

## Abstract

In modern biology, large scale is not just a slogan but a very active area of research. By parallelizing trials, new kinds of questions can be asked and questions examined with greater accuracy. For example, if you hope that a rare mutation will occur, you need a lot of time or luck to find it if you do not massively parallelize the experiment. My contribution to this area is the development of a new method for monitoring growth in a large number of microbial colonies in parallel. In itself, this is not new, but we believe that the quality of the data we collect is higher than comparable technologies, while the cost of setting up the system is kept relatively low. The development of this platform, Scan-o-matic, is described in articles one and two.

However, a technique is only relevant if it is used, and in article three we are using the large scale and the quality of measurement to determine what types of interactions between genes explain complex traits in yeast growth using an advanced breeding system. In article four we test, on a smaller scale, how yeast can evolve to withstand arsenite and how stable such adaptation is after it has been achieved if the yeast is allowed to live without arsenic for a while.