Modelling Robotic Cognitive Mechanisms by Hierarchical Cooperative CoEvolution

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Received (Day Month Year)
Revised (Day Month Year)
Accepted (Day Month Year)

Recently, many brain modelling efforts attempt to support cognitive abilities of artificial organisms. The present work introduces a computational framework to address brain modelling, emphasizing on the integrative performance of substructures. Specifically, we present an agent-based representation of brain areas, together with a hierarchical cooperative coevolutionary scheme, which is able to highlight both the speciality of brain areas and their cooperative performance. The inherent ability of coevolutionary methods to design cooperative partial structures supports the design of partial brain models and, at the same time, provides a consistent method to achieve their integration. As a result, the proposed approach proceeds in either an incremental or a compound mode. Furthermore, the performance of the model in lesion conditions is considered during the design process to enforce the reliability of the result. Implemented models are embedded in a robotic platform to support its behavioral capabilities.

Keywords: Coevolution; Brain Modelling; Robotics; Working Memory; Lesion Model.

1. Introduction

Contemporary approaches employ in many cases brain-inspired computational systems to support cognitive abilities of artificial organisms. Along this line, a large number of models have been proposed, as a means to explain and reproduce the functionality of partial brain areas[2,4,8,29,32,50]. Unfortunately, these approaches operate at different levels of description and explanation, based on different assumptions. Existing models seem to form a heterogeneous collection, where computational differences among them constitute their integration very difficult[52]. Thus, a consistent procedure to support design specifications and model integration is still lacking. The present work aims at addressing this issue. Specifically, we propose a computational framework to support brain modelling efforts, addressing at the same time the development of cognitive abilities in robotic platforms.

The central nervous system (CNS) of mammals consists of interconnected mod-

ules with different functionalities[20,5], implying that models with distributed architecture should be designed. Recently, we introduced an agent-based coevolutionary method to implement partial computational models of the mammalian CNS[29]. Our approach is based on the argument that mammalian cognition is a result of phylogenetic development, and subjective environmental experience[13]. In summary, each brain area is modelled by a self-organized agent[10,19], emphasizing the autonomy and the special features of the area. Each agent is represented by a neural network structure that captures the basic anatomical principles of the mammalian CNS. The design of each agent focuses on the emergence of brain area -like functionality, after a certain amount of robot - environment interaction[5,48]. Similar to a phylogenetic process, we employ an evolutionary approach to specify the computational details for each neural agent. Instead of using a unimodal evolutionary process, we employ a cooperative coevolutionary scheme which offers enhanced search abilities of agent components[38].

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 novel Hierarchical Cooperative CoEvolutionary (HCCE) scheme which allows the coevolution of a large number of species (populations) organized in gradually larger groups. By assigning a neural agent in each species, we are capable of emphasizing both the autonomous characteristics of the agents and their coupled performance. The ability to address systematically these two particular features - partial autonomy and cooperative performance - with a single design methodology, seems particularly appropriate for brain modelling. Both of them are provided by the proposed approach, as a direct consequence of combining the distributed modelling (specifically, agent-based modelling) with the distributed design mechanism (specifically, an HCCE-based scheme).

Following recent trends that study computational models in lesion conditions[1,14,31,36], our method facilitates systematic modelling of biological lesion experiments. Specifically, lesions can be easily simulated by deactivating appropriate agent structures. Thus, the pre- and post- lesion performance of the model is investigated during the coevolutionary design process. Furthermore, appropriate fitness functions are specified to guide the coevolution of partial structures, indicating the performance of the model when all components are present, and also indicating its performance when some components are deactivated. Following this approach, biological lesion results can be replicated by the coevolutionary design process, enforcing the similarity of the model to the brain prototype.

Additionally, the hierarchical approach facilitates the scalability of the modelling process, by providing a mechanism to combine groups of brain areas (partial models). In other words, the proposed hierarchical coevolutionary approach facilitates the design of cooperating components and, additionally, supports their further re-usability formulating composite structures with enhanced behavioral repertory. That is, an expanding CNS model can seamlessly result by integrating gradually

more neural agents. This particular feature, makes HCCE an efficient methodology to accomplish large scale brain modelling tasks. Other approaches that combine blocks of neural networks to model brain areas[47,21,23] have also appeared in the literature. However, they suffer in terms of scalability because they lack a systematic design methodology to support the re-usability of substructures (e.g. evolution[17]). Thus, they can not be utilized as a general purpose computational framework for brain modelling.

The rest of the paper is organized as follows. In the next section we formally present the agent structures employed for the implementation of partial brain models. Then, the motivation behind coevolutionary design of agents is discussed. In section 3 we present the hierarchical cooperative coevolutionary scheme which is utilized to design brain models consisting of autonomous but cooperating agents. Experimental results which follow the proposed computational framework are presented in section 4. Specifically, we demonstrate the implementation of a computational model which simulates posterior parietal cortex - prefrontal cortex - primary motor cortex - spinal cord interactions in a delayed response task. Two different approaches are illustrated to design the model by means of either a compound or an incremental process. Following research efforts which link cognitive capabilities of robots to brain science [44,45], the implemented CNS models are embedded in a simulated robot to furnish it with cognitive capabilities. The robotic platform supports interaction with the environment, and the assessment of the proposed approach. Finally, in the last section, the basic features of the proposed method are discussed, and directions for future work are highlighted.

2. Computational Model

Agents are deemed as an appropriate theoretical tool for modelling complex, distributed systems. At the same time, the brain is described as a group of cooperating specialists that achieve the overall cognitive function by splitting the task into smaller elements[41]. Thus, an agent-based approach seems suitable to support brain modelling, mainly due to the distributed organization of CNS. Agent technology facilitates the development of intelligent systems consisting of cooperative/interactive parts, supporting their flexibility, autonomy, subjectivity, and situatedness in a specific environment[10,34]. From a designer's point of view it supports problem decomposition, abstraction of partial models, and scalability of global problem solution[19].

We have implemented two different neural network based agents, to supply a general computational framework for brain modelling: (i) a computational cortical agent to represent brain areas, and (ii) a link agent to support information flow across cortical modules. The computational structures employed in the present study, constitute an enhanced version of our previous agents formulation[26,29]. The new agents follow a more flexible formulation which emphasizes their reusability, offering advanced modelling abilities of CNS performance.

We note that the proposed computational structures are not restrictive for the

coevolutionary design method, but rather serve as a guide on how coevolutionary approaches can be employed to support brain modelling tasks. The present work addresses primarily the development of a method to support CNS modelling for robotic applications, than presenting perfect models of mammalian brain areas. Currently, the employed computational structures have been formulated as simple configurations that are suitable for the task at hand. Additional constraints can be integrated to increase their biological reliability or, alternatively, a different neural structure with emphasis on biological features can be used, to implement brain models with enhanced biological reliability.

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. Thus, proper connectivity among modules can be defined, to simulate 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 agents 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 in the receiving plane. Thus, a link agent consists of axons terminating at any desired position of the receiving cortical agent. Cortical planes have a predefined dimension, and thus projecting axons are deactivated if they exceed the borders of the plane. Consequently, not all excitatory neurons project their outputs in the receiving plane. This is illustrated graphically in Fig 1(a), where active projections are represented by an $\times$ on their termination. Projections outside the cortical plane are illustrated without a terminal point, and thus they are deemed deactivated.

When the locations of axons in the cortical plane are defined, synapses between axon terminals and the excitatory or inhibitory neurons of the receiving plane can be formulated. The details of synapse specification are is described below.

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. Both sets of neurons, are uniformly distributed. Thus, an excitatory and inhibitory grid are defined on the cortical plane. Both types of neurons follow the Wilson-Cowan model with sigmoid activation, similar to[49]. Let x represent the firing rate of a neuron. It is updated based on the incoming signals, following the equation:

$$\mu \Delta x = -x + S(W_A A + W_E E - W_I I) \tag{1}$$

where μ presents the membrane time constant, W_A are the synaptic weights of the afferent axon signals, and W_E, W_I the synaptic weights of neighboring excitatory

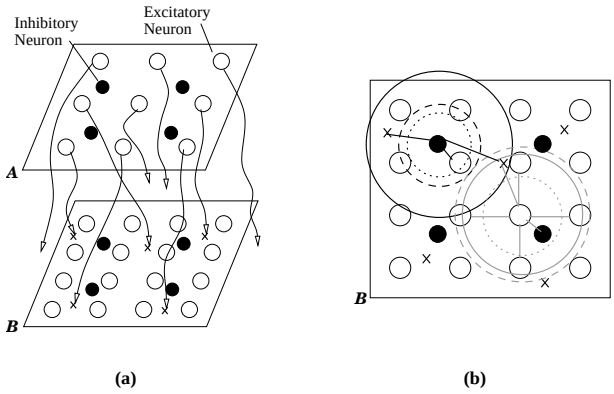

Fig. 1. Schematic representation of a computational model with cortical and link agents. Part (a) illustrates a link agent which supports information flow from cortical agent A to B. Part (b) illustrates synapse definition in cortical agent B. Neighborhood radii for (i) afferent axons are illustrated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

and inhibitory neurons. $S(y) = 1/(1 + e^{-\alpha(y-\beta)})$, is the non-linear sigmoid function where β and α stand for the threshold and the slope, respectively. All excitatory neurons of a cortical plane share common parameters μ_e, α_e, β_e. The same is also true for inhibitory neurons using parameters μ_i, α_i, β_i.

The axon terminals from the efferent projected cortical agents are also located on the same plane (Fig 1(b)). Three synapse types specify the connectivity of cortical agents. All neurons receive input information from (i) projecting axons, (ii) excitatory neighboring neurons, and (iii) inhibitory neighboring neurons. The connectivity of neurons follows the general rule of locality[40], and thus 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, that is radii $n1_e, n2_e, n3_e$, relative to the three synapse types. The same is also true for all inhibitory neurons employing neighborhood measures $n1_i, n2_i, n3_i$.

The performance of cortical agents is greatly specified by the experiences of the artificial organism, obtained through environmental interaction[34]. This is similar to epigenetic[a] learning which has an important contribution to the performance of the mammalian brain[48]. To enforce experience based subjective learning of robots, each set of synapses is assigned a Hebbian-like biologically plausible learning rule, similar to[9]. We have implemented a pool of ten Hebbian-like rules that can be appropriately combined to produce a wide range of functionalities. Learning rules are the same with those presented in our previous work[29], and thus they are omitted

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

here. Still, the architecture of agents is open and amenable to other learning rules with desirable characteristics in terms of either model performance or biological plausibility.

Each synapse is assigned a learning rule to adjust its synaptic weight during real-time performance. A separate rule is used for each of the three synapse types of a neuron (either with a projecting axon, or with a neighboring excitatory neuron, or with a neighboring inhibitory neuron), defining learning dynamics of the cortical plane. All excitatory neurons share common learning rules $r1_e, r2_e, r3_e$. The same is also true for all inhibitory neurons employing rules $r1_i, r2_i, r3_i$. Consequently, six rules are necessary to specify the learning process in each cortical plane.

The plasticity of agent structures, which stems from the assignment of learning rules, allows synaptic adjustment at run-time. This process highlights subjective understanding of the organism about the world, since a large number of synapses can be self-organized based on agent's internal dynamics and environmental experience. All synapses are classified in 6 categories (3 for excitatory and 3 for inhibitory neurons) to reduce the number of parameters. The most common, but harder to evolve, alternative of genetically-encoded synaptic strengths, results to a rather unmanageable problem complexity, and at the same time prevents experience based adjustment.

3. Hierarchical Cooperative CoEvolution (HCCE)

Recently there is a debate among genetics and neurobiology regarding the extent that brain organization and the associated cognitive functions are genetically predetermined, or emerge through patterns of developmental experience[5,7,48]. It seems that both genetically encoded features and subjective experience have a significant role in the formation of the animal's cognitive skills[13]. Phylogenesis determines the internal dynamics of brain structures that allow the epigenetic emergence of valuable behaviors. Besides the modulation of epigenetic learning by phylogenesis, the reverse interaction is also true. The well known since 1896 Baldwin effect, discusses the outcome of epigenetic learning on evolution, with the best able to learn organisms having larger numbers of offsprings[46].

Thus, an appropriate mechanism to perform structural specification of the components representing brain areas, should be based on the interactions of phylogenetic and epigenetic processes. Phylogenesis is represented computationally by an evolutionary process, while epigenesis is represented by online adjustment of agents[9]. The evolutionary process genetically determines the internal dynamics of partial brain models, which in turn allow the emergence of a valuable behavior during lifetime performance. This is the approach followed in the present work.

The majority of evolutionary algorithm applications involve a single solution representation to map genotypes to phenotypes. However, using this approach, it is not possible to sufficiently explore partial solutions, which correspond to partial specifications of the genotype[38]. To alleviate for that, coevolutionary algorithms have

been recently proposed that facilitate exploration in problems consisting of partial components[3]. 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. Each species is allowed to evolve separately, by using its own evolutionary parameters. Accordingly, increased search competencies are inherently available in coevolutionary algorithms, while the special characteristics of each species are also preserved. The brain modelling problem fits very well to coevolutionary approaches, because separate coevolved species (populations) can be utilized to perform design decisions for each model of a brain area, enforcing also the cooperation among brain modules.

Most of the coevolutionary approaches presented in the literature can be classified as competitive[42], or cooperative[38]. Competitive approaches are based on an antagonistic scenario, where the success of one species implies the failure of the other. In contrast, cooperative approaches follow a synergistic scenario, where individuals are rewarded when they successfully cooperate with individuals from the other species. Since brain modelling efforts aim at the cooperative performance of partial structures, in the following we only consider cooperative coevolution.

Despite the increased number of applications of cooperative coevolutionary algorithms, the significance of collaborator choice is usually overlooked[54,53]. The majority of existing applications consider only the ability of species to cooperate with the best individuals from the other species[22,38], or a randomly selected set of cooperators[3,15]. Evidently, the coevolutionary process could be supported by the maintenance of successful assemblies of cooperators[33].

We have introduced a two level evolutionary scheme[26,29] which aims at the successful selection of cooperators among species, as a means to improve the performance of coevolutionary algorithms. Besides species evolution, our method employs an additional evolutionary process, to select the proper individuals from each species that cooperatively are able to construct a good problem solution. The present work extends this method to a hierarchical multi-level architecture, developing a powerful Hierarchical Cooperative CoEvolutionary (HCCE) scheme. In the past, a hierarchical cooperative approach has been also presented by others[6]. However, compared to previous work[6], our approach is capable to coevolve groups of system components, and additionally address their specialized characteristics by utilizing multiple criteria to guide partial evolutionary processes.

In the following we present the proposed architecture, emphasizing its employment in brain modelling tasks.

3.1. *Hierarchical Organization*

The HCCE scheme is properly drawn to facilitate the design of systems consisting of partial components, organized in groups with complexity that gradually varies, from simple to more complex ones. Specifically, two different kinds of species encoding the configurations of either a Primitive agent Structure (PS) or a Coevolved agent

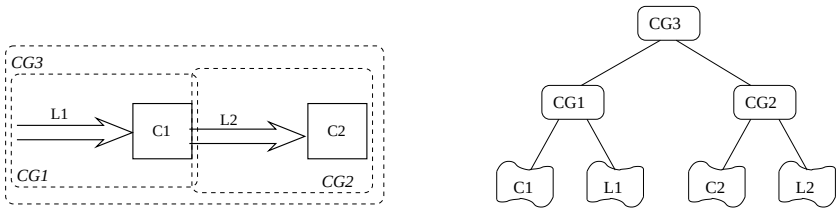

Fig. 2. The design of agents by cooperative coevolution. Part (a) represents a hypothetical connectivity of agents. Cortical agents are illustrated with blocks, while link agents are illustrated with double arrows. Part (b) represents the hierarchical coevolutionary scheme used to evolve partial structures. CGs are illustrated with rounded boxes, while PSs are represented by free shapes.

Group (CG) are employed. PS species specify partial elements, encoding the exact structure of either cortical or link agents. A CG consists of a group of cooperating PSs with common objectives. Thus, CGs specify configurations of partial solutions by encoding individual assemblies of cortical and link agents. Additionally, a CG can also be a member of another CG. Thus, several CGs are organized hierarchically in a tree-like architecture, with the higher levels enforcing the cooperation of the lower ones (Fig 2). However, different CGs can have different objectives, and consequently their evolution can be driven in different directions.

The details of the HCCE can be made clear by means of a specific example. Let us assume the existence of two cortical agents and two link agents representing their afferent projections (Fig 2(a)). We assume that agents $L1$,$C1$, have to support the fulfillment of task $T1$, while agents $L2$,$C2$, have to support the fulfillment of task $T2$. Thus, coevolutionary groups $CG1$ and $CG2$ are properly defined, each one classifying the structures supporting a respective task. At the same time, we assume that all structures have to cooperate to serve a third task $T3$. Thus, $CG3$ is also defined to enforce the cooperation among the groups $CG1$, $CG2$, aiming at the accomplishment of $T3$. This assumption is typical for mammalian CNS organization (e.g. different brain areas serve visual or motor competencies, which further cooperate to form advanced real life behaviors). The corresponding HCCE process which designs the structures of the current example, is illustrated in Fig 2(b). Four PS species are employed to evolve agent structures, while three CG species search for assemblies of cooperable individuals among PS species.

Following the HCCE approach, evolutionary exploration is performed concurrently in different spaces. The evolution of PS species facilitates search in the parameter space of sub-components. At the same time, the evolution of CG species searches within PS populations to identify suitable individuals in order to formulate successful assemblies of cooperators. Furthermore, CG species memorize good configurations of cooperating individuals across consecutive evolutionary generations. These configurations can be used as a basis to drive coevolution, since PS individuals are more likely to be members of good cooperating assemblies.

A snapshot of the HCCE process described above is illustrated in Fig 3. All individuals in all species are assigned an identification number which is preserved during the coevolutionary process. The identification number serves the definition of assemblies among different species. Each variable on the genome of a CG specifies the identification number of a partial solution at the lower level. The arrows connecting individuals among species illustrate how the HCCE builds the proposed compound solutions. For example individual with $id = 7$ of species $CG3$ specifies a solution consisting of partial assemblies with $id = 19$ at $CG1$ and $id = 3$ at $CG2$. Analyzing further the first assembly, it consists of the individual with $id = 14$ at $C1$ species, and individual with $id = 21$ at $L1$ species. In the same way, analyzing the assembly of $CG2$, it consists of the individual with $id = 4$ at species $C2$, and individual with $id = 5$ at species $L2$. It is clear that individuals at CG species might select some agents (or some assemblies of agent structures) multiple times. Following this mechanism, the cooperator selection process performed by the evolution of CG species, allows agents to participate in various assemblies aiming at the identification of a successful set of cooperators.

In order to test the performance of a complete problem solution, populations are sequentially accessed starting with the higher level. The genome values of CG-individuals at various levels are used as guides to select cooperators 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.

3.2. *Lesion Simulation*

The proposed HCCE is also able to consider the performance of the model at lesion conditions, by deactivating appropriate nodes in the tree hierarchy. Similar lesion conditions are typical in biological experiments related to the performance of mammalian CNS. Lesion simulation is performed in the level of CGs, since all lower level species share common objectives, and thus they are deactivated as a group. This is not restrictive to our model, since the deactivation of a single PS can be simulated, if necessary, by defining a CG with only one lower level PS species. As a result, the HCCE design process is able to consider the functionality of both the composite model, and any desired partial configuration, according to the needs of the brain modelling task.

Turning back to the example of Fig 2, a $CG3$ individual specifies the structure of the composite model which is tested on the accomplishment of task $T3$. Then, in order to simulate $C2$ lesion, the agents under $CG2$ are deactivated, and the remaining structures are tested on the accomplishment of task $T1$. Next, the respective agents from $CG2$ are isolated (lesion of $CG1$) and tested on the accomplishment of task $T2$. Fitness values are assigned in the respective individuals as it is described below.

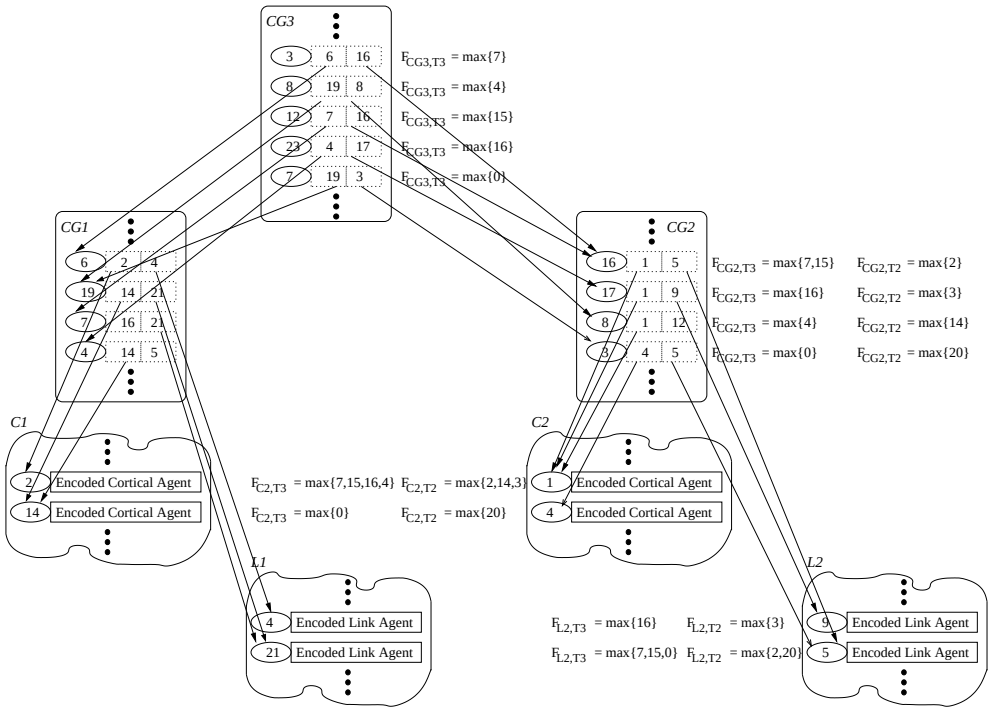

Fig. 3. A snapshot example of the hierarchical coevolution of species. The arrows illustrate definition of individual assemblies. See text for details.

3.3. *Fitness Assignment*

Although the majority of existing cooperative coevolutionary methods assume that all species share a common fitness function[3,22,54], the proposed approach allows the employment of separate fitness functions for different species. This is in accordance to the coevolution of agent structures, because different objectives can be defined for each agent.

When an assembly of cooperators is tested, the cooperative performance of all agent structures is evaluated. The fitness function of each agent species evaluates subjectively the overall performance, that is it evaluates the performance according to the objectives it is designed for. 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. For each species s, a fitness function f_s is designed to drive its evolution. Specifically, f_s is based on partial fitness functions $f_{s,t}$ evaluating the ability of a candidate solution to serve task t. The fitness values for the accomplishment of each task are combined in a multiplicative manner to estimate the global fitness value:

$$f_s = \prod_t f_{s,t} \tag{2}$$

For the agents which are not participating in the accomplishment of a task, the respective $f_{s,t}$ can be either omitted, or set equal to unity.

Since all PS species under a CG share common objectives, they also share the same fitness functions. For the example at hand the latter means that the fitness function of species $L1$, $C1$ on a task t, is equal to the fitness function of $CG1$ (e.g. $f_{L1,t} = f_{C1,t} = f_{CG1,t}$). The same is also true for species $L2$, $C2$ and $CG2$ (e.g. $f_{L2,t} = f_{C2,t} = f_{CG2,t}$). However the fitness functions of $CG1$, $CG2$ and $CG3$, do not have to be related in general.

The cooperator selection process at the higher levels of hierarchical coevolution will potentially select a component individual from the lower levels to participate in more than one complex assemblies. Similarly to most existing approaches, individuals of the coevolved species are assigned for each task the maximum of the fitness values achieved by all the solutions formed with their membership. Specifically, an individual of the s-th species is assigned for task t the value:

$$f_{s,t} = max_k\{f^k_{s,t}\} \tag{3}$$

where $f^k_{s,t}$ is the fitness value of the k-th solution formed with the membership of the individual under consideration.

The fitness assignment mechanism described by Eqs. (2) and (3), intuitively works as follows. First, Eq. (3) estimates the suitability of a component structure to support the accomplishment of a given task, by taking the maximum of the fitness values obtained with its membership. Then, based on the ability of a candidate solution to support each task, Eq. (2) calculates the overall fitness of the individual representing its aptness to all given tasks. We utilize multiplication to combine partial results, because it handles effectively measures of different ranges, and additionally penalizes sufficiently those individuals that perform poorly in at least one task.

The fitness assignment process is further explained by means of the example illustrated in Fig 3. We remind that according to the employed scenario, the composite model should accomplish task $T3$, the partial model of $C1$,$L1$ should accomplish task $T1$ (lesion of $CG2$), and the partial model of $C2$,$L2$ should accomplish task $T2$ (lesion of $CG1$). As a result, individuals of $CG3$ are evaluated for the accomplishment of task $T3$, individuals of $CG1$ and lower level PS species are evaluated for the accomplishment of both tasks $T3$ and $T1$, while individuals of $CG2$ and lower level PS species are evaluated for the accomplishment of both tasks $T3$ and $T2$. The assigned fitness values are illustrated in Fig 3, following the formulation introduced in Eqs. (2) and (3). For the sake of brevity, we present fitness assignment only on $CG2$ and its lower level species. For the same reason we also assume that $F_{CG3,T3} = F_{CG2,T3}$, while in general they can be different.

The top level species $CG3$ is sequentially accessed and fitness values are estimated regarding the accomplishment of $T3$. Let us now examine the individual of $CG2$ with $id = 16$, which participates in two cooperator assemblies of $CG3$. Its ability to serve task $T3$ will be evaluated with the maximum of the respective fitness

values. Additionally, $CG2$ individuals are assigned separate fitness values for the task $T2$ that they also serve. The same is also true for the individuals of lower level species $C2, L2$. For example, $C2$ individual with $id = 1$, has multiple participation in the accomplishment of tasks $T3$ and $T2$ and its partial fitness values regarding the two tasks are estimated by the maxima of the respective values.

We also note the fitness assignment of the individual with $id = 4$ of $C2$. Although it receives a high score for its participation in task $T2$, it receives zero for its participation in $T3$, and consequently its aggregative score according to Eq. (2) will be also zero. There are also individuals which receive a high aggregative score, even if none of the assemblies they participate perform successfully in all tasks. This is the case for individual with $id = 5$ of species $L2$. One of its cooperating assemblies receives a high score in $T1$ and a low score in $T2$, while the other receives a high score in $T2$ but a low score in $T1$. However, the individual under consideration is finally assigned two high scores, because according to the partial performances, it is able to successfully serve both tasks. At the snapshot of the HCCE scheme shown in Fig 3, individual 5 of species $L2$ does not participate in overall effective assemblies, since none of them accomplishes both tasks. However, its high aggregative score increases the probability of participating in better assemblies in the next generation. Additionally, by means of genetic operators, parts of its genotype will also be transferred in the following generations, producing even better offsprings.

3.4. *Encoding*

A general purpose genotype is employed for both the evolution of PS species, and the cooperator selection process at CG species. The genotype is designed in an abstract form, able to handle a variety of computational structures (Fig 4). Thus, neural agents of any level of biological plausibility can be encoded and evolved.

Each individual is assigned an identification number and encodes two different kinds of variables. The first kind is allowed to get a value from a set of unordered numbers (e.g. {1,5,7,2}, with the ordering of the elements being of no use). These variables are called *SetVariables* and they are employed to store identification numbers, encoding the relationship between various elements of the model. The second kind of variables is allowed to get a value within a range of values (e.g. [0,1]); therefore, they are called *RangeVariables* and they are employed to search the domain of parameters in partial structures. The values of SetVariables and RangeVariables are encoded in the genome by an integer and a real number, respectively, and they are graphically represented with dashed and solid boxes (Fig 4(a)).

Appropriately modified instances of the genotype are employed to encode the detailed structure of cortical and link agents. Following the description of link agents in section 2.1, their structure is specified by the (x, y) coordinates of axon projections. Thus, for a cortical structure with N_e excitatory neurons which employes a link agent to project on another cortical structure, $2N_e$ RangeVariables are necessary to encode the coordinates of link axons. The genotype used to encode link

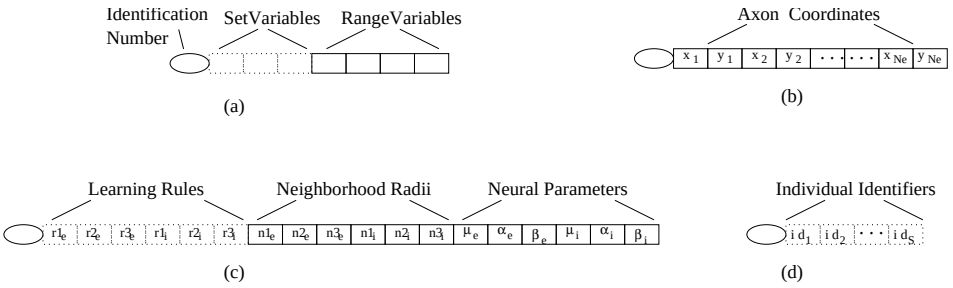

Fig. 4. A schematic representation of (a) the general genome structure, (b) link agent's genome structure, (c) cortical agent's genome structure, (d) CG genome structure.

agent structure is illustrated in Fig 4(b).

In accordance to the description of cortical agents in section 2.2, their structure is completely specified by 6 SetVariables encoding the identifiers of the learning rules employed to adjust synapse weights, 6 RangeVariables to encode neighborhood radii employed for synapse definition, and 6 RangeVariables to encode neural parameters (μ, α, β) separately for excitatory and inhibitory neurons. Thus, the genotype used to encode cortical agent structure is formulated as shown in Fig 4(c).

CG species encode assemblies of PSs (cortical or link agents) or other CGs (groups of cortical and link agents) located at the lower levels of the coevolutionary hierarchy. Thus, for the coevolution of S lower level species an equal number of SetVariables has to be utilized. Each SetVariable is joined with one lower level species, and its value can be any identification number id of the individuals from the species it is joined with. A graphical illustration of the genotype employed by CG's species is given in Fig 4(d).

3.5. *Genetic Operators*

Based on the genome structure, we have implemented crossover and mutation operators which perform seperately on each kind of variables. During the mate process, the usual single-point crossover is applied independently to SetVariables and RangeVariables. Moreover, different mutation operators are implemented for each kind of variables. Mutation corresponds to additive noise in the case of RangeVariables. Mutation of SetVariables is different for PS and CG individuals. As it has been described in section 3.4, in the case of PS, SetVariables encode learning rule identifiers. Thus, mutation corresponds to random assignment of a new learning rule. In the case of CG, SetVariables encode identifiers of individuals at the lower species. Thus, mutation corresponds to probabilistic selection of a new individual, based on the accumulative probabilities at the lower level species. Following this approach, the best fitted individuals are most probably selected to participate in assemblies of cooperators.

Replication Operator. Because of the probabilistic nature of the process, some individuals of the species at the lower level are multiply selected to participate in

many assemblies. However, having a large number of multiple cooperations is generally a drawback for the coevolutionary process. This is due to the fact that different cooperators would demand evolution of the same individual in different directions. At the same time, some individuals in the same species might exist, which are not offered any cooperation (termed *non-cooperative* henceforth). Non-cooperative individuals can be utilized to decrease the multiplicity of cooperations for those which are heavily reused. This is achieved by employing a new genetic operator termed "Replication" (introduced in our previous work[29]). In short, for each non-cooperative individual x of a species, replication identifies the fittest individual y with more than max_c cooperations. The genome of y is then copied to x, and x is assigned $max_c - 1$ cooperations of y, by updating the appropriate individuals of the population at the higher level. After replication, individuals x and y are allowed to evolve separately following different evolutionary directions. Thus, Replication enforces the evolutionary process to exploit the whole population of individuals in each species. We note that the application of Replication operator has no meaning for the species at the top level since there is no higher evolutionary process to select its individuals multiple times.

Evolutionary Step. In order to produce a new generation, each species is evolved independently. Initially, the individuals of a species are sorted according to their fitness values. Then, starting from the higher levels, each species is sequentially applied all genetic operators, as described above. At first, replication reduces the very large number of cooperations for individuals. Then, a predefined percentage of individuals are probabilistically crossed over. Finally, mutation is applied in a small percentage of the resulted population to subserve diversity.

4. Experimental Methodology

The effectiveness of the proposed approach is illustrated by modelling four modules of the mammalian central nervous system (CNS), namely posterior parietal cortex (PPC) - prefrontal cortex (PFC) - primary motor cortex (M1) - spinal cord (SC), addressing their role in the development and exploitation of working memory (WM). The implemented model is embedded in a simulated mobile robot that is furnished with cognitive abilities, proving the validity of results.

The aforementioned modules of the mammalian central nervous system are represented by 4 cortical agents which are appropriately connected via link agents (Fig 5). The connectivity of agent structures follows the organization of the brain prototype. Sensory stimuli are projected to both M1 and PPC. M1, SC are located in the lower levels of the motor hierarchy, encoding and expressing respectively basic motor commands. PPC-PFC reciprocal interaction operates in a higher level, in order to develop motor plans. PFC activation is passed to M1 which modulates its performance according to the higher level. SC is represented only by its descending pathway, specifying the details of motor actions. We note that the proposed model does not aim to be a detailed replica of the biological prototype (e.g. premotor areas

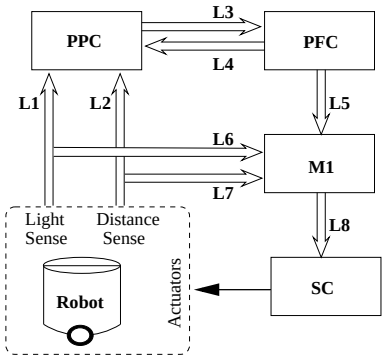

Fig. 5. A schematic overview of the model consisting of four cortical agent structures to represent posterior parietal cortex (PPC), prefrontal cortex (PFC), primary motor cortex (M1), and spinal cord (SC). Link agents are illustrated with double arrows.

are not represented). It is a rather simplified version which demonstrates how the agent-based coevolutionary framework can be employed to support brain modelling tasks.

Several biological experiments highlight the behavioral organization of the brain areas under discussion. These experiments are usually based on Delayed Response (DR) tasks which require animals to retain memory relative to a sample cue for a brief time period[37]. The trial begins by presenting to the animal a sample cue. After a brief delay period, the animal has to decide upon its behavioral response, according to a rule associated with the sample cue. A large number of PFC lesion studies in mammals (e.g. rats[16,39], monkeys[11]) have shown that animals with prefrontal lesions had significantly decreased scores in DR tasks, compared to pre-surgery levels. As a result neuroscientists conclude that PFC is responsible for the formation of WM, and its successful projection to the lower level motor structures.

Two different coevolutionary approaches are followed for modelling the interactions of the brain areas under discussion. First, an incremental process is followed. It starts by implementing separate computational models of both M1-SC and PFC-PPC interactions. These two models are further integrated by means of an additional coevolutionary scheme that operates on top of their results. In the second approach, a single coevolutionary process is employed to design from scratch the composite model illustrating the ability of HCCE to design complex models, consisting of independent but cooperating modules.

4.1. *Agent's Structure*

Each one of PPC, PFC, and M1 structures are represented by a cortical agent with 16 excitatory and 9 inhibitory neurons. SC is represented by another cortical agent with 4 excitatory motor neurons and 9 inhibitory neurons. The model is embedded in the YAKS environment, that simulates Khepera mobile robot functionality, facilitating environmental interaction[51]. The robot is equipped with uniformly dis-

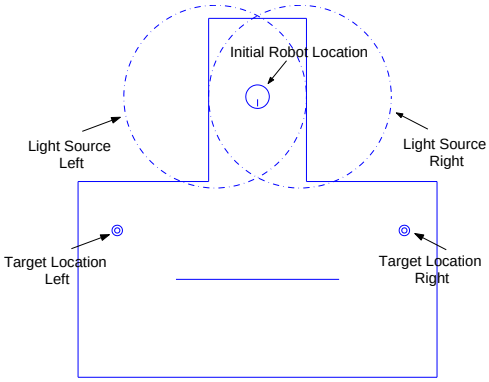

Fig. 6. A graphical representation of the experimental environment. Walls are illustrated with solid lines. Dashed circles illustrate the existence of two light sources employed for tasks $T2$, $T3$. Double circles represent the goal points for the two different cases of task $T3$.

tributed distance and light sensors. Each sense is supported by 8 sensors. Thus, link agents L1, L2, L6, L7 (Fig 5) are represented by the coordinates of 8 projecting axons. It is also reminded that for each projecting cortical agent only excitatory neurons formulate efferent axons to the receiving cortical agent. Thus L3, L4, L5, L8 are all represented by the coordinates of 16 projecting axons.

The motion of the mobile robot is supported by means of two wheels. We assume that a pair of agonist and antagonist muscles moves each robot wheel to the desired direction. Each excitatory motor neuron of the spinal cord activates either an agonist or an antagonist muscle. Wheel speed is specified by the activation difference within a pair of muscles. Thus, 4 excitatory motor neurons are utilized in SC (see above) to define muscle's activation, and by consequence the speed of the robot.

4.2. *Behavioral Tasks*

The design process aims at enforcing the behavioral similarity of the model with the biological prototype. The experimental environment is demonstrated in Fig 6. We have formulated a robot-based DR task and a lesion scenario which is in accordance to biological observations. Three different tasks serve the process of modelling PPC-PFC-M1-SC interactions enforcing the emergence of the desired functionality in each substructure. In the following we present the tasks and the brain area representing modules responsible for their accomplishment.

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. Since M1-SC are the modules of the mammalian CNS which serve basic motor commands and they are operative after lesion of the higher level structures[20], it is assumed that in the robotic task they are relevant for the accomplishment of wall avoidance navigation. Other models of M1 have been also developed[2,50], which, however, do not emphasize on the self-organized understanding of environmental

characteristics.

The second task $T2$ aims at the development of WM-like performance, related to the spatial presence of a light cue. Working memory (WM), is the ability to hold for a short time period input information in order to guide forthcoming actions. The prefrontal cortex (PFC) is the brain structure most closely linked to WM [8]. There are also more areas of the mammalian brain involved in WM, formulating a distributed network. One of the main components of this network is the posterior parietal cortex (PPC)[4], that is particularly relevant in accomplishing spatial tasks[35]. Thus, in the current model, PPC-PFC interaction aims at developing WM-like activation. More specifically, a light cue is presented to the left or right side of the robot (see Fig 6). WM functionality aims at encoding and memorizing the side of light appearance. In other words, $T2$ task is successfully achieved if persistent activity is observed in PFC, related each time to the side of the light cue. A large variety of WM computational models have been presented in the literature modelling PFC activity by means of recurrent circuits[4,8,18]. However, these models have been developed in isolation, in the sense that they are not linked to lower motor structures to affect their performance.

The third task $T3$, integrates the above behaviors to a more complex one where all substructures of the model are active, and WM-based orders guide the activity at the lower motor levels. Similar to the hierarchy of the mammalian motor brain areas, the memory held by PFC activation modulates M1 performance to develop goal directed motion[20,12]. The successful interaction of substructures 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 presence, and then make a 90^o turning choice approximating the goal position specified by the side of the light cue (Fig 6). Different WM models have been also presented in the literature[32,43,55]. Some of them[43,55], have been tested in tasks similar to $T3$. However, they all employ compact artificial neural network structures, without specifying any relationship with brain areas.

The accomplishment of the tasks presented above simulates the interactions of the brain areas under discussion, due to the following reasons. First, the overall computational structure performs similarly to animals in pre-lesion conditions, solving the DR task $T3$. Second, WM-like activation is developed in PPC-PFC. This is demonstrated by PPC-PFC performance in task $T2$. Finally, according to biological experiments shown that PFC lesion results to significantly reduced motion-planning ability, the robot navigates in a purposeless mode in task $T1$.

4.3. *Evaluation*

The successful accomplishment of the above tasks is measured by three evaluation functions E_1, E_2, E_3. In the following we present both the experimental setup of each task, and the quantitative measures evaluating their accomplishment.

Task T1. The wall avoidance navigation task, $T1$, is related to M1-SC interactions which account for robot motion avoiding crash on the walls. The robot is allowed to interact with the environment for M simulation steps, where its performance is observed. In the present study, experiments for $M = 1500$ simulation steps are performed. The successful accomplishment of the task is evaluated by the function:

$$E_1 = \left(\sum_M (sl + sr - 1) \cdot (1.0 - p^2) \right) \cdot \left(1 - \frac{2}{M} \left| \sum_M \frac{sl - sr}{sl \cdot sr} \right| \right)^3 \cdot \left(1 - 2\sqrt{\frac{B}{M}} \right)^3 \quad (4)$$

where $sl, sr \in [0, 1]$ are the instant speeds of the left and right wheel, $p \in [0, 1]$ 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 largest the value of E_1 the best the performance of the robot in wall avoidance navigation.

Task T2. The WM task involves interactions of PPC-PFC structures. The experiment proceeds as follows. The robot is located to a predefined position of the environment when a light source is turned on, either on its left or its right side, for 50 simulation steps. Then, the light source is turned off, and the robot interacts with the environment for $M = 300$ simulation steps. During this period, the robot has to memorize the side that the light source appeared.

We specify two different states l, r 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^l, a_j^r, are computed, with j identifying one of the N_e excitatory neurons at PFC. The activation of inhibitory neurons at PFC is not considered, since only excitatory neurons encode efferent information. The formation of separate WM patterns each one related to a side of light cue appearance, is evaluated by measuring the persistency of activation in PFC agent:

$$E_2 = \min \left\{ \sum_{j, a_j^l > a_j^r} \left(a_j^l - a_j^r \right), \sum_{j, a_j^r > a_j^l} \left(a_j^r - a_j^l \right) \right\} \cdot \left(\frac{v_l}{m_l} + \frac{v_r}{m_r} \right) \quad (5)$$

The first term of Eq. (5) supports the representation of the states l, r by a different set of active neurons at PFC. Furthermore, the second term enforces the consistency of PFC activation, with m_l, v_l, m_r, v_r being the mean and variance of average activation at the respective states:

$$m_l = \frac{1}{N_e} \sum_j a_j^l \quad v_l = \frac{1}{N_e} \sum_j \left| m_l - a_j^l \right|$$

$$m_r = \frac{1}{N_e} \sum_j a_j^r \quad v_r = \frac{1}{N_e} \sum_j \left| m_r - a_j^r \right|$$

If persistently few, but the same, neurons are activated during the observed period, the second term of Eq. (5) will get a high value. If activation is not consistent, different neurons are activated in different simulation steps, and the term under

discussion will get a low value. Overall, high values of E_2 indicate successful performance in the WM task.

Task T3. The experimental process of $T3$ describes a delayed response (DR) task, that has to be accomplished by the interaction of PPC-PFC-M1-SC structures. The robot is standing in a predefined position of the environment, when a light source is turned on for 50 simulation steps either on its left or its right side. Then, the light source is turned off, and the robot is allowed to move for $M = 300$ simulation steps. When the robot approximates the end of the corridor, it has to decide which side to turn. The DR task is completed successfully if the robot turns to the same side that the light source appeared.

Assuming a proper WM-like performance at PFC, different target locations are defined in corridor sides depending each time on the position of the initial light cue (Fig 6). During the response of the robot, it has to approximate one of the two target locations without crashing on the walls. The robot acts freely in the environment for $M = 300$ simulation steps, and then the euclidian distance d to the target is measured. The successful approximation to a target location x, is measured by:

$$G^x = \left(1 + 3\left(1 - \frac{d}{D}\right)\right)^3 \cdot \left(1 - 2\sqrt{\frac{B}{M}}\right)^2 \tag{6}$$

where 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 first term of Eq. (6) enforces target reaching, while the second addresses robot motion without bumps.

The accomplishment of $T3$ is evaluated by two subtasks which test separately robot turning regarding the right or left side of light cue presence. Thus, two evaluation measures G^l, G^r are obtained based on Eq. (6), employing each time the appropriate target location. The total accomplishment of the memory-guided behavioral task $T3$, is evaluated according to:

$$E_3 = G^l \cdot G^r \tag{7}$$

which implies high scores for both subtasks. The largest the value of E_3, the best the accomplishment of the DR task by the robot.

Having introduced the experimental procedure, we now turn to the distinct coevolutionary approaches followed to model the brain areas under discussion. Specifically, an incremental and a compound approach are demonstrated in the following two sections. In this presentation, the distinct features of the two approaches are highlighted.

4.4. *Incremental Modelling*

It is generally hard to accomplish large scale brain modelling by developing from scratch a very complicated model. An alternative approach could be based on implementing separate models of partial brain areas which are further integrated in

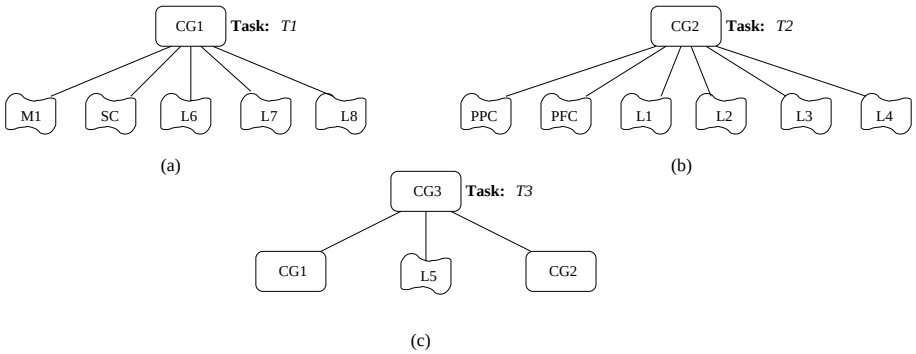

Fig. 7. A schematic overview of the incremental coevolutionary process. Part (a) illustrates the process employed to design the model of M1-SC interaction, part (b) illustrates the process designing the model of PPC-PFC interaction, and part (c) illustrates the coevolutionary process which serves their integration.

gradually more complex ones. Hence, the ability to proceed by means of an incremental approach, is a desirable feature for a successful brain modelling method. The proposed computational framework is capable of facilitating the incremental modelling process. Specifically, the agent-based representation of brain areas supports the decomposition of the problem to small tractable tasks. Additionally, the HCCE scheme can be utilized to attain each separate task, designing partial brain models. Then, the results of partial processes should be further integrated to develop a combined solution. Fortunately, the HCCE scheme can be employed again to support the integration process[27].

The incremental modelling approach is demonstrated by implementing a computational model of the brain areas illustrated in Fig 5. Two coevolutionary processes are performed independently, to design partial models of M1-SC, and PPC-PFC interaction (Fig 7). Each process is responsible to design the cortical and link agents involved in the respective partial model. When both processes are finished, a third coevolutionary scheme commences to design the intermediate link structure which integrates the two partial models in a composite one.

Specifically, the first coevolutionary process aims at the accomplishment of the wall avoidance navigation task $T1$, by M1-SC interactions. The hierarchical scheme coevolves five lower level species, each one encoding an agent structure (Fig 7(a)). Populations of 200 individuals evolve all component species, while a population of 300 individuals evolves the higher-level cooperator selection process. The fitness function of the present process evaluates the success on wall avoidance navigation. This is achieved by means of the E_1 measure. Following the formulation introduced in Eqs. (2), (3), the fitness function is defined by:

$$f_{CG1} = f_{CG1,t1} \text{ with } f^k_{CG1,t1} = E_1 \tag{8}$$

where k represents each membership of an individual in a proposed solution. After 70 epochs, the coevolutionary process converged successfully, and the robot could

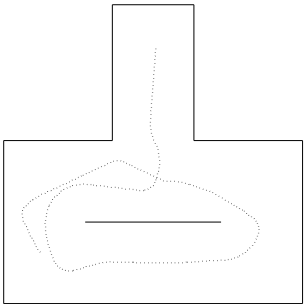

Fig. 8. A sample result of robot wall avoidance navigation.

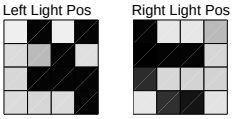

Fig. 9. The average activation of 16 excitatory neurons at PFC. The dark activation values indicate that the cell remain active during all the observed period, while light values indicate low activity in the same period. It is clear that each side of light cue presence is encoded in a different activation pattern.

be driven without bumping on the walls. A sample result is illustrated in Fig 8.

The second coevolutionary process aims at the accomplishment of $T2$ WM task, by PPC-PFC interactions (Fig 7(b)). Populations of 200 individuals evolve agent species, while a population of 300 individuals evolves the higher level species selecting cooperating agents. The employed fitness function equals to E_2, evaluating the success on WM-task, $T2$:

$$f_{CG2} = f_{CG2,t1} \text{ with } f^k_{CG2,t1} = E_2 \tag{9}$$

where k is as above. After 80 evolutionary epochs we got many computational models able to simulate WM performance. A sample result is illustrated in Fig 9.

The third coevolutionary process aims at the accomplishment of $T3$ delayed response task by the composite model. The third hierarchical scheme performs on the results of the previous two processes evolving the link agent $L5$ that supports their connectivity (Fig 7(c)). The ten best individuals of $CG1$ and $CG2$ species are used as candidate partial models, formulating a basis for the construction of the global model. The species of $CG1$ and $CG2$ are not evolved, and thus the ten best individuals of $CG1$ and $CG2$ remain unchanged. As a result, only two species need to be evolved. The first species, consisting of 200 individuals, is evolved at the lower level encoding the structure of $L5$ link agent. The second species addresses the formulation of succesfull assemblies. $CG3$ is evolved at the higher level employing 300 individuals. The coevolutionary process is driven by a fitness function that equals E_3, evaluating the success on $T3$ delayed response task:

$$f_{CG3} = f_{CG3,t1} \text{ with } f^k_{CG3,t1} = E_3 \tag{10}$$

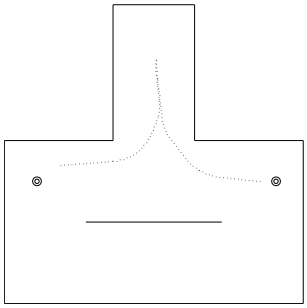

Fig. 10. A sample result of robot performance in the delayed response task. PFC activation successfully modulates M1 performance to drive the robot to the desired goal.

where k is as above. After 40 evolutionary epochs we got many computational schemes able to accomplish the memory guided behavioral response task. A sample result is illustrated in Fig 10.

In a last validation experiment, we test the performance of M1-SC model in the DR task (simulating PFC lesion functionality). The performance observed was unsuccessful as expected, and it looked very much like the first simulation steps of wall avoidance navigation (Fig 8). The robot moves without a tendency to turn. In particular, it moves straight, unless a wall is sensed. This makes the robot turn in the direction that avoids crash with the wall, irrespective of the side that the light cue appeared.

4.5. *Compound CoEvolutionary Modelling*

Following the incremental modelling approach, the partial models designed first, bias the implementation of those designed in the subsequent phases. As a result, there could be cases where the constraints imposed by the initial models can be too hard, harming the forthcoming integration processes. There could be also cases, where the interactive relationship among partial structures can be too complex to be modelled by separate phases. All these factors imply that many times complex models will be necessary to be designed in a single step.

The computational framework introduced in the present work is appropriately formulated to address such design considerations. The employment of neural agents representing brain areas, together with the HCCE scheme that utilizes different fitness functions to evolve each species, support the design of composite models, highlighting both the cooperative and the individual characteristics of substructures. The employment of a compound coevolutionary process for modelling the brain areas illustrated in Fig 5, is discussed below.

A three level hierarchical coevolutionary scheme is utilized. Agent structures are classified in CGs according to the artificial lesion scenario described in section 4.2. The specification of CGs, is illustrated graphically in Fig 11. The tasks served by each group of agents are illustrated at the right side of each CG. Specifically, the

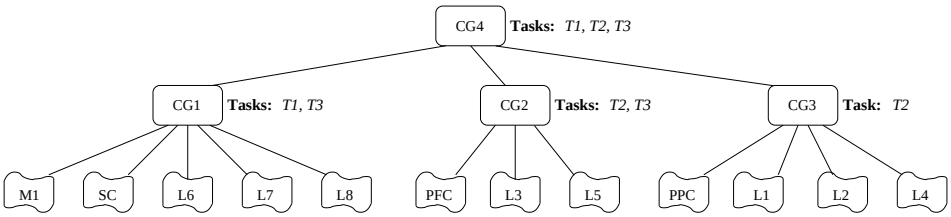

Fig. 11. A graphical illustration of the compound coevolutionary process.

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. They need to serve WM persistent activation, and the delayed response task. The structures under $CG3$ are related to PPC and its afferent projections which have to support WM activation only ($CG2$ structures are responsible for the proper formulation of WM and its projection to M1). Finally, a top level CG is employed to enforce cooperation within partial configurations supporting the accomplishment of all the three tasks[30].

The evaluation of candidate solutions starts by sequentially accessing the individuals of the top level species, which guides cooperator 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 WM 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 support the accomplishment of different sets of tasks. According to the lesion scenario, the agent structures grouped under $CG1$ need to 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. (2), (3):

$$f_{CG1} = f_{CG1,t1} \cdot f_{CG1,t2} \text{ with } f^k_{CG1,t1} = E_1,\ f^k_{CG1,t2} = \sqrt{E_3} \tag{11}$$

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

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

$$f_{CG2} = f_{CG2,t1} \cdot f_{CG2,t2} \text{ with } f^k_{CG2,t1} = {E_2}^2,\ f^k_{CG2,t2} = \sqrt{E_3} \tag{12}$$

where k is as above.

The structures under $CG3$ need to serve only the development of WM-like activation. Thus, the fitness function employed for the evolution of $CG3$ is defined

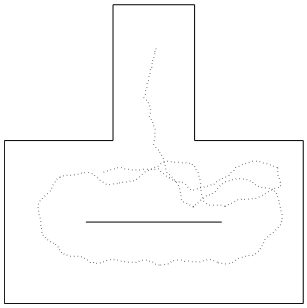

Fig. 12. A sample result of robot performance, driven by M1-SC. The robot moves in a purposeless mode without bumping on the walls.

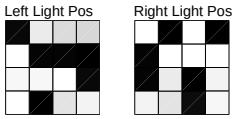

Fig. 13. The average activation of 16 excitatory neurons at PFC, for each light position. Activation is demonstrated with levels of grey.

by:

$$f_{CG3} = f_{CG3,t1} \text{ with } f^k_{CG3,t1} = E_2 \tag{13}$$

where k is as above.

Additionally, the top level evolutionary process $CG4$, enforces the integration of partial configurations in a composite model, aiming at the successful accomplishment of all three tasks $T1$, $T2$, and $T3$. The fitness function is defined accordingly, following the formulation introduced in Eqs. (2), (3), by:

$$f_{CG4} = f_{CG4,t1} \cdot f_{CG4,t2} \cdot f_{CG4,t3} \text{ with } f^k_{CG4,t1} = \sqrt{E_1},\ f^k_{CG4,t2} = {E_2}^2,\ f^k_{CG4,t3} = E_3 \tag{14}$$

where k is as above.

It is easily observed from Eqs. (11) - (14), that the formulation of fitness functions is based on the measures evaluating the performance of each task. Specifically, different species enforce the accomplishment of each task with a different weight. For example, compared to $CG1$, the fitness function which guides the evolution of $CG4$ enforces more the accomplishment of $T3$ than the accomplishment of $T1$ (see definitions of $f^k_{CG1,t1}$ - $f^k_{CG1,t2}$ 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 new generations, supporting the robustness of the evolutionary process. After 200 evolutionary epochs the process converged successfully.

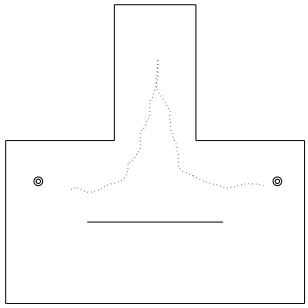

Fig. 14. A sample result of robot performance in the delayed response task, for two different sides of light cue presence.

Sample results of the performance on each task are illustrated in Figs 12, 13, 14. As it is indicated by the lesion scenario, M1-SC are able to drive the robot in a purposeless manner, following the wall avoidance policy (Fig 12). At the same time, PPC-PFC interaction encodes the side of light cue appearance, and memorize it for a short future period (Fig 13). Moreover, the composite model combines successfully the performance of partial structures to accomplish the DR task (Fig 14).

In a last validation experiment, the functioning of the model after PFC lesion is tested on the DR task. The performance observed is similar to the first simulation steps of wall avoidance navigation (Fig 12). The robot moves forward unless a wall is sensed, which makes it turn in the proper direction to avoid crash. This is a predicted performance since M1-SC agents adjust their functioning based only on the directly incoming sensory information, without considering higher level plans.

4.6. *Incremental vs Compound Modelling*

The previous paragraphs demonstrated how the proposed Hierarchical Cooperative CoEvolutionary (HCCE) scheme specifies the structure of neural agents, developing computational models of brain areas. The modelling can be achieved by following two different approaches, either by performing partial coevolutionary processes whose results are incrementally integrated, or by means of a compound coevolutionary process which designs in a single step the composite model. The qualitative differences among the two approaches can be revealed by close inspection of Figs 7 and 11, both of them related to Fig 5. In the following, we compare the two approaches in order to conclude regarding their usability.

First, we note that both approaches are capable of successfully modelling the areas under consideration. For example, examining the performance in task $T2$ (Fig 9 and Fig 13), we may conclude that in both cases, distinct activation patterns emerge to encode the side of light cue. Still, distinct characteristics may emerge in the solutions derived by the two design approaches, without however eliminating the effectiveness of the result. Specifically, with respect to wall avoidance navigation (Fig 8 and Fig 12), we observe that motion without unreasonable spinning is more

likely observed with the first approach. This is because in the incremental case, the design of M1-SC model aims only at the accomplishment of $T1$, while in the compound process the objective is more complicated aiming at the accomplishment of both $T1$ and $T3$. Similar motion patterns are observed in the delayed response task, as it is illustrated in Figs 10 and 12. This is because PFC has to exploit the performance of M1, which has its own spinning dynamics described just above. Thus, the re-usability of M1 affects the performance of the composite model. However, it is clear that PFC projection successfully adapts the performance of M1-SC, driving the robot according to the DR task.

Let us now proceed by examining the practical issues of the two approaches. From a designer's point of view, the incremental coevolutionary approach seems easier and rather preferable, because the objectives of partial processes are simple and well defined. Consequently, the fitness functions guiding the evolution of each species can be easily formulated. On the contrary, the design of the compound co-evolutionary scheme is a rather complicated process since each species must serve more than one objectives. This is a critical design factor, since the evolution of species with largely independent fitness functions will prevent their ability to cooperate, and the compound coevolutionary process will not converge satisfactorily. In order to formulate the fitness functions, the relative weight of the objectives have to be identified for all CGs (hence the square roots and power of two in Eqs. (11)-(14)). Still, a carefully designed compound coevolutionary process is able to highlight both the cooperation among the components of the model, and their autonomous roles in the performance of the composite system.

An important issue concerns also the usage of computational resources. Similar to the majority of evolutionary applications, the brain modelling process by means of HCCE is performed off-line. Following the incremental modelling approach, partial coevolutionary processes are completed in a relatively short time. This is because each of them has a very specific objective to satisfy (accomplishment of only one task), and a small set of agents to tune. Thus, only few generations are enough for a successful design. In contrast, following the compound coevolutionary scheme, more evolutionary epochs are necessary to accomplish the global objective. This is because the interactions within different species (each one having separate objectives), delay the convergence of the total hierarchical coevolutionary scheme. At the same time, following the compound coevolutionary approach, each epoch requires more computational resources, because individuals are tested in the accomplishment of many different tasks. As a result, the compound HCCE approach is computationally more expensive compared to the incremental one.

Based on the above comments, we can formulate guidelines on the usability of each approach. The employment of the incremental approach is suggested whenever the decomposition of the model is possible. This is because the incremental steps are more easily designed. In the case where the model consists of densely connected brain areas, then the specification of partial incremental tasks is difficult. Additionally, it is possible that the incremental integration process will get stalled, due to the

biases of initial models. In both cases, the compound approach should be followed, which however requires more experimental effort by the designer.

Additionally, a mixed approach can be followed. The designer can start with an indicative problem decomposition designing partial models which will be temporarily stored. Then, the results of these processes can be reloaded and used as a starting point of a compound coevolutionary process. This approach is different from the incremental one since partial results do not remain unchanged, but they can be further refined. At the same time, it is also different from the compound coevolutionary approach since the design process does not start from scratch, but by a meaningful set of parameter values, which speeds up coevolution. Due to the nearly-global search performed by evolutionary methods, the reloaded species do not harm the compound coevolutionary process which is not likely to get trapped in a local optimum. Along this line, our previous work[28] discusses how existing models can be redesigned based on the HCCE design mechanism.

5. Conclusions and Future Work

The computational framework introduced in the present work to support brain modelling bears a twofold contribution. First, appropriate agent structures are designed to represent brain areas and their connectivity. The agent-based representation is in accordance to the distributed nature of the biological prototype. Additionally, due to the inherent autonomy of agent components, it supports problem decomposition to small tractable and progressively solved tasks. Second, a distributed design mechanism is employed to specify the details of the model. We introduce a Hierarchical Cooperative CoEvolutionary (HCCE) scheme that designs autonomous substructures by utilizing separate fitness functions for their evolution. Furthermore, the coupled functioning of system components enforces their successful integration in a composite structure. We note that HCCE has been proved to outperform other coevolutionary and unimodal evolutionary procedures in designing complex distributed systems[24].

Overall, the agent-based coevolutionary framework facilitates the implementation of complex brain-like cognitive systems for robotic applications. More specifically, it accomplishes:

- the successful design of distributed partial brain models, by specifying the structure of their components,
- the integration of partial models to gradually more complex ones,
- the construction of complex behaviors from simple components,
- the implementation of large scale brain models by means of an incremental approach,
- the replication of biological lesion results.

It should be noted that the hierarchical design mechanism does not enforce the model to perform in a hierarchical mode. This can be easily deduced by comparing

Fig 5, with Figs 7 and 11. The performance of partial brain structures can be either hierarchical or completely parallel. Hence, the hierarchical coevolutionary design approach does not impose any constraints on simulating the connectivity of brain areas. In contrast, it facilitates significantly their modelling. Along this line, the HCCE design mechanism has been recently utilized to design a much larger distributed cognitive system for a humanoid robot, modelling overlapping observation/execution brain pathways[25].

The formulation of appropriate neural agents (improved versions of the ones presented in our previous work[29], as discussed in section 2) has an important contribution in designing successful models. Specifically, the ability of link structures to project their axons on any desirable position of the receiving cortical plane, has a considerably positive impact on modelling competencies of agents, emphasizing their re-usability. To verify this, we performed experiments similar to those demonstrated in the present work, by employing the previous computational modules[29]. These experiments were not successful due to the fact that the employed computational modules utilize axon projections at predefined locations.

Despite the successful accomplishment of the tasks described here, we emphasize that the existing computational structures are designed to support primarily abstract CNS modelling for robotic applications, than detailed modelling of mammalian brain areas. In the future, additional constraints can be integrated to the agent structures, enhancing the biological reliability of the model. This does not contradict in any sense with HCCE -based design, which is capable of encoding any desirable structure.

The similarity of the model with the biological prototype is further enforced by replicating the results of biological lesion experiments. This is achieved by exploiting the ability of HCCE to consider the performance of the model in pre- and post-lesion conditions, and additionally specify properly its operation in both cases. The results obtained in the current work are biologically plausible, but additional experiments are necessary to support their biological reliability. This constitutes one direction of our future work. The more biological data the model is able to reproduce, the more reliable the roles of agents in the composite model become.

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

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