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Generation of Diversity in a Reaction-Diffusion based Controller

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Abstract

A controller of biological or artificial organism (e.g. in bio-inspired cellular robots) consists of a number of processes that drive its dynamics. For a system of processes to perform as a successful controller, different properties can be mentioned. One of the desirable properties of such a system is the capability of generating sufficiently diverse patterns of outputs and behaviors. A system with such a capability is potentially adaptable to perform complicated tasks with proper parameterizations and may successfully reach solution space of behaviors from the point of view of search and evolutionary algorithms. This paper aims to have an early step towards exploring this capability at the levels of individuals and populations by introducing measures of diversity generation and by evaluating the influence of different types of processes on diversity generation. A reaction-diffusion based controller called AHHS (Artificial Homeostatic Hormone System) is

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studied as a system consisting of different processes with various domains of functioning, e.g. internal/external to the control unit. Various combinations of these processes are investigated in terms of diversity generation at both levels of individuals and populations and the effects of the processes are discussed representing different influences for the processes. A case study of evolving a multi-modular AHHS controller with all the various process combinations is also investigated representing the relevance of the diversity generation measures and practical scenarios.

Keywords: Diversity, reaction-diffusion based control, evolutionary computation, modular robotics, bio-inspired control

1 Introduction

Both biological and artificial systems represent high diversity in the patterns of outputs and behaviors that they present, i.e. visual patterns on the body of an animal or locomotion pattern of legs during a walk (see Figure 1 for some examples of biological and artificial organisms). In a biological organism consisting of several cells with identical genotypes, different behaviors and phenotypical traits are exhibited by the cells due to interactions of the cells with each other and with their local environment. For example, various parts of an animal's body are different in their shapes and functionalities. During development of an animal, patterns of protein concentrations are generated along the body and lead the development of the cells. It was found in embryogenesis of *Drosophila melanogaster* embryos [23, 27, 1] that protein gradients govern the segmentation process of the body. In the aggregated phase of the slime mold *Dictyostelium dicoideum*, waves of chemical gradients organize the "body" of the aggregated pseudo-organisms ("slug state") and also its motion is governed by spiral chemical waves [16, 8, 19, 35]. This fact was exploited also to generate swarm robotic applications by mimicking slime mold gradient formation [36]. Complex patterns are also found on the outer skins of many animals or in the growth process of tissue structures, some of them could be described by models of self-organizing "Turing processes" [41, 19, 31].

Diversity can be considered differently at individual level and at the level of a population: By the diversity at individual level, we mean the diversity of a phenotypical trait which is generated across different cells of an organism or in different time-slots. Diversity at individual level can be rephrased as *complexity of a phenotypical pattern* and can be investigated both spatially and temporally. Imagine a multi-cellular organism and consider a particular trait of its cells as an observable trait; for example a level of a particular protein in every cell or

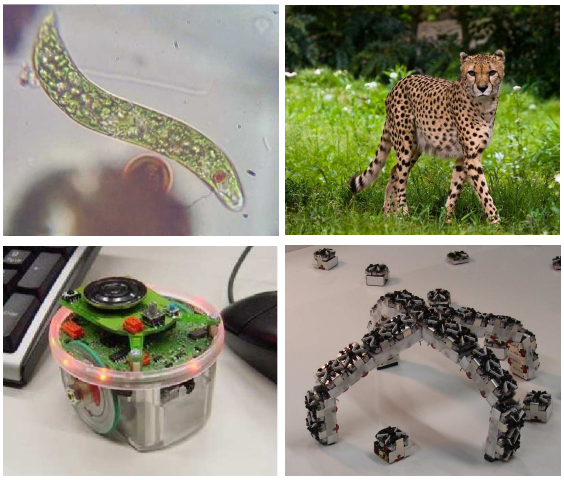


Figure 1: Examples of unicellular and multicellular organisms in biology and robotics. First row represents a unicellular organism (an euglena) and a multi-cellular organism (a cheetah). Second row represents a unicellular robot (ePuck) and a multi-cellular (modular) robot (symbricator). (The images of euglena and cheetah are adapted from Wikimedia Commons).

the color or shape of the cell. By taking a snapshot of the organism's body and considering complexity of the pattern of observable trait along the cells of the body, spatial diversity of the trait can be computed. Similarly, in a single or multi-cellular organism, by observing dynamics of a particular trait during time, temporal diversity can be computed for every single cell and also for the organism as a whole. Having the capability of generating spatial and temporal complex patterns means various behaviors of cells across the body and over time. It may give the organism the required flexibility for performing complicated tasks and dealing with dynamics of real world environments for both biological and artificial organisms.

In robotics, capability of generating diverse outputs is desirable for a controller to provide an adaptive behavior based on received sensory data (extrinsically forced), or based on internal dynamics (intrinsically forced) that may include internal states resulted from past behaviors and effects (memory induced).

A controller in a single-module robot needs to generate output patterns that change the behavior of the module from time to time. In multi-modular robots, different modules containing identical controllers usually need to behave differently based on their role and positioning in the robot. For example in a locomotion task for a modular robot with legged-shaped or snake-shaped configuration, the organism needs to move the legs or different body-segments in a rhythmic motion with different phase-shifts. For example CPGs (Central Pattern Generators) have been used as coupled oscillators generating proper rhythmic motion for body segments of modular robots [22]. As the task gets more and more complicated, the capability of a controller to make complicated output patterns becomes more important. A system that lacks the potential of generating diversity in output patterns of the controller clearly fails to achieve complicated behaviors. Diversity generation is also a remarkable issue from the point of view of Evolutionary Robotics (ER). For example, a modular robot at the beginning of a locomotion task, might be in a resting stance and the information provided by the sensors may not be sufficient for the local controllers to generate a coordinated movement. For such a robot in early generations of evolution, controllers that make even seemingly non-useful movements for the modules may lead to bootstrapping due to symmetry breaking and bring the robot to proper stances where sensory information is exploitable.

At population level, diversity is a feature of population that is measured between different members. It has been studied in the context of Evolutionary Computation (EC) in different areas such as optimization [42] and ER [30]. Various techniques have been investigated for measuring and preserving diversity in populations in order to prevent premature convergence of evolutionary algorithm and staying in local optimums in multi-modal fitness landscapes and also keeping the population adaptable to changes in its environment. The fo-

cus of the studies in population diversity concern with different aspects, i.e., diversity of genotypes [17, 34, 26], phenotypes [12] or as in some recent works in ER, diversity of behaviors [18, 25, 28].

From an evolutionary perspective, capability of generating diverse phenotypes or behaviors in a population means that more areas of the solution space are potentially reachable by the evolutionary process and it can lead to a richer exploration capability which is a necessary condition for a successful evolutionary search. Although it should be noted that for evolution to be successful, proper exploitation mechanisms should be considered as well.

In some areas including ER, where behavior is a result of both genotype and environment (e.g., physics of the body), it might not be enough for evolution to have genotypic diversity in the population while various genotypes may end up to similar behaviors. This is even of more importance within an initial population where bootstrapping the evolutionary process requires a sufficient diversity of behaviors between different individuals. In a set of processes that control dynamics of an organism, it is a desirable property to be able to make phenotypically or behaviorally diverse populations with diverse parameterizations of the processes (genotypical diversity).

In this paper, the capability of generating diversity at both individual and population levels are investigated in the context of a reaction-diffusion-based system called AHHS (Artificial Homeostatic Hormone System). The internal processes that control the dynamics of an AHHS are discussed and the effect of inclusion or exclusion of each process in the capability of generating diversity is investigated. The investigation is performed for a number of internal processes of AHHS that were introduced in the past and also an additional process, called *tunneling*, which is introduced here.

The results are compared with the capability of diversity generation in CTRNN

(Continuous-Time Recurrent Neural Networks) as a well-known adaptive Artificial Neural Network (ANN). CTRNN is chosen as a reference method because of its simplicity, neurobiological plausibility, and being a universal approximator of smooth dynamics [14]. It is also analytically tractable [4] and has been applied to a wide range of problems such as computer vision [10], audio applications [7] and of the most interest of us in adaptive behaviors and robotics, e.g. in Beer and Gallagher [6], Floreano and Mondada [13], Santos and Campo [33], Chiel et al. [9].

This study aims to provide a better understanding of quantitative and qualitative effects of the investigated processes in generating diversity in individual and population levels. The methods of diversity investigation in this work may be usable in the future for other processes of internal dynamics in other systems in order to evaluate and predict their influence in the space of behaviors which are potentially reachable by the system and lead to design systems suitable for generating particular behaviors with respect to the required amount of diversity.

The contribution of this paper that goes beyond the state of the art is summarized as follows:

- Dissection of internal processes of AHHS and analysing their properties.
- Proposing some metrics and methods for investigating diversity in the levels of individual and population from the viewpoint of EC.
- Introducing *tunneling* as a new internal process for AHHS.

2 Processes of dynamics in AHHS

AHHS (Artificial Homeostatic Hormone Systems) is inspired by the signaling network of unicellular organisms and is designed to be evolvable as a decen-

tralized controller applicable in the control of systems that consist of several agents e.g. modular robots. AHHS is a reaction-diffusion-based system which can be seen as a Gene Regulatory Network (GRN) augmented by special communication processes between the units, i.e. diffusion. The method is originally introduced by Schmickl and Crailsheim [37], Schmickl et al. [39] and an improved version is introduced in Hamann et al. [21]. For applications of AHHS in single and multi-modular robotic scenarios see Stradner et al. [40], Schmickl et al. [38], and Hamann et al. [20].

In this work, a restricted version of AHHS is implemented and an additional process of communication between adjacent units is introduced into the system. Considering the main focus of the work, the basic processes of dynamics in AHHS are included in the current implementation and their influence in generating spatial and temporal diversity in the phenotypes is investigated.

An AHHS as introduced before, consists of a set of *hormones* and a set of *rules*. Here in order to add an extra process of communication, a set of *tunnels* is also introduced into AHHS for the first time. Concentration levels of the hormones are state variables of the system and their dynamics are controlled by several processes. These processes include base production, decay, hormone-to-hormone reaction, diffusion and tunneling (see below for their functionality).

To each hormone in an AHHS, a base production rate and a decay rate are assigned. Base production rate indicates the constant increase rate of the hormone. Decay rate, determines the decrease rate of the hormone proportional to its current concentration level.

Process of hormone-to-hormone reaction is supported by *rules*. Each rule represents an influence of one hormone - called input hormone - in production rate of another hormone - called target hormone. Self-influence is allowed. Also,

several rules may contain the same input and target hormones. In that case the influence of the input hormone to target hormone equals to the total value of all the influences.

The diffusion of hormone concentration and the hormone transfer based on tunneling are the means of communication between the adjacent units in an AHHS. To every hormone in an AHHS, a diffusion rate is assigned that specifies the rate of diffusing a hormone from a unit to its neighbors.

In an analogy to intercellular communication in biological cells where adjacent cells connect to each other via tunnel-like junctions to transfer ions and molecules, process of tunneling is introduced to AHHS. In contrast to diffusion, tunneling can act against hormone gradients. Tunneling is implemented by using *tunnels*. Each tunnel represents the influence of a hormone in transfer rate of another hormone from a unit to one of its neighbors.

In a more formal representation of the processes above, the dynamics of hormone concentration H at time t is defined for hormone h as follows:

$$\begin{aligned}\frac{\Delta H_h}{\Delta t} =&\alpha_h + D_h \nabla^2 H_h(t) - \mu_h H_h(t) \\ &+ \sum_i \mathcal{L}_i(t) - \sum_i (\mathcal{T}_i(t) + \sum_n \mathcal{T}_i^n(t)),\end{aligned} \tag{1}$$

where α_h, D_h, and μ_h are base production rate, diffusion rate, and decay rate of hormone h respectively. $\mathcal{L}_i(t)$ is the influence of the linear hormone-to-hormone rule i, and $\mathcal{T}_i(t)$ is the influence of the tunnel i executed in the unit under consideration and $\mathcal{T}_i^n(t)$ is the influence of neighbor unit n to the unit under consideration when tunnel i is executed in the neighbor unit.

A linear hormone-to-hormone rule is defined as:

$$\mathcal{L}_i(t) = \theta(H_k(t))(H_k(t)\lambda_i + \kappa_i), \tag{2}$$

The output is applied to hormone concentration $H_h(t)$ and the input is $H_k(t)$ ($h = k$ is allowed). λ_i and κ_i are two parameters of the rule called dependent dose and fixed dose. These values are allowed to be negative. Trigger function θ determines whether or not the rule is executed.

$$\theta(x) = \begin{cases} 1 & \text{if } min_i < x < max_i \\ 0 & \text{else} \end{cases}, \tag{3}$$

for min_i and max_i as parameters of the rule (between 0.0 and 1.0 in this implementation).

A tunnel is defined with an equation similar to a linear hormone-to-hormone rule:

$$\mathcal{T}_i(t) = \theta(H_k(t))(H_k(t)\lambda_i + \kappa_i), \tag{4}$$

while the output of the equation determines the amount of hormone concentration that is transferred from the unit to one of its neighbors. The target neighbor is represented by a parameter of the tunnel determining the direction of the neighbor.

The basis of activity is different between processes that control the concentration level of a hormone. Some processes act solely upon the concentration level of the same hormone but in some processes other hormones may be involved. In addition, some processes act locally while in other processes other units (neighboring units) are also involved. Another aspect of difference in the processes is conservation of mass in the system. Conservation of mass can be considered for individual hormones or all the hormones together. In the former case, the total amount of every particular hormone throughout the system stays intact by the process. In the later case, the process may transform the proteins to each other but the total amount of the proteins altogether is fixed. In

AHHS, some of the processes maintain conservation of mass for every particular protein. Other processes do not maintain any conservation of mass. These processes may generate or destroy a protein within the system without compensating for this change by an opposite change in the amount of any other protein.

Based on these differences, dynamic processes of AHHS can be set in four groups (see Table 1 for a summary):

- The first group consists of processes which change a hormone's concentration value in a fixed rate or solely based on current value of the hormone itself in the local AHHS unit (no influence by other hormones or by the same hormone in the vicinity). Processes of base production and decay belong to this group. These processes have no conservation of mass. In an analogy with ANN, base production and decay processes are similar to bias and negative recurrent edge of a node in an ANN.

- The second group consists of processes that change a hormone's concentration value based on the value of the same hormone and other hormones (including itself) inside the containing AHHS unit. Hormone-to-hormone reaction belongs to this group. It has no conservation of mass. In an analogy with ANN, hormone-to-hormone reaction is similar to edges between nodes.

- The third group contains processes of implicit communication between units while a change in hormone's concentration depends on the same hormone in the two units. Diffusion process belongs to this group. Diffusion does not require interaction of hormones. It maintains conservation of mass and it only works in one gradient direction from units with higher concentration to units with lower concentration.

- The fourth group contains processes of implicit communication between units while a change in hormone's concentration depends also on other hormones in the other units. Tunneling belongs to this group. Tunnels involve hormone interaction and can act against the gradient. Tunneling maintains conservation of mass and the transfer amount of a hormone is basically defined by other hormones in the source unit and is limited by the amount of the hormone in the target unit.

Table 1: Processes can be grouped based on the hormones involved and whether their activity is internal or external to the unit.

	self-sufficient	other hormones involved
internal to the unit (local) and no conservation of mass	base production, decay	hormone-to-hormone reaction
external to the unit and with conservation of mass	diffusion	tunneling

3 Investigating Diversity

The diversity brought by a controller is a result of processes governing dynamics of the system and inputs from environment. Diversity can be investigated at two different levels: population level and individual level. For each level a proper evaluation metric is required.

In the following sections, we design experiments in order to get an evaluation of diversity at the two levels by using the patterns of generated outputs by AHHS organisms. At population level, we compute the diversity over a population of independent organisms. Each organism contains its own genotype. The diversity at population level is considered as the number of various behaviors generated in the population by different organisms. At individual level, diversity is an internal property of the output pattern generated by a single

organism. We define the individual diversity as the complexity of the output pattern generated by an organism across the organism's body and during time. A number of qualitative types are defined for output patterns considering the complexity in spatial or temporal dimension.
The experiments are performed for different combinations of processes of AHHS with the aim of investigating the effect of each process in generating the diversity for the system.
The results at individual level are compared with the diversity generated by a CTRNN system as a reference method.

3.1 Diversity at Population Level

In this section diversity is studied in population level over randomly generated individuals. We claim that from evolutionary algorithms perspective, a high capability of generating diversity at population level is a desirable property of a system of processes that control behavior of an organism. A diverse initial population means a diverse set of starting points for the searching procedure and is a better initial covering over the search space. Also, the capability of making a high range of phenotypical traits and behaviors means a broad reachable area in search space and increases probability of reaching the solution space. It should be noted that we are aware of the fact that for a system aiming to evolve towards a solution space its not enough to make highest rates of diversity. A controller that generates a purely random behavior over time can generate a high diversity but it is not a controller space that we would like to search in. There need to be a trade off between the exploration capability provided by the high potential of generating diversity and exploitation capabilities of the system to limit the search. The difference between the diversity generation of a purely random generation controller and what we are search-

ing for is that the dynamics of our systems are bound and controlled by a set of restricted processes defined in the system and therefore the randomness is constrained.

In order to evaluate the diversity, first we define a *behavior*. A *behavior* is a sequence of consecutive states of an arbitrary phenotypical trait of an organism that is observed during a limited time. Figure 2 represents example *behaviors* for three AHHS organisms in the first 100 time-steps. In a population of organisms, phenotypical diversity is computed based on the number of different *behaviors* observed in the population.

We set up the experiments with all combinations of AHHS processes of dynamics and in two levels of population-size: First a large population of randomly parameterized AHHSs, namely overall population, is generated. By a *large population*, we mean a population with a size of several times greater than the size of *behavior* space. In order to assess the influence of different AHHS processes in generating diversity in the population, for every combination of AHHS processes, the processes are activated in the system and diversity of the population is evaluated.

In another level of population-size, the overall population is randomly divided into small subpopulations with a fixed size and the same process of diversity evaluation for combinations of processes is repeated for every subpopulation. A subpopulation is considered a typical population that is subjected to evolve in an evolutionary task and its size is chosen respectively.

The diversity of overall population is a representative of the fraction of *behavior* space which is reachable by the system of processes. The maximum diversity in this case is reached if every *behavior* of the *behavior* space is presented by at least one of the individuals in the population. On the other hand, diversity of subpopulations represents diversity of a randomly generated population in a

typical evolutionary task. The maximum diversity within a subpopulation is reached if every individual exhibits its unique *behavior* which is different than *behavior*s of the others.

In addition to the overall and subpopulation diversities, performing a comparison between the two diversities might also be useful. Comparing the diversity in the overall population and its subpopulations gives a measure to assess phenotypical similarity between the subpopulations. For example, if a set of processes of dynamics leads to a set of subpopulations with high internal diversity but the overall diversity (the diversity in the overall population) is comparatively low, it means that the subpopulations are phenotypically similar to each other although they are diverse internally. On the other hand, with the same internal diversity for the subpopulations and a high diversity for the overall population, we can conclude that the subpopulations are phenotypically variant. By applying this analysis, the efficiency of using island models of evolution can be assessed for evolving the system. From the point of view of island models in evolutionary algorithms [43], having a high similarity between the subpopulations (islands) means similar starting points (initial conditions) for individual islands. It might prevent to have a set of islands that each island follows its unique search trajectory and therefore the system fails to benefit from using island models.

3.2 Simulation at Population Level

An AHHS organism is set up consisting of two adjacent AHHS units, say $unit_0$ and $unit_1$. $unit_1$ is observed for a phenotypical trait. Both units contain an identical instance of an AHHS genome and maintain three hormones. The concentration levels of the hormones change in the interval of $[0.0, 1.0]$ under the control of dynamic processes of AHHS. The initial concentration levels are

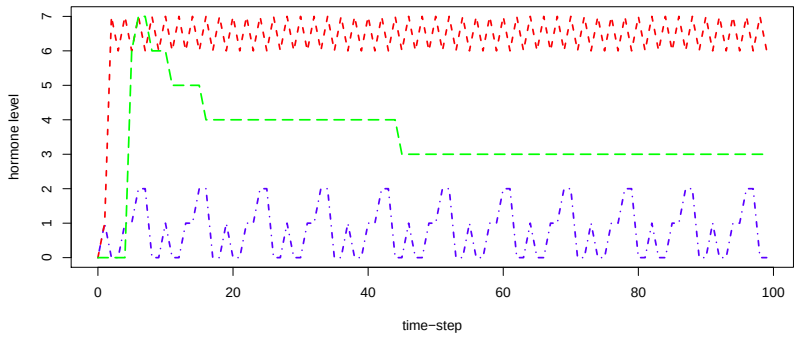


Figure 2: Example *behaviors* for three AHHS organisms in the first 100 time-steps. The observed phenotypical trait in this case is a hormone concentration.

set to 0.5 in $unit_0$ and to zero in $unit_1$. One of the 3 dynamic hormones is arbitrarily chosen and its concentration levels are observed as a phenotypical trait.

The number of rules is 30 and is chosen based on preliminary experiments for maximum diversity generation (data is not shown) and also matches previous experiments with AHHS [21]. The number of tunnels is chosen 3 arbitrarily.

3.3 Results and Discussion at Population Level

A *behavior* is defined as a sequence of phenotypical trait (concentration levels of a chosen hormone) of $unit_1$ in five consecutive time-steps (time-steps 95 to 100). The value range of the trait is discretized into eight bins. Therefore, the size of the behavior-space is 8^5, i.e. 32768. Note that the number of bins (eight) and the size of the sequence (five) are chosen arbitrarily by taking computational plausibility into account.

A large population of 1,000,000 randomly generated AHHSs are created. The arbitrary size of population is chosen to be reasonably higher than the size of

behavior space such that the computed value for overall diversity is statistically meaningful. The population is then divided into 10,000 subpopulations of size 100. The size of subpopulations is again arbitrarily chosen based on a typical population-size of AHHSs in an evolutionary robotic task.

Diversity in a population is computed as the number of various *behaviors* that are achieved by at least one individual of the population divided by the maximum number of possible *behaviors* in the population. Note that if the size of population is greater than the size of *behavior* space, the maximum possible *behaviors* in the population equals the size of behavior state, otherwise the value equals the population-size. This means, with a *behavior* space of size 32768, the maximum number of possible *behaviors* in a subpopulation of size 100 is 100, but the maximum number is 32768 for the overall population of size 1,000,000.

The diversity is evaluated for all the different combinations of AHHS processes in all of the subpopulations and the overall population. In order to do that, for every combinations of AHHS processes, a randomly generated population (of size 1,000,000) is created, and the diversity of the overall population as well as its subpopulations are computed (as described above).

Figure 3 represents the average diversity for subpopulations, the diversity of overall population, and a value, called "ratio". This value is a factor of ratio between the overall and subpopulation diversities and is used to facilitate comparison between the two diversities in order to assess phenotypical similarity between the subpopulations and consequently to assess the usefulness of applying island models for the system. The value is calculated as the number of various *behaviors* achieved in the overall population divided by the averaged number of various *behaviors* achieved in the subpopulations and scaled by a factor of 100. Although this ratio is not an accurate measure of similarity between the subpopulations it makes an impression about the concept

especially when two combinations of processes show a significant difference between their ratios.

ANOVA test is executed on the data for diversity generation of subpopulations. The results are represented in Table 2 suggesting a high importance for hormone-to-hormone-reaction and base-production processes, and then diffusion and decay, and lowest importance for tunnels in making diversity in population level.

The combinations of processes are arranged in Figure 3 by the increasing order of overall diversity. For the clarity of the figures, the processes *hormone-to-hormone reaction*, *decay*, *base-production*, *diffusion*, *tunneling* are encoded as r, c, a, d, t respectively.

Respective to diversity in overall population, three groups of process combinations can be detected in Figure 3. Process combinations that show no diversity and basically make a single *behavior* of "doing nothing" make the no-diversity group. The rest of process combinations are grouped into low overall-diversity and high overall-diversity generators. A jump in overall diversity representing an increase in the reachable *behavior* space is starting from process combination $\{rct\}$ and distinguishes the two groups.

The following observations are implied by Figure 3:

- Process combinations of $\{c\}$, $\{r\}$, $\{rc\}$, and *no process* are in no-diversity group.
- The process combinations in high overall-diversity group also represent high "ratio" value in comparison to the group of low-overall-diversity that means there is low similarity between the subpopulations.
- Since the observed unit is initially empty, in order to generate some diversity, the process combinations need to include a communication process

enabling transfer of the hormones from outside of the unit (*d* or *t*), or an internal process that initiates production of hormones out of nothing (*a*).

The combinations that do not have any of these processes make no diversity and place in "no diversity" group

- Processes *a*, *d* and *t* can make some diversity on their own.

  For $\{a\}$, concentration of the observable hormone independently increases in $unit_1$ with a constant rate [1]. Due to randomized parameterizations of individuals in the population, the rate of increase may be different in various individuals making diversity in the population.

  In the case of $\{d\}$, the hormone is diffused from $unit_0$ to $unit_1$ with various rates until the concentrations of the hormone become equal in the two units. Therefore, again increase of the hormone might be detectable in $unit_1$ with different rates for different individuals. [2].

  In $\{t\}$, the hormone is first transferred from $unit_0$ based on the parameters of tunnels in the individual. At the same time other hormones may have also been transferred from $unit_0$ to $unit_1$ that would lead to a back-transfer of the observable hormone from $unit_1$ to $unit_0$. Diversity is generated based on the parameters of the tunnels in every individual.

- "Ratio" in Figure 3, shows a higher value for $\{t\}$ comparing $\{a\}$ and $\{d\}$ indicating less similarity between the subpopulations controlled only by $\{t\}$.

- All the combinations in the group of high overall-diversity contain *r*. Since *r* is an internal process with no ability of generating hormones out

[1] The concentration ends up to the maximum concentration level (1.0), but in the interval of observation it might not be still saturated for some values of constant production rate.

[2] The diversity is lower than $\{a\}$ because the maximum possible value for the concentration level in this case is half of the initial concentration level of the hormone in $unit_0$ ($0.5/2$)

of nothing, in the process combinations in this group, a communication process (d or t) or a process that is able to independently initiate hormone production (a), is included. As in the figure, all combinations that include r together with such a process, is in the group of high overall-diversity, except for $\{rt\}$ although $\{rt\}$ still represents a high "ratio" comparing other combinations in its group (low-overall-diversity) representing comparatively low similarity between subpopulations.

- In the group of high overall-diversity, the combinations that include d make higher diversity in both subpopulation and overall population in contrast to their counterpart combinations with no d. These combinations also show lower similarity between subpopulations (high "ratio") that implies usability of employing island models of evolution in searching the *behavior* space. This is not necessarily the case for the combinations in low-overall-diversity group.

- Similar points as above can be mentioned for the combinations that include c.

- Another point that is implied by focusing at subpopulation diversity is that combinations with a make higher subpopulation diversities comparing their counterparts with no a, except for $\{adt\}$ which makes slightly less diversity.

3.4 Diversity at Individual Level

Diversity at individual level is defined as a property of every individual organism and is computed for an observed phenotypical trait. Diversity of a phenotypical trait (e.g. output of a controller) which is generated by a system over

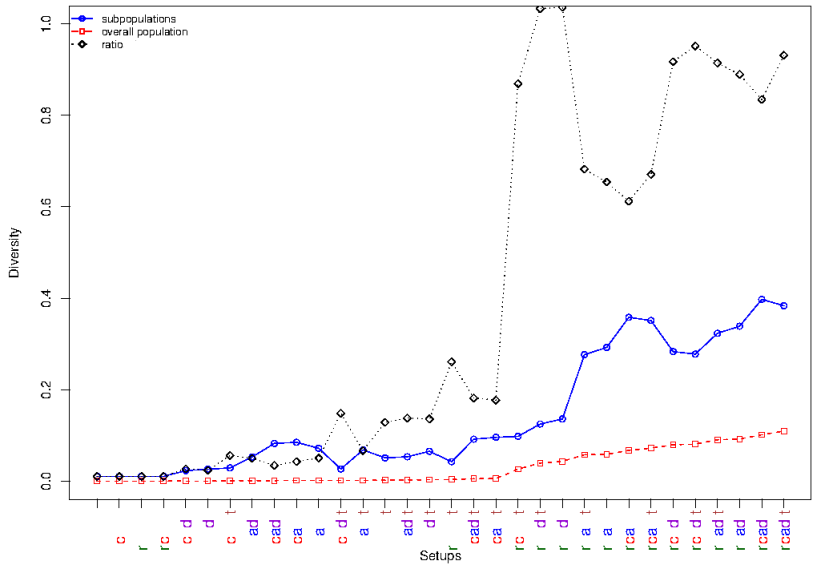


Figure 3: Diversity of behaviors averaged over all subpopulations (solid line), diversity in the whole population (dashed-line), and the ratio between number of various behaviors achieved in the whole population and the averaged number of various behaviors achieved in the subpopulations (dotted-line). r, c, a, d, t indicate hormone-to-hormone reaction, decay, base production, diffusion, and tunneling, respectively.

Table 2: ANOVA test is used to statistically compare the influence of every underlying process in diversity generation of the system at population level. The significantly high values of *r* and *a* suggest a high importance for these processes. The values suggest the next level of importance for *d* and *c*, and the lowest importance for *t*.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
reaction (*r*)	1	25625873.17	25625873.17	3549429.14	0.0000
decay (*c*)	1	1363111.01	1363111.01	188803.94	0.0000
production (*a*)	1	13772313.32	13772313.32	1907597.45	0.0000
diffusion (*d*)	1	2131198.84	2131198.84	295191.47	0.0000
tunnels (*t*)	1	90217.96	90217.96	12496.05	0.0000
Residuals	319968	2310078.34	7.22		

time and over units of the organism is investigated by defining some measures of complexity for the spatiotemporal pattern of the trait.

The word *complexity* has been used in scientific works with many different meanings and in different applications (for a review on complexity measures see Badii and Pliti [2], Daw et al. [11]). Complexity can be measured based on entropy with its information theory definition [32]. The metrics can consider aspects of entropy together with properties of dynamical systems [3]. Other methods are related to Komologrov complexity [24] and measure algorithmic complexity of the pattern.

Here we are interested in measuring irregularities of an observed trait along both spatial (organism's body) and temporal axes. With some similarity to a work by Fusco and Minelli [15] in measuring morphological complexity, number of consecutive monotonic subsequences with non-zero slopes are used as an estimate of irregularity.

For a sequence $\mathbf{X}$ of observed traits:

$X = X_1 \frown X_2 \frown ... \frown X_N$

where X_i is a monotonic subsequence of X and the sign of slope for every X_i and X_{i+1} are different, complexity is defined as:

$$Cs(\mathbf{X}) = \begin{cases} 0 & \text{if } slope(X) = 0 \\ N & \text{else} \end{cases} \tag{5}$$

In this work, an organism is set up as a row of adjacent units with identical controller and observe it for an arbitrary trait during a fixed period of time. A spatiotemporal matrix is generated out of the observed values while every row in the matrix represents the state of the observed trait for the organism in a single time-step. In the same way, every column of the matrix represents the state of the trait in a single unit over time (see Figure 4 for some examples). Note that in this study the system i not interacting with environment and therefore there is no input from the outside. Therefore, all the generated diversity comes from inside and demonstrates the intrinsic capability of the system for diversity generation.

Table 3: Type assignment to a spatiotemporal pattern by using Eq. 5

Static-flat	$\forall i : Cs(a_{i,*}) = 0$ and $\forall j : Cs(a_{*,j}) = 0$
Dynamic-flat-monotone	$\forall i : Cs(a_{i,*}) = 0$ and $\forall j : Cs(a_{*,j}) = 1$
Dynamic-flat-nonmonotone	$\forall i : Cs(a_{i,*}) = 0$ and $\forall j : Cs(a_{*,j}) > 1$
Static-complex-monotone	$\forall i : Cs(a_{i,*}) \leq 1 \wedge \exists i : Cs(a_{i,*}) = 1$ and $\forall j : Cs(a_{*,j}) = 0$
Static-complex-nonmonotone	$\forall i : Cs(a_{i,*}) > 1$ and $\forall j : Cs(a_{*,j}) = 0$
Dynamic-complex	$Cs(a_{i,*})$ is increasing or is not monotonic over i; or $Cs(a_{i,*})$ is fixed and $\exists j : Cs(a_{*,j}) > 0$
Transient-flat	$\forall i : Cs(a_{i,*}) \leq 1 \wedge \exists i : Cs(a_{i,*}) = 1$ and $\forall j : Cs(a_{*,j}) \leq 1 \wedge Cs(a_{*,j}) = 1$
Transient-complex	$\exists i : Cs(a_{i,*}) > 1$ and $\forall j : Cs(a_{*,j}) \leq 1 \wedge Cs(a_{*,j}) = 0$
Vanishing	$Cs(a_{i,*})$ is decreasing over i

Qualitative types of Spatiotemporal patterns We define a set of qualitative types for spatiotemporal patterns. The behavior of the complexities along both spatial and temporal coordinates are considered in these definitions.

- *Static-flat*: no diversity in any direction i.e. identical value for the trait all over the organism and during the whole time (Figure 4a).
- *Dynamic-flat-monotone*: no spatial complexity and low temporal complexity, i.e. identical value for the trait along the organism's body and the value changes monotonically over time (Figure 4b).
- *Dynamic-flat-nonmonotone*: no spatial complexity and temporal complexity, i.e. no difference between the units of organism along the body but the behavior of the units has non-monotone dynamics and shows some ups and downs in the value. (Figure 4c).
- *Static-complex-monotone*: low spatial complexity while the value of the trait changes monotonically along the body. The body-pattern does not change over time (no temporal complexity) (Figure 4e).
- *Static-complex-nonmonotone*: spatial complexity while the change is non-monotone along the body. The body-pattern does not change over time (no temporal complexity) (Figure 4f).
- *Dynamic-complex*: a complex body-pattern that changes over time and does not loose complexity (Figure 4d).
- *Transient-flat*: very low spatial and temporal complexity with a monotonic change over the time and along the body. It eventually converges to either a flat pattern or a static-complex-monotone pattern (Figure 4h).
- *Transient-complex*: very low temporal complexity with a monotonic change but a spatial complexity with non-monotonic change along the body.

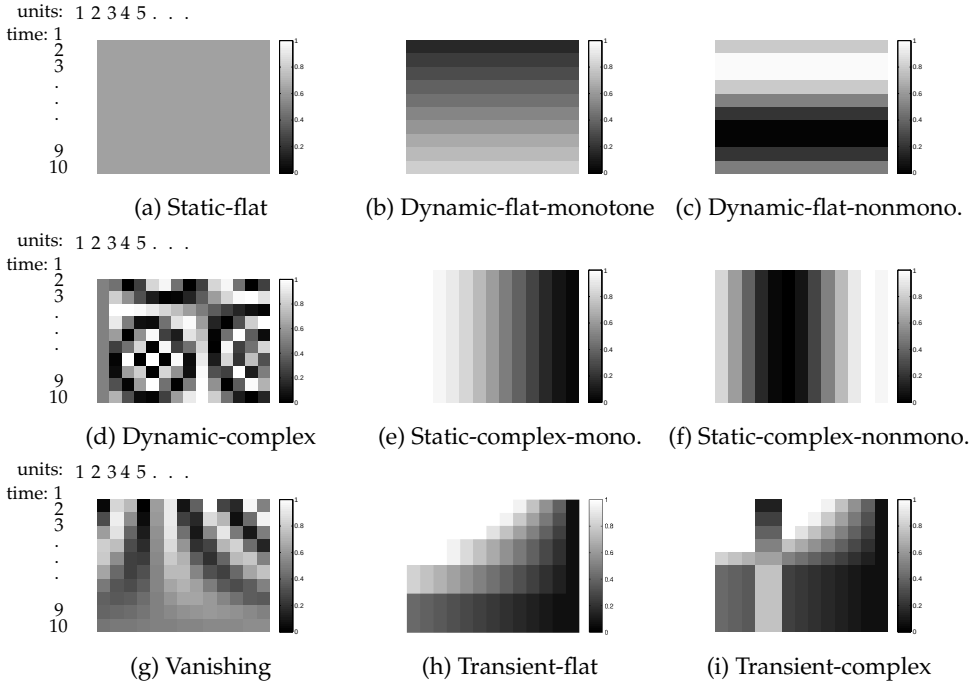
It eventually ends up to an either monotone or non-monotone static-complex pattern (Figure 4i).

- *Vanishing*: spatial complexity decreases over time. It may eventually converges to zero and represents a flat pattern or may end up in a dynamic-complex pattern with a spatial complexity which does not change over time (Figure 4g).

As mentioned, a *vanishing* pattern may eventually converge to other pattern types. In the same way for a *dynamic-flat-monotone*, since the trait values are bounded, a monotonic change (either increasing or decreasing) is a transient pattern that may end up at *static-flat* pattern, or it might be a part of very slow *dynamic-flat-nonmonotone* pattern. We have chosen the number of observation time-steps comparatively long in respect to the number of bins (20 to 8, see section 3.6). Therefore, we suspect that most of the *dynamic-flat-monotone* patterns are transient patterns ending up to *static-flat*.
In order to make an impression of usefulness of different types of patterns, it might be interesting to think of some ways of exploiting the patterns in a simple application. The non-transient patterns in a limited locomotion of a modular robot may be a good example:

- Based on the definition of the type of dynamic-complex patterns, it comprises many different patterns including traveling waves. Modular robots can benefit from traveling waves along the body (as it is exploited in CPGs [22]), e.g. modular robot in a snake configuration or a legged organism.

- Static complex patterns (either monotone or nonmonotone) are similar to body pattern in biological embryos [23, 27, 1]. In a similar way as embryos, these patterns can be used for structuring and discrimination



(a) Static-flat (b) Dynamic-flat-monotone (c) Dynamic-flat-nonmono.

(d) Dynamic-complex (e) Static-complex-mono. (f) Static-complex-nonmono.

(g) Vanishing (h) Transient-flat (i) Transient-complex

Figure 4: Examples of different qualitative types of a spatiotemporal patterns. Horizontal coordinate represents the units along the organism's body and vertical coordinate represents time.

between different modules of a robot and assigning different roles to different modules. For example, having an oscillation generator in the modules, a static pattern can be used to assign different phase-shifts to different modules such that a traveling wave is generated along the body.

- A non-monotone dynamic flat pattern basically means an oscillation over time where all the units perform the same behavior. By externally assigning different phase shifts to different modules, a traveling wave can be produced generating a proper locomotion for the modular robot.

In order to assign a type to an spatiotemporal pattern that is represented by a matrix $\mathbf{A}$, complexity is measured for every row and every column of the matrix by using Eq. 5. Let $Cs(a_{i,*})$ be the measured complexity of i^{th} row of $\mathbf{A}$

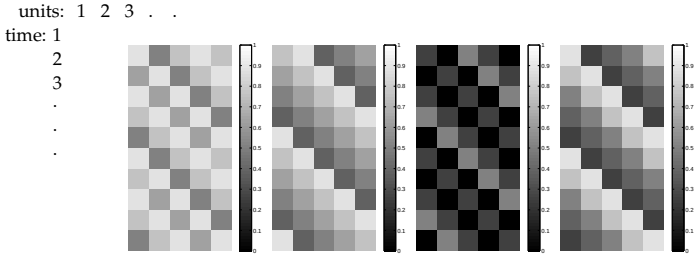


Figure 5: four example patterns evolved for generating a traveling wave by AHHS.

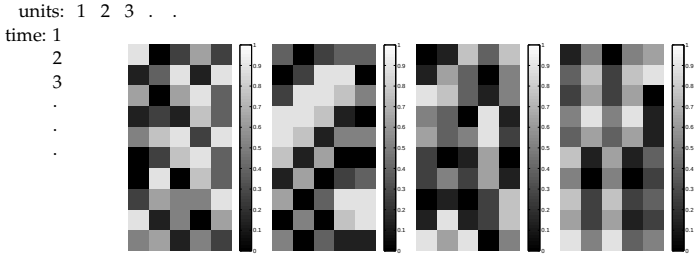


Figure 6: four example patterns evolved for maximum overall complexity by AHHS.

and $Cs(a_{*,j})$ be the measured complexity of j^{th} column of $\mathbf{A}$. Table 3 describes the method for assigning a type to a spatiotemporal pattern.

The number of spatiotemporal patterns of each type are counted in populations of organisms with randomly parameterized controllers. Independent experiments are performed for controllers of all combinations of AHHS processes and also for CTRNN controllers (see below) and the results are compared.

Figure 5 represents some patterns generated by AHHS exhibiting traveling waves. As another example of spatiotemporal patterns generated by AHHS, Figure 6 represents patterns with maximum total complexity that is measured along both spatial and temporal dimensions.

3.4.1 CTRNN

CTRNNs (Continuous-Time Recurrent Neural Networks) are Hopfield continuous networks with unrestricted weights matrix. They are networks of biologically inspired neurons that have been shown to be universal approximators of smooth dynamics and exhibit complicated dynamical behaviors [14]. A neuron i in the network is of the following general form:

$$\tau_i \dot{y_i} = -y_i + \sum_{j=1}^{N} w_{ji}\sigma(g_j(y_j + \theta_j)) + I_i \tag{6}$$

where y_i is the state of the ith neuron, τ_i is the neuron's time constant, w_{ji} is the weight of the connection from the jth to ith neuron, θ_i is a bias term, g_i is a gain term, I_i is an external input, and $\sigma(x) = 1/(1 + e^{-x})$ is the standard logistic output function.

3.5 Simulation at Individual Level

AHHS settings for the experiment An AHHS organism comprises of six adjacent AHHS units is created, say $unit_0$ to $unit_5$. All units contain an identical instance of an AHHS genotype and maintain three hormones. Hormones' concentration levels may change in the interval of $[0.0, 1.0]$. Initially, the concentration levels of all the three hormones are set to 0.5 in $unit_0$ and to zero in other units. One of the 3 hormones is observed as the phenotypical trait in $unit_1$ to $unit_5$.

CTRNN settings for the experiment In the same way as AHHS organism, an organism of six adjacent CTRNN units is created, say $unit_0$ to $unit_5$. Every CTRNN unit consists of three nodes which assimilates the three hormones of the AHHS implementation. Every unit is connected to its immediate neighbors by an incoming and outgoing edge for every peer node in the two units. Initial

Figure 7: An example spatiotemporal pattern generated by an AHHS organism of size five in 20 consecutive time-steps.

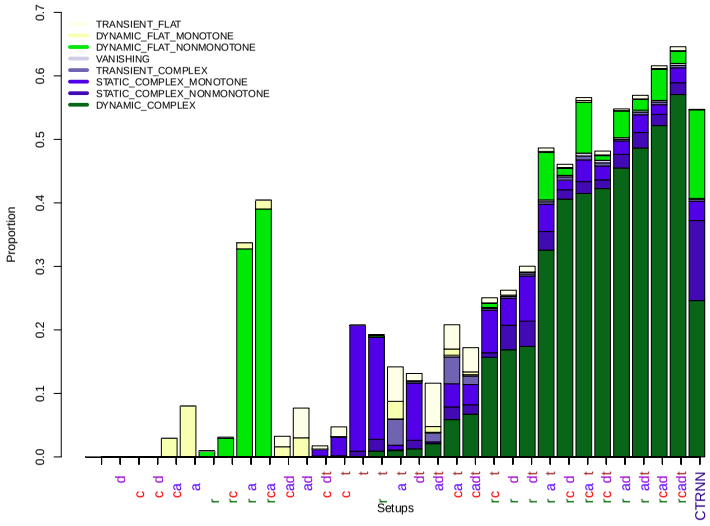
value of each node is set to 0.5 in $unit_0$ and set to zero in other units. I_i is set to zero for all the units. Weights are randomly initialized. By considering the study of the parameter space structure of CTRNN by [5], the values of the θs are set based on the weights such that the richest possible dynamics is achieved. One of the 3 nodes is observed as the phenotypical trait in $unit_1$ to $unit_5$.

3.6 Results and Discussion at Individual Level

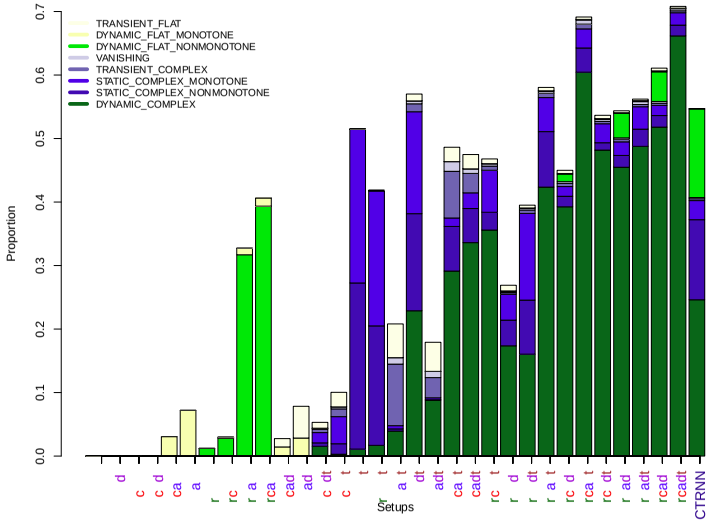
For every combination of AHHS dynamics processes as well as CTRNN, 10,000 randomly generated organisms are independently generated and run for 100 time-steps. The arbitrarily chosen phenotypical traits are observed in time-steps 80 to 100. Similar to the experiments at population level, the value range of the observed trait is discretized into eight bins. A *spatiotemporal pattern* is formed as a 20×5 matrix representing the state of the trait observed in the five units of the organism in 20 consecutive time-steps. Figure 7 demonstrates an example *spatiotemporal pattern*.

Figure 8a represents the number of patterns of different types for the different AHHS combinations of processes and for CTRNN. The numbers are represented proportional to the size of populations. The values for the type *static-flat* patterns are not represented for the sake of clarity.

In order to get an evaluation of the influence of number of tunnels in generation of different spatiotemporal patterns, the experiments are repeated for AHHS



(a) for three hormones, 30 rules, and three tunnels.



(b) for three hormones, 30 rules, and 30 tunnels.

Figure 8: Pattern types for all combinations of processes of AHHS and for CTRNN. *Static-flat* patterns are not shown (the rest of each bar up to 1.0). r, c, a, d, t indicate hormone-to-hormone reaction, decay, base production, diffusion, and tunneling processes, respectively.

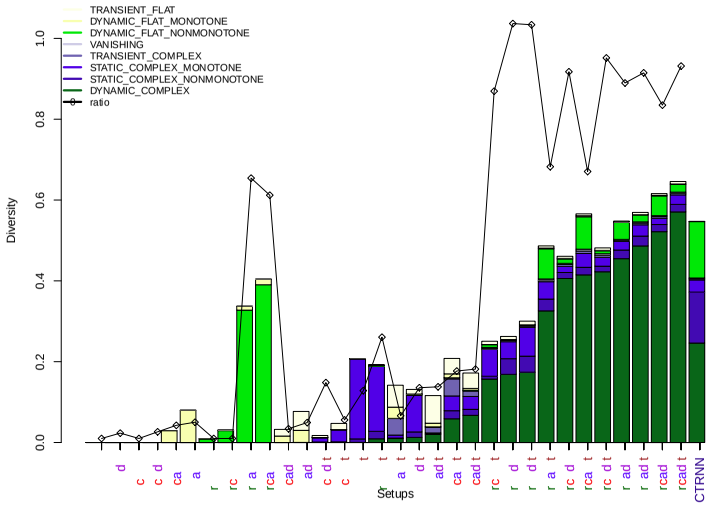


Figure 9: Results from both population level and individual level in a same figure. The setting is three hormones, 30 rules, and three tunnels. r, c, a, d, t indicate hormone-to-hormone reaction, decay, base production, diffusion, and tunneling processes, respectively

combinations of processes while the number of tunnels are set to 30 and the number of hormones and rules stay unchanged (3 and 30 respectively). Figure 8b represents the results.

The following observations are implied by Figure 8a and Figure 8b:

- Only a negligible number of patterns generated by CTRNN exhibit the transient pattern types (*dynamic-flat-monotone*, *vanishing*, *transient-flat*, and *transient-complex*). Most of the patterns of types *static-complex* are non-monotone which means an static oscillatory-shape pattern over the body.

- Process combinations $\{d\}$, $\{c\}$, $\{cd\}$, and *no process* do not generate any interesting pattern (only *static-flat* pattern that is omitted from the figure, or *dynamic-flat-monotone* which is a transient pattern).

- Since all the units of the organism except $unit_0$ that is not observed, start with the same initial hormones' concentration levels of zero, a communication process is necessary to transfer some hormones from $unit_0$ in order to initiate symmetry breaking. Therefore, process combinations with no *d* or *t* only generate patterns with no spatial diversity (*flat* patterns).

  Due to that, process combinations $\{ca\}$, $\{a\}$, $\{r\}$, $\{rc\}$, $\{ra\}$, $\{rca\}$, generate *dynamic-flat-monotone* and *dynamic-flat-nonmonotone* patterns. Since *dynamic-flat-monotone* is a transient pattern, $\{ca\}$ and $\{a\}$ eventually end up to *static-flat* patterns. That is because *a* and *c* respectively increase and decrease the value of the observed hormone by a constant rate. If the rate of decrease is higher than the increase-rate, the hormone level never raises from zero. If the increase-rate dominates the rate of decrease, the hormone concentration level eventually ends up at saturation level (1.0) for all the units making *static-flat* pattern.

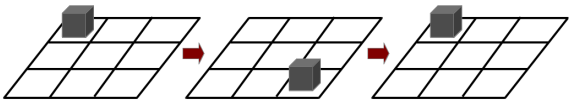
  On the other hand, process combinations $\{r\}$, $\{rc\}$, $\{rca\}$ and $\{ra\}$ are

capable of generating *dynamic-flat-nonmonotone* patterns due to inclusion of r while $\{rca\}$ and $\{ra\}$ generate rather high number of *dynamic-flat-nonmonotone* due to inclusion of a along with r which enables more possibilities in the values by raising the hormone levels.

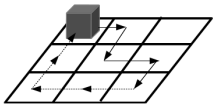
- The only process that is able to generate *static-complex* and *dynamic-complex* patterns on its own is $\{t\}$ according to both Figure 8a and Figure 8b.
- r represents an important effect in generating *dynamic-complex* patterns although it requires to be combined with a communication process (d or t). The only exception is the process combination $\{rt\}$, that represents low number of *dynamic-complex* patterns although the number of *static-complex* patterns are rather high.
- The low number for *dynamic-complex* patterns in comparison with *static-complex* patterns in $\{rt\}$ is also valid in Figure 8b where the number of tunnels is much higher.
- The highest amount of diversity generation is associated to the process combinations that include both r, a, and d while the combinations that include all r, a, and t generate considerably high diversity especially if the number of tunnels are high (Figure 8b).
- Comparison of Figure 8a and Figure 8b implies that the increase in the number of tunnels makes a considerable impact in the diversity generation of the system in favor of *dynamic-complex* patterns.

4 Evolving for a Task

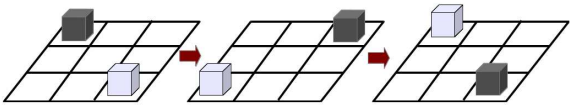
In this section, different settings of AHHS are evolved for a multi-modular controller in order to give an impression of the relevance between the diversity



(a) Conveyor for a single box.



(b) A potential path for transporting the single box.



(c) Conveyor for two boxes.

Figure 10: Demonstration of the conveyor experiments.

measures described in the previous sections and evolutionary tasks in practice. The scenario is about a special conveyor consisting of a 3×3 grid. Every cell of the grid has a value that can be considered the height of the cell (or a potential level). Every cell's height is controlled by an AHHS controller. At the beginning of the task, a box(s) stands on a specific cell(s) of the grid. The task is to convey the box from the starting point to two target points one after the other (Figure 10). The box is moved to one of the Von Neumann neighbouring cells if the height of the neighbour is lower than the height of the current cell (the difference needs to be more than a specific threshold). If there are several neighbours with sufficiently low height, the box moves to the neighbour with the lowest height.

AHHS configuration All the AHHS controllers are genetically identical with 3 hormones, 3 tunnels, and 30 rules. One of the hormones is chosen to directly determine the controller's output value. Hormone concentrations are variable between zero and one. At the beginning of an evaluation, all the hormone

concentrations are set to 0.5 in the cell (0,0) and to zero in other cells.

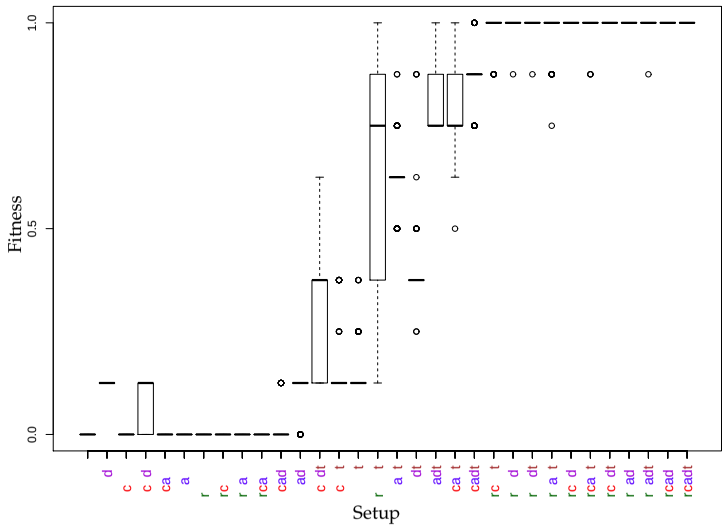
Evolutionary algorithm configuration For every experiment, a population of 30 randomly initialized AHHS are evolved for 1000 generations. Elitism is applied for 3 best individuals. The rest of the population are selected by linear proportional selection and mutated to make the next generation (for the details of evolutionary operators of AHHS see [20]).

4.1 Experiments

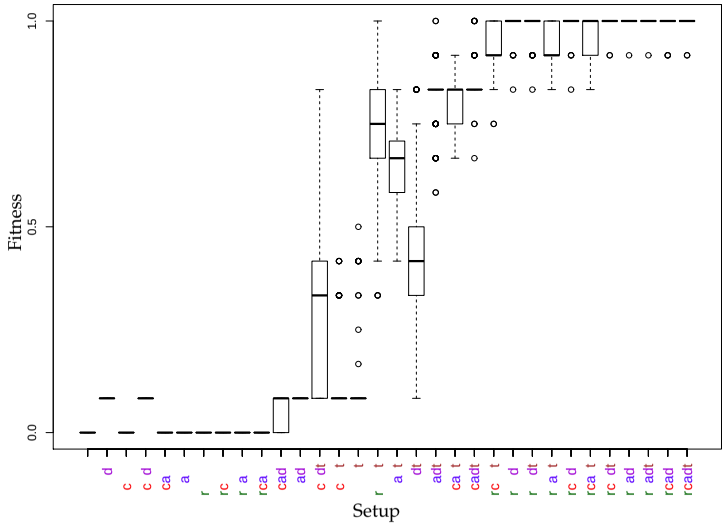
AHHS is evolved for generating controllers for two experiments with the special conveyor. A difference of $+0.02$ between the output value of a cell holding the box and one of its Von Neumann neighbours would be enough for pushing the box to the neighbouring cell. In the first experiment, a single box has to be transported. The box starts at cell (0,0) and is supposed to move to (2,2) (as it's first target) and moves back to (0,0) (as the second target) in maximum 10 time-steps overall. Figure 10a represents the first experiment and Figure 10b represents a potential path of the box generated by the conveyor. Note that in every move of the box, the value of current cell has to be more than the next cell (with a value of 0.02) and therefore the output pattern has to be changed during time.

In the second experiment, two boxes are placed at cells (0,0) and (2,2) and have to be conveyed at the same time. The boxes are supposed to move to the first targets at (2,0) and (0,2) respectively and then to their second targets at (2,2) and (0,0). The process is allowed to take 6 time-steps overall. Figure 10c demonstrates the second experiment.

Fitness values are calculated at the end of each experiment as follows:



(a) Fitness values for the conveyor experiment for a single box



(b) Fitness values for the conveyor experiment for two boxes

Figure 11: Fitness values of the conveyor experiments for all combinations of processes of AHHS. Box-plots indicate median and quartiles, whiskers indicate minimum and maximum, circles indicate outliers (values are collected from 100 independent runs in each case).

$$Fitness = 1 - \frac{\sum_{i=1}^{n} d_i}{8} \tag{7}$$

where n is the number of boxes, and d_i is defined as follows:

$$d_i = \begin{cases} dist(t_1, t_2) + dist(c, t_1) & \text{if } t_1 \text{ is not met} \\ dist(c, t_2) & \text{else} \end{cases} \tag{8}$$

where t_1, t_2, and c are the coordinations of the first and second targets and the final position of the box, and $dist(a, b)$ is the distance between a and b in terms of minimum number of steps necessary for reaching b starting from a.

In both experiments, the AHHS controllers need to make dynamic and complex patterns to fulfill the tasks. Note that, the system we have here is a 2D system which is different than the experiments of diversity measures.

Both experiments are repeated for 100 independent runs for all possible combinations of AHHS processes and the results are demonstrated in Figure 11a and Figure 11b. The order of the results for the demonstrated combinations of processes is the same as Figure 9.

By comparison of Figures 11a and 11b with Figure 9, we conclude that process combinations which are able to generate high numbers of *complex-dynamic* patterns are more successful in producing proper behaviour for the two investigated tasks. On the other hand, the combinations which were detected as poor diversity generators fail to produce the desired behaviours. Another interesting result of these comparison concerns the process combination $\{rt\}$. In both experiments, this combination is successful while, for example, $\{at\}$ and $\{dt\}$ with higher numbers of *complex-dynamic* patterns failed to evolve for the desired behaviours. In a similar way, $\{cdt\}$ seems to be more evolvable towards the desired behaviors comparing its neighboring process combinations. This might be explainable by looking at the $ratio$ factor of the diversity in popula-

tion level (in Figure 9). $ratio$ values are considerably higher for $\{rt\}$ and $\{cdt\}$ in comparison with their neighbouring process combinations representing that evolution is more successful in finding the desired behaviours (if exist) due to intrinsic diversity of the populations with these settings.

5 Conclusion

In this article, capability of generating diversity is investigated as a desirable property of controller systems with non-trivial behaviors, e.g. in evolutionary robotics, where a known problem of bootstrapping of the evolutionary process can be reduced by having behavioral diversity in the population [29].

The controller system that is investigated here is AHHS. The implemented AHHS system includes the processes of *hormone-to-hormone-reaction*, *decay*, *base-production*, and *diffusion* which were introduced before [37, 39], and a newly defined process called *tunneling*. These processes that drive dynamics in an organism that is controlled by AHHS are described and discussed based on their scope of functioning and their influence on generating diversity.

Metrics of diversity are introduced in different levels: population level and individual level. The metrics at population level evaluate diversity of behaviors generated by different organisms in a random population. The evaluation is performed for populations of both big and small sizes in respect to the size of behavior-space. For a big population (namely, overall population) the results demonstrate that to what extent a particular combination of processes covers the behavior space. For a small population it demonstrates that how much of phenotypical variance is achieved by a random initialization that in turn influences the efficiency of starting an evolutionary algorithm from the population. By comparing results from both sizes of populations, we have a measure of similarity between different random small populations which can be used as

an indicator of whether or not employing island models in evolutionary algorithms is proper for the system.

A metric is also introduced for diversity evaluation in individual level where the spatiotemporal patterns generated by organisms are considered. In this level several qualitatively different types are defined while every spatiotemporal pattern is belonged to one of these types. For all different combinations of AHHS processes that are involved in controlling a random organism and for a large number of controllers, generated spatiotemporal patterns are classified in these types and the number of patterns in every type is calculated. The experiment is performed for randomly initialized controllers consisting of different combinations of AHHS processes and also by CTRNN and the calculated numbers are compared in these different cases.

As a summary of the evaluated capabilities of diversity generations, Figure 9 represents the diversity values at both population and individual levels at the same figure. Although there are some differences in the configurations for the two levels due to the requirement of computability in the study of population level and spatial dimension in stapiotemporal patterns at individual level, the results might still be interesting to be represented in the same figure.

All in all, the effects of the investigated internal processes of AHHS can be summarized as follows:

- *hormone-to-hormone-reaction* is a process that may generate or degenerate a hormone depending on its present concentration value and the concentration values of other hormones in the same unit. This process is similar to feedback loops in recurrent neural and regulatory networks. This process is intuitively suspected to generate high diversity and as it is admitted by the results, it is the most important process in order to make diversity at both population and individual levels. All the pro-

cess combinations that make high population diversity (including $ratio$ of overall to subpopulation) contain hormone-to-hormone-reaction and the same combinations generate comparatively high degrees of diversity at individual level.

- By combining *base-production* process with *hormone-to-hormone-reaction* process without adding any communication process, a comparatively high diversity can be generated. For example, in process combinations {*hormone-to-hormone-reaction*,*base-production*} and {*hormone-to-hormone-reaction*, *decay*, *base-production*} a rather high number of *dynamic-flat-nonmonotone* patterns which are spatiotemporal patterns with no spatial complexity and a rhythmic change in temporal dimension are generated.

- Combining *diffusion* process as an implicit communication process with *hormone-to-hormone-reaction* process produces a proper complexity in temporal dimension. This effect is not detectable for *tunneling* as another process of implicit communication.

- Processes *hormone-to-hormone-reaction*, *base-production*, and *diffusion* together make the highest number of non-*static-flat* patterns in general and *dynamic-complex* patterns in particular. They also demonstrate highest achievability of *behavior* space implied by high diversity in overall population at population level.

- The effect of *diffusion* process can be also investigated by comparing process combinations {*decay*, *base-production*, *diffusion*} and {*base-production*, *diffusion*} with their counterparts without *diffusion* ({*decay*, *base-production*} and {*base-production*}). In the cases where *diffusion* are included, spatial dimension of complexity is added to the produced spatiotemporal patterns that changes the type of the patterns, while no significant change

in the population diversity is generated neither in subpopulations nor in the overall population.

- Inclusion of *decay* process along with *hormone-to-hormone-reaction*, *base-production*, and *diffusion* in a process combination also increases both individual and population diversities.

- *tunneling* is the only process that is able to generate *static-complex* and *dynamic-complex* patterns on its own ($\{t\}$). On the other hand, although *tunneling* process seems to have some similarities with *hormone-to-hormone-reaction* in terms of influence of other hormones in the target hormone and with *diffusion* in terms of being an implicit communication process between neighbor units with conservation of mass, it contributed differently in the dynamics of the system. It can be clearly observed by comparing the process combinations {*hormone-to-hormone-reaction, tunneling*} and {*hormone-to-hormone-reaction, diffusion*}. The difference is visible at both population and individual levels, while the individual level represents large proportions of *static-complex* patterns implying that *tunneling* has a high spatial influence that can dominate the temporal influence of *hormone-to-hormone-reaction*. The high spatial influence of *tunneling* is also observable in the combinations {*hormone-to-hormone-reaction, tunneling*} and {*hormone-to-hormone-reaction*} in Figure 8b. We suspect that the high spatial influence of *tunneling* dominates its temporal influence and reduces its overall effect in the dynamics of the system.

In order to get an impression of the relevance between the described metrics of diversity generation and evolutionary tasks in practice, an evolutionary task for a multi-modular system of AHHS is investigated. The evolutionary behaviour of all the possible combinations of processes are demonstrated admit-

ting a correlation between the capability of diversity generation and evolvability of the system for the given task.

Similar methods and metrics as used in this work might be applicable for making a deeper understanding about processes that are considered to be included in AHHS or other control systems and investigation of their effects in generating target behaviors.

In the future, the generated spatiotemporal patterns especially *dynamic-complex* patterns will be further partitioned qualitatively into sub-types and investigated in more details in order to provide more information about the type of behaviors that can be generated by the controllers and the processes that need to be included in a system for producing particular target behaviors. Similarly, some processes can be investigated in more abstract or more detailed way, for example considering *r* process as a feedback loop, it can be abstracted into two different processes with positive and negative feedback effects and their influences in the diversity generation for the system can be studied separately.

The diversity generation capabilities of the processes will also be investigated in the future in a closer relation with evolutionary algorithms. The effects of these capabilities of the system can be investigated in more details and for more variations of tasks while evolutionary algorithms (both regular and island models) are applied in order to evolve for specific types of behaviors and patterns in real tasks especially in the context of evolutionary robotics.

Acknowledgment

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