Supplementary Information: Model Description.

A basic model of the mRNA and protein products of a single gene (Fig. S1) was built to explore the logical consequence of half-life and inventory size on mRNA and protein dynamics in bacterial cells.

In the single cell model (Panels A and C), ~10 mRNAs transcription events occur in the cell over a 24 h (1440 min) period at random intervals. Under steady state conditions, each random transcription event produces a single mRNA molecule (mRNA inventory is plotted on the left axis in Fig. 3) that gives rise to a translation burst of 7 proteins (plotted on the right axis in Fig. 3) (Arkin *et al.,* 1998; Xie *et al.,* 2008; Taniguichi *et al.,* 2010). During upregulation (the four hour period marked in light blue in Panel C), each random transcription event instead produces three mRNAs. mRNA and protein inventories decay exponentially at 1 minute time steps. For the run presented in Figure 3, half-lives are parameterized as 1.5 min for mRNA and 12 h for protein (Fig. S1), and starting per cell inventories are 900 for protein (http://bionumbers.hms.harvard.edu) and 0 for mRNA.

In the population model (Panels B and D), the basic single cell module is replicated 100 times and each is driven by independent randomly-generated transcription events. mRNA and protein contents are averaged across all cells at each time step.

Sensitivity analyses were conducted that varied parameters for the frequency of transcription events, mRNA burst size, protein burst per message, and macromolecule half-lives. Changes to these parameters produced runs with varying sizes of mRNA and protein pools, but mRNA and protein inventories were poorly synchronized under dynamic extrinsic conditions whenever there was a substantial difference in half lives.

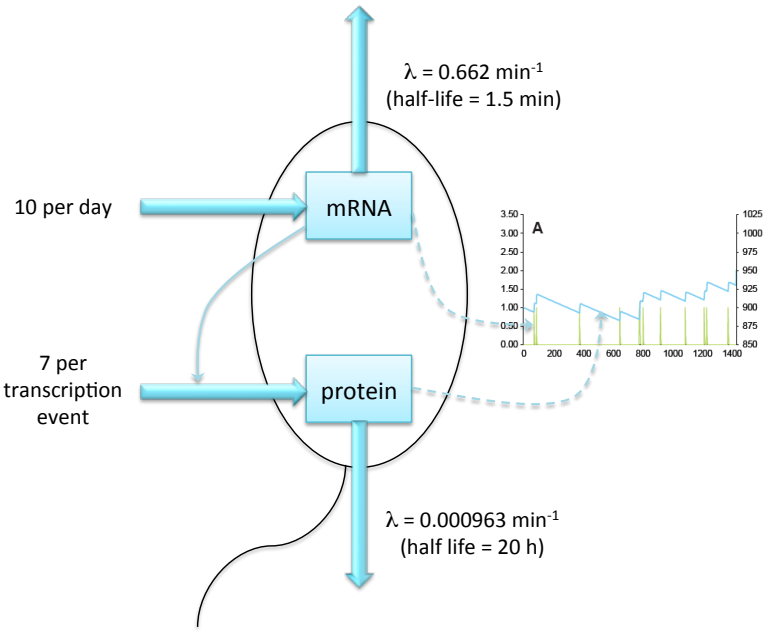

Fig. S1. Single cell module for a basic model exploring effect of macromolecule half-life on the synchrony of mRNA and protein levels in a bacterial cell. Parameters shown are those used in the run shown in Fig. 3, Panel A.

References:

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Taniguchi Y, Choi PJ, Li G-W, Chen H, Babu M, Hearn J, Emili A, Xie XS. (2010). Quantifying *E. coli* proteome and transcriptome with single-molecule sensitivity in single cells. *Science* **329:** 533-538.