

In [1]:

```
from IPython.display import Image
```

## 2 Dimensional scenarios - dispersing over a chain of cells

In this experiment we check the sensitivity of the model to the initial conditions. The sine curve representing the fluctuating environmental conditions can impose significant bias in short runs. Thus the simulation was started at different places on the sine curve. The full cycle is completed in 50 steps, the numbers indicate the starting time out of the 50.

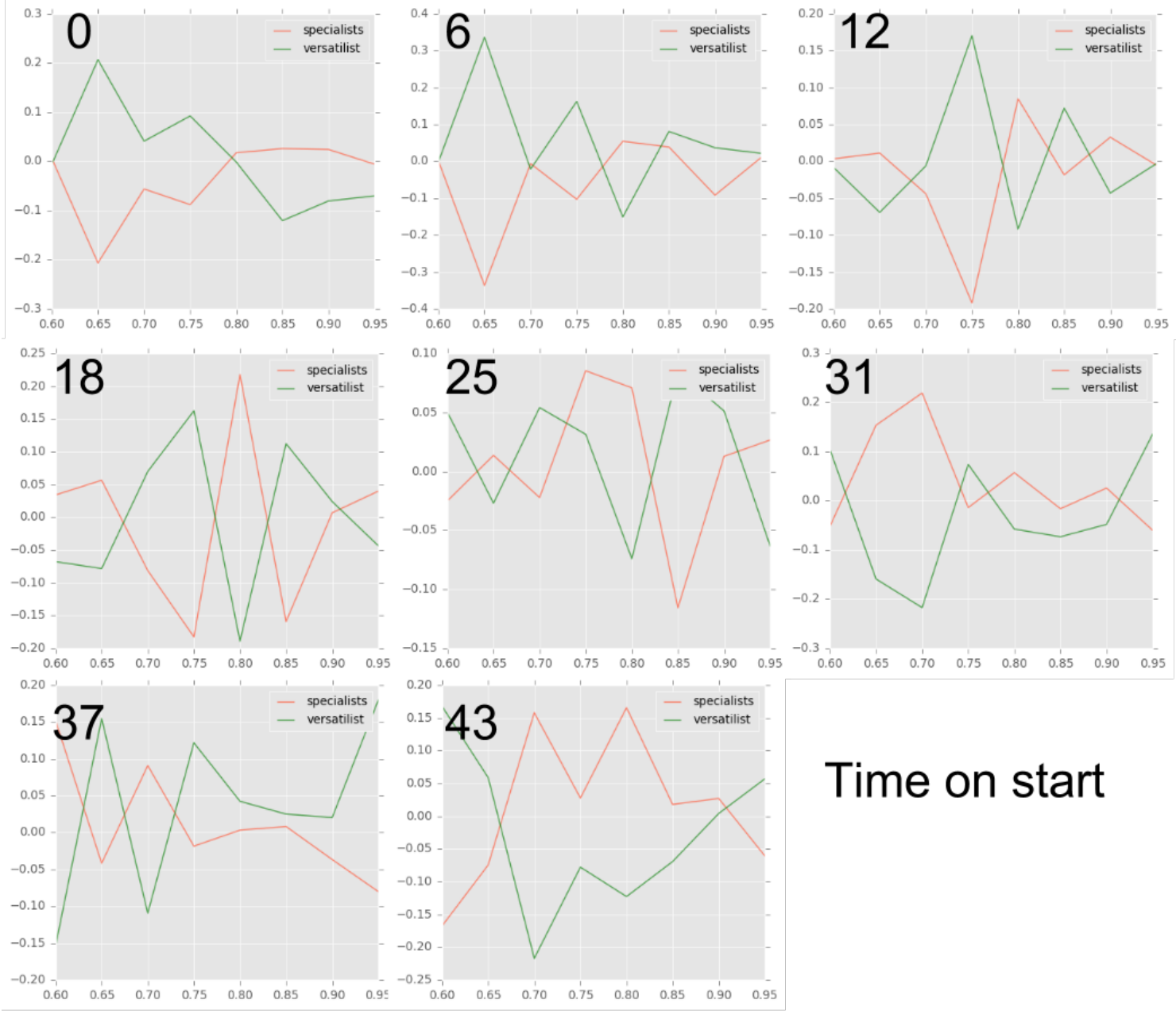
This is where we disperse the population along a chain of cells (2D scenarios), the middle of which is a 'barrier' cell, i.e., it has cc of 1/10th of the other cells. We then record the composition of the population before and after the barrier cell.

In all cases the pattern look completely random.

In [2]:

```
Image(filename='/Users/iar1g09/Dropbox/IZA/PHD/case_studies/variability_case_study/figures/barrier_scenarios.png')
```

Out[2]:

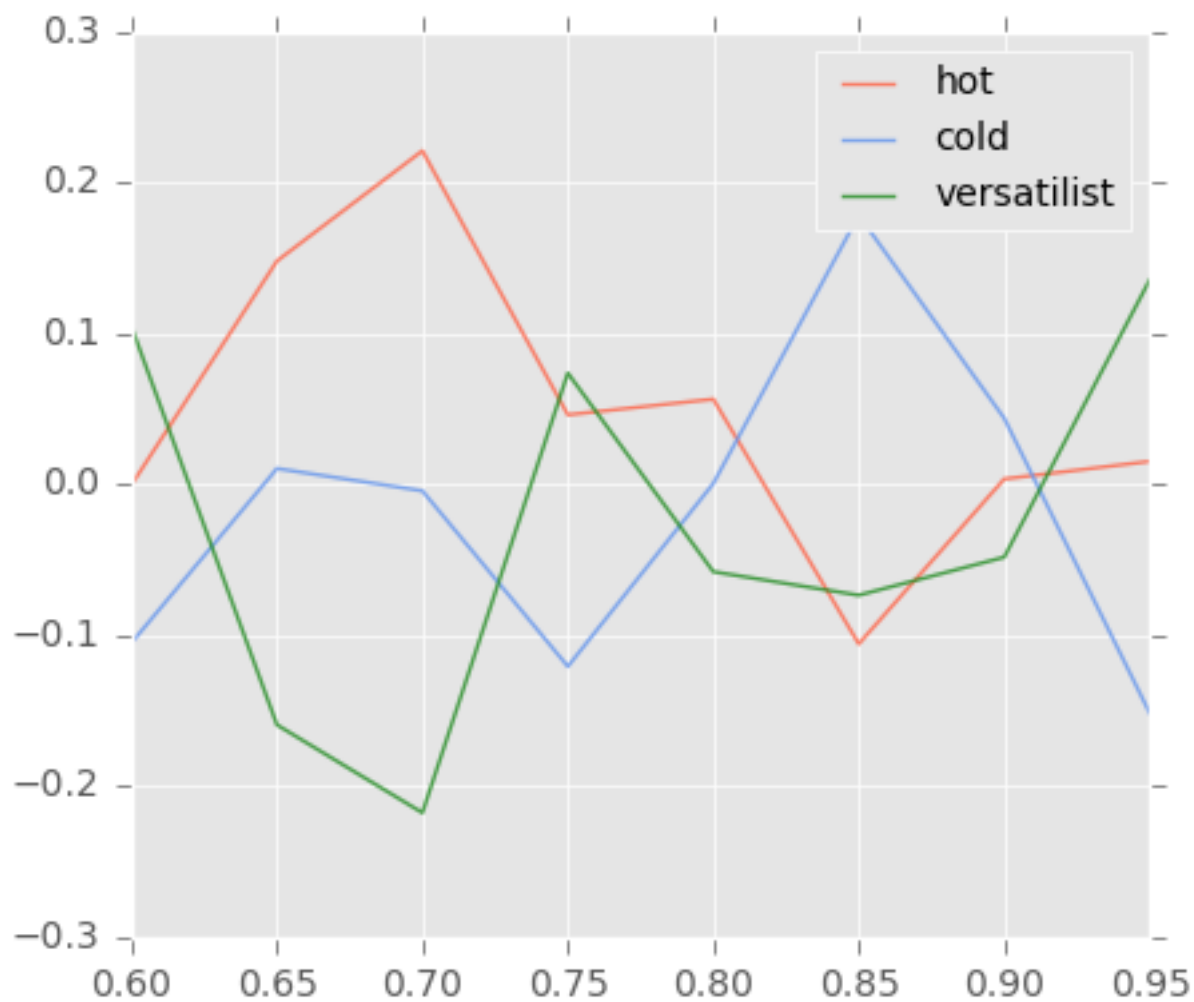


When broken down to each gene, it doesn't look any better. This is an example (start time 31 from a range of 0-50).

In [3]:

```
Image(filename='/Users/iarlg09/Dropbox/IZA/PHD/case_studies/variability_case_study/2D_all_sep_start31.png')
```

Out[3]:



**Conclusion: given the current experiment design no significant trends have been detected.**