Biological networks: fungal network extraction, testing of model predictions and transport in physarum slime mould

By Freya Way – July 2019

I am grateful to have received funding to undertake research experience this summer. Over a month at the Plant Sciences Department, I studied the strange world of fungal mycelium and slime mould plasmodium. These organisms specialise in breaking down biological matter in dark damp places such as woodland soil and leaf litter. As they grow, forage and deplete their resources, they create impressively self-organised biological networks, which have evolved and optimised over millions of years, and may be able to provide us with exciting insights into the efficient design of spatial networks and transport systems.

Each day consisted of a variety of tasks, from practical lab work to computer-based analysis. I started by learning the practical aspects of maintaining the slime mould culture, which needs to be kept alive and healthy so that samples can be taken for experiments under the microscope (i.e. firing florescent beads into the specimen to measure the direction and speed of its internal transport flows). However, the slime mould is vulnerable to bacterial attack and humidity fluctuations and needed regular plating onto new agar as well as twice daily feeding, making this surprisingly challenging, but a good way to develop lab skills and sterile technique. I also designed and conducted slime mould feeding experiments to assess what food regime generates the most healthy and abundant slime mould plasmodium [image top]. In addition, the light microscopes themselves were fascinating to use –incredibly complicated in terms of features and incredibly expensive– but allowing a live specimen to be studied through a field of view wide enough to observe its mesoscale network behaviour.

Also on the practical side, I learnt to set up fungi growth experiments consisting of an inoculum in a petri dish of compressed sand. We injected the fully-grown mycelium with radioactive carbon and visualised its decay using scintillation screen and imaging equipment. This gave tantalising insights to into their internal transport, including elusive oscillating pulses. Additionally, I photographed the fungi each day under specialised lighting so we could monitor their growth through time. It felt valuable to learn the technicalities of imaging material to the high standard necessary for quantified image analysis -the computerized way to process and compare large data sets of images.

Aside from lab work I undertook image processing and analysis using MATLAB programs developed by Mark Fricker’s lab. This involved performing careful visual alignments of time series images, sub-setting images of fungal mycelium from their background, and converting the networks to digital graphs [image middle and bottom]. The digital versions are data that can be used in the future to test the mechanisms responsible for fungal growth. The model under investigation is the ADD model of growth-induced mass flow (a biophysical advection/diffusion/delivery model), that predicts resource translocation in fungi. Complementing this, I was taught skills in MATLAB including manipulating data for graphics and image digitalisation and processing.

Overall, this was an incredibly useful experience in which I developed skills in using a wide range of equipment, performing practical lab tasks, and computational quantified analysis techniques, which will be invaluable for future research endeavours. I enjoyed delving further into the study of biological networks, which is to me an exciting field in the way it ranges incredibly from cell biology right up to physiology and ecology. In addition, this was a great opportunity to experience working full time in a lab and research setting, where I enjoyed being exposed to the wide-ranging research and ideas of the international group.