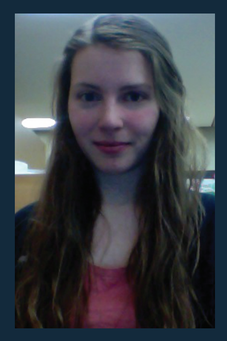
Anticipating environmental changes through dynamic gene expression



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Concentrations of cellular components were previously thought to remain steady, and change only in accordance with their surroundings. Recent single cell observations have revealed dynamic protein production patterns in genetically identical cells kept in constant conditions [1].

Sigma factors are bacterial proteins which play a crucial role in specifying which proteins are switched on [2]. Their own expression, shown in figures 1 and 2, occurs in discrete random pulses distributed randomly in time, and across the popuation. We are interested in how this dynamic behaviour is regulated, and how it contributes to cell survival and propagation.

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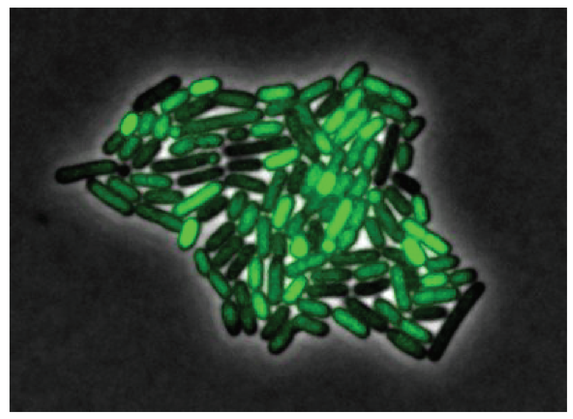
Figure 1. Snapshot of a Bacillus subtilis colony containing a fluorescent reporter for sigma B.



The intensity of green fluorescence indicates the amount of sigB in a cell. This varies across the population, and also within an individual cell dynamically over time.

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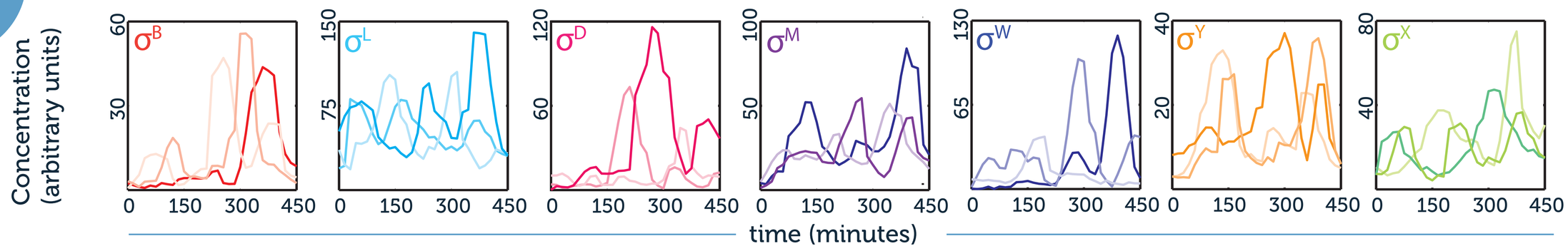

Figure 2. Expression pulses for a range of sigma factors in Bacillus subtilis. Different colour intensities show levels in different cells.

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- We hypothesise that pulsatile sigma factor expression enables more efficient allocation of a shared, and limited resource.
- This is inspired by what we know about signalling dynamics in communications technology from the analog to digital movement.
- We constructed a model simulating multiple sigma factors which all compete for a limited resource, a typical sigma factor pathway from the model is shown in figure 3.

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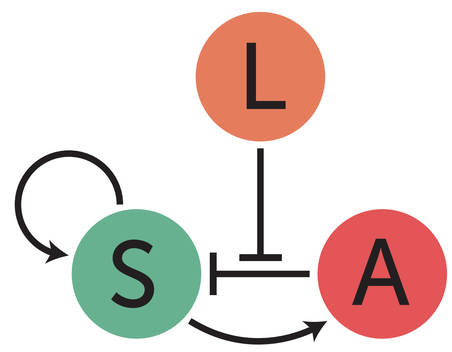
Figure 3. Sigma factor pathway structure in simulations. All pathways share a key resource, and each pathway includes a sigma factor (S), its own anti-sigma factor (A) which it activates, and a ligand species which surpresses the anti-sigma factor action.

Arrows indicate positive interactions (activation) and truncated lines indicate negative interactions (repression).



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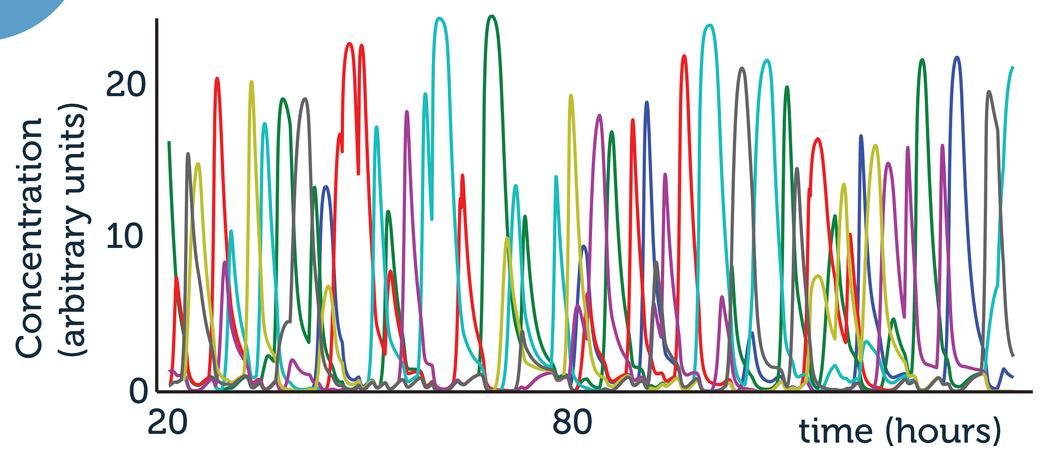

Figure 4. Pulsing sigma factor simulations.

Pulses of high expression are distributed over time such that no two sigma factors are expressed simultaneously. This supports a time-sharing hypothesis.

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By studying dynamic expression patterns we hope to understand the underlying networks which control and propagate biological signals.

In future work we will test whether this form of dynamic expression can confer a bet-hedging fitness advantage whereby sub-populations of cells are able to anticipate environmental change by expressing a different set of genes.

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[1] Locke, J. C. W., Young, J. W., et al. (2011), Science 334 (6054), 366–369

[2] Haldenwang, W. G. (1995), Microbiological Reviews 59 (1), 1–30.

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