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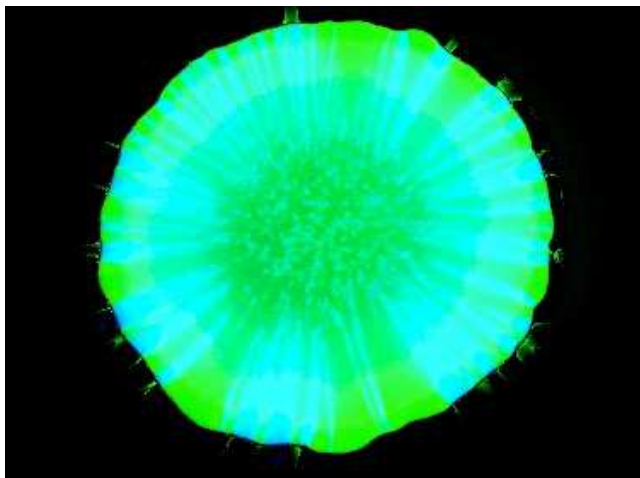
# Experimenting with evolution: adaptation in spatially structured environments

**Supervisors:** Chris Knight (University of Manchester, Life Sciences, <http://tinyurl.com/knightFLS>), Daniela Delneri (University of Manchester, Life Sciences, <http://tinyurl.com/DelneriFLS>).

**Contact:** [chris.knight@manchester.ac.uk](mailto:chris.knight@manchester.ac.uk) +44 (0)161 2755378

## Introduction

Understanding how spatial structure influences evolution is vital to describing, understanding and predicting the likely impacts of environmental change on biodiversity. This is particularly true for microbes, which occupy environments with a wide range of spatial structuring from the fine-structure of soil to the fluid structure of the atmosphere. The fact that many microbes may readily be brought into the laboratory and studied with approaches developed in cell biology enables questions of ecology and evolution to be addressed in ways impossible in other systems (e.g. see Replansky et al. 2008). However, this is typically done using unstructured, shaken liquid cultures, *uncharacteristic* most natural environments. Novel approaches are being developed to high throughput growth of microbes in spatially structured colonies on agar plates (Bean et al. 2014). Here we will combine the power of such high throughput analysis with approaches to assessing competitive fitness within microbial colonies (Hallatschek and Nelson 2010, see Figure), to address fundamental questions about the role of spatial structure in microbial evolution.



**Figure: Quantifying microbial competition in a spatially structured environment.** Two yeasts, distinguished by colour, growing together on an agar plate. The yellow strain starts in a minority but is fitter in this environment than the cyan strain. This is apparent from the larger amount of yellow at the periphery than near the centre, by the curvature of the sector edges and from the bulges around the periphery at the yellow sectors. Competitive fitness may be quantified by measuring any of these features. (©Daniel Smith, Knight lab).

## Project Summary

We have recently acquired a robot that can propagate >6,000 microbial colonies on a single agar plate ([www.singerinstruments.com](http://www.singerinstruments.com)). The student will use this robot to carry out experimental evolution in spatially structured environments and to test the fitness effects of specific beneficial mutations. This will build on, and involve direct comparison with, existing work in the lab using unstructured environments to identify the influences of the environment on evolution. Specifically we have used budding yeast (*Saccharomyces cerevisiae*) and alcohol, as a stressor important in yeast evolution, to test the genetic basis of adaptation in the lab. Such approaches, combined with whole-genome sequencing and analysis will enable the student to ask questions such as 'What is the effect of spatial structure on the rate, fitness

effects and nature and of beneficial mutations?', which leads into wider issues of understanding phenotypic plasticity and environmental change (Chevin et al. 2010). The ideal student will have a background in evolutionary biology and genetics, with good quantitative skills and be willing to learn and develop a range of experimental and analytical techniques. Experience of microbiology and computational expertise would be advantageous.

## References

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