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published in

GECCO '20
2020

DOI (link to publisher)

[10.1145/3377929.3390032](https://doi.org/10.1145/3377929.3390032)

document version

Publisher's PDF, also known as Version of record

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citation for published version (APA)

De Carlo, M., Ferrante, E., & Eiben, A. E. (2020). Comparing indirect encodings by evolutionary attractor analysis in the trait space of modular robots. In *GECCO '20: Proceedings of the 2020 Genetic and Evolutionary Computation Conference Companion* (pp. 73-74). Association for Computing Machinery, Inc. <https://doi.org/10.1145/3377929.3390032>

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Comparing Indirect Encodings by Evolutionary Attractor Analysis in the Trait Space of Modular Robots

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ABSTRACT

In evolutionary robotics, the representation of the robot is of primary importance. Often indirect encodings are used, whereby a complex developmental process grows a body and a brain from a genotype. In this work, we aim at improving the interpretability of robot morphologies and behaviours resulting from indirect encoding. We develop and use a methodology that focuses on the analysis of evolutionary attractors, represented in what we call the *trait space*: Using trait descriptors defined in the literature, we define morphological and behavioural Cartesian planes where we project the phenotype of the final population. In our experiments we show that, using this analysis method, we are able to better discern the effect of encodings that differ only in minor details.

CCS CONCEPTS

• **Computing methodologies** → **Evolutionary robotics**; **Artificial life**; **Generative and developmental approaches**; • **Computer systems organization** → Evolutionary robotics;

KEYWORDS

Evolutionary Robotics, Indirect encodings, Evolutionary Attractors

ACM Reference Format:

Matteo De Carlo, Eliseo Ferrante, and A.E. Eiben. 2020. Comparing Indirect Encodings by Evolutionary Attractor Analysis in the Trait Space of Modular Robots. In *Genetic and Evolutionary Computation Conference Companion (GECCO '20 Companion)*, July 8–12, 2020, Cancún, Mexico. ACM, New York, NY, USA, 2 pages. <https://doi.org/10.1145/3377929.3390032>

1 INTRODUCTION

In Evolutionary Robotics, evolving simultaneously the morphology (body) and the controller (brain) of the robot is particularly interesting [1]. The encoding of an individual, and the corresponding mapping from genotypes to phenotypes, can be direct or indirect. Direct encoding imply that genotypes are directly translated into phenotypes, while indirect involve a process for building the robot body and its controller. Indirect encodings allow for the exploitation of geometrical properties like symmetry [9] and/or the reuse of some genotypical information in multiple parts of the body or brain [3]. Other studies have found that indirect encoding improve

evolvability in certain situations [4]. Indirect encodings are complex, hard to control and analyse, as the mapping process is multi-step and difficult to backtrace. Changes to any step of the process may or may not produce effects on the final outcome.

The aim of this paper is to introduce a new way to analyse the effects of different genotype-phenotype mapping processes on the evolved robots. To this end, we specify a system of several morphological and behavioural descriptors [7] that span a multi-dimensional space and use projections and dimension reduction techniques to analyse the outcome of the evolutionary process in this space. We show that, with this approach we can attribute the frequency of specific attractors to a specific choice regarding the genotype-phenotype mapping.

2 EXPERIMENTAL SETUP

Our robot system is based on RoboGen [1]. The bodies of the robots are modular, composed of three modules: a core brain module, a brick module and an active joint module. The robot brains (controllers) have a network structure where each joint of the body has a coupled oscillator that drives it, and neighboring joints are connected to each other. The design of the controller is based on Central Pattern Generators (CPG) [5, 6]. The genotype is divided into two separate sections: the body and the brain. The body section is adapted from [7], using a Lindenmayer-System inspired process. We define two minor variations in this encoding, that different in whether we allow joint modules to adjacently appear through direct connections between them, or, we force blocks in between joints.

The structure of the brain is fully determined by the body [6], and only the weights of the connections must be specified in the brain section of the genotype. We use CPPNs as genotypes for the brain. The setup is a standard HyperNEAT [2, 10], with speciation disabled. The substrate of the nodes in the CPG is the space containing all the positions of the joints corresponding to the CPG nodes.

We carried out experiments in two different experimental setups. Each setup was evaluated 10 times. We evolved a population of size $\mu = 100$ for 200 generations using a steady state evolutionary algorithm. In each generation $\lambda = 50$ offspring were created by choosing 50 pairs of parents through binary tournament selection and producing 1 offspring for each pair. With probability 0.8, the offspring is obtained with the crossover operator from a pair of parents and then mutated. Instead, with probability 0.2, the second parent is not considered and the offspring is just a mutation of the first parent of the pair. In both cases the mutation probability is set to 0.8. From the resulting set of $\mu + \lambda$ individuals, 100 individuals are selected for survival, again using binary tournament selection. The total number of resulting robots produced in each run is $50 + 200 \cdot 50 = 10050$. Each individual is evaluated for 30 seconds in a

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GECCO '20 Companion, July 8–12, 2020, Cancún, Mexico

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ACM ISBN 978-1-4503-7127-8/20/07...\$15.00

<https://doi.org/10.1145/3377929.3390032>

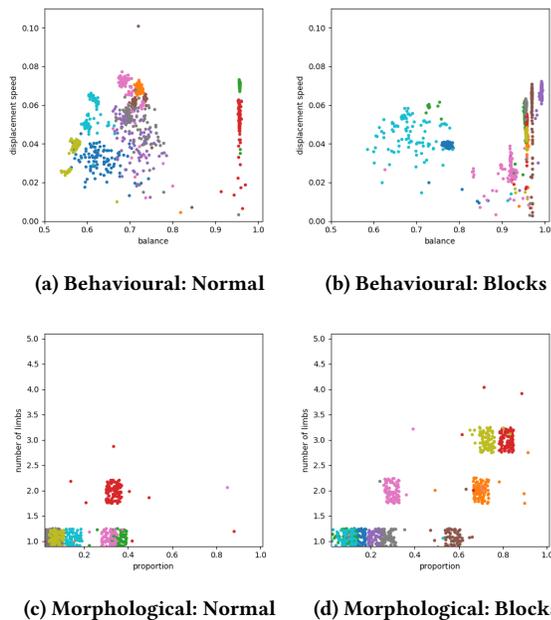


Figure 1: Scatter plots of some measurements of robots in the last generation. Each color represents a single run. In 1a and 1b we plot some behavioural measurements against each other. In 1c and 1d we plot some morphological measurements instead. We added jitter in the morphological plots to better visualize overlapping data.

flat plane. For the fitness of the individual, we measure the total displacement of the robot and divide by 30 seconds to obtain the average speed.

3 RESULTS

Our results (not shown) present a multi-modal distribution of the fitness of the final generation. We hypothesize this corresponds to variations between runs, that is each run converges to a single stable attractor, and not by variations within same run. To confirm this, and to perform our more detailed analysis, we now perform the analysis of the individuals of the final generation projected in the morphological and behavioural trait space hereby defined.

We use a set of descriptors derived from the work in [8]. To this end, we define a trait space as a Cartesian plane where the axis are represented each by one of the morphological or behavioural descriptors. For the behavioural space (Figure 1a and Figure 1b), we choose two descriptors that are weakly correlated with each other: “displacement speed” and “balance” (note that in our experiments displacement speed corresponds to fitness). To represent the morphological trait space of the individuals, the two more weakly correlated descriptors were “number of limbs” and “proportion”.

By analyzing the trait space in Figure 1, we first confirm that the attractors are indeed unimodal, as each run converged to a different region for both the behavioural and morphological trait space. We also observe that there seems to be no linear relationship between displacement speed and balance: a better balance does not

intrinsically mean a better or worse speed of the robot. However, the data seem to show two big clusters of points. We are calling these two clusters “evolutionary attractor groups”, because these must represent each a unique set of behavioural traits. When focusing on one single encoding at the time (as in Figure 1a and Figure 1b), we can observe that the different encodings had different frequency of convergence to the two attractor groups: For example, with the normal encoding only 2 out of the 10 runs converged to the rightmost group, while with the encoding that forced blocks in between joints saw 8 of the 10 runs converge to the same group.

By analyzing the morphological trait space (Figures 1c, 1d) we observe that in the normal encoding an entire class of robots is absent: the more proportionate robots with a number of limbs ≥ 3 . The encoding that is imposing blocks has instead generated many runs where robots with multiple limbs emerged.

Concluding, we can use the trait spaces to visualize evolutionary attractors in a way to have insights on the evolved robot solutions. This analysis disclosed differences between the two encodings that would not be obvious otherwise.

We showed that the encoding that forces blocks within joints seems a minor change but it makes a huge difference: Not only the evolved morphologies were different, but, when blocks were forced, evolution produced more robots that created balanced crawling gaits. In summary, in this paper we have obtained useful insights about encoding the morphologies of evolvable robots and we have showcased a method for investigating evolutionary robotics systems. The method is general, it can be used in a variety of applications. It can also be naturally extended by the addition of controller features.

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