Appendix S1: Modelling details

Model equations

The full core (non-reporter-specific) equations are:

$$\frac{da}{dt} = A(ql - a)$$

$$\frac{dt_m}{dt} = O_t + \frac{L_t + R_a a}{1 + L_t + R_a a + (R_c E_c c_N)^{H_t}} - Y_t t_m$$

$$\frac{dt_I}{dt} = S_t t_m - \left(l K_{t,l} + (1-l) K_{t,d}\right) t_I$$

$$\frac{dt_A}{dt} = \left(l K_{t,l} + (1-l) K_{t,d}\right) t_I - \left(l D_{t,l} + (1-l) D_{t,d}\right) t_A$$

$$\frac{dc_m}{dt} = O_c + \frac{\left(\left(l R_{c,l} + (1-l) R_{c,d}\right) E_t t_A\right)^{H_c}}{1 + \left(\left(l R_{c,l} + (1-l) R_{c,d}\right) E_t t_A\right)^{H_c}} - Y_c c_m$$

$$\frac{dc_C}{dt} = S_c c_m - K_c c_C - \left(l D_{c,l} + (1-l) D_{c,d}\right) c_C$$

$$\frac{dc_N}{dt} = K_c c_C - \left(l D_{c,l} + (1-l) D_{c,d}\right) c_N$$

The parameters O_t and O_c can be made non-zero to simulate overexpression of either gene. The parameter $E_c = 1$, except that for the CCA1-LUC reporter, $E_c > 1$ if the CCA1-LUC fusion protein is active in regulation. The same applies to E_t for TOC1-LUC. To simulate experiments with transcriptional reporters we add variables for LUC and its mRNA. For pTOC1::LUC the extra equations are:

$$\frac{du_m}{dt} = \frac{L_t + R_a a}{1 + L_t + R_a a + (R_c c_N)^{H_t}} - Y_u u_m$$

$$\frac{du}{dt} = u_m - D_u u$$

For pCCA1::LUC they are:

$$\frac{du_m}{dt} = O_c + \frac{\left(\left(l R_{c,l} + (1-l) R_{c,d}\right) t_A\right)^{H_c}}{1 + \left(\left(l R_{c,l} + (1-l) R_{c,d}\right) t_A\right)^{H_c}} - Y_u u_m$$

$$\frac{du}{dt} = u_m - D_u u$$

For experiments with translational reporters, we instead add variables for the luciferase-fused mRNA and the active luciferase-fused protein species. For TOC1-LUC:

$$\frac{dt'_m}{dt} = \frac{L_t + R_a a}{1 + L_t + R_a a + (R_c c_N)^{H_t}} - Y_t t'_m$$

$$\frac{dt'_I}{dt} = S_t t'_m - \left(l K_{t,l} + (1-l) K_{t,d} + D_u\right) t'_I$$

$$\frac{dt'_A}{dt} = \left(l K_{t,l} + (1-l) K_{t,d}\right) t'_I - \left(l D_{t,l} + (1-l) D_{t,d} + D_u\right) t'_A$$

For CCA1-LUC:

$$\frac{dc'_m}{dt} = O_c + \frac{\left(\left(l\,R_{c,l}+(1-l)\,R_{c,d}\right)t_A\right)^{H_c}}{1+\left(\left(l\,R_{c,l}+(1-l)\,R_{c,d}\right)t_A\right)^{H_c}} - Y_c\,c'_m$$

$$\frac{dc'_C}{dt} = S_c\,c'_m - K_c\,c'_C - \left(l\,D_{c,l}+(1-l)\,D_{c,d}+D_u\right)c'_C$$

$$\frac{dc'_N}{dt} = K_c\,c'_C - \left(l\,D_{c,l}+(1-l)\,D_{c,d}+D_u\right)c'_N$$

We have assumed that the deactivation rate of luciferase in TOC1-LUC and CCA1-LUC equals its total rate of deactivation and degradation in the transcriptional lines, D_u, because luciferase is only subject to slow non-specific protein degradation.

Model cost function

For the transcriptional reporters, the observable to be fitted is u, whereas for the translational reporters it is the sum over the two forms or compartments, $t'_I + t'_A$ or $c'_C + c'_N$. Consider a single data set of N points. Let $\bar{y}$ be the measured time series and $\bar{y}'$ the simulated one, with measurements taken at timepoints $\bar{t}$. Find for each timepoint i the window of $N \cdot \min\left(1, (t_{end}-t_0)/72\right)$ points that is centered (as far as possible) on t_i. For all points j, j' in that window, calculate the weight matrix

$$W_{i,j} = \frac{w_i(t_i - t_j)\,y_j}{\sum_{j'} w_i(t_i - t_{j'})\,{y_{j'}}^2},$$

where the weights are

$$w_i(\Delta t) = \left(1 - \left(\frac{|\Delta t|}{r_i}\right)^3\right)^3,$$

where r_i is the greatest $|\Delta t|$ within the window.

The cost for a single data set is

$$E_e = \frac{\sum_i \left(\frac{y'_i}{\overline{W}_i \cdot \bar{y}'} - y_i\right)^2}{N \sum_i \left(\|\overline{W}_i\|^{-1} - y_i\right)^2},$$

where the denominator normalizes the cost so that a value of 1 means “as good as a straight line”.

The total cost is

$$E = \sqrt{\frac{\sum_e z_e E_e}{\sum_e z_e}},$$

where z_e is the weight of each data set. This weight is set to 3 for LL data and 1 for all other data sets (see Table S2).