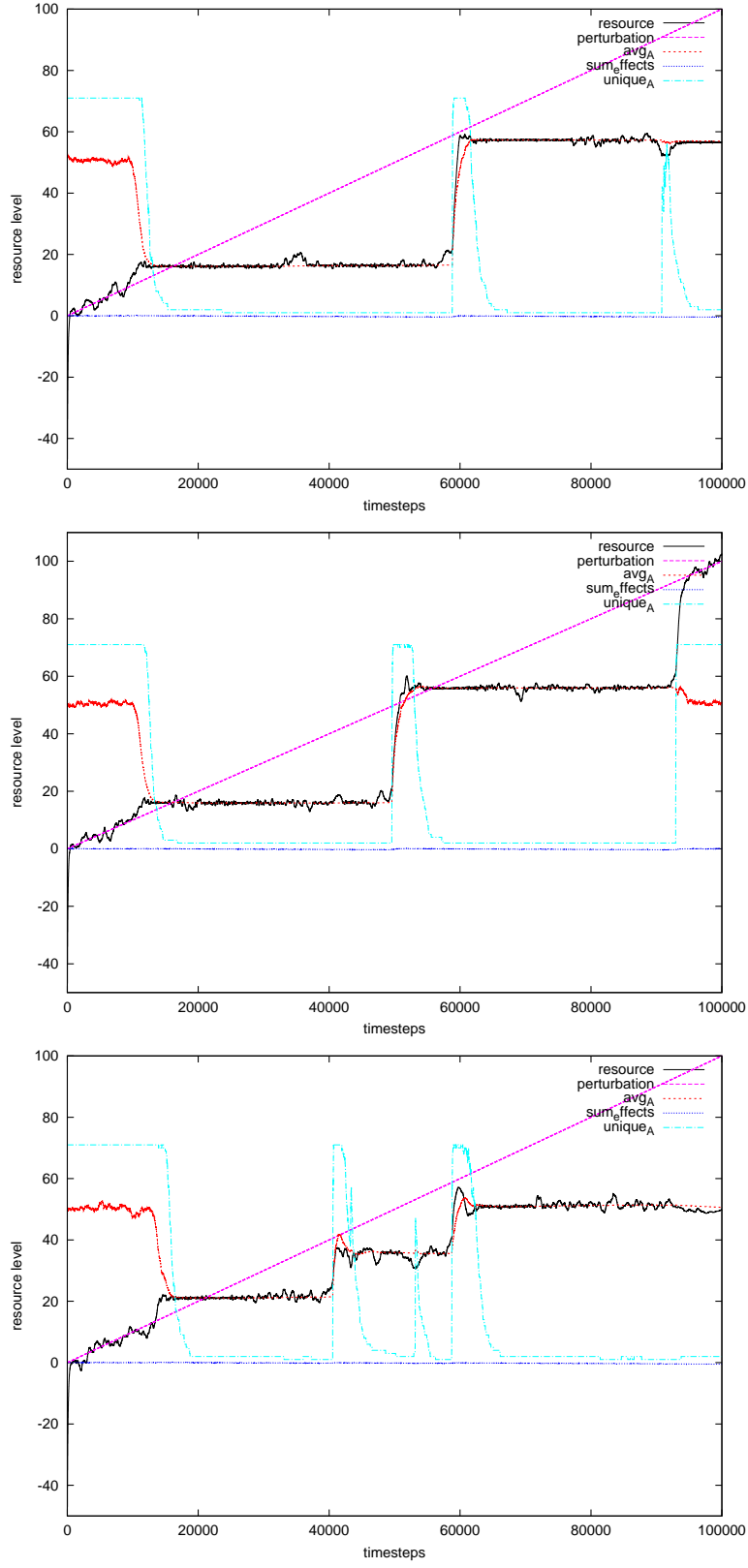


Figure 3: Sample runs of the JTB version with the mutation rate set respectively to $\mu = 0.1$, $\mu = 0.3$ and $\mu = 0.8$

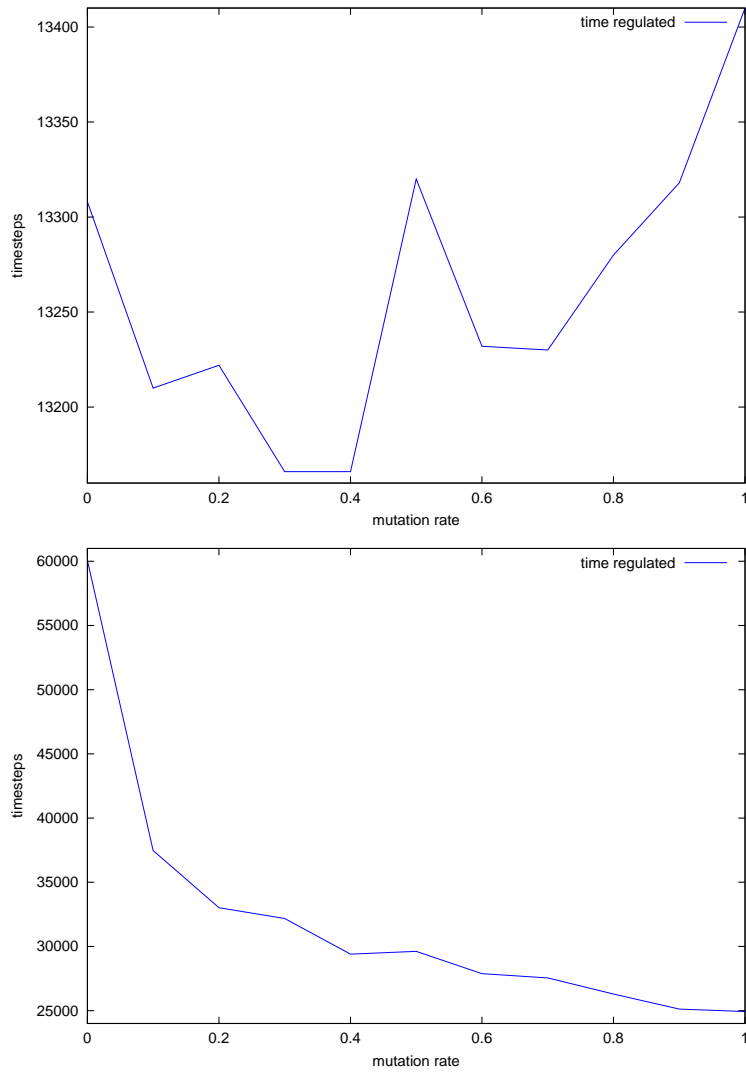


Figure 4: Sample runs of 100 simulations for both the the ECAL and the JTB versions of daisyworld over different mutation rates

resource at a certain value much longer.

Mutation rates of 0.8, however, become “unpredictable”: in the graph showed the resource is not kept stable but oscillates around the valued marked by the mean A trait. Further simulations, though, showed that with high mutation rates the resource might never be regulated all – or might even get pushed to values beyond the actual perturbation, which would mean a totally ineffective process of regulation.

This is probably due mainly to the high randomness of such a system. For high mutation rates every new individual brought into the population is mutated with near certainty; this leads to a much diverse population but with less power of keeping the resource at a stable level (*resistance* to perturbation).

The fact, however, that the system is not capable of any *resistance* for any mutation rate (not even on average – see figure 4) might be due to the same reasons that are making the graphs noticeably different from the one showed in the original article. Further analysis on this issue is done in section 7.

As the graphs show, also, as soon as the number of unique individuals drops to a value around 1, the resource will begin its regulatory phase: in fact, by reducing the biodiversity of the system, all individuals can exercise the same effect on the resource; the overall result is a massive regulation for a longer timespan.

The graphs for the JTB simulation showed in figure 3, on the other hand, show clearly how the regulatory epochs appear when biodiversity increases. Each epoch is visible as a “step” in the resource level. Moreover, different mutation rates show a different number of steps and a different stability in the resource level.

For example, for lower mutation rates (around 0.1) there are only two major steps, each one showing how the resource is regulated on a very stable value for two relatively long time frames. It is noteworthy to point out, however, how with high mutation rates (as showed in the third graph with $\mu = 0.8$) the resource keeps oscillating around the mean A trait, but is regulated in three different epochs. There is even a single perturbation in the population between timestep 50000 and 60000: it is clearly identified by a spike of the cyan line, showing perhaps a mutation that created a new niche of individuals - that, however, was not fit enough to survive at the current resource value, and thus was suddenly taken off the population.

When observing the cyan line showing the number of different individuals care must be taken to interpret correctly the y axes as the actual *number* of individuals, and not as a resource value.

The JTB graphs for $\mu = 0.3$ and $\mu = 0.8$ also point out how any sudden increase in the biodiversity can provide a possible new regulatory epoch. However, the “effort” required to establish a new population able to regulate the resource is the same: the number of different individuals jumps from a few to around 70 every time a new niche is created. Speculating about this fact one could observe how biodiversity has always a high price; the number of species that are *sufficient* to control a resource is much lower than the number *necessary* to permit a new regulatory epoch. Speculating even more this could perhaps explain how, by a mechanism similar to what is known as “mass extinction”, an ecosystem could perhaps allow certain species to survive longer than others, only to move then to different species as soon as the resource becomes more perturbed.

This could perhaps become an interesting feature to be pursued in more studies, perhaps by linking it with the known mass extinctions / explosions

(such as the “Cambrian Explosion”) in Earth’s history.

The graphs from the JTB version of the simulation are much more closer to the results shown in the relative paper. In the next section probable reasons for this will be discussed.

Figure 4 show how an increase in the mutation rate brings the average time during which the resource is regulated to lower rates. The timescale on the y axes of the first graph, however, shows how – even on an average of 100 simulations – the ECAL model implemented does not really display any difference in the time regulated. The JTB version, however, does clearly show that with an increasing mutation rate the resource is regulated less; this is an indication of the *resistance* of the resource, i.e. the ability to resist a perturbation to the current state.

7 Testing

The two set of graphs are sometimes slightly different from their counterparts in the respective papers. Several tests have been made to understand what has gone wrong for the ECAL implementation, but none of them has showed any noticeable result. Some of the most relevant parameters in the ECAL version have been changed to those used by the JTB version (such as α , β , the population size, the death rate), with no improvement. A different tournament, where the winner would replace the loser and not a random individual in the population, has been implemented and tested in the ECAL version but showed no great improvement with the current algorithm. Reflexion has been tried for the mutation but did not show any better result.

The whole set of 100 simulations has been tried several times with different seeds for the random number generator but the overall result did not

differ much from those showed here.

This situation has led to the development of the JTB version, which used the same source code of the ECAL model - modified only where the JTB paper stated clearly the differences with the previous versions. The fact that the JTB version yields to results very similar to those presented in the paper is probably suggesting that the “malfunction” in the ECAL simulation is probably due to a combination of all differences between the two models. Further work will have to be pursued in order to completely rule out software bugs and to find exactly where the two models differ from each other.

A Source Code

The source code attached to this document is 11 pages long. All code is available under the GNU General Public License [?] unless otherwise specified. The SFMT library is the work of Saito and Matsumoto [7]. The FCMP library is copyrighted by Belding under the GNU Library Public License [8].

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