Symbiogenesis as a Mechanism for Building Complex Adaptive Systems: A Review*

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Abstract

In 1996 Daida *et al.* reviewed the case for using symbiosis as the basis for evolving complex adaptive systems [6]. Specific observations included the impact of different philosophical views taken by biologists as to what constituted a symbiotic relationship and whether symbiosis represented an operator or a state. The case was made for symbiosis as an operator. Thus, although specific cost benefit characterizations may vary, the underlying process of symbiosis is the same, supporting the operator based perspective. Symbiosis provides an additional mechanism for adaption/ complexification than available under Mendelian genetics with which Evolutionary Computation (EC) is most widely associated. In the following we review the case for symbiosis in EC. In particular, symbiosis appears to represent a much more effective mechanism for automatic hierarchical model building and therefore scaling EC methods to more difficult problem domains than through Mendelian genetics alone.

1 Introduction

Evolutionary Computation (EC) has long been associated with a Darwinian model of evolution in which natural selection represents a metaphor for performance evaluation and the motivation for maintaining a population of candidate solutions, whereas metaphors from Mendelian genetics are generally invoked to support the specifics of the representation and provide a model for credit assignment [13]. As such this mirrors the classical development of biology, with recent extensions including the introduction of developmental evolution – therefore reinforcing the use of Mendelian genetics – to the widespread use of coevolution, particularly cooperative and competitive models. Indeed, even calls for the use of more accurate biological models in EC have generally focused on the genetics, thus reinforcing discoveries such as the process of transcription [4]. Conversely, symbiosis as a coevolutionary process has been much less widely studied in the EC literature.

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Symbiosis was defined by De Bary in 1879 as the living together of organisms from different species c.f., "unlike organisms live together" [8] (see [24, 6, 20] for current surveys of the concept). As such the process can encompass both exploitive parasitic relationships and co-operative mutualistic associations. However, central to symbiosis is a requirement for long-term, but not necessarily physical, association between partnering entities. The nature of the association, and therefore the degree of antagonism versus mutualism linking different partners, will vary as a function of environmental factors (see for example the closing commentary in [6]). When the symbiotic association leads to a long-term relationship that, say, converts an initially exploitive relationship into one of co-operative dependence *resulting in a new species* then the process is considered to be that of symbiogenesis [26, 27, 25].

The core components include: (1) partners entering in a relationship from different species/ organisms; (2) partners adapting phenotypically under selection pressure as a result of the symbiotic relationship, and; (3) a long term association which facilitates the creation of a new species of organism(s). The first two points are sufficient for symbiosis, whereas all three points provide symbiogenesis. The result is therefore increased functionality in the case of the final host entity, through the learning or application of traits developed independently by the symbiont(s) [26, 27, 25]. Conversely, a Darwinian model emphasizes the vertical inheritance of genetic variation through sexual reproduction of partners from the same species [19, 25]. From an EC perspective symbiogenesis is a form of coevolution that has the potential to provide the basis for hierarchical/ component-wise model building; whereas competitive coevolution provides a mechanism for scaling EC to problem domains with truly vast state spaces and cooperative coevolution supports processes by which parallel problem decomposition / diversity is emphasized. Indeed systems utilizing multiple forms of coevolution are beginning to appear in EC (e.g., [38, 21]), whilst the interaction of multiple evolutionary mechanisms in biology is widely acknowledged [19]. In the following we review biological properties of symbiosis – thus revisit a general abstract model of symbiosis that appears to be particularly useful under an EC context – as well as recent attempts to make use of symbiotic style algorithms in EC.

2 Biological Context

Despite De Bary's early recognition of symbiosis, it was not until the 1970's that the phenomena received more widespread recognition. In particular Lynn Margulis was instrumental in promoting Serial Endosymbiosis Theory as the mechanism by which evolution from prokaryote to eukaryote took place [23]–[27]. Moreover, most autopoietic entities require symbiotic (as well as Darwinian) models of development [25]. From the perspective of theoretical biology, John Maynard Smith was an early proponent, abstracting the concept of symbiogenesis as a mechanism by which complexity may be increased [28]. Figure 1 summarizes his model in which: Individuals (symbionts) from candidate species
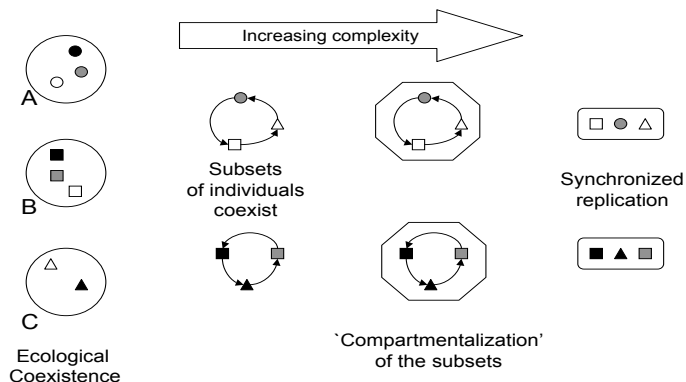
Figure 1: Abstract model of Symbiogenesis: Complexification as a process of compartmentalization (adopted from [28]). Individuals from independent species A, B, C already under an ecological coexistence (far left) form an increasingly intimate coevolutionary partnership resulting in a 'compartment' (center) that supports the coordinated replication of symbionts (right).

currently coexisting in a common genepool/ population/ ecosystem become enclosed within a 'compartment' such that a subset of individuals interact, thus identifying the partners. Over time, the interaction results in a mechanism being established for the replication of the partners i.e., the interaction is beneficial as measured by natural selection. Thus, the specific form of a symbiotic coevolutionary interaction was not emphasized, but rather the key factors were that different species were involved and that the process establish an intimate association over a 'significant time period.' Note also that the concept of a 'host' is quite abstract; the host may or may not be a currently existing entity.

Given this definition for the generic process of symbiogenesis – effectively establishing symbiosis as an operator rather than a state [6] (i.e., outcomes are independent of the coevolutionary interaction) – a wide range of 'resolutions' exist that provide specific examples of symbiosis in nature: **(1) Endosymbiotic:** Interactions that take place within a host potentially resulting in symbiogenesis. *Intracellular* – in which integration at the cellular level takes place. Symbiont cells enter the host, survive, reproduce and successfully appear in the host offspring e.g., as in the case of prokaryote to eukaryote transfers; *Extracellular* – symbionts establish themselves between the host cells (as opposed to within them) or within cavities of the host e.g., as in the case of the mammalian gut (host) and *E. coli* (symbiont) a relation that enables mammals to digest food. **(2) Entosymbiotic:** Represent symbiotic relationships that do not enter the host 'body' and to date lack complete histories supporting symbiogenesis [20]. Daida *et al.* separate this into two forms [6]: *Attachment Symbiosis* – the host and symbiont undergo a permanent/ semi-permanent attachment e.g., as in the case of sea anemones riding the shells of hermit crabs. As such the relationship tends to be one-to-one; *Behavioral Symbiosis* – rely on communication as the

medium to establish the basis for the symbiotic association. As such, relationships can be much more flexible with hosts being served by different symbionts over time e.g., the tooth cleaning relationship between crocodiles and birds.

In addition to this, intracellular endosymbiosis can be augmented by other processes such as horizontal gene transfer (HGT) [1]. Classically, HGT was associated with the transfer of plasmids – bacterial genes not in the main chromosome; where genetic material in the plasmid is known to confer resistance to antibiotics through the combination of high rates of plasmid exchange and a 'noisy' process of transcription [1]. The process frequently appears in bacteria, but also considered to result in the migration of plastids and mitochondria between bacteria, archaea and eukarya [33]. From the view of molecular evolution, both HGT and symbiosis imply that molecular development did not follow a tree of life, but a network of life metaphor in which there is much more inter-breeding of the gene pool [33, 25]. However, the underlying message is that the process of variation is that of Lamarckian inheritance augmented with mutation [26].

The above two level ontology is by no means the only scheme for distinguishing between different forms of symbiosis. Indeed, we maintain in this work that it is the relationship supporting the process of compartmentalization (Figure 1) that more effectively summarizes developments under EC. Thus, five basic categories of relationship might be identified (adapted from [24]): **(1) Spatial relationships** – what degree of physical proximity is necessary to support the identification of potential partners e.g., commensalism (a very intimate integration of partners) versus mutualism (a purely behavioral compartment in which participants maintain physical independence); **(2) Temporal relationships** – defines over what period of the participant's lifetime the compartmentalization exists e.g., whether a compartment is only established following: appropriate communication (therefore symbiosis is an occasional behavioral activity), under a periodic model of reformation and disengagement, or be permanent through the lifetime of participants; **(3) Metabolic relationships** – to what degree a third party host is necessary to provide the compartmentalization, in contrast with symbionts relying on a nonphysical identification (of compartmentalization). This might raise secondary factors such as to what degree participants provide mutually beneficial food sources; **(4) Genetic relationships** – To what degree specific protein(s)/ gene(s) of a participant are transfered to others; and, **(5) Coevolutionary relationships** – symbionts need not be purely mutualistic in their interaction [26, 27, 6]. Indeed coevolutionary relationships could fall under the categories of amensalism, commensalism, competition, predation or mutualism.

Finally, we note that more recent observations from the field of theoretical biology have increasingly emphasized that symbiosis is associated with conferring robustness to the resulting biological entity. The resulting hypothesis of 'self extending symbiosis' refers to a process by which [18]: "evolvable robust systems continue to extend their system boundary [a.k.a compartmentalization] by incorporating foreign biological forms to enhance their adaptive capability against environmental perturbations and hence improve their survivability and

reproduction potential." In short, Mendelian genetics is associated with providing the genomic architecture, whereas symbiosis extends the host through new 'layers of adaptation' [18].

3 Summary of EC models supporting Symbiogenesis

In the following we review examples from EC in which symbiogenesis has played a central role. Particular attention is given to the relationship supporting compartmentalization (spatial, temporal, metabolic, genetic or coevolutionary). That is to say, it is the *combination of relations* that promotes the state of symbiosis as opposed to the *relative resolution* at which symbiosis takes place.

3.1 Learning Classifier Systems (LCS)

Initial research used the control of a 4 legged robot as the environment to consider issues such as [3]: (1) the allocation of rules from a fixed sized population to one of the four robot legs (speciation); (2) symbiosis as used to control the identification of genetic information transferred between pairs of LCS rules. Thus speciation controls the number of legs to which members of the rule population are mapped, whereas symbiosis provided an operator for pairing rules initially associated with each leg. The authors continue with this theme in later work [34]. They note that in order to promote the identification of effective serial combinations of rules, the symbiotic operator needs to focus on rules from different niches and be biased towards matching the rules that were sequentially successful. Moreover, additional controls were necessary in order to build suitable mechanisms for effective credit assignment – or temporal persistence – when using symbiosis. Once integrated, the model was able to provide favorable solutions under a suite of 'Woods' reinforcement domain problems. The focus of the earlier work was necessarily directed towards the impact of assuming different mechanisms for establishing the 'compartmentalization' of symbionts (or the *spatial* relationships of Section 2), while simultaneously providing the basis for providing solutions to a specific problem domain. Conversely, under the later work, the key factor was the use of *temporal* relationships as the mechanism for establishing stable compartments. Both approaches make use of macro operators for selecting individuals to appear in the host compartment and assume a relatively loose model of *metabolic* relation.

3.2 Symbiogenesis and genetic linkage learning

The overall goal of these algorithms is to establish a mechanism for dealing with deceptive linkage/ epistasis in binary representations i.e., correlation of gene changes with fitness is highly non-linear. As such, the participants take the form of a Genetic Algorithm (GA) and most emphasis is placed on establishing relevant *metabolic* and *genetic* relationships for compartmentalization to take

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place. Conversely, the spatial and temporal relationships remain intimate and permanent respectively. The process involved takes the form of either reordering the genes of the host [32] or providing mechanisms for inserting different genetic information within the context of an initial host individual [11, 37, 35]. In the latter case, the work of Dumeur defines a structure for building solutions out of multiple symbionts in which the frequency of seeing similar values in the same gene location makes the utility of that value more probable [11]. The process for promoting symbiont membership is driven by how 'open' a host is to incorporating new symbionts. The 'weaker' a host, the more likely that it will accept new symbionts and vice versa.[1] The GA representation utilizes a pair of values <gene location, gene value> where gene values are binary i.e., implementing a binary GA.

A different approach is taken by the 'composition' model of Watson and Pollack [37]. Again a binary GA is considered in which individuals only specify subsets of the genes. Other genes are considered 'neutral' to that individual: such neutral genes have no contribution other than to establish the alignment of the remaining genes. Fixed length individuals are assumed in order to establish gene alignment for the sharing of genetic material during symbiosis. Symbiosis is the sole mechanism by which individuals are combined to produce a child. To do so, a rule for combining non-neutral genes is established (referred to as 'composition'). In a later work this is combined with a Pareto based competitive coevolutionary model for determining whether a (symbiotic) child is retained [38, 36]. Thus a child is retained if it is better than the parents, in the Pareto sense, over a random sample of training scenarios (i.e., a test for symbiogenesis). Thus, children are only accepted if they are explicitly better than the parents.

Further efforts have been made to provide a more formal structure by which composition may evolve solutions to problems with higher orders of linkage [9]. Recent results are along these lines [10] i.e., hierarchical model building . Additional refinements to the composition model have also been introduced [15]: (1) mutation for supporting population diversity (2) initial population limited to single (non-neutral) genes but allowed to incrementally increase, thus making the hierarchical gene linkage learning more explicit; and, (3) maintenance of a worst case tabu list of poorly performing genomes to bias against revisiting poor states during symbiosis. Moreover, the same process was also employed for evolving fuzzy rules under a LCS context [2]. Watson has also continued to develop the model, with a particular focus on the criteria for detecting 'good' symbiotic partners [29], dropping the requirement for children to strictly better their parents. Finally, a 'Symbiogenetic Coevolutionary' framework also concentrates on the linkage learning problem under binary GAs with symbionts having the capacity to 'inject' themselves into the host chromosome, over-writing sequences of bits [35]. Again binary deceptive problems were used to illustrate the effectiveness of the approach under a fixed length representation.

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[1] Incidentally, the early GA model of Daida *et al.* also made use of 'switches' to indicate whether the corresponding gene of the host can be 'infected' with a symbiont of a 'type' also declared by the host [7].

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3.3 Pairwise symbiogenesis and coevolution of symbiont behaviors

Kim *et al.* develop a model for the pairwise construction of symbionts [17]. Emphasis was placed on the exchange process for mapping participants between independent symbiont and component populations i.e., *spatial* and *temporal* relationships are used to control the mapping from independent species to compartmentalization (and viceversa). However, a natural penalty for this is that there is no process for combining more than two partners in a symbiotic relation. The pairwise limitation also appears in the 'linear' model of Morrison and Oppacher [31]. What is particularly interesting in their linear model is that different pairwise associations are initialized to represent different *coevolutionary* relation: amensalism, commensalism, competition, predation and mutualism. Moreover, the relative 'strength' of an association can be pre-specified as a design parameter. Defining the relevant strength parameter, however, was observed to be problem dependent. Eguchi *et al.* address this by letting the association itself evolve, this time under a multi-agent context [12]. Specifically, pairs of agents are selected – 'self' and 'opponent' – as well as the children of the 'self' individual. Pairwise evaluation under a Pareto framework is then performed under each of the models of symbiotic association to establish their preferred relation. (In an earlier work the authors describe an approach based on fuzzy rules [16]).

3.4 Models with dissimilar representations and multiple populations

The evolution of neural networks provided an early example in which different representations are employed for compartment and symbiont or hierarchical Symbiotic Adaptive Neuroevolution [30]. Specifically, a 'blueprint' population in this case expresses the compartment by indexing (symbiont) neurons from an independent neuron population; thus model building is a combinatorial search over the set of symbionts i.e., a *spatial* relationship. Similarly, the symbiogenetic evolution of Genetic Programming (GP) has also been considered for 'teaming' – that is forming teams of programs which collectively evolve to provide solutions [21]. The Symbolic Bid-based (SBB) GP framework utilizes a GA to conduct a combinatorial search for effective GP symbionts; thus each GA (host) individual defines a compartmentalization. Central to this model is an explicit separation of learning when to act (the bid or a *temporal* relation) and what to do (the action) or Bid-based GP. Without this, the context under which each symbiont program operated would be lost. Results demonstrate effectiveness at problem decomposition under classification [21] and reinforcement learning domains [22]. Moreover, the symbiont population (Bid-based GP) content evolves under mutation and a variable size population model in order to support symbiogenesis in the best compartments (teams) with fitness sharing providing additional support for diversity. Finally, under a Tree structured GP context the evolution of constants using a separate GA representation/ population was considered [5].

As such this may be interpreted as symbiosis where multiple GP populations are evaluated using constants suggested by the GA population.

4   Discussion

A characterization of the form of symbiosis employed in EC is established through emphasizing the nature of relationships used to support compartmentalization. As such, *genetic* and *metabolic* relationships appear to be the norm in (binary) GAs with symbiogenesis having strong implications for solving problems with hierarchical relationships. LCS augment *genetic* relationships with *temporal* relationships. The result is better properties for either constructing combinations of rules (LCS) or much stronger mechanisms for resolving complex gene linkage (GA), as illustrated in the case of solutions under binary deceptive or hierarchical building block style problem domains. *Spatial* and *temporal* relationships appear as a central element to the model of Kim *et al.*, whereas the other pairwise models of symbiosis emphasize the evolution of the degree of mutualism versus competition or the *coevolutionary* relationship. When multiple populations are employed with different representations – as in Neural Evolution or GP – then *spatial* and *temporal* relationships again establish the relevant model of compartmentalization for symbiogenesis to take place.

Common to symbiosis in general is the explicit support for a divide and conquer approach to evolution. EC frequently assumes sexual recombination (crossover) as the principle mechanism for making use of modularity. However, as demonstrated by the work of Watson [36], crossover requires very favorable gene orderings for addressing problems with high orders of gene linkage. Likewise, EC models making use of symbiosis require support for suitable contextual information. Models of gene alignment play a significant role in GAs supporting symbiogenesis whereas for the GP setting of SBB the concept of bidding is central to enforcing a relevant behavioral context. Moreover, diversity maintenance in the symbiont population must be explicitly addressed in order to avoid premature convergence [15, 29]. Indeed, any scheme of model building through symbiosis must be augmented by suitable variation operators. This brings the discussion back to the relation between Darwinism and Symbiogenesis. It is increasingly apparent that mutation operates at many levels – micro, macro, mega [26] – with symbiosis often considered a form of mega mutation, whereas more gradualist forms of adaptation are associated with micro and macro models of mutation [26]. With this in mind Watson considered 'compositional evolution' in general as support for combining genetic material that was "semi-independently preadapted in parallel" [36]. This covers more than just symbiotic models, including specific forms of sexual recombination (implying that specific conditions for population diversity and genetic linkage exist [36]) and horizontal gene transfer (see for example 'Transgenetic Algorithms' [14]).

Finally, from the perspective of future developments, the advent of recursively applied symbiotic operators is likely. Specifically, hosts reaching symbiogenesis may themselves become candidate symbionts for the continued devel-

opment of more complex individuals. This is particularly likely when the host (compartment) population make use of cooperative coevoluationary mechanisms, such as fitness sharing, to encourage diversity at the host level. The next (recursive) application of symbiosis would use (some subset of) a previously evolved host population as the candidate symbionts for building new host compartments (see for example the diversity in host/ team behaviors illustrated by [22]); thus, providing an automated process for 'layered learning.'

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