File S1: Selection of model parameters

Cell volume: Bacterial cell volume varies with growth phase, increasing to 3 μm^3 during exponential phase but falling to 1 μm^3 in stationary phase[1]. We therefore adopted a value of 1 μm^3 (= 10^{-15} L) for cell volume during stationary phase. With this value, 1 molecule/cell = 1.66 nM.

Total RNA polymerase, σ^{70}, σ^{38} and Rsd per cell: Measured values for total RNA polymerase and sigma factors have varied greatly depending upon cellular growth phase and growth rate. A list of values measured under various conditions is given in[2]. As we are modeling conditions during stationary phase, we have adopted values measured during stationary phase in *E. coli* MG1655 using quantitative western blotting[3].

Total 6S RNA per cell: Wassarman and Storz[4] showed that 6S RNA increases steadily throughout growth and stationary phase, from 1000 molecules/cell in exponential phase to 10,000 molecules/cell in late stationary phase (24 hours). Our data also indicates that the concentration of 6S RNA continues to increase throughout stationary phase. We therefore adopted a value of 8000 molecules/cell ≈ 13000 nM, consistent with an earlier time point in stationary phase.

$K_{E\sigma 70}$, $K_{E\sigma 38}$: Measured values for E-σ dissociation constants have varied greatly with temperature and ionic conditions, although all measurements agree that E-σ^{70} binding is considerably stronger than E-σ^{38}. A list of measured values under various conditions is given in[2]. We have used values measured under high-salt conditions in the presence of glutamate, similar to cellular conditions in stationary phase[5]. However, we have also run the model with values from other studies[6,7], and obtained similar results.

K_{6S}: The dissociation constant for *E. coli* 6S RNA and RNA polymerase has not been measured to our knowledge. However, a dissociation constant of 131 nM has been measured for the binding of RNA polymerase and 6S RNA -1 from *Bacillus subtilis*, which is similar in structure and expression pattern to *E. coli* 6S RNA[8]. Increasing or decreasing this parameter by 5-fold does not substantially affect our findings.

Nonspecific binding: E. coli has ~4.6 × 10^6 base pairs per genome, each of which can potentially be a non-specific binding site. Assuming that stationary phase cells have a single copy of the genome, we adopted this as the number of non-specific DNA binding sites. *In vitro* experiments[9] under ionic conditions similar to physiological conditions found that the non-specific dissociation constants of Eσ^{70} and core were comparable (10^{-3} – 10^{-4} M). We assumed that the non-specific binding affinity of Eσ^{38} would be similar to these, and used a value of 10^{-4} M for all non-specific binding.

Promoter binding and transcription: In the *E. coli* genome, it is estimated that ~1000 promoters are under the control of Eσ^{70} and ~200 under Eσ^{38} (RegulonDB database). However, not all promoters are active at any time, and many can be bound by both holoenzymes. In particular, the activity of Eσ^{70} promoters is strongly reduced during stationary phase. We therefore adopted a value of 200 active promoters/cell for each sigma factor. Promoter binding affinities were chosen to be comparable with values in[10] and[11]. The promoter clearance rate was also chosen to be comparable with values in [2] and[12]. For simplicity, we have assumed that the sigma factor is released immediately upon initiation, as shown below.

$$E\sigma + P \underset{k_{bE\sigma P}}{\overset{k_{fE\sigma P}}{\rightleftharpoons}} E\sigma^{70}P_{70} \xrightarrow{c} \mathrm{E}_e + \sigma + P$$

In steady state, this must satisfy the equation:

$$\frac{k_{bE\sigma P} + c}{k_{fE\sigma P}} = \mathrm{K}_{E\sigma P}$$

We assumed that the promoter clearance rate is considerably smaller than $k_{bE\sigma P}$ and thus approximated:

$$\frac{k_{bE\sigma P}}{k_{fE\sigma P}} \approx K_{E\sigma P}$$

Transcription Elongation: The rate of elongation by RNA polymerase depends on growth conditions and the transcribed sequence, and is reduced in stationary phase. Proshkin et al.[13] measured elongation rates of 42 nt s^{-1} in exponential phase and 21 nt s^{-1} in stationary phase. Assuming an average operon length of 1000 nt, the transcribing RNA polymerase would be released at a rate of 21/1000 = 0.021 s^{-1}.

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