Table S1: Model parameters

		Value	Reaction	Propensity	References and Comments
k_{-a}	MarA-promoter dissociation rate	$1.8\ (\text{min})^{-1}$	$P_{10} \xrightarrow{k_{-a}} P_{00} + A$ $P_{11} \xrightarrow{k_{-a}} P_{01} + A$ $P_{12} \xrightarrow{k_{-a}} P_{02} + A$	$k_{-a} \cdot P_{10}$ $k_{-a} \cdot P_{11}$ $k_{-a} \cdot P_{12}$	Other feedback operons: 1.8 min^{-1} [1], 2.4 min^{-1} [2]. The stochastic pulsing is not disrupted for a wide range of k_{-a} and k_{-r} values.
k_a	MarA-promoter association rate	$\frac{k_{-a}}{1500}\ (\text{molecules} \cdot \text{min})^{-1}$	$P_{00} + A \xrightarrow{k_a} P_{10}$ $P_{01} + A \xrightarrow{k_a/\beta} P_{11}$ $P_{02} + A \xrightarrow{k_a/\beta'} P_{12}$	$\frac{1}{V} \cdot k_a \cdot P_{00} \cdot A$ $\frac{1}{V} \cdot \frac{k_a}{\beta} \cdot P_{01} \cdot A$ $\frac{1}{V} \cdot \frac{k_a}{\beta'} \cdot P_{02} \cdot A$	Dissociation constant for MarA = 25nM = 1500 molecules/cell [3]. V is the ratio between the volume of the cell at a given time and the average volume of *E. coli* considered in the paper ($1\ \mu m^3$).
k_{-r}	$MarR_2$-promoter dissociation rate	$1.8\ (\text{min})^{-1}$	$P_{01} \xrightarrow{k_{-r}} P_{00} + R_2$ $P_{02} \xrightarrow{2 \cdot k_{-r}} P_{01} + R_2$ $P_{11} \xrightarrow{k_{-r}} P_{10} + R_2$ $P_{12} \xrightarrow{2 \cdot k_{-r}} P_{11} + R_2$	$k_{-r} \cdot P_{01}$ $2 \cdot k_{-r} \cdot P_{02}$ $k_{-r} \cdot P_{11}$ $2 \cdot k_{-r} \cdot P_{12}$	Other feedback operons: 1.8 min^{-1} [1], 2.4 min^{-1} [2]. The stochastic pulsing is not disrupted for a wide range of k_{-a} and k_{-r} values.
k_r	$MarR_2$-promoter association rate	$\frac{k_{-r}}{150}\ (\text{molecules} \cdot \text{min})^{-1}$	$P_{00} + R_2 \xrightarrow{2 \cdot k_r} P_{01}$ $P_{01} + R_2 \xrightarrow{k_r} P_{02}$	$\frac{1}{V} \cdot 2 \cdot k_r \cdot P_{00} \cdot R_2$ $\frac{1}{V} \cdot k_r \cdot P_{01} \cdot R_2$	Dissociation constant for $MarR_2$ = 2.5nM = 150 molecules/cell [4-6].

			$P_{10} + R_2 \xrightarrow{2 \cdot k_r / \alpha} P_{11}$ $P_{11} + R_2 \xrightarrow{k_r / \alpha'} P_{12}$	$\frac{1}{V} \cdot \frac{2 \cdot k_r}{\alpha} \cdot P_{10} \cdot R_2$ $\frac{1}{V} \cdot \frac{k_r}{\alpha'} \cdot P_{11} \cdot R_2$	
α_{00}	Transcription rate with no $MarR_2$ molecules and no MarA molecules bound to the promoter	$0.40\,(\min)^{-1}$	$P_{00} \xrightarrow{\alpha_{00}} P_{00} + M + R_{uf} + A_{uf}$	$\alpha_{00} \cdot P_{00}$	From other systems: 0.36 min^{-1} [1], 0.1 min^{-1} [2]. α_{00}, $\beta_{(a/r)}$ and c_{Act} are chosen to match the experimental data (10,000 molecules if $MarR_2$ binding sites are eliminated, 500 molecules in the basal level – See Supplementary Methods).
α_{01}	Transcription rate with one $MarR_2$ molecule and no MarA molecules bound to the promoter	$\alpha_{00} / c_{Inh1}\,(\min)^{-1}$	$P_{01} \xrightarrow{\alpha_{01}} P_{01} + M + R_{uf} + A_{uf}$	$\alpha_{01} \cdot P_{01}$	One molecule of $MarR_2$ is bound; the transcription rate is modified by c_{Inh1}.
α_{10}	Transcription rate with no $MarR_2$ molecules and one MarA molecule bound to the promoter	$\alpha_{00} \times c_{Act}\,(\min)^{-1}$	$P_{10} \xrightarrow{\alpha_{10}} P_{10} + M + R_{uf} + A_{uf}$	$\alpha_{10} \cdot P_{10}$	One molecule of MarA is bound; the transcription rate is modified by c_{Act}.
α_{11}	Transcription rate with one $MarR_2$ molecule and one MarA molecule bound to the promoter	$\alpha_{00} \times c_{Act} / c_{Inh1}\,(\min)^{-1}$	$P_{11} \xrightarrow{\alpha_{11}} P_{11} + M + R_{uf} + A_{uf}$	$\alpha_{11} \cdot P_{11}$	One molecule of MarA and one molecule of $MarR_2$ are bound; the transcription rate is modified by c_{Act} / c_{Inh1} .
α_{12}	Transcription rate with two $MarR_2$ molecules and one MarA molecule bound to the promoter	$\alpha_{00} \times c_{Act} / (c_{Inh1} \times c_{Inh2})$ $(\min)^{-1}$	$P_{12} \xrightarrow{\alpha_{12}} P_{12} + M + R_{uf} + A_{uf}$	$\alpha_{12} \cdot P_{12}$	One molecule of MarA and two molecules of $MarR_2$ are bound; the transcription rate is modified by $c_{Act} / (c_{Inh1} \times c_{Inh2})$.

α_{02}	Transcription rate with two $MarR_2$ molecules and no MarA molecules bound to the promoter	$\alpha_{00}/(c_{Inh1} \times c_{Inh2}) \ (\min)^{-1}$	$P_{02} \xrightarrow{\alpha_{02}} P_{02} + M + R_{uf} + A_{uf}$	$\alpha_{02} \cdot P_{02}$	Two molecules of $MarR_2$ are bound; the transcription rate is modified by 1 / ($c_{Inh1} \times c_{Inh2}$).
c_{Act}	Activation factor	80			From another system: 20 [1]. *marRAB* is expressed strongly after induction [7]. α_{00}, $\beta_{(a/r)}$ and c*Act* are chosen to match experimental data from this study (10,000 molecules if $MarR_2$ binding sites are eliminated, 500 molecules in the basal level – See Supplementary Methods).
c_{Inh1}	Repression factor for the first $MarR_2$ binding	800			$MarR_2$ binding impairs RNA polymerase binding and progression [5,8]. The system is robust to changes in this parameter.
c_{Inh2}	Repression factor for the second $MarR_2$ binding	10			$MarR_2$ binding impairs RNA polymerase binding and progression [5,8]. The system is robust to changes in this parameter.
λ_M	mRNA degradation rate	$\ln(2) / 24 \ (\min)^{-1}$	$M \xrightarrow{\lambda_M} 0$	$\lambda_M \cdot M$	[9],Stochastic pulsing behavior is robust to changes in this parameter.
β_a	*marA* translation rate	$0.34 \times 20 \ (\min)^{-1}$	$M \xrightarrow{\beta_a} M + A_{uf}$	$\beta_a \cdot M$	Translation rate = 34% of the *lacZ* translation rate [7]. *lacZ* translation rate: 18.8 min^{-1} [10], *lacZ* initialization every 3.2 sec [11].
β_r	*marR* translation rate	$0.044 \times 20 \ (\min)^{-1}$	$M \xrightarrow{\beta_r} M + R_{uf}$	$\beta_r \cdot M$	Translation rate = 4.4% of the *lacZ* translation rate. [7].
k_{fa}	MarA folding rate	$5 \ (\min)^{-1}$	$A_{uf} \xrightarrow{k_{fa}} A$	$k_{fa} \cdot A_{uf}$	Fast, due to the small size of the protein and the coupling of this process with translation *in vivo* [12]. The system is robust to changes in this value.

					Other examples: 60 min^{-1} for Cytochrome C [13], 0.9 min^{-1} for the synthetic oscillator [1].
k_{fr}	MarR folding rate	$5\,(\min)^{-1}$	$R_{uf} \xrightarrow{k_{fr}} R$	$k_{fr} \cdot R_{uf}$	Fast, due to the small size of the protein and the coupling of this process with translation *in vivo* [12]. The system is robust to variations in this value. Other examples: 60 min^{-1} for Cytochrome C [13], 0.9 min^{-1} for the synthetic oscillator [1].
k_{dr}	MarR dimerization rate	$0.01\,(\text{molecules}\cdot\min)^{-1}$	$2\times R \xrightarrow{k_{dr}} R_2$	$\frac{1}{V}\cdot k_{dr}\cdot\frac{R\cdot(R-1)}{2}$	Assumed to be consistent with the cI protein in *E. coli*, 0.01 mol^{-1} min^{-1} [14]. The system is robust to variations in this value. Another example: 0.18 min^{-1} for the synthetic oscillator [1].
k_{-dr}	$MarR_2$ dimer disruption rate	$k_{dr}/50\,(\min)^{-1}$	$R_2 \xrightarrow{k_{-dr}} 2\times R$	$k_{-dr}\cdot R_2$	Assumed to be consistent with the cI protein in *E. coli*, $k_{dr}/50$ min^{-1}. The system is robust to variations in this value. Other example: $k_{dr}/100$ min^{-1} for the synthetic oscillator [1].
λ_{auf}	Unfolded MarA degradation rate	$\lambda_r\,(\min)^{-1}$	$A_{uf} \xrightarrow{\lambda_{auf}} 0$	$\lambda_{auf}\cdot A_{uf}$	We assumed only folded MarA to be actively degraded by Lon protease [15], setting the degradation rate for unfolded MarA at a reduced level, comparable to what we used for degradation of the folded $MarR_2$ protein. There is only a small amount of unfolded protein; as a result, the system is robust to variations in this parameter.
λ_a	MarA degradation	$\ln(2)\ (\min)^{-1}$	$A \xrightarrow{\lambda_a} 0$	$\lambda_a\cdot A$	[15]
λ_{ruf}	Unfolded MarR degradation rate	$\lambda_r\,(\min)^{-1}$	$R_{uf} \xrightarrow{\lambda_{ruf}} 0$	$\lambda_{ruf}\cdot R_{uf}$	We assumed the same degradation rate as the folded $MarR_2$ protein. There is only a small amount of unfolded protein; as a result, the system is robust to variations in this parameter.

λ_r	MarR and $MarR_2$ degradation	$\ln(2)/24\ (\text{min})^{-1}$	$R \xrightarrow{\lambda_r} 0$ $R_2 \xrightarrow{\lambda_r} 0$	$\lambda_r \cdot R$ $\lambda_r \cdot R_2$	We assumed the protein to be stable, using a degradation time that matches the dilution rate due to cell division in rich medium [16]. Changes in the parameter do not disrupt stochastic pulsing.
k_{sal}	$MarR_2$ allosteric inhibition rate	20 $(\text{molecules} \cdot \text{min})^{-1}$	$Sal + MarR_2 \xrightarrow{k_{Sal}} MarR_2\text{-}Sal$	$\frac{1}{V} \cdot k_{Sal} \cdot MarR_2 \cdot Sal$	Selected to fit experimental data from [17] and [18]. The system is robust to changes in this parameter.
k_{-sal}	$MarR_2$-Salicylate complex disruption rate	0.5 $(\text{min})^{-1}$	$MarR_2\text{-}Sal \xrightarrow{k_{-Sal}} Sal + MarR_2$	$k_{-Sal} \cdot MarR_2\text{-}Sal$	Selected to fit experimental data from [17] and [18]. The system is robust to changes in this parameter.
		As detailed in Supplementary Methods, the parameters given below are used to fit the model to the following experimental data: 3.3-fold repression with only one $MarR_2$ site active and a 20-fold repression with both sites active [7,19]; competition in the binding between MarA and $MarR_2$ [5], either by sliding block [20] or alignment of the marbox with the -35 box [8]; approximately 9,000 molecules with 5mM of salicylate induction [4] and maximum expression with salicylate of 10,000 molecules ([17] with the data from [4]); basal expression of 500 molecules (Maximum level / Repression fold with both sites active).			
α	Inhibition in the binding of the first molecule of $MarR_2$ when MarA and no $MarR_2$ are bound	1000	$P_{10} + R_2 \xrightarrow{2 \cdot k_r/\alpha} P_{11}$		
α'	Inhibition in the binding of the second molecule of $MarR_2$ when MarA and $MarR_2$ are bound	1.5	$P_{11} + R_2 \xrightarrow{k_r/\alpha'} P_{12}$		
β	Inhibition in the binding of MarA when one $MarR_2$ molecule is bound	1.5	$P_{01} + A \xrightarrow{k_a/\beta} P_{11}$		

β'	Inhibition in the binding of MarA when two $MarR_2$ molecules are bound	1.5	$P_{02} + A \xrightarrow{k_a/\beta'} P_{12}$		

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