

# Colonization strategies in a 3D environment

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## Abstract

The Biosphere is a bountiful source of inspiration for the biologically inclined scientist, though one may be seized by the twists and turns of its complexity. Artificial Life emerged from the conundrum of condensing this overwhelming intricacy into a tractable volume of data.

To tackle the challenge of studying long-term dynamics of artificial ecosystems we focused our efforts on plant-plant interactions in a 3D setting. Through an extension of K. Sims' directed graphs, we devised a polyvalent genotype for artificial plants development. These individuals compete with one another in a shared plot of earth with the environment playing a crucial part in the phenotype's expression. We illustrate and analyze how the use of multi-objective fitnesses generated a panel of diverse morphologies and strategies some of which exhibiting self-reproduction capabilities.

## Introduction

Natural ecosystems are staggering by virtue of their intricate interactions networks and seemingly endless detail levels. Adaptation, co-evolution and arming races are a small subset of the myriad evolutionary strategies observed in the outside world. In order to translate this onto an artificial medium, one has to address three key issues.

The first is finding functional, adaptive and yet computationally tractable representations for both the genomic and phenotypic aspects of the 'creatures'. Then, genetic variation and discrimination methods, the keystones of Darwin's natural selection process, ought to be devised. Ultimately, environmental pressure, whether coming from the inanimate (abiotic) or living (biotic) surroundings, should be strong enough so that diversity can emerge without excessively narrowing the viable behaviors range.

## Morphogenetic engineering

A number of models have been devised to tackle the problem of artificial morphogenesis starting with the L-Systems which successfully generated plant morphologies in both 2-D (Prusinkiewicz and Lindenmayer, 1991) and 3-D environments (Bornhofen, 2008), as well as mobile creatures (Hornby and Pollack, 2001).

In a similar fashion the directed graphs from (Sims, 1994), define distinct organs and the relationship between them, allowing for very compact encoding of motile morphologies. Closer to biology is the use of Genetic Regulatory Networks (Banzhaf, 2003) to control cellular building blocks. By using such a finer-grained representation it was possible to evolve cell clusters towards specific shapes (Joachimczak and Wróbel, 2008) or generate creatures with self-organized organs in non-trivial environments, e.g. (Disset et al., 2016).

## Replicators

With rules as simple as the one in the Game of Life (Gardner, 1970), elaborate ecosystems emerged with no use of evolutionary techniques. Other contributions such as (Adami and Brown, 1994), simulated self-reproducing computer programs into a 2D memory grid where the organisms had their duplication mechanism embedded into their life-cycle.

Further complexification of the phenotypic space led to ecosystems such as (Metivier et al., 2002; Ventrella, 2005) where the environment was a 2D continuous grid and the 'animals' had to manage their reproduction cycle by actively searching for mates in their surroundings.

## Biotic vs Abiotic

In case of co-evolution or competition (e.g. (Miconi, 2008)), there is a biotic component to the ecosystem in the sense that from the viewpoint of an individual, every other entity is a hard-to-control part of its environment.

When considering the abiotic, i.e. non-living, component of earth's ecosystems it has been shown that, with only water availability and temperatures, it is possible to model most of the biodiversity observed in nature (Woodward and Williams, 1987). The same holds true for artificial simulations where the impact of environmental factors can be a driving force for the speciation process as in (Bornhofen et al., 2011). Additionally, dynamically changing the local constraints pushes individuals out of local minimums and promotes adaptability (Canino-koning et al., 2016).

Our project is to design a virtual ecosystem which tackles all three points by modeling both plants and animals in a

shared environment thus inducing complex interactions and survival/reproduction strategies starting, in this paper, with the growth of vegetals. The following section details the use of an extended version of the directed graphs (hereafter named ‘Graphtals’) from (Sims, 1994) to produce functional morphologies starting from a single seed. We then devised a reproduction scheme to allow for the continuous generation of new plants in an environment whose genotype should, in time, also be evolved thus providing a wide range of external conditions. We then explore various outcomes stemming from this implementation in terms of growth and adaptation strategies before considering the impact of the evolution process itself and highlighting the necessary extensions to this model.

## Self-reproducing vegetals

Here, individuals are not only expected to develop interesting morphologies but also to adapt to an unknown, and potentially precarious, environment.

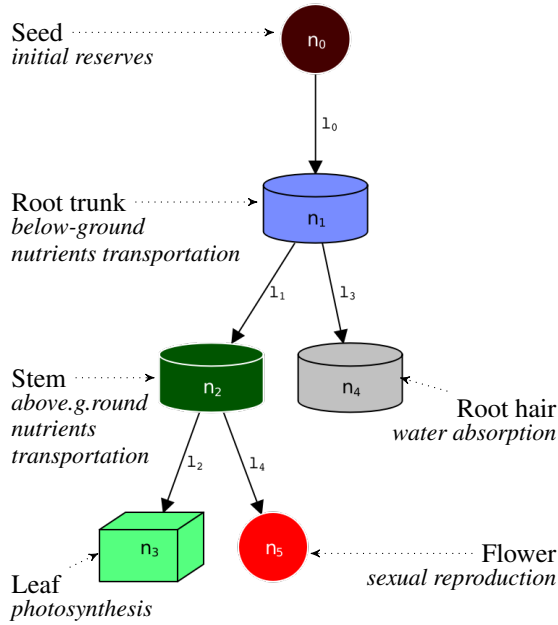


Figure 1: Base graphtal in all following experiments

## Graphtal fields

To this end, the genotype is composed of both structural and behavioral instructions as depicted with the example in figure 1. Each node  $n_i$  describes an abstract sub-organ and is composed of an *id* and a set of parameters  $n_i^d$  specifying its skill which in turn defines its shape (sphere, box, cylinder). Furthermore, it also codes for the initial dimensions, density, color and maximal growth factor of the corresponding organ.

Behavior is controlled by two tuples  $\mathbf{A}, \mathbf{S} \in [0, 1]^E$  with  $E$  the number of elements (limited to water and glucose in this work).  $\mathbf{A}$  models an organ’s balance between production and consumption: a value of 0 (resp. 1) indicates a source (resp. sink) for this specific element.  $\mathbf{S}$  enables quiescent behavior by imposing a threshold below which no growth or budding actions can be performed.

A link  $l_i : n_1 \rightarrow n_2$  expresses a *growth relationship* from  $n_1$  (the parent node noted  $l^i$ ) to  $n_2$  (the ‘child’ node noted  $l^o$ ) and, also, contains a set of parameters noted  $l^d$ . This contains, amongst others, the position on the parent’s surface and the relative orientation. A special field  $r$  is used to regulate recurrent connections by imposing a maximal depth ( $r > 0$ ) or indicate a terminal node ( $r = -1$ ).

To easily code for the highly regular structures observed in nature, each link can select a repetition pattern from:

- *none* no repetition
- *radial*( $\mathbf{V}, N$ )  $N-1$  copies evenly rotated around  $\mathbf{V}$
- *random*( $N, S$ )  $N-1$  copies randomly placed

Ultimately, a handful of plant-wide parameters are stored separately. Namely the growth speed and maximal size factor, the individual’s sex and two sets of parameters  $dW$  and  $\{\mu, \sigma^i, \sigma^o\}$  that will be detailed more thoroughly in following sections.

## Metabolism

At the beginning of a simulation, plants’ seeds are filled with a limited amount of nutrients, i.e. water and glucose, to start the growth process but longer-term survival requires a strategy to maintain comfortable resource levels. Organs die from starvation if any of their nutrient reserves are exhausted. In these experiments, the environment contains only two types of resources from which nutrients can be extracted: water and light.

The first one is extracted through below-ground root hair and must be dispatched through the plant and more importantly to the leaves. Indeed these later require both resources to produce glucose according to Equation (1).

$$G_i = .025 * S_i * \mathbf{L} \cdot \mathbf{N}_i \quad (1)$$

where  $\mathbf{L}$  points to the sun,  $S_i$  the leaf’s photoreceptive surface and  $\mathbf{N}_i$  the  $z$  axis in its local coordinates system.

Resources distribution is implemented through a decentralized mechanism which follows the gradient of nutrient. Every simulation step, organs share a portion of their reserves according to the transport equation (2).

$$d_{A \rightarrow B}^e = \frac{k_{AB}^e * \text{stored}(A) * \text{needs}(B)}{\sum_{o \in C(A)} \text{needs}(o)} \quad (2)$$

where  $\text{needs}(x)$  (resp  $\text{stored}(x)$ ) is the need (resp. stored amount) in nutrients in an organ  $x$ ,  $C(x)$  the set of organs connected to  $x$  and  $A, B$  two organs so that  $0 \leq \text{needs}(A) < \text{needs}(B) \leq 1 \wedge B \in C(A)$ .

Backpropagation is enacted through the  $k_{AB}^e$  term. It is a connection width coefficient which provides finer control over resources allocation at the plant level and is meant to allow for greater adaptability to changing environmental conditions. Every tick, all organs are marked based on their participation in the plant's well-being which is then used to update the width of their connections according to the formulas (3-5).

$$m^e(A) = \frac{(stored_t(A) - stored_{t-1}(A))}{volume(A)} \quad (3)$$

$$cm^e(A) = \frac{P_A^e * m^e(A) + \sum_{o \in C(A)} cm^e(o)}{P_A^e + |C(A)|} \quad (4)$$

$$\frac{dk_{AB}^e}{dt} = 1 - cm^e(B) * dW \quad (5)$$

where  $P_A^e$  indicates whether or not organ  $A$  produces element  $e$  (i.e. root hair for water and leaf for glucose) and  $dW$  an inertia factor, first set to 0, stored in the plant's genome.

Tropisms are another mechanism for adaptive behavior. They are enabled by a number of tropic coefficients ( $w \in [-1, 1]^3$ ), in each graphal link, which indicate how a given stimulus  $t \in \{\text{light, gravity, neighborhood}\}$  should affect an organ's relative orientation. With  $\mathbf{l}$  the average light direction during the last 24 hours,  $\mathbf{g}$  the gravity,  $\mathbf{d}$  the negative density gradient and  $dR = \pi/8$ , the details are given by equation (6).

$$dO = \sum_{t \in T} \mathbf{t} * w_t * dR \quad (6)$$

## Autonomous reproduction

**Data:**  $P$ , set of plants

$M \leftarrow \{p \in P/p \text{ is male}\};$

**for**  $m \in M$  **do**

$G_m \leftarrow genotype(M);$

**for**  $s_m, stamen \in m$  **do**

$f \leftarrow \text{random female, with pistils, in range of } m;$

$G_f \leftarrow genotype(f);$

$A \leftarrow align(G_m, G_f);$

$C_{mf} \leftarrow compatibility(A, G_f);$

**if** random toss with probability  $C_{mf}$  **then**

            delete  $s_m$ ;

$p_f \leftarrow \text{random pistil from } f;$

$p_f \leftarrow \text{Fruit}(\text{Mutate}(\text{Cross}(A, G_m, G_f)));$

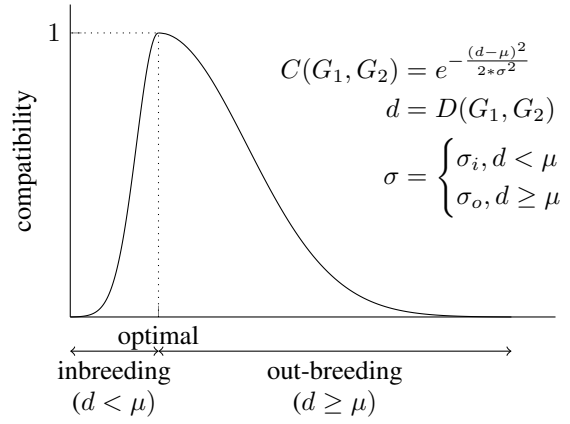
**end**

**end**

**end**

**Algorithm 1:** Mating process

One of the most powerful tools available to Life is its ability to adapt through the process of natural selection. Over



**Figure 2:** Genetic compatibility function

the course of history numerous propagation scheme have been developed. We chose to focus, in this work, on sexual reproduction because of its greater degree of interactions and inter-species diversity.

The subset of a plant's genotype devoted to reproduction includes its sex, compatibility metrics  $\{\mu, \sigma_i, \sigma_o\}$  and sexual organs. These interact with one another according to algorithm 1. Given  $G_1 = (N_1, L_1)$  and  $G_2 = (N_2, L_2)$  the alignment procedure creates three subsets:

- $M_a = \{\{l_1, l_2\}, l_1^{id} = l_2^{id} \wedge l_1^i = l_2^i \wedge l_1^o = l_2^o\}$
- $M_{ia} = \{\{l_1, l_2\}, l_1^{id} = l_2^{id} \wedge (l_1^i \neq l_2^i \vee l_1^o \neq l_2^o)\}$
- $M_i = \{l_1 \in L_1, \nexists l_2 \in L_2, l_1^{id} = l_2^{id}\} \cup \{l_2 \in L_2, \nexists l_1 \in L_1, l_2^{id} = l_1^{id}\}$

which highlight the structural similarities between both individuals. The genetic distance  $d$  is then computed based on the average field-by-field difference of comparable node and link data, i.e. those in  $M_a$  and  $M_{ia}$ . Links in  $M_i$  are given the maximal distance of 1. The total sum is given by equation (7).

$$d(l_1, l_2) = \frac{1}{3}(d(l_1^i, l_2^i) + d(l_1^o, l_2^o) + d(l_1^d, l_2^d)) \quad (7)$$

$$D(G_1, G_2) = \sum_{\{l_1, l_2\} \in M_a \cup M_{ia}} d(l_1, l_2) + |M_i|$$

This crossover operator differs from those commonly found in the literature (Sims, 1994; Bornhofen, 2008; Disset et al., 2016) on three points: 1) it can fail early on, 2) is biased by the *female* genome and 3) has low resistance to large structural differences. The rationale behind point 3 is that, instead of devising a robust operator that can produce a somewhat viable offspring from two completely unrelated individuals, a minimalist alignment procedure is better suited to sexual reproduction of same species creatures in

which the population is mostly homogeneous. Indeed, point 1 guarantees that the more both genomes are different the less likely it is that crossing will be attempted at all.

Having the compatibility function embedded into the genome gives each species a segregation scheme which is of utmost importance as the number of nodes/links is not fixed, thus requiring the optimal genetic distance to be adapted as evolution goes. Furthermore having both in-/out-breeding coefficients allow for the specification of the search spaces with adaptive plants accepting a broader range of incoming genetic material while more conservative ones could instead focus on controlled inbreeding to solidify their alleles.

## The environment

Selective pressure should emerge on its own from the interaction between self-interested individuals. However the environment could play a pivotal role in guiding the complexification process whether by imposing harsh restrictions on the amount of available resources or by displaying a range of (from a creature's point of view) semi-random dynamics.

For this work, the only varying part of the environment is the sun, which produces season cycles through the following set of parameters: day (100 simulation steps) and year (300 days) lengths, latitude ( $\pi/4$ ) and declination ( $\pi/8$ ), i.e. typical values for a European climate. Additionally, the ground was a 10m flat square divided into 400 voxels with a constant supply of water in each of them.

## Population process

A complete ecosystem genotype is composed of both a description of the environment (currently not evolved) and a set of plants 'templates'. Each of these latter represents whole species whose strategies for survival will be pitted against one another in their shared piece of earth.

The procedure to translate these templates into a densely populated ecosystem is straightforward. First the environment is divided into as many cells as the requested number of plants (100 in this experiment) and the largest seed size is tested against half the cell size. If this fails, the whole ecosystem is deemed non-viable and the simulation is aborted, thus preventing plants from having too large initial reserves. Otherwise, each cell is subdivided once more in four and a plant is placed in a single subcell with a random genome from the set of templates and a random vertical rotation. This leaves enough room for autonomous reproduction to place offspring even when the initial population has not entirely died out.

In the current experimental settings, the number of plants is set to 100 and only one species is considered. Furthermore, every random number used during the simulation (plants position, ions, iteration, etc.) is generated from a fixed seed provided by the genotype (not evolved but randomly set).

## Colonization dynamics

### Evolution protocol

This work comes within the scope of studying long-term evolutionary trends in elaborate 3D ecosystems. However, evolving, from scratch, such systems with a non-trivial degree of complexity would require a prohibitive amount of computational resources. Stemming from this intent, the following experiment was designed to generate usable individuals to seed an environment with. Viable plants would thus have to develop strategies to both survive and reproduce so that their genetic material does not die off.

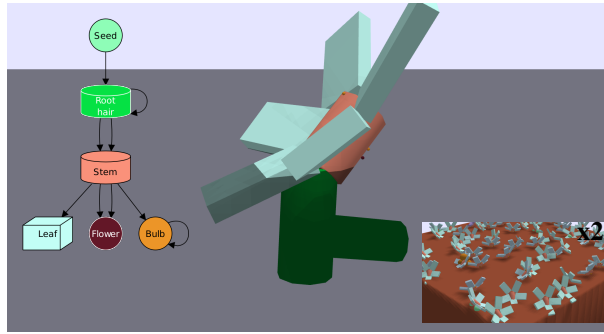
The evolution protocol relied on a standard genetic algorithm where the genotypes underwent single point mutation on all of the fields mentioned in section Graphical fields. The environment was kept constant throughout the  $N = 60000$  simulation steps (2 years). As we aimed for both efficiency and diversity, we devised a range of fitness functions  $F_*$  as described below.

$$\begin{aligned}\nu &= \frac{1}{NP} \\ F_b &= \nu \sum_{t \in N} \sum_{p \in P} biomass(p, t) \\ F_p &= \nu \sum_{t \in N} \sum_{p \in P} production(t, p) \\ F_c &= \frac{\nu}{W^2} \sum_{t \in N} surface(t) \\ F_a &= \nu \sum_{p \in P} lifespan(p) * 2^{-\alpha_p}\end{aligned}$$

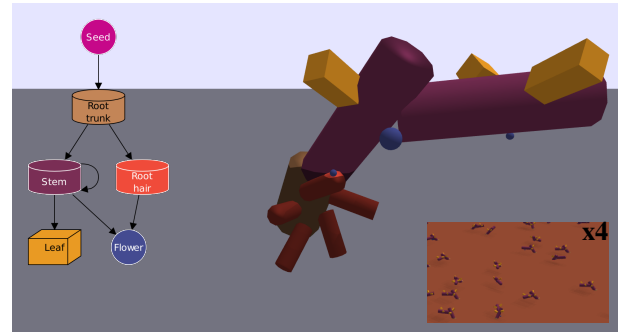
Where  $surface(t)$  corresponds to the total surface covered by plants at time  $t$  and  $\alpha_p$  is designed to provide a smoother gradient towards reproduction. Plainly put, these aim at producing plants which are:  $F_b$  large,  $F_p$  many-leaved,  $F_c$  wide,  $F_a$  fast reproducers. Given that every fitness is likely to be exploited into non-desired behaviors, a fifth one  $F_m$  is introduced that evaluates genomes on all four criteria at the same time.

Furthermore, in order to prevent local optimum a novelty metric is used as proposed in Lehman and Stanley (2008). An individual's 'footprint', i.e. its synthetic behavioral description, is  $(F_a, F_b, F_p, R, G, S)$ , with  $R$  the number of successful autonomous reproductions,  $G$  the number of autonomous generations and  $S$  the seed size.

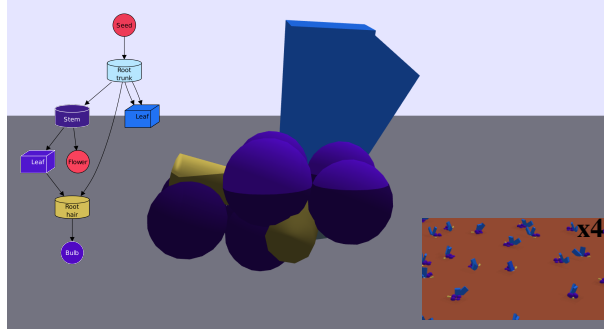
In each scenario, plants are evaluated on two to five criteria using a tournament selection where 3 participants are randomly selected from the population and compete on a random objective as described in Disset et al. (2016).



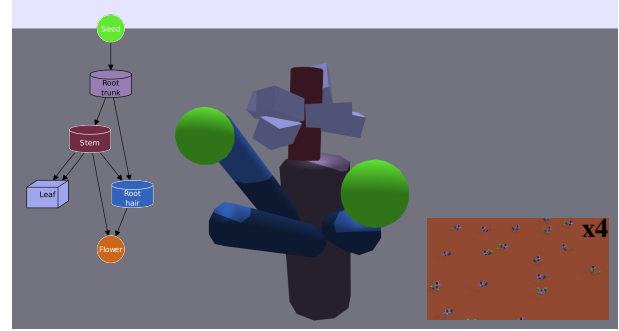
(a) Radial -  $F_c$



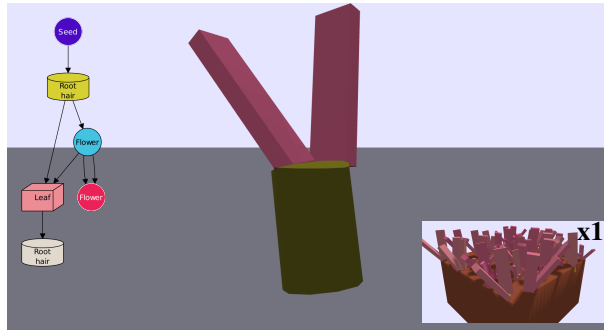
(b) Balanced -  $F_{ma}$



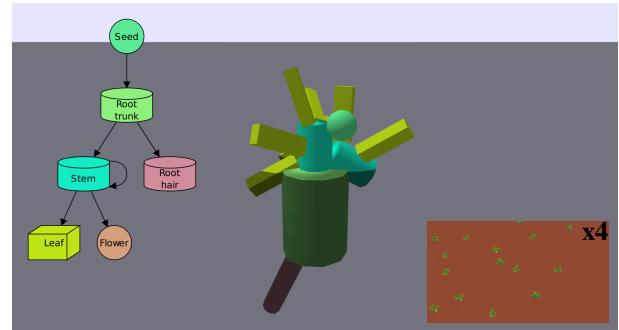
(c) Storage -  $F_{mb}$



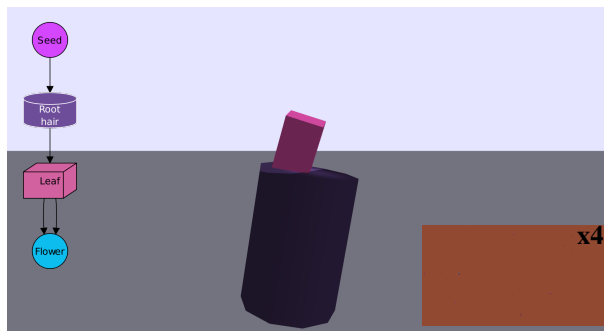
(d) Shoots -  $F_a$



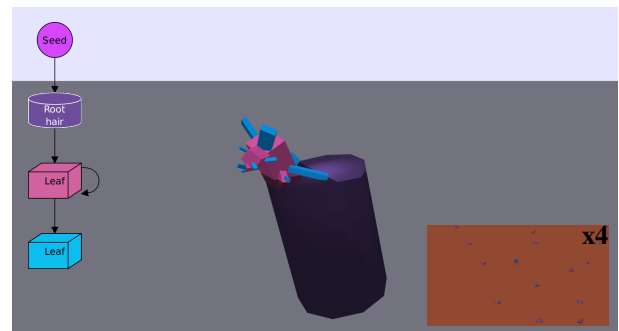
(e) Massive -  $F_b$



(f) Scattered -  $F_{pa}$



(g) Reproduction -  $F_{ma}$



(h) Survival -  $F_{mb}$

Figure 3: Examples of the morphologies developed. a to f are at the 20th day and h is at the 30th. From left to right: Genome, Single individual, Ecosystem. The fitness that produced this individual is indicated in the caption with  $F_{ma}$  indicating the age criterion of the multi-objective fitness  $F_m$ . Videos of these individuals' full ecosystem can be seen on <https://vimeo.com/album/5075632>.

## Morphologies

While three out of the five fitnesses performed an average of two evolutions in the given time frame ( $F_a = 2.4$ ,  $F_c = 2.5$ ,  $F_m = 1.8$ ), the remaining two behaved very differently: while  $F_b$  produced 8.4 'champions' per run,  $F_p$  did not manage to bring a single one to the 250 generations threshold (min=93, max=199). This can be explained by observing the evaluation times of those final individuals which range from 12 milliseconds up to 10+ minutes.

In order to gain a further grasp on the situation, we manually examined the phenotype of the 40 best champions (out of a total of 215) that is 5 for every single objective fitness and another 5 for each criterion in  $F_m$ . Summarized in figure 3 are the morphologies of the most interesting creatures.

As one can see these evolutions produced very different strategies to cope with the environment and their respective fitness. Variation in the sun's position and the plants' relative orientation led to either having large leaves so that production is maximized during short favorable moments (3a, 3c, 3e), or numerous, evenly spread, leaves so that sunlight can be efficiently gathered throughout the day by different parts of the plant (3d, 3f, 3h).

Root morphology was not thoroughly investigated, due to the uniform water distribution exerting only very limited evolutionary pressure, and most individual manage with a simple root trunk connected to a handful of capillary tubes (3b, 3d, 3f). Some even went as far as to completely forsake the former (3a, 3e, 3g).

As the autonomous reproduction process starts from flowers, their growth is of utmost importance for a species' permanence. All plants except two from figure 3 actually generate at least one such organ, though only 3g, 3e, 3a manage to bring them to maturity.

## Strategies

From these morphologies and their associated dynamics graphs we can extract three main strategies: quiescence, expansion and reproduction as illustrated in figure 4.

The first one (in red) is quite straightforward in its survival method. One can see on the graphs that after a short burst of activity, early on in the simulation, this type of individual goes into a quiescent state, keeping its metabolic value in a comfortable range so that most plants make it to the end of simulation.

The expansionist (in blue) however, adopts a radically different approach: instead it tries to reach as fast as it can a mature state which, depending on the plant, can take up to a full year. This allows the ecosystem to compensate for the extremely high mortality rate: in the example depicted, 96% of the population dies in the first hundred days.

Finally, the reproduction strategy (in green) relies on having the smallest possible morphology, i.e. a small seed and a single root hair directly connected to the leaf. Resources are mostly directed towards producing mature fruits as quickly

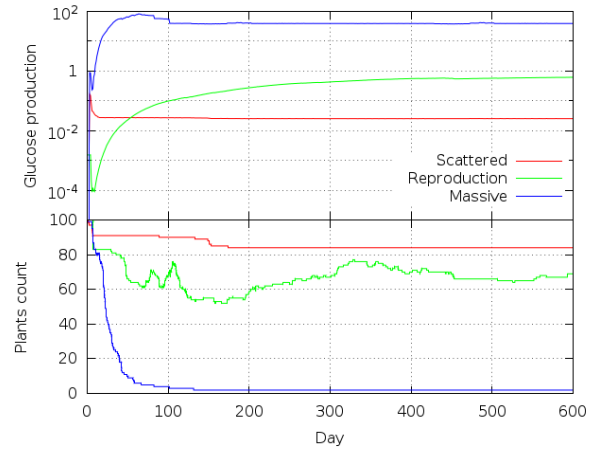


Figure 4: Typical examples of the three strategies' dynamics. Individuals are taken from figure 3 with the red, green and blue curves corresponding to 3f, 3g and 3e

as can be, thus maintaining a population in a safe range ([60, 80] in this case).

It is extremely interesting to compare these behaviors with those obtained in (Bornhofen et al., 2011) where varying environmental factors led the emerge of CSR triangle (Grime, 1977). Indeed a plant population under favorable conditions should evolve towards individual competition while with, decreasing resources availability, a slower, more conservative, metabolism is expected. If exposed to recurrent, localized uncontrolled deaths, the ruderals would thrive with their fast life cycle and colonization approach.

Though with some differences, this experiment exhibited all three strategies with the same environment, hinting at how these populations perceived their surroundings with respect to the local optimum they started their evolution in.

## Reproduction

Given that having creatures that can populate an unknown environment on a long-term scale are a prerequisite for the emergence of complex ecosystems, we investigated whether or not the evolved genomes successfully used the tools they had. Autonomous reproduction was actually a relatively rare occurrence because of the multiple checkpoints required: 39% of the runs failed to produce sexual organs at all. The rest is divided between those that successfully obtained fecundated fruits but did not pursue further (27%) and those that also brought them to maturation (31%). This only leaves 5 runs (3%) with champions that actually mated in their simulation. Furthermore, 4 of them only did so for a couple generations which hints at a behavior still under optimization.

The individual in figure 3g, however, managed to self-reproduce for seven generations with an average maturation period of 75 days and 3 offspring per plant.

This 'species' mutated its genetic compatibility function

so that diversity would be favored. More specifically, for such a compact genotype and considering the small mutational differences, its optimal genetic distance of  $\mu = 1.33$  facilitates reproduction between individuals with a single link addition/suppression. An observation comforted by the large out-breeding tolerance  $\sigma^o = 2.9$  (opposed to  $\sigma^i = .5$ ).

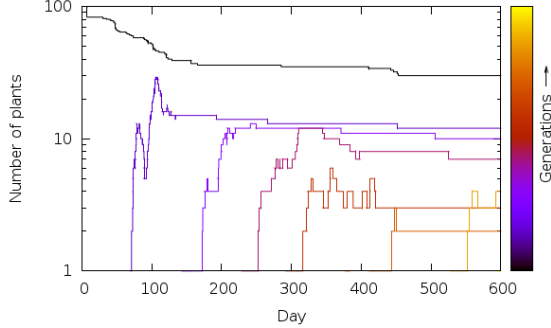


Figure 5: Population dynamics per autonomous generation

Moreover, the population underwent a process of natural ‘trimming’ with its less adapted members rapidly dying as depicted in figure 5. In the first 150 days, the initial population shrinks by 60% quickly replaced by offspring from the first generation. As time goes by we can see that individuals are more and more adapted to their environment with the average survival time steadily increasing.

### Adaptivity

Another point of interest was the use of the backpropagation and various tropisms to sense the environment both for nutrients and competition. The population was dominated by genotypes with non-zero values, however this did not imply that they had any impact on the phenotype (e.g. a phototropism on an underground link).

To measure how well the evolution managed to find meaningful values for these adaptive behaviors, we reevaluated each genome after disabling either the backpropagation (plant level) or all tropisms for a given stimulus (link level). The average InterQuartile Range of the fitness variation observed for the organisms that exhibited non-zero values is 0.07%: almost all reevaluations were squeezed into a narrow band around 100% (i.e. no fitness variation).

For the handful of individuals that performed differently, we can see that the photo-tropism is the least meaningful one with the most impacted simulation still producing 96% of its original performance. This could, in part, be explained by the relatively uniform access to sunlight in the environment where vertical competition did not have time to develop.

On the other side of the spectrum both gravitropism and backpropagation proved quite useful with a maximal fitness drop exceeding 50%. The former was used in its negative form to provide an upward growth of above-surface organs

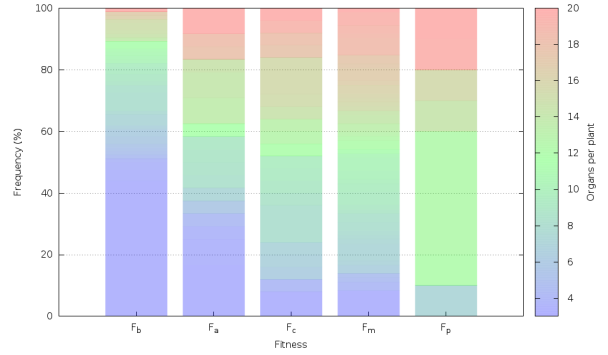


Figure 6: Repartition of average organ count per fitness.

thus increasing light absorption while, in the latter, this parameter allows a redirection of resources towards expansion by reducing the communication canals with less growth-oriented parts of the plant. Furthermore, in the case of individual 3e, loss of this component induces a rapid decline by the 150th day which leads to an untimely extinction event a year later.

### Influence of evaluation criteria

We now turn our attention to the evolution procedure itself and more specifically the contribution of our fitness functions set. The diversity of criteria used induced a similar amount of variability in the obtained genomes as one can see the range of morphologies and behavior obtained.

All fitnesses, however, did not perform equally both in terms of complexity (see figure 6) and relevance. Indeed, while  $F_b$  produced plants that could grow at a sustained pace, they proved quite simplistic, morphologically speaking, with almost 60% of the population growing less than five organs. Given that every random graph starts with this specific amount, it shows that evolution discovered that the bigger one wants to grow, the smaller the genotype.

We can observe a similar trend in  $F_a$ , though with a slight offset caused by the necessity of having sexual organs. The global strategy for this fitness is as described in details for individual 3g: small genome, small plant, fast mating.

This tendency is reversed in  $F_p$ , with no instance in the ‘Minimalist’ section of the phenotypic space. Indeed, as glucose production requires both efficiently positioned leaves and sufficient water uptake, evolution favored genotypes with repetitive structure. On the downside, this also led to extremely long evaluation times which prevent all runs to reach 250 generations with no overwhelming advantages over the competing fitnesses.

The coverage-oriented evaluations performed by  $F_c$  led to a more balanced distribution of organ count between minimalism and over-complexification. While this is the less biologically inspired criterion, it proved more robust to being exploited by the genetic algorithm and, paradoxically,



brought more life-like individuals about, such as 3a.

Finally, the multi-objective fitness  $F_m$  generated more all-rounder creatures, that did not suffer from over-optimization. Indeed when looking at 3c, 3b or 3f, one can observe plausible morphologies made functional by the contradictory pull of all individual fitnesses. Furthermore, it settled in a complexity landscape similar to that of  $F_c$ , though with less exploration of the uppermost region.

## Conclusion

This experiment showed the viability of our bail-out crossover algorithm, though on a reduced scale, and highlighted the difficulty of developing a balanced strategy between survival and reproduction. Furthermore, we observed that the size of the genotypic space was large enough to, in itself, create a speciation phenomena solely based on the starting point of an evolutionary run. However diverse the morphologies we obtained, this problem must be addressed to open the way of population dynamics study across time and space. We additionally noticed the positive impact of a multi-objective evaluation criterion to promote robustness of demeanor by simultaneously selecting from a larger range of viable mutations.

Though already quite complex our model currently lacks any sort of environmental pressure from the temperature at ground level. As mentioned in the opening section of this paper, it is an essential component in earth's biodiversity and, thus, should be included in our future experiments. It could also be used to provide the plants with some form of temporal perception. This would allow adaptive behaviors such as delaying the growth of a seed until a more favorable season or restarting leaf production comes 'spring'.

The environment itself was kept mostly static for this experiment with the exception of the sun. There is ongoing development to add more diversity both topological, e.g. changing the altitude of different patches, and temporal, e.g. varying the hygrometry. These changes would induce stress in the ecosystem, thus promoting adaptation and diversity. By evolving these environments and selecting for those with the most stimulating patterns, we could obtain simulations with highly adapted yet clustered populations.

A further step in this direction would bring about co-evolution and competition by increasing the number of species used to seed the environment. We could then observe the richness of interaction between multiple strands of individuals, both plants and animal, on a long time-scale (as introduced in <https://vimeo.com/godinduboisalife/futureworks>). The use of graphpal to grow plants being straightforward to extend to animals, as this technique is extensively used in the literature.

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