

Automated analysis of *Physarum* network structure and dynamics

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ABSTRACT

We describe software tools to extract the network architecture from time-series of *Physarum* development using intensity-independent, phase-congruency tensors and watershed segmentation to give a set of weighted adjacency matrices with the physical dimensions of each tube. The network can also be interrogated to map the phase, amplitude and frequency of the oscillations using windowed Fourier techniques. This work was presented at PhysNet 2015.

Categories and Subject Descriptors

J.3 [Life and Medical Sciences]: Biology and Genetics

Keywords

Physarum, network dynamics, phase congruency tensors

1. INTRODUCTION

Plasmodial slime molds (myxomycetes), such as *Physarum*, and mycelial fungi form elaborate interconnected networks that are highly responsive to local environmental conditions [6]. These networks have no central controller, but develop as the organism forages for new resources in a patchy environment. They must transport nutrients between spatially separated source and sink regions, and also maintain their integrity in the face of predation or random damage. The challenges that these conflicting demands place on the network organization have strong parallels with those faced in the design of other biological transport networks (see [4] and

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anthropogenic infrastructure networks. The balance they have achieved between cost, efficiency and resilience may represent a good compromise to such a combinatorial optimization problem, and may yield useful insights into the design of delocalized, robust infrastructure networks [6]. This presumes that solutions adopted by biological networks will exemplify useful generic theoretical principles, such as persistence, robustness, error-handling or appropriate redundancy, as they have been honed by evolution. A range of network architectures, development and dynamics can be found within the fungi and myxomycetes, suggesting a comparative approach may be instructive. However, the constraints imposed by the components used to construct the network (i.e. branching tubes) and the limited information that can inform developmental fate may have a profound effect on the possible network organization and dynamics, so that any result can only be generalized to a very limited set of real-world problems (see for example [3]).

2. NETWORK ARCHITECTURE

One of the major advances needed to aid both biological understanding and development of bio-inspired algorithms for other domains, is development of high-throughput methods to extract the network architecture and dynamics, to allow comparison between treatments and species, and provide empirical data to support quantitative modelling.

In response to this need, we have developed a set of novel methods to characterize the biological networks of fungi and slime molds [8]. For high-throughput measurements, with thousands of tubes on each image, manual network delineation is not a viable option, especially if time-series are analyzed. Furthermore tubes typically show variation in contrast, both through uneven illumination, and also because of considerable variation in thickness (see Fig. 1a). To overcome these limitations, we have developed a set of image analysis procedures based on intensity-independent contrast enhancement using phase-congruency tensors (Fig. 1b), followed by watershed segmentation and cost-based pruning to characterize *Physarum* and fungal networks at high resolution. The local vector information from the PCT enhancement can also be incorporated in the cost-function to

improve network pruning. Finally, a graph representation of the weighted network is constructed, including additional procedures to redefine the part of the graph corresponding to resource positions. Additional information, such as the arena boundary, can be used to define quasi-euclidean distances throughout the microcosm. Local tube thickness is estimated using gray-scale granulometry (Fig. 1c).

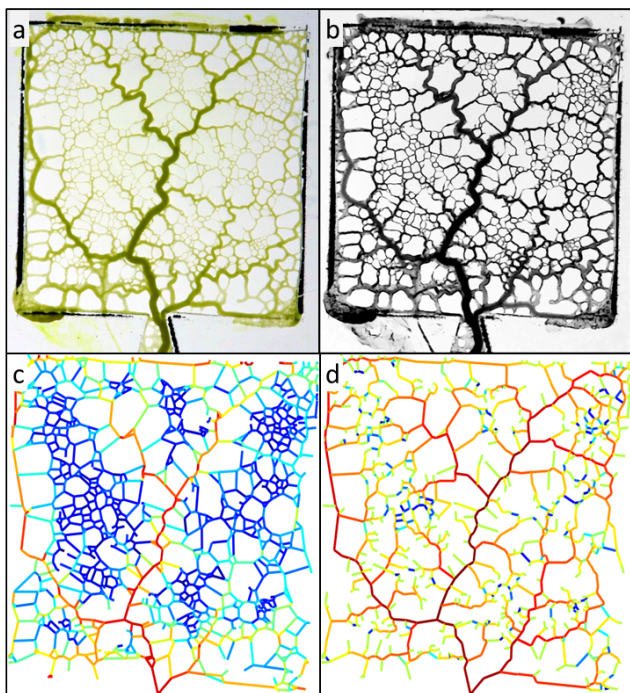


Figure 1: Automated analysis of a developing *Physarum* network. (A) Original image (B) inverted and contrasted-enhanced image (C) weighted network, color coded by edge thickness (D) network color-coded by betweenness centrality

Using these approaches, we are now able to automatically and rapidly extract networks with $10^5 - 10^6$ branches which permit species comparisons of network architecture, development, and behaviour using graph-theoretic network measures, such as edge betweenness centrality (Fig. 1d), flow models [2] or biophysical circuit analog models [7].

3. OSCILLATORY BEHAVIOR

Physarum displays marked actin-myosin based contractions that drive reciprocating shuttle streaming over different temporal and spatial scales. Fourier analysis provides a compact description of such oscillations in terms of their frequency, magnitude and phase. In a single colony, the oscillations self-organise to achieve a single wavelength across the whole colony irrespective of size, which is optimal for mixing the cytoplasmic contents [1]. Here we describe a software tool to map oscillatory phenomena in both the time and frequency domains [5]. Key parameters of interest, such as phase (see Fig. 2a-c) or amplitude (see Fig. 2d-f) of the oscillations, are presented as the hue in pseudo-colour coded maps. This maintains the spatial information in the image and facilitates understanding of complex propagating waves or oscillatory domains with distinct behavior.

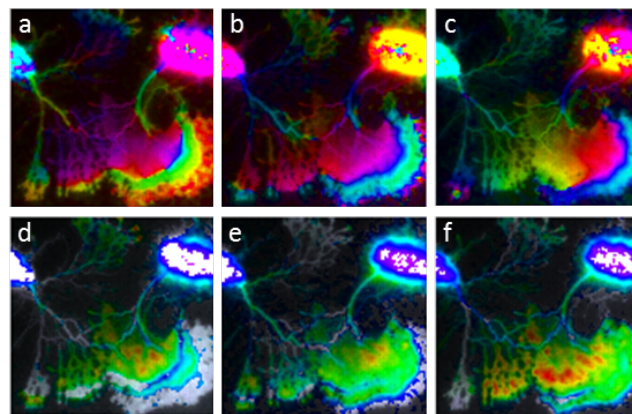


Figure 2: Spatial mapping of changes in phase (a-c) and amplitude (d-f) using windowed Fourier analysis during colony fusion. Oscillations were analysed after de-trending and smoothing with a Hanning window using sliding 30 min blocks. Images are shown at 2h (a,d), 2.5h (b,e) and 3h (c,f).

Both software interfaces have been written in MatLab and available as standalone packages from: www.markfricker.org MatLab libraries for the network program are available from: community.dur.ac.uk/boguslaw.obara/research/software/

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5. REFERENCES

- [1] K. Alim, G. Amsellem, F. Peaudecerf, M. P. Brenner, and A. Pringle. Random network peristalsis in *Physarum polycephalum* organizes fluid flows across an individual. *PNAS*, 110:13306–11, 2013.
- [2] W. Baumgarten and M. Hauser. Functional organization of the vascular network of *Physarum polycephalum*. *Physical Biology*, 10:026003, 2013.
- [3] W. Baumgarten, T. Ueda, and M. Hauser. Plasmodial vein networks of the slime mold *Physarum polycephalum* form regular graphs. *Phys. Rev. E*, 82:046113, 2010.
- [4] A. Fessel, C. Oettmeier, E. Bernitt, N. Gauthier, and H.-G. Döbereiner. *Physarum polycephalum* percolation as a paradigm for topological phase transitions in transportation networks. *Phys. Rev. Lett.*, 109:078103, 2012.
- [5] M. D. Fricker, M. Tlalka, D. Bebbler, S. Takagi, S. C. Watkinson, and P. R. Darrach. Fourier-based spatial mapping of oscillatory phenomena in fungi. *Fung. Gen. Biol.*, 44:1077–1084, 2007.
- [6] L. Heaton, B. Obara, V. Grau, N. Jones, T. Nakagaki, L. Boddy, and M. D. Fricker. Analysis of fungal networks. *Fung. Biol. Rev.*, 26:12–29, 2012.
- [7] L. L. Heaton, E. Lopez, P. K. Maini, M. D. Fricker, and N. S. Jones. Advection, diffusion, and delivery over a network. *Phys Rev E*, 86:021905, 2012.
- [8] B. Obara, V. Grau, and M. D. Fricker. A bioimage informatics approach to automatically extract complex fungal networks. *Bioinformatics*, 28:2374–2381, 2012.