Distributed Brain Modelling by means of Hierarchical Collaborative CoEvolution

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Abstract- The current work addresses the development of cognitive abilities in artificial organisms. In the proposed approach, neural network-based agent structures are employed to represent distinct brain areas. We introduce a Hierarchical Collaborative CoEvolutionary (HCCE) approach to design autonomous, yet cooperating agents. Thus, partial brain models consisting of many substructures can be designed. Replication of lesion studies is used as a means to increase reliability of brain model, highlighting the distinct roles of agents. The HCCE is appropriately designed to support systematic modelling of brain structures, able to reproduce biological lesion data. The proposed approach effectively designs cooperating agents by considering the desired pre- and post- lesion performance of the model. In order to verify and asses the implemented model, the latter is embedded in a robotic platform to facilitate its behavioral capabilities.

1 Introduction

Cognitive abilities of animals are supported by the performance of their Central Nervous System (CNS), which consists of several interconnected modules with different functionalities [1]. Even if the detailed, exact properties of each brain area are not clear yet, many computational models have been proposed capturing their basic characteristics [2, 3, 4, 5]. These efforts support the long-term vision of developing artificial organisms with mammal-like cognitive abilities.

We have recently introduced a systematic method to design computational models of partial CNS structures [6, 7]. In accordance to the distributed organization of the mammalian CNS, an agent-based modelling approach is followed to enforce the autonomy of brain areas. Specifically, the model consists of a collection of neural network agents, each one representing a CNS area.

Similarly to an epigenetic learning process, the performance of agents is specified by environmental interaction. The dynamics of epigenetic learning are designed by an evolutionary process which simulates phylogenesis, similar to [8, 9]. Following the phylogenetic/epigenetic approach, the objective adopted during the evolution of agents, is to furnish them with abilities to develop similar performance to the respective brain areas, after a certain amount of environmental interaction. As a result, both genetically encoded features and subjective experience have their own role in the formation of model's performance.

Instead of using a unimodal evolutionary process we employ a collaborative coevolutionary approach which is able to highlight the specialties of brain areas represented by distinct agents [10]. Additionally, the coevolutionary approach facilitates the integrated performance of substructures in the composite model. The combination of these two particular features (partial autonomy and collaborative performance) in a single design method seems particularly appropriate for brain modelling.

In the present work, we propose a hierarchical extension of this approach, which exploits the inherent ability of coevolutionary methods to integrate partial structures. We introduce a Hierarchical Colaborative CoEvolutionary (HCCE) scheme which supports the coevolution of a large number of species (populations). Specifically, evolutionary processes at lower levels are driven by their own dynamics to fulfill the special objectives of each brain area. The evolutionary process at the higher levels, tunes lower level coevolutionary processes to achieve the integrated performance of partial structures. The architecture of multiple coevolutionary processes tuned by a higher level evolution can be repeated for as many levels as necessary, forming a tree hierarchy.

It should be noted that the composite model does not have to perform in a hierarchical mode. The performance of partial CNS structures can be either hierarchical or completely parallel, depending on the biological prototype. Hence, the hierarchical coevolutionary approach does not imply any further constraints. It is introduced only to support the design process of brain modelling.

Furthermore, following recent trends aiming at the study of computational models in lesion conditions [11, 12, 13], we adapt our method to accomplish systematic modelling of biological lesion experiments. The agent-based representation of brain areas facilitates lesion simulation by simply deactivating appropriate agent structures. Thus, the performance of the model in pre- and post- lesion conditions can be tested. Furthermore, appropriate fitness functions can be specified for the evolution of partial structures, to indicate the performance of the model when all substructures are present, and also indicate the performance when some partial structures are eliminated. Following this approach, biological lesion data can be considered during the coevolutionary design process, while the computational structures are properly formulated to replicate pre- and post- lesion performance of the biological prototype. Consequently, in-

creased reliability is offered to the final model.

The rest of the paper is organized as follows. In the next section, we present the structure of neural agents employed for the representation of CNS areas. In section 3 we introduce the hierarchical collaborative coevolutionary scheme which supports agents' design. The results of the proposed approach in a brain modelling task are presented in section 4. Specifically we demonstrate the design of a computational model of posterior parietal cortex (PPC) - prefrontal cortex (PFC) - primary motor cortex (M1) - spinal cord (SC) interactions in the mammalian brain. The model is embedded in a robotic platform, to support environmental interaction and prove the validity of results. The model emphasizes on working memory usage in delayed response tasks, replicating the performance of the biological prototype in pre- and post- lesion conditions. Finally, conclusions and suggestions for future work are drawn in the last section.

2 Computational Model

We implement two different neural agents, to supply a general computational framework: (i) a cortical agent to represent brain areas, and (ii) a link agent to support information flow across cortical modules.

2.1 Link Agent

The structure of link agent is appropriately designed to support connectivity among cortical modules. Using the link agent any two cortical modules can be connected, simulating the connectivity of brain areas.

Each link agent is specified by the projecting axons between two cortical agents (Fig 1(a)). Its formation is based on the representation of cortical modules by planes with excitatory and inhibitory neurons (see below). Only excitatory neurons are used as outputs of the efferent cortical agent. The axons of projecting neurons are defined by their (x, y) coordinates on the receiving plane. Cortical planes have a predefined dimension and thus projecting axons are deactivated if they exceed the borders of the plane. This is illustrated graphically in Fig 1(a), where only the active projections are represented with an $\times$ on their termination. As a result, the proposed link structure facilitates the connectivity of sending and receiving cortical agents supporting their combined performance.

2.2 Cortical Agent

Each cortical agent is represented by a rectangular plane. A cortical agent consists of a predefined population of excitatory and inhibitory neurons, which all follow the Wilson-Cowan model with sigmoid activation as it is described in [6]. Both sets of neurons, are uniformly distributed, defining an excitatory and an inhibitory grid on the cortical plane. On the same plane there are also located the axon terminals from the efferent projected cortical agents.

All neurons receive input information either from i) projecting axons, or ii) excitatory neighboring neurons, or iii) inhibitory neighboring neurons. The connectivity of neurons follows the general rule of locality. Synapse formation is based on circular neighborhood measures. A separate radius for each of the three synapse types, defines the connectivity of neurons. This is illustrated graphically in Fig 1(b), which further explains the example of Fig 1(a). All excitatory neurons share common neighborhood measures. The same is also true for all inhibitory neurons.

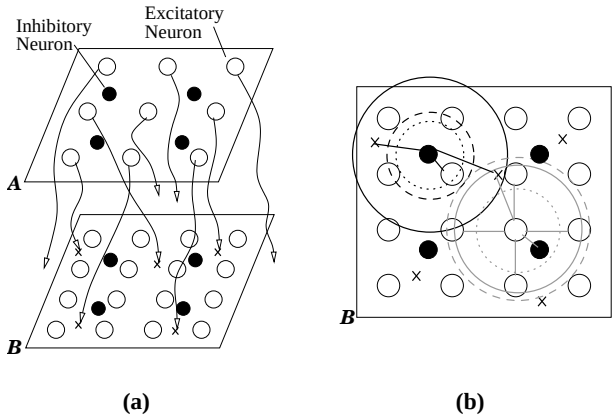

Figure 1: Schematic representation of the computational model. Part (a) illustrates a link agent which supports information flow from cortical agent A to B. Part (b) illustrates synapse definition in cortical agent B. Neighborhood radius for i) afferent axons is illustrated by a solid line, for ii) neighboring excitatory neurons by a dashed line, and for iii) neighboring inhibitory neurons by a dotted line. Sample neighborhoods for excitatory neurons are illustrated with grey, while neighborhoods for inhibitory neurons are illustrated with black.

The performance of cortical agents is adjusted by the experiences of the artificial organism obtained through environmental interaction, similar to epigenetic[1] learning [14]. To enforce experience-based subjective learning, each set of synapses is assigned a Hebbian-like learning rule defining the self-organization internal dynamics of the agent. We have implemented a pool of 10 Hebbian-like rules that can be appropriately combined to produce a wide range of functionalities. The employed learning rules are the union of those employed in [15, 6], and thus they are omitted here due to space limitation. Agent's plasticity allows synaptic adjustments at run-time based on environmental interaction. This is in contrast to the most common alternative of genetically-encoded synaptic strengths which prevents experience based learning.

3 Hierarchical Collaborative CoEvolution (HCCE)

Similar to a phylogenetic process the specification of parameter values for all agents is approached in a systematic way by using an evolutionary mechanism, as it has been suggested in [8, 9]. However, using a unimodal evolution-

[1] Epigenesis here, includes all learning processes during lifetime.

ary approach, it is not possible to explore effectively partial solutions, which correspond to brain structures.

To alleviate for that, coevolutionary algorithms have been recently proposed that facilitate exploration, in problems consisting of many decomposable subcomponents [10]. They involve two or more coevolved populations with interactive performance. Distinct populations are usually referred as *species* in the coevolutionary literature, and thus this term will be employed henceforth.

The brain modelling problem fits very well to coevolutionary approaches, because separate coevolved species can be used to perform design decisions for each partial model of a brain area. As a result, reliable models can be implemented, because both the special features of each area and the cooperation within computational brain modules can be highlighted.

We have presented a new evolutionary scheme to improve the performance of collaborative coevolutionary algorithms, by explicitly addressing the collaborator selection issue [6, 7]. The present work extents this scheme to a hierarchical multi-level architecture. Our method combines the hierarchical evolutionary approach [16], with the maintenance of successful collaborator assemblies [17], to develop a powerful coevolutionary scheme.

We employ two different kinds of species to support the coevolutionary process encoding the configurations of either a Primitive agent Structure (PS) or a Coevolved agent Group (CG). PS species specify partial elements of the model, encoding the exact structure of either cortical or link agents. A CG consists of groups of PSs with common objectives. Thus, CGs specify configurations of partial solutions by encoding individual assemblies of cortical and link agents. The evolution of CG modulates partly the evolutionary process of its lower level PS species to enforce their cooperative performance. A CG can also be a member of another CG. Consequently several CGs can be organized hierarchically in a tree-like architecture, with the higher levels enforcing the cooperation of the lower ones.

The HCCE-based design method for brain modelling is demonstrated by means of an example (Fig 2). We assume the existence of two cortical agents connected by three link agents representing their afferent and efferent projections (Fig 2(a)). One hypothetical HCCE process employed to specify agent structure is illustrated in (Fig 2(b)).

Similar to [16, 6] all individuals in all species are assigned an identification number which is preserved during the coevolutionary process. The identification number is employed to form individual assemblies within different species. Each variable in the genome of a CG is joined with one lower level CG or PS species. The value of that variable can be any identification number of the individuals from the species it is joined with. PSs encode the structure of either cortical or link agents. The details of the encoding have been presented in [6, 7], and thus they are omitted here due to space limitations. CGs enforce cooperation of PS structures by selecting the appropriate cooperable individuals among species. Additionally, a new genetic operator, termed Replication [6], exploits the most able to cooperate

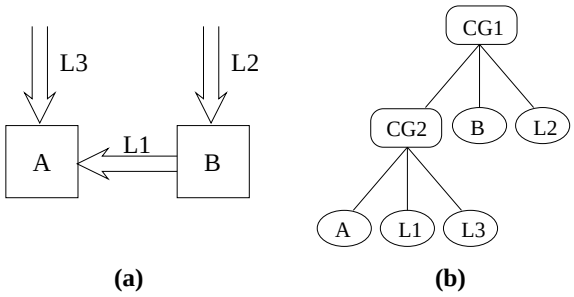

Figure 2: Hierarchical collaborative coevolutionary design of agents. Part (a) represents schematically a hypothetical connectivity of agents. Part (b) represents the hierarchical coevolutionary scheme utilized to evolve partial structures. CGs are illustrated with oval boxes, while PSs are represented by ovals.

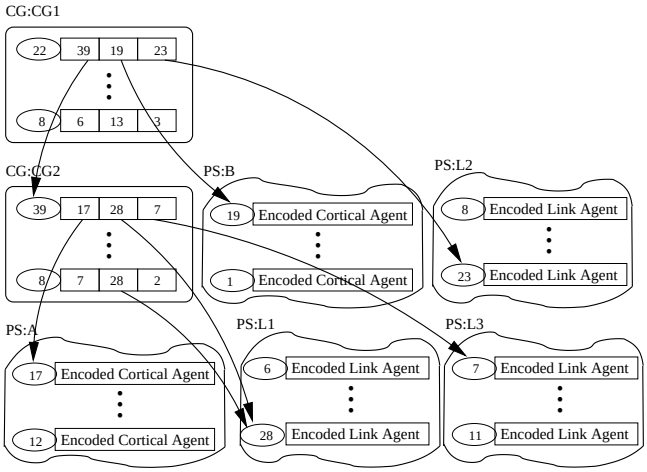

Figure 3: An overview of the hierarchical coevolutionary scheme, with CG species tuning the evolutionary processes of PS species. Identification numbers are represented with an oval.

individuals in each partial species. A snapshot of the exemplar HCCE process described above is illustrated in (Fig 3).

In order to test the performance of a complete problem solution, populations are sequentially accessed starting by the higher level. The values of CG individuals at various levels are used as guides to select collaborators among PS species. Then, PS individuals are decoded to specify the structure of cortical and link agents, and the performance of the proposed overall solution is tested on the desired task.

The proposed hierarchical scheme is able to support the simulation of lesion conditions which is a typical case for biological experiments. Specifically, by deactivating a CG together with the PS structures corresponding to its lower level species, we can easily simulate lesion of the respective brain areas. As a result, all necessary lesion conditions can be considered during the evolutionary process, and the role of each partial structures in the composite model can be highlighted.

Furthermore, even if the majority of existing collabora-

tive coevolutionary methods assume that all species share a common fitness function [18, 19, 20], our method allows the employment of separate fitness measures for different species. This matches adequately to the distributed agent-based modelling of brain areas, because different objectives can be defined for each partial structure preserving their autonomy. This special feature of HCCE, facilitates additionally the modelling of biological lesion data, because properly formulated fitness functions can be utilized to specify the desired pre- and post- lesion performance of the model.

For each species s, a fitness function f_s is designed to drive its evolution. All PS species strictly under a CG (that is PSs that have level difference 1 from the CG) share a common f_s. The fitness function is formulated to evaluate the performance of the model in different conditions, which corresponds to the pre- and post- lesion state of the model. Specifically a partial fitness function $f_{s,t}$ evaluates the ability of an individual to serve task t, while the overall fitness function is estimated by:

$$f_s = \prod_t f_{s,t} \tag{1}$$

Furthermore, the collaborator selection process at the higher levels of hierarchical coevolution will probably select an individual to participate in many assemblies. (e.g. the case of individual 28 of PS species L1, of Fig 3). Let us assume that an individual participates in K assemblies which means that it will get K fitness values $f_{s,t}$ on its ability to serve task t. Then, similar to most existing coevolutionary approaches the individual will be assigned, the maximum of the fitness values achieved by all the solutions formed with its membership:

$$f_{s,t} = max_k\{f_{s,t}^k\} \tag{2}$$

where $f_{s,t}^k$ is the fitness value of the k-th $(k = 1...K)$ solution formed with the membership of the individual under discussion. This value represents the ability of the individual to support the accomplishment of the t-th task.

The above equations describe fitness assignment in each species of the hierarchical coevolutionary process. Just after the testing of collaborator assemblies and the assignment of their fitness values, an evolutionary step is performed on each species independently, to formulate the new generation of its individuals. First, individuals of the species are sorted according to their fitness values. Then, a predefined percentage of individuals are probabilistically crossed over. An individual selects its mate from the whole population, based on their accumulative probabilities. Finally, mutation is performed in a small percentage of the resulted population. This process is repeated for a predefined number of evolutionary epochs, driving each species to the accomplishment of each own objectives and additionally enforcing their composite cooperative performance.

4 Results

The effectiveness of the proposed approach is illustrated on the design of a partial brain computational model, which simulates posterior parietal cortex (PPC) - prefrontal cortex (PFC) - primary motor cortex (M1) - spinal cord (SC) interactions, emphasizing on working memory (WM) usage (Fig 4). We note that the proposed model does not aim to be a detailed replica of the biological prototype (e.g. premotor areas are not represented), but it serves as a guide on how the proposed computational framework can be employed to support brain modelling.

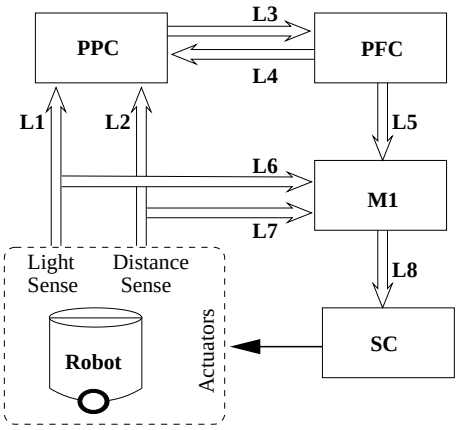

Figure 4: A schematic overview of the Primary Motor Cortex model. Cortical agents are illustrated with blocks, while link agents are illustrated with a double arrow.

In order to design a reliable model, we focus on the distinct role of each area in the mammalian brain. Several years of experimentation with biological organisms in delayed response (DR) tasks, has shed light on their behavioral organization [21]. M1 encodes primitive motor commands which are expressed to actions by means of SC. PPC-PFC reciprocal interaction operates in a higher level encoding WM [22], to develop plans regarding future actions. PFC activation is then passed to M1 which modulates its performance accordingly. As a result, all the above mentioned structures cooperate for the accomplishment of a DR task by the organism. Additionally, several experiments highlight the performance of these structures in lesion conditions. Specifically, PFC lesion affects planing ability of the organism, resulting in purposeless motion [23], while M1 lesion eliminates motion ability of the organism [1].

Computational models regarding the structures under discussion have been also presented in the literature. For example computational models of M1 have been developed in [2, 4], which however, do not emphasize on the self-organized understanding of environmental characteristics by the robot. Existing PFC computational models emphasize on WM activity by means of recurrent circuits [22, 24]. However, these models are not operative, in the sense that they are not linked to other structures to affect their performance. A computational model aiming at the accomplishment of memory guided tasks has been proposed in [25], which however employs a compact artificial neural network structure, without specific assumptions for the performance of partial brain areas.

The present work employs the hierarchical collaborative coevolutionary approach to design a model of the areas un-

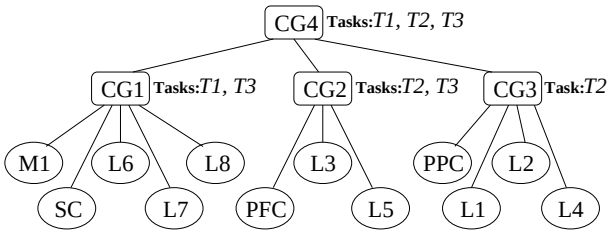

Figure 5: A graphical illustration of the coevolutionary process.

der discussion, which performs in real-time. In this endeavor, environmental interaction is of utmost importance, since it is difficult to investigate CNS areas functionality without embedding the models into a body to interact with its environment. Thus, a simulated mobile robot is utilized to support environmental interaction, while at the same time the model enriches the behavioral repertory of the robot. Specifically, we employ a two wheeled simulated robotic platform equipped with 8 uniformly distributed distance and light sensors.

The experimental process aims at reproducing a lesion scenario which is in agreement to the biological data presented above. The composite computational model aims at the accomplishment of a DR task, developing a behavior similar to the one described in pre-lesion performance of animals [21]. This is further supported by two partial behaviors. The first accounts for the development of WM-like activation in PPC-PFC which are the brain structures most closely linked to WM [22]. The second accounts for purposeless motion by M1 when lesion occurs on the higher level structures [23]. Both partial and composite models are embedded on the robotic platform to furnish it with cognitive abilities and prove the validity of results.

The employed scenario is properly adjusted to the needs of robotic applications. Three tasks are designed to demonstrate the effectiveness of the computational procedure and also highlight the role of each agent in the model.

The first task $T1$, accounts for primitive motion abilities without purposeful planning. For mobile robots, a task with the above characteristics is wall avoidance navigation. Thus, for the needs of the present study, M1-SC structures aim at wall avoidance navigation. The successful accomplishment of the task is evaluated by the function:

$$\begin{aligned} E_1 &= \left(\sum_M (sl+sr-1)*(1.0-p^2)\right) \\ &* \left(1-\frac{2}{M}\left|\sum_M \frac{sl-sr}{sl*sr}\right|\right)^3 \\ &* \left(1-2\sqrt{\frac{B}{M}}\right)^3 \end{aligned} \quad (3)$$

where we assume that the robot is tested for M steps, sl, sr are the instant speeds of the left and right wheel, p is the maximum instant activation of distance sensors, and B is the total number of robot bumps. The first term seeks for forward movement far from the walls, the second supports straight movement without unreasonable spinning, and the last term minimizes the number of robot bumps on the walls.

The development of WM-like performance specifies the second task $T2$. Working memory (WM) is the ability to hold and manipulate goal-related information to guide forthcoming actions. In the present experiment, a light cue is presented in the left or right side of the robot. WM performance aims at persistent PFC activity, related each time to the respective side of light cue presentation.

Two different states l, r are defined associated to the left or right side of light source appearance. For each state, separate activation-averages over the time of M simulation steps, a_j, are computed, with j identifying excitatory neurons of PFC agent. The formation of WM related to the side of light cues is evaluated by measuring the persistency of activation in PFC:

$$\begin{aligned} E_2 &= \frac{1}{2}\left(\frac{v_l}{m_l}+\frac{v_r}{m_r}\right) \\ &* \min\left\{\sum_{j,a_j^l>a_j^r}\left(a_j^l-a_j^r\right), \sum_{j,a_j^r>a_j^l}\left(a_j^r-a_j^l\right)\right\} \end{aligned} \quad (4)$$

where m_l, v_l, m_r, v_r are the mean and variance of average activation at the respective states. The first term seeks for consistent PFC activation, and the second supports the development of a distinct set of active neurons for each state.

Finally, a third task $T3$, aims to combine the above behaviors formulating a complex model. The successful interaction of all partial structures is demonstrated by means of a delayed response (DR) task. Specifically, a light cue is presented on the left or right side of the robot. The robot has to move at the end of a corridor memorizing the side of sample cue appearance, and then make a choice related to 90^o turn left or right, depending on the side of light cue presence. A target location is defined on each side of the corridor depending on the position of the initial light cue. The robot has to approximate the target location without crashing on the walls. The successful approximation to the target location is estimated by:

$$G = \left(1+3.0*\left(1-\frac{d}{D}\right)\right)^3 * \left(1-2\sqrt{\frac{B}{M}}\right)^2 \quad (5)$$

where d is the minimum euclidian distance between the target and the robot, D is the euclidian distance between the target and the starting location of the robot, and B is the total number of robot bumps. The accomplishment of $T3$ is evaluated by means of two subtasks testing separately the right or left turn of the robot for the respective positions of the light cue, employing each time the appropriate target location:

$$E_3 = G^l * G^r \quad (6)$$

We turn now at the design of the model by means of the HCCE process. In accordance to the lesion experiment followed in the present study, each agent needs to serve more than one tasks. This guides the classification of the respective PSs in CGs. The tasks served by each group of agents

are illustrated in (Fig 5), at the right side of each CG. Specifically, the structures under $CG1$ are related to M1-SC interactions, and they need to serve both the wall avoidance and the delayed response task. The structures under $CG2$ are related to PFC and its afferent and efferent projections, which need to serve working memory persistent activation, and the delayed response task. The structures under $CG3$ are related to PPC and its afferent projections which have to support working memory activation only ($CG2$ structures are responsible for the proper formulation on working memory and its projection to M1). Finally, a top level CG is employed to enforce cooperation within partial configurations aiming to support the accomplishment of all the three tasks.

The testing phase for the individuals of the coevolutionary scheme proceeds as follows. The top level species is sequentially accessed. Each individual of $CG4$, guides collaborator selection among its lower level CG and PS species. Individuals of PS species are decoded to detailed agent structures. The composite model is tested on the accomplishment of DR task $T3$. Next, PPC-PFC interaction is isolated by deactivating the agents under $CG1$. The remaining structures are tested on working memory task $T2$. Finally, $CG1$ agents are activated back, and now $CG2$ structures are deactivated to simulate PFC lesion. The remaining agents are tested on the accomplishment of wall avoidance navigation.

The fitness functions which guide the evolution of species are designed accordingly to support the accomplishment of the respective tasks. Individuals are assigned a combination of evaluation indexes, for the accomplishment of tasks where the composite model is performing, and the accomplishment of tasks with performance of the eliminated model. It is reminded that all PSs share the same fitness functions with their higher level CG.

The agent structures grouped under $CG1$ serve the success on tasks $T1$, $T3$. Thus, the fitness function employed for the evolution of $CG1$ and its lower level species is based on the measures evaluating the success of the respective tasks. Following the formulation introduced in eqs. (1), (2):

$$\begin{array}{l} f_{CG1} = f_{CG1,T1} * f_{CG1,T3} \text{ with} \\ f^k_{CG1,T1} = E_1, \;\; f^k_{CG1,T3} = \sqrt{E_3} \end{array} \tag{7}$$

where k represents each membership of an individual in a proposed solution.

Similarly, $CG2$ design aims to support both the accomplishment of $T2$ and $T3$ tasks. Thus, the fitness function which guides the evolutionary process is defined by means of the respective evaluation measures:

$$\begin{array}{l} f_{CG2} = f_{CG2,T2} * f_{CG2,T3} \text{ with,} \\ f^k_{CG2,T2} = {E_2}^2, \;\; f^k_{CG2,T3} = \sqrt{E_3} \end{array} \tag{8}$$

where k is as above.

The third group $CG3$, consists of PPC and all link agents projecting on it. These structures need to serve only the development of working memory activation in PFC. Thus, the objective of $CG3$ design, is the accomplishment of $T2$. The fitness function employed for the evolution of $CG3$ is

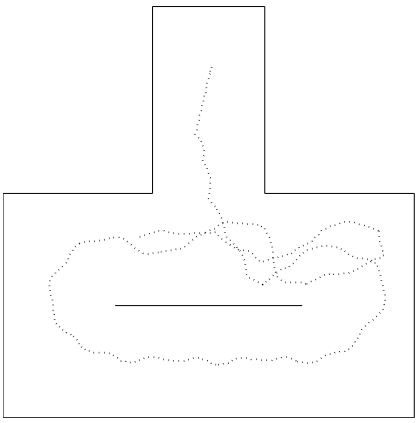

Figure 6: A sample result of robot performance, driven by M1-SC. The robot moves in a purposeless mode without bumping on the walls.

defined by:

$$\begin{array}{l} f_{CG3} = f_{CG3,T2} \text{ with,} \\ f^k_{CG3,T2} = E_2 \end{array} \tag{9}$$

where k is as above.

Additionally, the top level evolutionary process $CG4$, enforce the integration of partial configurations in a composite model, aiming at the successful accomplishment of all the three tasks. Thus, the top level $CG4$ consists of all lower level CGs. The fitness function employed for the evolution of $CG4$ supports the concurrent success on wall avoidance task $T1$, working memory task $T2$, and DR task $T3$. It is defined accordingly, following the formulation introduced in eqs. (1), (2), by:

$$\begin{array}{l} f_{CG4} = f_{CG4,T1} * f_{CG4,T2} * f_{CG4,T3} \text{ with,} \\ f^k_{CG4,T1} = \sqrt{E_1}, \; f^k_{CG4,T2} = {E_2}^2, \; f^k_{CG4,T3} = E_3 \end{array} \tag{10}$$

where k is as above.

The exact formulation of the above fitness functions (eqs (7) - (10))is a result of a trial and error procedure. Following this approach, different species enforce the accomplishment of each task with a different weight. For example, compared to $CG1$, the fitness function which guides $CG4$ evolution, enforce more the relative accomplishment of $T3$ than $T1$ (see definitions of $f^k_{CG1,T1}$ - $f^k_{CG1,T3}$ and $f^k_{CG4,T1}$ - $f^k_{CG4,T3}$).

The coevolutionary process described above employed populations of 200 individuals for all PS species, 300 individuals for $CG1$, $CG2$, $CG3$, and 400 individuals for $CG4$. Additionally, an elitist evolutionary strategy was followed in each evolutionary step with the 7 best individuals of each species, copied unchanged in the respective new generation, supporting the robustness of the evolutionary process. As a result, after 200 evolutionary epochs the process converged successfully and the cooperation of agent structures with completely different objectives (e.g. those under $CG1$ and those under $CG3$) is achieved.

Sample results of robot performance on each task are illustrated in Figs 6, 7, 8. As it is indicated by the lesion scenario, M1-SC are able to drive the robot in a purpose-

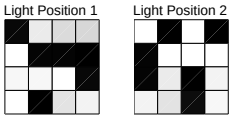

Figure 7: The average activation of 16 excitatory neurons at PFC, for each light position. Activation is demonstrated with levels of grey.

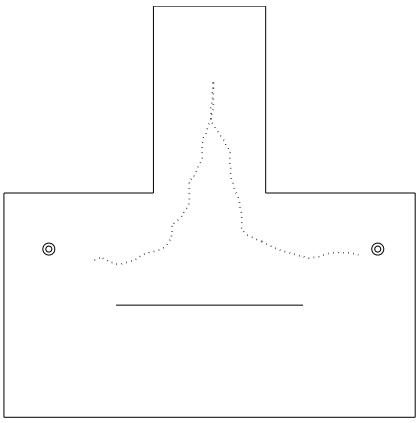

Figure 8: A sample result of robot performance in the delayed match-to-sample task, for two different sides of light cue presence. Goal positions are illustrated with double circles.

less manner, following a wall avoidance policy (Fig 6). At the same time, PPC-PFC interactions are able to encode the side of light cue appearance and memorize it for a brief future period (Fig 7). Moreover, the composite model combines successfully the performance of partial structures to accomplish the DR task (Fig 8).

Consequently, the results observed by biological lesion experiments related to delayed response tasks, are successfully replicated by the model. This is achieved by means of the powerful HCCE process, which specifies the performance of the model in pre- and post- lesion conditions. By simulating lesion effects in biological organisms, realistic models can be developed, while at the same time, the role of each agent in the composite model can be highlighted.

5 Conclusions

The work described in this paper, addresses the development of cognitive abilities in artificial organisms by means of brain modelling. Specifically, we introduce a systematic computational framework for the design and implementation of brain models.

The proposed approach is based on the employment of neural agent modules to represent brain areas, which are connected using appropriate link agent structures. The agent-based modelling is in accordance to the distributed nature of mammalian CNS. Furthermore, it facilitates the autonomy of brain areas, and consequently allows the investigation of model performance in lesion conditions supporting its reliability.

Agent structures are adjusted in real-time by following a self-organized process which simulates epigenetic learning of biological organisms. The dynamics of epigenetic learning are designed following an evolutionary approach which simulates phylogenesis. As a result, both genetically encoded features and environmental experience specify the performance of the model.

We employ a hierarchical collaborative coevolutionary (HCCE) approach to support design specification of agent structures. The collaborative coevolutionary process is suitable for agents' design because it offers increased search abilities of partial components, and is able to emphasize both the specialty of brain areas and their cooperative performance.

The hierarchical organization of the coevolutionary process facilitates the elimination of agent structures to simulate lesion experiments. Thus, the role of each partial structure in the composite model can be examined. Additionally, by employing independent fitness functions for the evolution of each species, HCCE supplies a mechanism to specify the performance of the model in pre- and post- lesion conditions. Consequently, the proposed method seems particularly appropriate for implementing reliable models of brain areas, with the ability to replicate biological lesion data.

Following this approach, the distinct role of each agent structure in the composite model is highlighted. This has been confirmed with the results shown in the previous section, as well as other results obtained in our experiments (not presented here due to space limitations). Evidently, further work is needed to fully ascertain the general applicability and validity of our approach.

We also note that by adopting the coevolutionary method for design specification, our approach is inherently furnished with the ability to integrate partial brain models. The proposed hierarchical collaborative coevolutionary scheme can be also utilized to integrate the performance of partial brain models, by introducing an appropriate number of additional higher level evolutionary process. Thus, the incremental integration of gradually more partial brain models on top of existing ones constitutes the main direction of our future work. We believe that by exploiting the proposed approach, a powerful method to design large scale reliable brain models can emerge.

Finally, it is noted that the proposed coevolutionary approach can be also utilized in contexts different than brain modelling, such as the design of cooperating robot teams, or the research on economic and social behaviors. Thus, it can be potentially employed as a general purpose method for the design of distributed complex systems.

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