Diversity Control in Evolution of Movement

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Abstract

In this work we investigate how various techniques of diversity control employed during evolution of 3D agents influence the velocity they achieve, and how these techniques influence the diversity of behaviors across multiple independent evolutionary runs. Three evolutionary settings are compared: a standard generational evolutionary process where fitness is velocity, a niching technique, and pure novelty search. Two genetic encodings (lower and higher level) and two environments (land and water) are used in experiments. To diversify behaviors, seven properties of movement introduced earlier are calculated for each individual during evolution. Best individuals obtained from evolution in each setting are compared both in terms of their fitness and the similarity of their movement patterns.

Introduction

Although the natural evolution produces a vast variety of morphologies, they often follow a similar general structure – especially in the case of animals, bodies of which typically consist of a trunk with limbs placed symmetrically on both sides of the trunk. This is because similar environmental pressures may lead to the convergence of similar morphologies during the evolutionary process, a phenomenon known as convergent evolution (McGhee, 2011). Likewise, the movement strategies employed by these morphologies often represent one of the attractors of the most effective modes of locomotion. For example, movement on land is usually performed with legged locomotion (although the number of legs and the gaits vary), with some exceptions such as snakes or snails. Although specific morphologies are usually linked to specific movement strategies, nature can find very innovative ways of controlling bodies when the environment demands it; an example of such a situation are rolling spiders which can be found in the Namib Desert of Southern Africa (Armour and Vincent, 2006).

Unfortunately, even though artificial evolution employed in the field of evolutionary design can efficiently discover fast-moving agents, behaviors found over repeated experiments are often similar to each other. Because of that, one misses a wide variety of behaviors that might be just as interesting, while having only slightly lower quality in terms of their fitness value. There are many reasons behind this problem, such as the lack of diversity in the simulated environments, and the restrictive nature and simplicity of genetic representations, which can make it difficult to escape from local optima. There exist some popular techniques – such as niching (Sareni and Krahenbuhl, 1998) – which are often employed in evolutionary algorithms to counter the problem of converging to “easy attractors”. These methods are designed to maintain the diversity of individuals in the population, which can often lead to finding individuals which are not only more diverse, but are also more fit for the environment.

An inspiration for the niching techniques comes from biology. A niche can be formed around a shared location in the environment, but also around a shared morphology or behavior – for example, different lengths and shapes of beaks allow Darwin’s finches to target specific sources of food effectively (Grant, 1999). Organisms that occupy the same niche compete with each other, but less so with organisms that occupy other niches. This principle is modeled by the “fitness sharing” technique (Holland, 1992; Goldberg and Richardson, 1987), where the fitness of individuals in the population is decreased proportionally to the aggregated (e.g., averaged) similarity to other individuals in this population. This forces the individuals to spread out in the space of all possible genotypes, increasing diversity and fitness at the same time.

While niching punishes individuals for being too similar to one another, it does not directly encourage diversity. In contrast, novelty search (Lehman and Stanley, 2008, 2011a) is a technique which abandons any direct attempt to improve the fitness altogether. In this technique, the probability of reproduction of an individual depends only on its novelty, i.e., on its dissimilarity to a few of the most similar individuals in a population. Despite this radical approach, novelty search tends to find surprisingly fit individuals when the space of the possible phenotypic traits (e.g., morphologies or behaviors in the case of artificial life and robotics) is limited, and one of the properties of phenotypes co-occurs with the desired trait of an individual.
The idea of novelty search was later developed further into a family of methods known as quality diversity (QD) algorithms (Pugh et al., 2016). QD algorithms focus on covering the entire phenotypic space with unique individuals, similarly to novelty search, but they also allow for local competition between similar individuals, which prompts the search to not only look for individuals which are novel, but also high quality according to the fitness function. Some of the most popular QD algorithms include novelty search with local competition – NSLC (Lehman and Stanley, 2011b) and MAP-Elites (Mouret and Clune, 2015).

Niching and novelty search both require a measure of similarity between two individuals to be defined. It is usually discouraged to base such a measure on the similarity between the genotypes of the individuals, as such a measure would heavily depend on the genetic representation used, and would not correlate with the lifespan performance of these individuals. Another possibility is to base the measure of dissimilarity on the fitness of individuals, as it was done in the past in hierarchical fair competition (Hu et al., 2005), fitness uniform selection scheme (Hutter and Legg, 2006), or convection selection (Komosinski and Ulatowski, 2017). This however does not necessarily encourage the diversification of useful behaviors, but serves to help overcome the valleys in the fitness landscape in order to discover the best behavior. It is often most desirable for the measure of similarity to compare the similarity of behaviors of individuals directly.

Unfortunately, traditional measures of movement – which could be used to encourage diversity of movement strategies – are often tied to specific morphologies, such as tetrapods (Biewener, 2006) or hexapods (Full et al., 1991). In our previous work we introduced a set of behavioral measures that can be applied to agents or robots with bodies modeled as graphs (Komosinski and Miazga, 2019), and can also be calculated for solid or soft morphologies. In this paper we use these behavioral measures for the purpose of evolving various behaviors. We investigate whether the use of niching and a simple version of novelty search (without local competition) improves the quality of individuals, but also whether the use of these techniques can lead to a higher diversity of emerging behaviors over multiple evolutionary runs. Although in this work we do not verify the usefulness of the proposed behavioral measures for the purpose of QD algorithms, these measures could be used there too as a behavior characterization (Pugh et al., 2016).

Simulation and evolution model

Simulations reported here have been performed using the Framsticks environment (Komosinski and Ulatowski, 2021a, 2009). This software environment is available as a native application for most desktop and mobile platforms, and also as a library that can be used in various programming languages. The simulation uses two models: elastic “sticks” or rigid bodies. In this work we used the former simulation model called MechaStick with collisions of body parts within a single creature disabled. Individuals are controlled by neural networks of arbitrary topology, and multiple sensors and effectors are available as shown in Fig. 1. The computational experiments were performed on Linux machines and the evolutionary processes were programmed in python (Komosinski and Ulatowski, 2021c), with the native Framsticks library performing mutation, crossover, simulation, recording of raw movement data, and evaluation of the performance of individuals.

Framsticks supports multiple genetic encodings (representations) ranging from direct, low-level ones to indirect, complex ones (Komosinski and Ulatowski, 2021b). In this work we use two genetic representations denoted \( f_0 \) and \( f_1 \).

- The \( f_0 \) genetic representation stores directly all the values of parameters of each component of body and brain except for default values. Each line of text in this representation corresponds to one element of the individual. Lines starting with \( p: \) denote parts (points with mass), \( j: \) corresponds to joints (links between parts), \( n: \) is for neurons and \( c: \) is for neural connections. However, the specifics of this genetic encoding are not particularly important because genetic operators (mutation and crossover) do not modify this textual representation. Instead, mutation and crossover modify phenotypes directly. Mutation changes individual aspects of the phenotype: moves parts randomly, adds or removes them, swaps joints, adds or removes joints, adds or removes neurons and neural connections, changes properties of neurons and weights of neural connections. Crossing over cuts two parent bodies in half using a random plane and then, to produce two offspring, it merges halves from different parents reconstructing broken links. \( f_0 \) is therefore a low-level, direct genetic encoding.

- The \( f_1 \) genetic representation, compared to \( f_0 \), is a higher level encoding, but still a direct one – i.e., there is a one-to-one mapping between genes and phenes. Most
genes (symbols) in the genotype sequence corresponds to a single element in the phenotype. The X symbol produces a stick (two parts connected with a joint). Parentheses ( ) denote a branching of the body structure, with commas inside a parenthesis separating descriptions of individual branches. Branches can be nested, so X (X, X) denotes a three-pointed star with equal angles, X (X, X, X) denotes a cross, and X (X, X (X, X, X), X) resembles a double dagger (a cross stemming from another cross). Additional symbols are used to modify properties of sticks: L and l increase and decrease length, F and f adjust friction, R and z rotate the branching plane by 45 degrees in either direction, etc. Each neuron is described by a sequence of symbols and values enclosed in square brackets. The sequence encodes the type of the neuron, its parameters, relative indexes of neuron inputs and values of connection weights. Mutations remove or add random symbols, add or remove neural connections, or change values by adding a random value drawn from a normal distribution. Two-point crossing over is used. A repair mechanism is employed to fix simple errors like mismatched parentheses.

While the fl encoding is higher level, it also imposes a restriction that is not present in f0: fl is not capable of describing cyclic bodies where joints constitute closed loops, so only tree-like structures can be represented. The space of all possible morphologies is also less restricted in f0 than in fl, because in f0 continuous values can be used for most properties of the body, while in fl most values are quantized. These differences make the two genetic encodings and the corresponding search spaces worthy of comparison.

For the evolutionary experiments, the fitness criterion was velocity, with details described in the following section. Both body and brain were encoded in genotypes and evolved simultaneously.

**Experiments and results**

**Properties of movement**

Experiments reported in this paper use the properties of movement from (Komosinski and Miazga, 2019) as the behavioral descriptors of the creatures.

Simulation of each creature yields three series of values C, D_{xy} and D_z defined as follows:

- C – the center of gravity: a series of triplets c = (x, y, z).
- D_{xy} – the dispersion in the xy plane: a series of values d_{xy}.
- D_z – the dispersion in the z dimension: a series of values d_z.

For each creature we calculate its “dispersion” in a given plane as the weighed standard deviation (Bland and Kerry, 1998) of its body parts. For the center of gravity c and the set containing all body parts P, the dispersion in the xy plane is evaluated as follows:

\[ d_{xy} = \sqrt{\frac{\sum_{p \in P} w(p) \cdot ((p_x - c_x)^2 + (p_y - c_y)^2)}{\sum_{p \in P} w(p)}} \]  

where w(p) is the importance of part p; in the following experiments it was the mass of p. The dispersion in the z dimension is calculated analogously.

We use C to compute two additional descriptors of movement, \( \Delta C \) and \( F \). Let \( E(p_1, p_2) \) denote the Euclidean distance between points \( p_1 \) and \( p_2 \). Then,

\[ \Delta C = \{c'_i : c'_i = E(c_i, c_{i+1}); c_i \in C, i = 1..|C| - 1\} \]  

is a vector of instantaneous speed of a creature, and

\[ F = \text{DFT}(\Delta C) \]

is the discrete Fourier transform of \( \Delta C \).

We use the following properties the descriptors of creature’s behaviors:

1. Average error of linear regression of position in the xy plane (err_{line,xy}).

To calculate this measure it is necessary to find the Euclidean regression line \( y = ax + b \) (Stein, 1983). This is the line for which the sum of the squares of distances from the points of the trajectory is minimal. The average error \( \text{err}_{line,xy} \) is calculated as the mean over all \( \varepsilon_i \), where

\[ \varepsilon_i = \left| y_i - \left( ax_i + b \right) \right| \sqrt{a^2 + 1} \]

2. Horizontal oscillation factor (var_{dis,xy}), calculated as a coefficient of variation of dispersion in the xy plane.

\[ \text{var}_{dis,xy} = \frac{\sigma(D_{xy})}{d_{xy}} \]

3. Vertical oscillation factor (var_{dis,z}), calculated as a coefficient of variation of dispersion in the z dimension.

\[ \text{var}_{dis,z} = \frac{\sigma(D_z)}{d_z} \]

4. Vertical-to-horizontal oscillation ratio (sd_{dis,z,xy}). Calculated as a mean ratio of dispersion in z to dispersion in xy, it compares the range of movement in vertical dimension to the range of movement in the horizontal plane.

\[ \text{sd}_{dis,z,xy} = \frac{\sigma(D_z)}{\sigma(D_{xy})} \]
5. Mean instantaneous speed in \(xyz\) \((\text{inst}_\text{speed})\).

\[
\text{inst}_\text{speed} = \frac{\Sigma C}{\#} \quad (8)
\]

6. Spectral flatness measure \((\text{sfm})\) defined as a geometrical mean of frequency domain of the \(xyz\) instantaneous speed divided by its arithmetical mean.

\[
\text{sfm} = \frac{\sqrt{\ln(F)}}{F} \quad (9)
\]

The value of \(\text{sfm}\) depends on the length of the recorded series of values. If a creature does not move, \(\text{sfm}\) is assumed to be 0.

7. The highest non-zero frequency in the spectrum of the creature’s speed \((f_{\text{max}})\).

\[
f_{\text{max}} = \arg\max_f F[f] \quad (10)
\]

**Experimental parameters**

The fitness criterion during evolution was velocity. Each individual was simulated for 5000 steps, and the value of velocity was calculated as the distance the center of mass of an individual’s body moved between birth and death divided by 5000. For water environment, water level was set to 20 (where 1 is the length of the default “stick”) and the creature was initially placed in the middle between the bottom and the surface. Neural networks of water creatures were simulated immediately starting from the first simulation step, whereas for the land environment, an additional stabilization period was introduced. This period ended once the center of mass of an individual moved for the distance lower than 0.01 during 100 consecutive simulation steps, and only after this period was the neural network simulated. This way the initial movements of the body caused by gravity and a particular shape of the body were not included in velocity calculation and in the analysis of movement properties.

In the experiments, we employed all possible combinations of different genetic encodings, environments, and diversity maintenance techniques, listed below together with their abbreviations used later in the paper. For each setting, the experiment was repeated ten times.

- **genetic representations:**
  - \(f\)\(0\)
  - \(f\)\(1\)

- **environment:**
  - Water
  - Land

- **diversity maintenance technique:**
  - none (None)
  - niching (Niche)
  - simple novelty search (Novel)

During evolution, in each generation, for all individuals, the seven movement properties described earlier were first independently standardized so that their mean is zero and their standard deviation is 1. When the novelty search or the niching technique was employed, the dissimilarity between two individuals was calculated as the sum of absolute differences of these standardized movement properties. For the simple novelty search, the fitness of each individual was the sum of dissimilarities to all other individuals in the population, so the velocity was disregarded. For the purpose of our experiments, we did not use the archive of the most novel past individuals when calculating the fitness of an individual. For niching, fitness of each individual was its measured velocity multiplied by \((1 + \text{the sum of dissimilarities to all other individuals in the population})\). This way, individuals more dissimilar to others in the population were able to achieve higher fitness, which promoted diversification.

In the evolutionary experiments, the population size was constant \((100)\) and the number of generations was fixed \((5000)\). When creating a new population, it was first filled with individuals selected from the old population using the tournament selection with a tournament size of 5. Then, individuals in the new population were grouped into pairs, and 20% of these pairs were replaced by their offspring (two complementary genotypes), resulting in the crossover rate of 20%. Finally, 90% of individuals were mutated.

Since we did not want evolved agents to depend on particular properties of the simulation engine, we added random noise by initializing the values of states of each neuron in each simulated creature with a random value according to the uniform distribution \([-0.01, 0.01]\). Because of this, the evaluation of creatures is no longer fully deterministic, but the evolved agents become more robust. We keep a set of best individuals found in evolution (a “hall of fame”) and once the evolutionary process ends, each individual in this set is evaluated 100 times, and its average fitness is calculated. The individual with the highest average fitness is considered the outcome of the evolutionary process.

Genetic operators may occasionally produce invalid genotypes. When the repair procedure for such genotypes fails, they are not added to the population and genetic operators are used until the entire population consists of valid genotypes.

Given the number of settings enumerated above (the genetic encoding, the environment, and the diversification technique) and the fact that we get one individual from each evolutionary run and there were 10 evolutionary runs per single experimental setting, for further analyses we get \(2 \cdot 2 \cdot 3 \cdot 10 = 120\) individuals.
Figure 2: Dissimilarity in properties of movement between best evolved individuals projected to 2D (fraction of variance preserved is, left to right, top to bottom: 61.6%, 69.6%, 53.6%, 66.3%). Rows are environments (top: land, bottom: water). Columns are genetic encodings (left: $f_0$, right: $f_1$). 3-10 individuals in each plot. Diversity control: none (black circle), niching (green square), novelty (red triangle).
Figure 3: Fitness of the best evolved individuals. Rows are environments (top: land, bottom: water). Columns are genetic encodings (left: $f_0$, right: $f_1$). 3 · 10 individuals in each plot. Diversity control: none, niching, novelty search. Each boxplot demonstrates 10 runs with horizontal line corresponding to the median, boxes representing interquartile range (IQR), whiskers reaching to the farthest results within the range of $[Q_1 - 1.5 \cdot IQR; Q_3 + 1.5 \cdot IQR]$ (where $Q_1$ is the first quartile and $Q_3$ is the third quartile) and outliers being the results beyond this range.
Results

Fig. 2 shows the distances between the best evolved individuals calculated as the difference in 7 properties of movement and projected to 2D with the use of multidimensional scaling (MDS) (Cox and Cox, 2008). Variance preserved within the two most significant dimensions ranges from 50% to 70%, which indicates that a significant part of the variance present in the original distance matrix is not captured in the plots. Despite that, we can make some observations based on these plots.

As novelty search does not select for high fitness, but rather purely for the diversity of behaviors, one could expect that the distribution of behaviors found for this type of diversity control will cover the space of the possible behaviors fairly evenly. Therefore, we can expect movement behaviors discovered by novelty search to be spread most widely. In contrast, as we expect the evolution without any sort of diversity control to often fall into one of the “easy” attractors in the space of all behaviors, we would expect it to show the least diversity.

These expectations are not always, however, met in practice. While the lack of diversity control often leads to the appearance of clusters of similar behaviors (like the relatively tight clusters for the \(f_0\) encoding and the goal of finding a high velocity on land or in water), the range of behaviors found by a simple evolutionary algorithm can still be quite high. The novelty search can also lead to clusters of behaviors (for example for \(f_1\) encoding and the land environment), which, while surprising, can be explained by the fact that the behaviors yielding high velocity may be quite rare, and thus underexplored by the novelty search, while both the standard evolution and the evolution with niching can find such movement strategies, as these two techniques are focused on improving the fitness of individuals. A number of movement techniques selected from the enormous wealth of strategies evolved in these experiments are illustrated in the video: https://youtu.be/L21_AdzvpGc.

Fig. 3 compares the quality of the best individuals found by employing different diversity control techniques. Niching appears to be beneficial for most combinations of encodings and environments. It suggests existence of local optima — niching can help escape these optima or avoid them altogether. An exception is a combination of \(f_0\) encoding and the water environment, where niching is unable to improve upon the results of a regular evolution. It may indicate, that \(f_0\) representation is unfit for the tasks of evolving creatures in water, where the best individuals often consist of a long chain of sticks. While creating such long, snake-like creatures is much simpler in \(f_1\) representation, \(f_0\) is better at creating more complex, interconnected and branching body plans. It seems, however, that in a water environment exploring the possibilities provided by the \(f_0\) encoding might not be the most effective approach.

Novelty search often finds surprisingly fit individuals when the evolution of velocity on land is considered, however it does not perform well for the task of finding creatures with high velocity in water. It is likely due to the fact in a water environment the most effective individuals tend to be rather simple. For this environment, novelty search tends to consistently find creatures of low quality.

Fig. 4 presents the change in the fitness of the best individual found during the course of evolution for all three types of diversity control (or lack thereof). The fitness value rises most consistently for the standard evolution — when there is no diversity control in place, it is rare for the fitness to deteriorate, as the selective pressure acts directly on velocity. Compared to the lack of diversity control, niching leads to a more chaotic improvement over time, with fitness rising and falling on short time scales. Overall, improvements found with niching tend to be more gradual than the rapid spikes in the fitness of the best individual which can be observed when the diversity control is missing. The quality of individuals found with the help of novelty search is highly unstable, as there is no selective pressure that would prevent the loss of good genotypes. Despite that, novelty search sometimes finds surprisingly good individuals, even though they are usually removed from population very quickly.

Conclusions

While the techniques of diversity control can help find individuals of higher fitness than it would be possible with standard evolution, high fitness is not always the only aspect of creatures that we are interested in. Often, especially in artificial life, we are interested in diversity of behaviors and in finding alternative ways of accomplishing a specific task. In such a situation, using the descriptors of behavior – such
as the general properties of movement employed here – as the basis for the diversity-guided search may be beneficial as demonstrated by this work.

In the future, we would like to build upon the work presented in this paper. We plan to further investigate the advantages of diversity control for a small set of fixed morphologies. In such a scenario, only the neural network controlling the movement of the body undergoes evolution. This way we will be able to identify more precisely how individual properties of movement influence the movement patterns emerging from evolutionary processes.

Additionally, we would like to experiment with the weights of the movement properties used while computing the dissimilarity between pairs of individuals. In this paper we assumed that all the properties are equally important, without considering the correlations between their values nor their general impact on the fitness of individuals. A better choice of weights of the properties could lead to finding creatures with even more interesting movement patterns.

Finally, we plan to use the proposed measures of movement as behavior characteristics in the quality diversity algorithms such as novelty search with local competition and MAP-Elites.

The experiments conducted in this paper were time-consuming, however for such a complex task, to fully benefit from the diversity control techniques and to discover their limitations, these experiments should be larger in scale, i.e., larger population sizes and a higher number of generations would be advantageous.

References


