Fungi as Metaphors for Resource Management

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***Abstract*—Modern societies are heavily dependent upon a number of critical infrastructure networks that allow our societies to function, including water, power and transportation. These networks are open to failure through a range of processes including shortage of essential resources, breakdowns at key nodes and surges in demand and this means that effective management of such networks is challenging. The fungi, an entire kingdom of life, epitomise successful networks in nature, demonstrating pervasive growth in harsh environments and a capacity to optimise resource distribution in space over time. We detail a graph-based implementation of an established model of fungal colony growth and recycling that provides a scheme for efficient resource allocation and distribution. Local processes of uptake of resource, growth and biomass recycling lead to non-local emergent patterns of biomass distribution and colony functioning. This colony growth and recycling in response to changes in resource supply leads to highly flexible spatio-temporal resource balancing in the natural world. In our simulations, we identify fungal colonies that have genotypes that maximise throughput from prescribed sources to sinks in a spatial environment, and provide a biological interpretation to reveal the link between the observed macro-scale pattern and the micro-scale processes that effect a given solution. This interpretation is then contextualised in the domain of critical infrastructure management.**

***Keywords*-adaptive systems; critical infrastructure; biological metaphors.**

I. INTRODUCTION

Modern societies are heavily dependent upon a number of critical infrastructures, including energy, transport, water and telecommunications, that allow our societies to function in an effective manner [1]. These infrastructures are interconnected and often have common resource dependencies [2], and have often evolved over long periods of time without foresight of the extent of future demands or system interconnectivity [3]. Rinaldi et al. characterise this interconnected, interdependent mix of networks as a complex adaptive system [4] where the behaviour of the whole system is not describable in terms of the component parts alone but in terms of emergent properties of the whole system. Ulieru highlights that to preserve functioning across this adaptive system, a management system must be able to dynamically reconfigure itself through self-organisation and self-repairing processes to effect resilience to perturbation [5], and in later work suggests that natural systems may offer routes to solutions [6] since natural systems have many of the properties sought after in complex adaptive systems management.

The use of biological metaphors to inspire algorithms for solving complex problems is already a well developed field with a long history [7]. Ant colonies have been used as a metaphor for routing algorithms in telecommunications networks [8]. Recent work in this field has extended the metaphor to consider ad-hoc networks [9] and trust provision in wireless networks [10]. Other biological metaphors for network management include bees [11] and cell biology [12]. In the field of biological metaphors, a little explored but highly successful organism that exhibits features that are desirable for protecting societys critical infrastructures are fungi.

Fungi are an entire kingdom of life and are one of the most successful organisms on the planet, with estimates suggesting that there may be as many as 1.5 million species of fungi globally [13]. A fungal colony is a highly successful organism, demonstrating pervasive growth through and survival in harsh environments such as soil. They achieve this through their capacity to operate in a decentralised manner, reacting locally to changes in context while interoperating at the colony scale and with other organisms and the environment [14].

Fungi are decentralised transport networks of hyphae that grow and branch at micrometre scales through the tortuous porous structure of soils [15]. Resource is taken up locally through the tips of the hyphae and then redistributed globally through translocation within the colony [16]. Colonies can recycle biomass: resource that is converted into hyphal structure may be remobilised through degradation of local regions of hyphae and translocated elsewhere in the colony [17]. This provides fungi with a highly plastic phenotype, where biomass investment may be dynamically linked to external resource availability, and local behaviour impacts on and is impacted by non-local behaviour in the colony resulting in emergent phenotypes [14].

Bebber et al. recognise that understanding how decentralised, highly flexible fungal colonies that are capable of pervasive growth, emergent behaviour and self-healing may inform the design of man-made networks [18]. They show that fungal colonies are effective transport networks that allocate limited resource efficiently. However, models of fungal colonies from which algorithms may be developed are scarce [19].

Like fungi, critical infrastructures can be modelled as graphs [20], i.e. a set of vertices and edges that represent the critical infrastructure components and connections. Graphs provide a proven way of representing critical infrastructures under a wide range of configurations and for many different domains [2], [20], [21].

Given the superior resource management strategies fungi adopt we expore the fungi as a metaphor for efficient resource management in critical infrastructure networks. Here, we examine the trait set that could lead to the development of a novel bio-inspired algorithm based on [17] for resource allocation in network structures, exploiting key properties of fungal colonies to establish a decentralised resource management. Consequently, an important first step is to generalise the formulation of the computational model from the existing 3D lattice implementation to a graph-based implementation. We show that modelled graph-based fungal colonies still exhibit the essential emergent phenomena that make fungal colonies such attractive metaphors.

In our first simulations, we identify the genotypes of fungal colonies that perform well with regards to network throughput and provide a biological interpretation to reveal the link between the observed performance and the model parameters that effect a given result. This interpretation is then contextualised in the domain of critical infrastructure management.

II. METHODOLOGY

As a fundamental step in understanding the origins of the fungal phenotype we developed a model of fungal colony dynamics and interactions that includes an explicit account of the physiology of organisms in order to link properties of the emergent phenotype to underlying physiological processes [17]. The model formulation represents individual mycelial networks growing in the environment as comprising three fractions: insulated biomass, non-insulated biomass and mobile biomass. These essentially relate to but are not limited to older inactive biomass, active hyphal tips and internal resource respectively. The relative proportion of these components is dynamic and determined by four physiological processes: uptake, inter-conversion between mobile and insulated/non-insulated phases (recycling of biomass), redistribution of mobile biomass and growth. Further, a fungal individual is characterised by a trait set (genotype) which regulates the physiological processes and its interaction with the environment. The model is based on a set of partial differential equations (Figure 1) which represent the interdependencies amongst the types of biomass - non insulated (b_n), insulated (b_i) and mobile biomass (n) and external resource (s) - and how these change over space and time [17].

$$\frac{\partial b_i}{\partial t}=\zeta[\Delta b_n+\beta_2(\alpha_n\pi^{\theta}-\beta_n\pi)]+\beta_2(\alpha_i\pi^{\theta}-\beta_i\pi)b_i$$

$$\frac{\partial b_n}{\partial t}=(1-\zeta)[\Delta b_n+\beta_2(\alpha_n\pi^{\theta}-\beta_n\pi)b_n]$$

$$\frac{\partial n}{\partial t}=\Delta b_n-\beta_1((\alpha_n\pi^{\theta}-\beta_n\pi)b_{ni}+(\alpha_i\pi^{\theta}-\beta_i\pi)b_i)+(\lambda_1 b_n+\lambda_2 b_i)s$$

$$\frac{\partial s}{\partial t}=\omega(s_{max}-s)-(\lambda_1 b_{ni}+\lambda_2 b_i)s$$

Figure 1. Mathematical model describing colony growth and resource management based on [17]

The continuous model outlined above was discretised and solved using a square lattice. In order to obtain a discrete graph based approach to fungal colony growth space is now represented as a hexavalent lattice. The colony is represented by a set of edges constrained by the architecture of the hexavalent lattice and each edge may contain all three fractions of biomass: insulated, non-insulated and mobile as detailed above. The edges can also possess a prescribed level of external resources. The key biological processes described by Falconer's model [17] are also implemented over the graph based colony.

Here, simulation of the dynamics of a single colony is performed and measurement is carried out using resource sources and sinks. Sources of resource, loosely simulating patches of concentrated organic material, can be placed in set locations in the colony allowing the uptake process to take place and mobile biomass to be introduced to the colony. Resource sinks represent areas of the colony investing in, for example, fruiting bodies or colony defenses and remove mobile biomass at a constant rate. Strategically placed sources and sinks are used to measure the throughput and response of the colony.

The complex interplay between the trait values and the size of the search space led to a genetic algorithm being used to find the genotypes which performed best. During the simulation, external resource was introduced into colony through three sources. Three sinks on the opposite side of the colony were set up to remove all mobile biomass that diffused into them. Because the amount of resource going into the colony was constant, the fitness used was simply the total amount of biomass that came through the sinks. Table I lists the traits that were being altered and the meaning of each. Selection was performed using linear rank selection and stochastic universal sampling [22].

A population of 40 individual colonies were used in each generation of the genetic algorithm. With regards to simulation time, two scenarios were examined: 100 and

Trait	Description
α_i	Insulated immobilisation [0-1]
α_n	Non-insulated immobilisation [0-1]
β_i	Insulated mobilisation [0-1]
β_n	Non-insulated immobilisation [0-1]
ζ	Insulation of non-insulated biomass [0-1]
θ	Non-linear term [1-3]

Table I
ANNOTATED LIST OF TRAITS (WITH SEARCHABLE RANGES) FROM THE COMPUTATIONAL MODEL OF [17] WITH RESPECT TO THE EQUATION SET IN FIGURE 1

300 time steps. These values were derived from preliminary studies (not shown). The initial run of 100 time steps resulted in individuals that had a peak of sink activity just before simulation termination. To determine whether other trait sets would outdo the fittest in this scenario if given more time to become established, the genetic algorithm was also run with the simulation for each individual being run for 300 time steps.

III. RESULTS

Falconer et al. (2005) reproduced observable growth patterns in fungal colonies and demonstrated plausible emergent behaviour. Qualitative comparison of fungal phenotypes using the same parameters as in Falconer et al., 2005 also showed good correspondence between the continuous and graph-based implementations (figure 2). In particular, we looked for the continuous model's "fairy ring" pattern and concentric rings (Figure 2) as well as a plateau biomass profile. These patterns were also observable in the discretised graph-based model.

In both scenarios, the average fitness in a generation of the genetic algorithm went up over time. While we tried a run using 200 generations, we found that the average fitness plateaued before reaching 100 generations and so the results from this are not included. While the actual values of the traits of the fittest individuals differ, when the ratio of α_i/α_n and β_i/β_n (insulated/non-insulated immobilisation and mobilisation traits) are viewed by fitness, a clear separation is found. Figure 3 shows each individual's immobilisation and mobilisation ratios against their fitness and shows that fit individuals tend to have an immobilisation ratio of between 0 and 1 and a mobilisation ratio between 1 and 2. No strong trends were found involving the two remaining traits, ζ and θ.

IV. DISCUSSION

Different colony foraging strategies, i.e. the way in which the colony extends itself in space over time and the manner in which the colony growth pattern responds to resource acquisition - are reflected in the physiological trait set. Consequently, different trait sets may be defined to determine different resource management strategies - manifest through dynamic patterns in growth - in critical infrastructures.

We demonstrate the use of a genetic algorithm search to identify colony trait sets that provide optimised solutions to a specific resource management task. Here, in our initial exploration to determine the most efficient trait sets associated with maximising throughput with constant source-sink relationships the recycling trait ratios (α_i/α_n, β_i/β_n) converged to [0 -1] and [1-2] respectively across the multiple runs of the GA.

For this scenario we may interpret this as the fastest investment (in terms of spatial extent) into a fixed and evenly distributed infrastructure. This even distribution occurs via the reallocation of resources from places where it already exists (recycling of insulated structural biomass, i.e. $\alpha_n > \alpha_i$) to areas where it is required to be established (periphery of colony, i.e. $\alpha_n > \alpha_i$). This localised, dynamic recycling behaviour thus maximizing throughput at the global level.

We expect this relation to be different, or at least the magnitude of the ratios to be different, for maximum throughput associated with changing source-sink relationships and/or damage to the network. In these contexts the resource allocation and distribution mechanism must be adaptive in space over time. We propose that our framework provides a platform to explore how the colony traits may interact to promote plasticity in form. This plasticity can allow rapid switches in foraging strategy and we suggest that a fungal colony inspired resource management approach may offer potential in protecting societys critical infrastructures.

V. CONCLUSIONS AND FUTURE WORK

The results reported here consider only a static environment and the capacity of a dynamic colony structure to optimise resource throughput. Clearly, a static solution may be identified a priori to such a problem. The most compelling motivation for using fungi as a metaphor for resource management in critical infrastructures is the capacity of colonies to react dynamically to a changing resource regime.

Importantly, our modelling framework does indeed allow configuration of dynamic environments and simulation of colony behaviour in that dynamic environment. We will use the same discretised colony growth and recylcing model coupled to the genetic algorithm search approach to optimise traits for dynamic, challenging problems. In particular, we will consider two main classes of problems. First, we will identify colonies that are able to deal well with the challenges of load balancing. To explore this we must vary over time the level of resource at the sources and measure, as here, the resource at the sinks. The genetic algorithm search may optimise throughput in the same way as detailed here.

Second, and more interestingly, we will identify colonies that are resilient to damage. Damage will be effected by removing sections of the network and again optimising on throughput. In both cases, we will undertake systematic experimentation and seek biological interpretations of the resulting optimised trait sets.

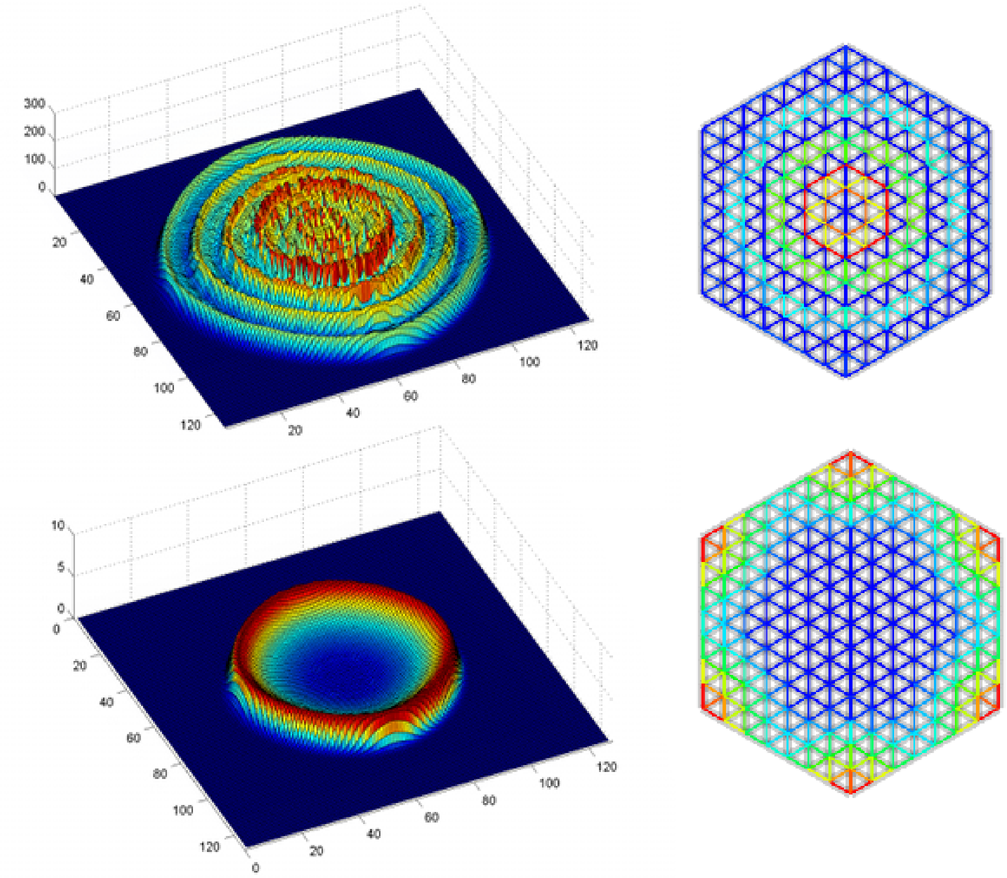

Figure 2. Comparison between continuous model (left) and graph based model (right).

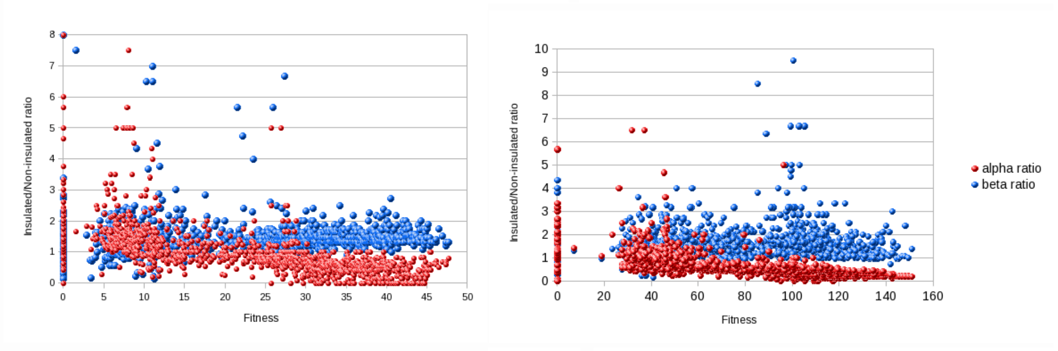

Figure 3. Trait ratios - 100 time step (left) and 300 time step (right) scenarios

It is anticipated that these analyses will reveal fungi to be a useful, versatile scheme upon which to base management algorithms in network-based contexts characterised by uncertainty and variance in demand loading and by the requirement to function in the face of partial failure.

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