

Supporting information

Edge detection

The method of solving for \mathbf{B} and $\boldsymbol{\mu}$ closely follows the steps in [1] with a few minor adjustments to account for the differences in our model structure.

The log-likelihood function of the model defined in Eq (3) is:

$$L(\mathbf{Y}|\mathbf{B}, \boldsymbol{\mu}) = \frac{-MN}{2} \log[2\pi\sigma^2] + N \log[\mathbf{I} - \mathbf{B}] - \frac{1}{2\sigma^2} \|\mathbf{Y} - \mathbf{B}\mathbf{Y} - \boldsymbol{\mu}\mathbf{1}^T\|_F^2. \quad (\text{S1})$$

By removing terms that do not depend on \mathbf{B} and adding a regularization term, the sparse maximum likelihood (SML) function becomes:

$$\begin{aligned} \hat{\mathbf{B}} = \arg \max_{\mathbf{B}} N \log[\mathbf{I} - \mathbf{B}] - \frac{1}{2\sigma^2} \|\mathbf{Y} - \mathbf{B}\mathbf{Y} - \boldsymbol{\mu}\mathbf{1}^T\|_F^2 - \lambda \|\mathbf{B}\|_{1,\mathbf{W}} \\ \text{s.t. } B_{ij} = 0 \forall (i, j) \in \mathcal{S}_q. \end{aligned} \quad (\text{S2})$$

Where \mathcal{S}_q contains the set of row and column indices of the entries of \mathbf{B} constrained to 0, and $\|\mathbf{B}\|_{1,\mathbf{W}} := \sum_{i=1}^M \sum_{j=1}^M w_{ij} |B_{ij}|$. The weights w_{ij} are chosen as $\frac{1}{\tilde{B}_{ij}}$, where \tilde{B}_{ij} is from a preliminary estimate of \mathbf{B} using ridge regression (Eq (S3)). These weights are added to the regularization term to improve estimation accuracy in line with the adaptive lasso [1, 2]. Additionally, the sample variance from the ridge regression estimate is used as the estimate of σ^2 in Eq (S2).

$$\begin{aligned} \tilde{\mathbf{B}} = \arg \min_{\mathbf{B}} \frac{1}{2} \|\mathbf{Y} - \mathbf{B}\mathbf{Y} - \boldsymbol{\mu}\mathbf{1}^T\|_F^2 + \rho \|\mathbf{B}\|_F^2 \\ \text{s.t. } B_{ij} = 0 \forall (i, j) \in \mathcal{S}_q. \end{aligned} \quad (\text{S3})$$

Both the ridge regression and SML estimates, $\tilde{\mathbf{B}}$ and $\hat{\mathbf{B}}$ respectively, can be solved on a row by row basis. This allows us to remove the experiments that targeted the i^{th} component when solving for $\mathbf{b}_i^T = [B_{i1} \ \cdots \ B_{iM}]$, the i^{th} row of \mathbf{B} . Removing these experiments for each component prevents fitting \mathbf{b}_i^T to data where an outside influence is controlling the abundance of the associated component.

Ridge Regression

For the ridge regression, this becomes

$$\begin{aligned} \tilde{\mathbf{b}}_i = \arg \min_{\mathbf{b}_i} \frac{1}{2} \|\mathbf{y}_i^i - \mathbf{b}_i^T \mathbf{Y} - \mu_i \mathbf{1}^i\|_2^2 + \rho \|\mathbf{b}_i\|_2^2 \\ \text{s.t. } B_{ij} = 0 \forall (i, j) \in \mathcal{S}_q. \end{aligned} \quad (\text{S4})$$

Where the overset i implies the variables adjusted for the removed targeted experiments (e.g., \mathbf{y}_i^i is the abundances for component i from the experiments that it was not targeted, and $\mathbf{1}^i$ is a $1 \times N$ vector of ones, with N^i is the number of experiments that do not target component i).

Minimizing Eq (S4) w.r.t μ_i^i gives

$$\mu_i^i = \bar{y}_i^i - \mathbf{b}_i^T \bar{\mathbf{y}}^i \quad (\text{S5})$$

where $\bar{y}_i^i = \sum_{j=1}^i \mathbf{y}_{ij}^i / N$ and $\bar{\mathbf{y}}^i = \sum_{j=1}^i \mathbf{Y}_j^i / N$. Eq (S4) then becomes

$$\begin{aligned} \tilde{\mathbf{b}}_i &= \arg \min_{\mathbf{b}_i} \frac{1}{2} \|\tilde{\mathbf{y}}_i^i - \mathbf{b}_i^T \tilde{\mathbf{Y}}^i\|_2^2 + \rho \|\mathbf{b}_i\|_2^2. \\ \text{s.t. } B_{ij} &= 0 \forall (i, j) \in \mathcal{S}_q. \end{aligned} \quad (\text{S6})$$

where $\tilde{\mathbf{y}}_i^i = \mathbf{y}_i^i - \bar{y}_i^i \mathbf{1}^i$ and $\tilde{\mathbf{Y}}^i = \mathbf{Y}^i - \bar{\mathbf{y}}^i \mathbf{1}^i$.

The constraint $B_{ij} = 0 \forall (i, j) \in \mathcal{S}_q$ can be applied directly by removing the j^{th} element(s) from \mathbf{b}_i^T and the j^{th} row(s) from $\tilde{\mathbf{Y}}^i$. Let $\check{\mathbf{b}}_i^T$ and $\check{\mathbf{Y}}^i$ represent these adjustments. Then Eq (S6) becomes

$$\tilde{\mathbf{b}}_i = \arg \min_{\mathbf{b}_i} \frac{1}{2} \|\check{\mathbf{y}}_i^i - \check{\mathbf{b}}_i^T \check{\mathbf{Y}}^i\|_2^2 + \rho \|\check{\mathbf{b}}_i\|_2^2. \quad (\text{S7})$$

This has a close form solution

$$\tilde{\mathbf{b}}_i = (\check{\mathbf{Y}}^i \check{\mathbf{Y}}^i + \rho \mathbf{I})^{-1} (\check{\mathbf{Y}}^i \check{\mathbf{y}}_i^i) \quad (\text{S8})$$

Sparse Maximum Likelihood

Using the cyclic block-coordinate ascent iteration algorithm from [1], we define the matrix $\hat{\mathbf{B}}(B_{ij})$ to be a matrix equal to $\hat{\mathbf{B}}$ except for the (i,j)th entry which is replace by B_{ij} , such that $\hat{\mathbf{B}}(B_{ij}) := \hat{\mathbf{B}} + \mathbf{e}_i \mathbf{e}_j^T (B_{ij} - \hat{B}_{ij})$. Eq (S2) can then be expressed as

$$B_{ij} = \arg \max_{B_{ij}} N \sigma^2 \log[|\mathbf{I} - \hat{\mathbf{B}}(B_{ij})|] - \frac{1}{2} \|\check{\mathbf{Y}}^i - \hat{\mathbf{B}}(B_{ij}) \check{\mathbf{Y}}^i - \check{\boldsymbol{\mu}} \mathbf{1}^i\|_F^2 - \lambda w_{ij} |B_{ij}| \quad (\text{S9})$$

Similar to the ridge regression, maximizing Eq (S9) w.r.t $\check{\boldsymbol{\mu}}^i$ gives

$$\check{\boldsymbol{\mu}}^i = (\mathbf{I} - \hat{\mathbf{B}}(B_{ij})) \check{\mathbf{y}}^i \quad (\text{S10})$$

Substituting into Eq (S9),

$$B_{ij} = \arg \max_{B_{ij}} N \sigma^2 \log[|\mathbf{I} - \hat{\mathbf{B}}(B_{ij})|] - \frac{1}{2} \|\check{\mathbf{Y}}^i - \hat{\mathbf{B}}(B_{ij}) \check{\mathbf{Y}}^i\|_F^2 - \lambda w_{ij} |B_{ij}| \quad (\text{S11})$$

Following the steps from [1], by rearranging and removing constant terms, this becomes

$$B_{ij} = \arg \max_{B_{ij}} N \sigma^2 \log[|\alpha_0 - c_{ij} B_{ij}|] + \alpha_1 B_{ij} - \frac{1}{2} \alpha_2 B_{ij}^2 - \lambda w_{ij} |B_{ij}| \quad (\text{S12})$$

where c_{ij} represents the (i,j)th co-factor of the matrix $\mathbf{I} - \hat{\mathbf{B}}$, and

$$\begin{aligned} \alpha_0 &:= |\mathbf{I} - \hat{\mathbf{B}}| \\ \alpha_1 &:= \left[(\mathbf{I} - \hat{\mathbf{B}} + \mathbf{e}_i \mathbf{e}_j^T \hat{B}_{ij}) \tilde{\mathbf{Y}} \tilde{\mathbf{Y}}^T \right]_{ij} \\ \alpha_2 &:= \|\tilde{\mathbf{Y}}^T \mathbf{e}_j\|_2^2 \end{aligned}$$

The value of B_{ij} can then be solved for as described in equations (12)-(16) and the associated text in [1].

Regularization parameters

The regularization parameters ρ and λ , were found using 5-fold cross-validation while stepping through a set range of values for ρ and λ in the ridge regression and SML algorithms respectively. To improve stability, the cross-validations were run multiple times and the ρ and λ resulting in the lowest mean error across the testing folds were selected and used to solve for $\tilde{\mathbf{B}}$ and $\hat{\mathbf{B}}$ in Eq (S3) and Eq (S2).

Algorithm implementation

The Matlab code for the SML algorithm provided by [1] was modified based on the changes described above. Additionally, the abundances of the monolignol transcripts and proteins ranged from on the order of 10^{-1} nM and 10^4 nM. For this reason, we included a function to scale each transcript and protein by its maximum value in the training data to bring the range of each transcript and protein to between 0 and 1 when solving for $\tilde{\mathbf{B}}$ and $\hat{\mathbf{B}}$. The coefficients of the returned $\tilde{\mathbf{B}}$ and $\hat{\mathbf{B}}$ were then accordingly untransformed to work with un-scaled data.

References

- [1] Cai X, Bazerque JA, Giannakis GB. Inference of Gene Regulatory Networks with Sparse Structural Equation Models Exploiting Genetic Perturbations. *PLoS Computational Biology*. 2013;9(5):e1003068. doi:10.1371/journal.pcbi.1003068.
- [2] Zou H. The Adaptive Lasso and Its Oracle Properties. *Journal of the American Statistical Association*. 2006;101(476):1418–1429.