

Supplement

1 ILP Formulation

The input dataset is a $N \times M$ matrix C of Boolean values representing trajectories, where N corresponds to the number of genes whose expression level was measured, and M corresponds to the number of experiments. $C_{i,j}$ denotes the observed Boolean value of gene i at experiment j . The formulation for steady states is nearly identical and is discussed in the main text. For every gene, a candidate set of regulators is provided, denoted for simplicity as g_1, g_2, \dots, g_k , although the identity and the number of candidates can be different for different genes. The gene itself is denoted as g_{k+1} . The output of the logic function is denoted by $I(w_1, w_2, \dots, w_k)$, where $w_l \in \{0, 1\} \forall l \forall i \in \{1, \dots, N\}, \forall j \in \{1, \dots, M-1\}, \forall (w_1, w_2, \dots, w_k) \in \{0, 1\}^k$ we add the constraints:

$$\begin{aligned} & \sum_{r=1}^k (C_{r,j} \cdot (w_r + (1 - 2 \cdot w_r) \cdot B_{g_r,j})) \\ & + (1 - C_{r,j}) \cdot ((1 - w_r) + (2 \cdot w_r - 1) \cdot B_{g_r,j})) \\ & + C_{k+1,j+1} \cdot B_{g_{k+1},j+1} + (1 - C_{k+1,j+1}) \cdot (1 - B_{g_{k+1},j+1}) \\ & < (2 - I(w_1, w_2, \dots, w_k)) \cdot (k + 1) + D_{g_{k+1},j+1} \end{aligned} \quad (1)$$

$$\begin{aligned} & \sum_{r=1}^k (C_{r,j} \cdot (w_r + (1 - 2 \cdot w_r) \cdot B_{g_r,j})) \\ & + (1 - C_{r,j}) \cdot ((1 - w_r) + (2 \cdot w_r - 1) \cdot B_{g_r,j})) \\ & + C_{k+1,j+1} \cdot (1 - B_{g_{k+1},j+1}) + (1 - C_{k+1,j+1}) \cdot B_{g_{k+1},j+1} \\ & < (I(w_1, w_2, \dots, w_k) + 1) \cdot (k + 1) + D_{g_{k+1},j+1} \\ & 1 - (C_{k+1,j+1} * (1 - B_{g_{k+1},j+1}) + (1 - C_{k+1,j+1}) * B_{g_{k+1},j+1} \\ & - (C_{k+1,j} * (1 - B_{g_{k+1},j}) + (1 - C_{k+1,j}) * B_{g_{k+1},j})) >= D_{g_{k+1},j+1} \end{aligned} \quad (2)$$

$$\begin{aligned} & 1 - (C_{k+1,j+1} * (1 - B_{g_{k+1},j+1}) + (1 - C_{k+1,j+1}) * B_{g_{k+1},j+1} \\ & - (C_{k+1,j+1} * (1 - B_{g_{k+1},j+1}) + (1 - C_{k+1,j+1}) * B_{g_{k+1},j+1})) >= D_{g_{k+1},j+1} \end{aligned} \quad (3)$$

$$D_{g_{k+1},1} \leq \sum_{i \in \{1, \dots, k\}} R_i \quad (4)$$

where $B_{i,j}$ are Boolean variables defined for each of the entries of matrix C , and $D_{g_{k+1},j}$ are Boolean variables defined for every gene and state (column of C) except the last. We also add the constraints:

$$\begin{aligned}
& \forall (w_1, w_2, \dots, w_k), (w'_1, w'_2, \dots, w'_k) \in \{0, 1\}^k, I(w_1, w_2, \dots, w_k) \neq I(w'_1, w'_2, \dots, w'_k) : \\
& \sum_{i:w_i \neq w'_i} R_i \geq I(w_1, w_2, \dots, w_k) - I(w'_1, w'_2, \dots, w'_k) \\
& \sum_{i:w_i \neq w'_i} R_i \geq I(w'_1, w'_2, \dots, w'_k) - I(w_1, w_2, \dots, w_k) \\
& V_w \geq \sum_{j \in \{1, \dots, k\}} \frac{R_j}{k} - \frac{\max\{0.5, w-1\}}{k}
\end{aligned}$$

where R_i are Boolean variables defined for each regulator included in a gene's candidate regulators list, and V_w are Boolean variables defined for every gene and every $w \in 1, \dots, k$, k being the number of candidate regulators of a gene. The value of the objective function is then the sum of the weights of variables that are set to 1 in the solution, i.e.:

$$\sum_{i=1, j=1}^{N, M} (B_{g_i, j} + W(V_{g_i, j}) \cdot V_{g_i, j} + D_{g_i, j}) \quad (6)$$

where W is a function that maps between a V variable and the weight assigned to it.