


A Hybrid of Metabolic Flux Analysis and Bayesian Factor Modeling for Multiomic Temporal Pathway Activation

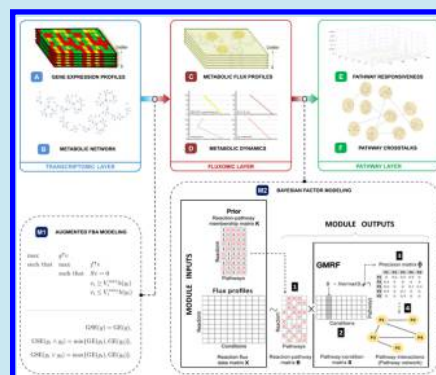
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 Supporting Information

ABSTRACT: The growing availability of multiomic data provides a highly comprehensive view of cellular processes at the levels of mRNA, proteins, metabolites, and reaction fluxes. However, due to probabilistic interactions between components depending on the environment and on the time course, casual, sometimes rare interactions may cause important effects in the cellular physiology. To date, interactions at the pathway level cannot be measured directly, and methodologies to predict pathway cross-correlations from reaction fluxes are still missing. Here, we develop a multiomic approach of flux-balance analysis combined with Bayesian factor modeling with the aim of detecting pathway cross-correlations and predicting metabolic pathway activation profiles. Starting from gene expression profiles measured in various environmental conditions, we associate a flux rate profile with each condition. We then infer pathway cross-correlations and identify the degrees of pathway activation with respect to the conditions and time course using Bayesian factor modeling. We test our framework on the most recent metabolic reconstruction of *Escherichia coli* in both static and dynamic environments, thus predicting the functionality of particular groups of reactions and how it varies over time. In a dynamic environment, our method can be readily used to characterize the temporal progression of pathway activation in response to given stimuli.

KEYWORDS: multiomics, flux-balance analysis, *Escherichia coli*, Bayesian factor modeling, pathway correlation, temporal pathway activation



The recent availability of high-throughput data regarding multiple layers of biological organization (“omics”) allows cellular processes to be mapped at the levels of mRNA, proteins, and metabolites. Analogously, the growing number of defined pathways, where reactions are classified into groups, allows us to better understand the particular functionality achieved by a series of reactions. To date, the study of interactions between pathways taken as single entities has been already applied to genes through gene expression analysis.¹ Such interactions, also known as *pathway cross-correlations*, are important to produce appropriate response to external stimuli and are assumed to be the underlying mechanism describing the response to dynamic environments. This suggests that studying biological systems requires a holistic approach that takes the concerted activities of molecules into account.² Previous studies inferred cross-correlations from gene expression data^{3–5} and others from protein–protein networks.⁶ Another recent study applied a Bayesian network inference to identify causal relationships among the most influential reactions.⁷ However, methods to infer cross-correlations between pathways from reaction fluxes, and therefore making use of the metabolism and its reaction–pathway associations, are still missing.

In the last 25 years, high-quality genome-scale reconstructions of metabolic networks have been combined with constraint-based optimization in order to analyze micro-

organisms at steady state. To improve the predicting capability of a metabolic model, one can include multiple “omic” layers, such as gene expression, codon usage, protein abundance, and the interaction between these layers. The interdependence among gene expression levels, protein production, and growth rate has been analyzed thoroughly by Scott et al.,⁸ highlighting a linear relation between the RNA–protein ratio and the growth rate of the bacterium. Other methodologies regarding how to improve the model predictions by means of gene expression have been recently proposed.⁹

Arguably, flux-balance analysis (FBA) is the most widely used constraint-based technique to predict flux distributions and network capabilities in large biochemical networks.¹⁰ FBA has proved to be useful thanks to its ability to handle large networks: it requires information about biochemical reactions and stoichiometric coefficients, but it does not involve kinetic parameters. This makes it well suited to studies that enumerate and characterize perturbations such as different substrates or genetic interventions (e.g., knockouts) leading to obligatory coupling between the growth rate and the production of a desired metabolite.¹¹ Recently, more than 1000 prokaryotic

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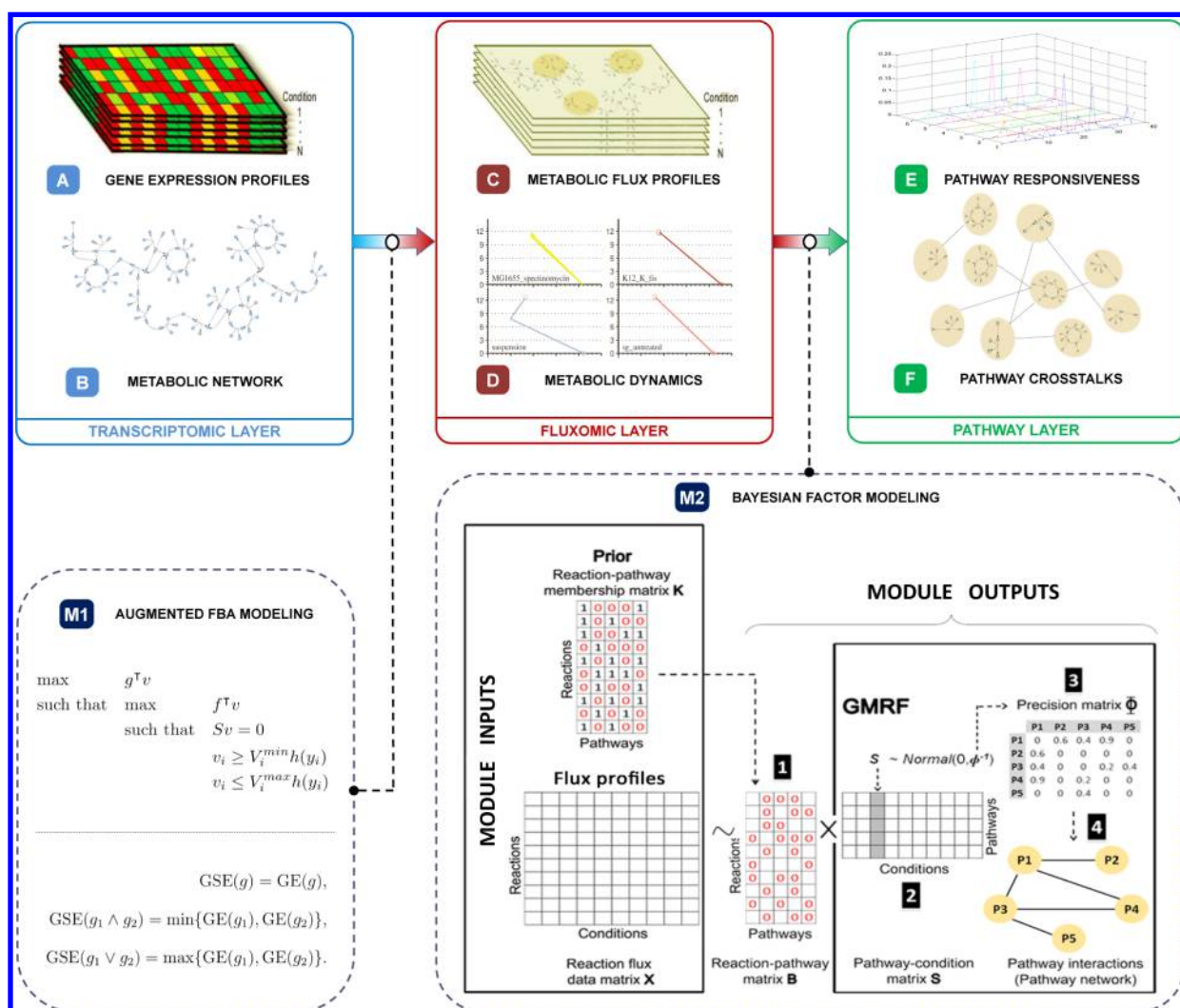


Figure 1. Our modeling framework combines Bayesian machine learning and metabolic flux modeling to analyze metabolic pathways from gene expression data. First, we propose an augmented FBA method (M1) to map gene expression data (A) on the metabolic network (B). The method includes a bilevel maximization framework in the case study of biomass-acetate objective space, therefore producing optimal flux profiles in different environmental conditions (C). Using a set of conditions with time-series gene expression profiles, we use our framework to elucidate the metabolism dynamics, involving rearrangements in the objective space during growth (D). Finally, we perform Bayesian factor modeling (M2) on the reaction flux distribution by taking predefined reaction-pathway memberships as prior knowledge. This enables us to infer the pathway responsiveness to each environmental condition (E) and the cross-correlations between pathways (F), elucidating the underlying mechanisms of bacterial response to dynamically changing environments.

genomes have been fully sequenced, thus allowing FBA models to incorporate also information on enzymes and genome, including the relationships among genes, proteins, and reactions (*GPR mapping*). To date, more than 90 genome-wide metabolic reconstructions have been published.¹²

In this study, we propose a methodology to predict the cellular response to environmental conditions from a pathway-based perspective. The classification of metabolic reactions into pathways allows us to understand or predict the functionality of particular groups of reactions under given growth conditions. However, since the interactions at the pathway level cannot be measured directly, we propose to apply a hierarchical Bayesian framework, which supports latent variable models in order to take pathway information into account.⁵ We focus on the cellular activity of *Escherichia coli* on the genomic, fluxomic, and pathway levels in different environmental settings by integrating an augmented metabolic model with a machine learning technique applied at the fluxomic level. Integrating a FBA

model and a Bayesian factor model leads to determining the degree of metabolic pathway responsiveness and to detecting pathway cross-correlations, starting from gene expression profiles (Figure 1).

The aim of this article is to combine a Bayesian machine learning technique and a multiomic flux model augmented with gene expression profiles in order to integrate and analyze data representing heterogeneous biological levels of organization. Our method highlights complex interactions between components of the model at different layers. We start with the investigation of the genome-scale model by using metabolic flux analysis in a bilevel setting, namely, the maximization of growth rate and acetate production. Through a Bayesian factor approach, we detect pathway cross-correlations that are assumed to be a static, intrinsic property of *E. coli* underlying its response behavior. Furthermore, we infer pathway activation profiles as a bacterial response to an ensemble of environmental conditions. Finally, we use time series of gene expression

profiles combined with our hybrid approach in order to investigate changing pathway responsiveness.

1. FLUX-BALANCE ANALYSIS WITH CONTINUOUS GENE EXPRESSION

Flux-balance analysis (FBA) is a linear programming technique that models the steady-state conditions in a chemical reaction network.¹³ The combination of flux-balance constraints and capacity constraints on the metabolic fluxes is a system of linear homogeneous equations and inequalities; thus, its solution space is a convex polyhedral cone representing the feasible flux distributions. The flux-balance constraint is represented by the equation $dX/dt = Sv = 0$, where X represents the vector of the concentrations of all metabolites of the network, S is its stoichiometric matrix, and v is the vector of flux rates. This constraint can be thought of as Kirchoff's laws applied to any node representing a metabolite in the network. The flux through a metabolite must be constant, namely, the input flux equals the output flux. If one allows the concentrations of metabolites to increase linearly, then the conditions become $dX/dt \geq 0$, which is equivalent to $Sv \geq 0$. This approach represents Von Neumann's optimal growth scenario and may be useful when one has to ensure that some metabolites are available also outside of the chemical reaction network modeled (e.g., when modeling only a compartment of a larger organism¹⁴ or when applying external optimization algorithms to maximize or minimize the metabolite concentration¹⁵).

To analyze the effects caused by the change of external media and conditions in which an *E. coli* strain was grown, we map each gene expression array (microarray profiles) to the acetate-biomass space of objective functions. We take these two fluxes as objectives because of the common assumption that microorganisms tend to optimize their metabolic network in order to maximize the growth rate, and possibly produce additional chemicals, in order to cope with multiple, sometimes conflicting, objectives to optimize simultaneously.¹⁶ As well as being an important target for biotechnology, with multiple industrial applications,¹⁷ acetate is central to many pathways in both aerobic and anaerobic *E. coli*. Being an intermediate metabolite, it is representative of processes not directly related to growth and therefore it is highly indicative of metabolic flexibility for possible reorganizations that need to be performed during adaptations to environmental changes. When acetate is present at high levels, it inhibits cell growth and recombinant protein productivity.¹⁸

The gene regulation process in bacteria is used to respond to the variations taking place in the metabolism or in the external environment. Here, we take into account 466 *E. coli* Affymetrix Antisense2 microarray expression profiles collected in various media and conditions,¹⁹ such as low or high glucose, aerobic or anaerobic environment, pH changes, antibiotics, and heat shock. For the dynamical analysis of growth, we will consider 41 growth conditions, each of which has been sampled at four time steps (164 microarray profiles in total).

Each expression profile is mapped to the *E. coli* model,²⁰ which we have augmented with a map from gene expression (GE) to constraints for metabolic fluxes. First, in order map a gene expression profile to a *gene set expression* (GSE) profile, we use recursively the following rules valid for the three basic cases of gene set:

$$\begin{aligned} \text{single gene:} & \quad \text{GSE}(g) = \text{GE}(g) \\ \text{enzymatic complex:} & \quad \text{GSE}(g_1 \wedge g_2) = \min\{\text{GE}(g_1), \text{GE}(g_2)\} \\ \text{isozymes:} & \quad \text{GSE}(g_1 \vee g_2) = \max\{\text{GE}(g_1), \text{GE}(g_2)\} \end{aligned} \quad (1)$$

Then, we solve the two-level maximization problem

$$\begin{aligned} \max & \quad g^T v \\ \text{such that} & \quad \max \{f^T v \mid Sv = 0, v_i \geq V_i^{\min} h(y_i), v_i \leq V_i^{\max} h(y_i)\} \end{aligned} \quad (2)$$

where V_i^{\min} and V_i^{\max} are the default lower and upper bounds for each flux, respectively, and v, f , and g are n -dimensional Boolean arrays that select the fluxes to be maximized (in this article, only one flux is selected for each level of the maximization problem). The gene set expression $y_i = \text{GSE}_i$ represents the "expression" of the i th reaction of the model.

The map from each gene set to the associated flux upper and lower bounds is defined as

$$h(x) = \frac{\gamma(1 + \log(x))^{sgn(x-1)}}{\sigma_i^2} \quad (3)$$

(and $h(x) = \gamma/\sigma_i^2$ if $x = 1$), where $sgn(x-1) = (x-1)/|x-1|$; γ is the weight for the variance σ^2 , which is the variance of the gene set, computed from the variance of its genes using the same rules (eq 1) used for the gene set expression (Figure 1-M1).

The importance of a gene, and therefore the ability to change the reaction flux of the corresponding reaction in the FBA model, is inversely proportional to the variance of that gene across all of the experimental conditions. The idea underlying this assumption is that those genes whose expression is only slightly varied across conditions must be regarded as key genes for the organism.²¹ We adopt γ as a multiplicative factor for the inverse of the variance of each gene, representing the weight attributed to the variance as an indicator of the importance of a gene. Here, γ was chosen as the value that causes the smallest loss of information (quantified using a normalized root-mean-square error, NRMSE) when using the Bayesian factor model. However, if further experimental data is available (e.g., protein abundance, translation rate, codon usage, or post-translational modifications), then we expect this parameter to be varied individually for each reaction.

The reasons for choosing this mathematical structure are as follows. First, a recent model suggests a protein synthesis rate that grows fast with increasing mRNA abundance but a decreasing growth speed for high values of mRNA abundance.²² Second, there is empirical evidence that logarithmic maps are useful to map biological processes.²³ Third, the approximation of this behavior with a logarithmic function simplifies the task of avoiding the translation of unrealistically high values of measured gene expression levels into overly weak constraints. The correlation between gene expression and metabolic phenotype is still a matter of debate, but recent evidence suggests that protein abundance is mainly determined by the transcript level.^{24,25} Therefore, we use the logarithmic map only to set constraints, whereas we solve the bilevel linear program (eq 2) to find the final flux distribution under each condition. The solution of the bilevel problem is a pair representing the maximum natural objective (biomass) allowed by the constraints and the maximum second objective (acetate) possible in the computed biomass-maximizing flux

distribution. Each experimental condition is associated with a gene expression array and therefore with a bilevel problem.

2. PATHWAY-BASED BAYESIAN FACTOR MODELING

Factor modeling is an unsupervised learning technique in a family of latent variable models, assuming that high-dimensional data are generated from the hidden lower-dimensional factors that are shared across data samples. Specifically, matrix factorization assumes that an observed $R \times C$ data matrix can be explained by two low-rank matrices with the dimension of $R \times P$ and $P \times C$, where $P \ll R, C$. Moreover, under Gaussian Markov random field (GMRF) properties, assuming a Gaussian distribution on the underlying factors in the matrix factorization process can capture the dependency between each element in P .

Here, we regard pathways as the latent factors underlying bacterial flux responses. We assume that the observed flux rates arise from specific combinations of pathways that are activated by a stimulus. In particular, the values of a flux rate for each reaction depends on the degrees of pathway activation and on the association strength between that reaction and the activated pathways. Having obtained the $R \times C$ flux rate matrix from the bilevel FBA, where R and C are the number of reactions and conditions, respectively, we use the Bayesian matrix factorization modeling with GMRF to perform pathway analysis. Specifically, we decompose the flux rate data matrix into two low-rank matrices whose dimensions are $R \times P$ and $P \times C$ as well as a $P \times P$ correlation matrix, where P is the number of latent pathways. Note that, in general, we take a pathway into account if it is associated with at least one reaction in R . Figure 1-M2 demonstrates the factor model graphically and mathematically. On the basis of the rationale of matrix factorization, the $R \times P$ matrix represents the association strength between reaction fluxes and pathways, whereas the $P \times C$ matrix denotes the association strength between pathways and conditions, suggesting degrees of pathway responsiveness. In addition, the correlations between metabolic pathways are denoted by the $P \times P$ matrix.

Formally, let R , C , and P be the number of reactions, conditions, and pathways, respectively. The flux data matrix $\mathbf{X} \in \mathbb{R}^{R \times C}$ is decomposed into two matrices: $\mathbf{X} \sim \mathbf{B}\mathbf{S}$. The first matrix $\mathbf{B} \in \mathbb{R}^{R \times P}$ denotes the membership strength of reactions in each pathway. The second matrix $\mathbf{S} \in \mathbb{R}^{P \times C}$ corresponds to the degree of pathway responsiveness specific to each condition. We transform the predefined reaction-pathway memberships of the *E. coli* model into the binary matrix $\mathbf{K} \in \{0,1\}^{R \times P}$ in order to guide the clustering of reactions into pathways in \mathbf{B} . On the basis of our assumption of pathway cross-correlations, we model pathway dependencies by assuming a Gaussian distribution on \mathbf{S} with a zero mean and a precision (inverse covariance) matrix $\Phi \in \mathbb{R}^{P \times P}$ from which the correlations between pathways are computed.

On the basis of the GMRF framework, the off-diagonal elements of the precision (inverse covariance) matrix can be interpreted as the partial correlations between any two random variables as follows.²⁶ The zero pattern in the precision matrix encodes the independence relations of two variables generated by a Gaussian distribution conditioned on the other random variables. Therefore, the precision matrix can be used to form a pathway cross-correlation network, where nodes represent individual pathways and neighboring nodes represent highly correlated pathways. More precisely, since we assume that for any given condition c , the pathway responsiveness vector $s_c \sim$

$\text{normal}(0, \Phi^{-1})$ is randomly drawn from a P -dimensional multivariate Gaussian with a zero mean μ and a precision matrix Φ , we can form an undirected graph $\mathcal{G}(\Phi) = (V, E)$, with vertices V corresponding to the random variables (pathways) $V_1, V_2, V_3, \dots, V_P$ and edges E satisfying $(V_i, V_j) \in E$ if and only if $\phi_{ij} \neq 0$. If $\mathcal{N}(i) = \{j: (i, j) \in E\}$ denotes the set of neighboring nodes of i in the graph \mathcal{G} , then the independence correlation of $V_i \perp V_u | V_{\mathcal{N}(i)}$ holds for any node $u \notin \mathcal{N}(i)$ that is not a neighbor of V_i . Moreover, the correlation strength between V_i and V_j is calculated as

$$\text{corr}(V_i, V_j | V_{\setminus ij}) = \left| \frac{\phi_{ij}}{\sqrt{\phi_{ii}\phi_{jj}}} \right| \quad (4)$$

where the subscript “ $\setminus ij$ ” indicates all nodes except V_i and V_j . Consequently, the correlation strength will range from zero to one, indicating the weakest correlation (conditional independence) and strongest correlation, respectively. The remarkable characteristic of the GMRF is that the conditional independence can be interpreted directly from the precision matrix. More importantly, it can encode any arbitrary structure of a graph.

Having observed the data matrix \mathbf{X} , the goal is to make inference on \mathbf{S} , \mathbf{B} , and Φ . Our interest for biological interpretation is only on \mathbf{S} and Φ , which indicate the degree of pathway responsiveness to each condition and the cross-correlations between pathways, respectively. At each time step, we use the inferred cross-correlations as the underlying mechanism of the *E. coli* system to predict the temporal progression of pathway activation.

In order to infer all unknown variables, we apply a Bayesian approach starting from the construction of a full probabilistic model, in which all relevant entities (i.e., observed data, latent variables, and nuisance variables) are treated as random variables having uncertainties described by a probability distribution. To avoid the optimization of the parameters, we apply the Bayesian hierarchical modeling, in which each parameter is given a prior distribution with a set of fixed hyperparameters.

The model is mainly based on Gaussian distributions containing two parameters, a mean and a precision (an inverse variance). According to the matrix factorization method, \mathbf{X} is modeled with a mean $\mathbf{B}\mathbf{S}$ and a precision τ_c (eqs 5 and 6).

$$\mathbf{x}_{rc} = \sum_{p=1}^P b_{rp} s_{pc} + \epsilon = \mathbf{b}_r \mathbf{s}_c + \epsilon; \quad \epsilon = \text{random noise}, \epsilon \in \mathbb{R} \quad (5)$$

$$\epsilon \sim \text{normal}(0, \tau_c^{-1}) \quad (6)$$

where \mathbf{b}_r is the r th row of \mathbf{B} and \mathbf{s}_c is the c th column of \mathbf{S} . Equations 7 and 8 illustrate that the latent variables \mathbf{B} and \mathbf{S} are modeled with a zero mean because of the sparsity constraints. While elements in \mathbf{B} are assumed to be independently distributed with a precision τ_B , elements in \mathbf{S} are presumably correlated within each column with a precision matrix Φ , expressing the hypothesis of pathway cross-correlations.

$$b_{rp} = \begin{cases} 0, & \text{if } k_{rp} = 0 \\ \text{normal}(b_{rp}|0, \tau_B^{-1}), & \text{if } k_{rp} = 1 \end{cases} \quad (7)$$

$$\mathbf{s}_c \sim \text{GMRF}(0, \Phi^{-1}) \quad (8)$$

All parameters (τ_e , τ_B , and Φ) are given conjugate priors with their own fixed hyperparameters (α_e , β_e , α_B , β_B , ν , Ψ), which are a gamma distribution for τ_e and τ_B and a Wishart distribution for Φ (eqs 9–11).

$$\tau_e \sim \text{gamma}(\alpha_e, \beta_e) \quad (9)$$

$$\tau_B \sim \text{gamma}(\alpha_B, \beta_B) \quad (10)$$

$$\Phi \sim \text{Wishart}(\nu, \Psi) \quad (11)$$

The set of eqs 5–11 entirely specifies each model entity with its probability distribution.⁵ The use of conjugate priors makes the inference computable analytically.

Upon the model specification, inference of unknown quantities can be made through the computation of the posterior distribution, which is composed of the probability conditioned on the observed data, known as likelihood, and its prior. Due to the conjugacy, we apply a Gibbs sampling algorithm, where each unknown variable is alternately sampled until the convergence is satisfactory. In order to reduce autocorrelation between samples, every 10 iterations we collect the samples of the matrix \mathbf{S} for the comparison between conditions and over time and those of Φ for the analysis of pathway cross-correlations.

3. RESULTS AND DISCUSSION

We first applied FBA modeling to map 466 gene expression data profiles, plus 164 time-series data profiles, into 2583 reaction flux rates of the *E. coli* metabolic network, subject to the maximization of acetate and biomass production. Next, we performed Bayesian factor modeling on those reaction fluxes by taking predefined reaction-pathway memberships as prior knowledge to infer the responsiveness degree of the 37 pathways of the *E. coli* model.

3.1. Sensitivity and Mean-Square Error Analysis. On the basis of a normalized root-mean-square error (NRMSE), as shown in eq 12, we performed a convergence analysis indicating how well the model fits the data. We compute the error as

$$\text{NRMSE} = \frac{\sqrt{\sum_{r,c} (x_{rc} - \mathbf{b}_r \mathbf{s}_c)^2 / (R \times C)}}{x_{\max} - x_{\min}} \quad (12)$$

where x_{\max} and x_{\min} are the highest and lowest values in \mathbf{X} .

More specifically, the NRMSE indicates how much the estimated flux rates inferred from the model assumption according to eq 5 are deviated from the original flux rate data matrix. In other words, it intuitively represents the information loss we expect if we use this model in place of the actual flux rates. The smaller the error is, the better the model fits the data. Figure 2 shows that the error decreases to approximately 0.853% at the stationary state.

We also performed a sensitivity analysis on γ in order to show the robustness of our approach by testing the perturbation of the flux rates induced by various perturbations of γ . Specifically, small changes of γ (1%) caused a very small average perturbation of 0.0079 mmol h⁻¹ gDW⁻¹ of the flux rates, 0.024 mmol h⁻¹ gDW⁻¹ for acetate, and 0.0009 h⁻¹ for biomass. A stronger (10%) perturbation of γ yields an average perturbation of 0.0081 mmol h⁻¹ gDW⁻¹ of the flux rates, 0.2200 mmol h⁻¹ gDW⁻¹ for acetate, and 0.0085 h⁻¹ for

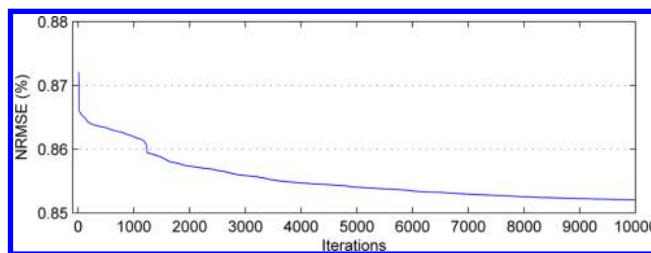


Figure 2. Normalized root-mean-square error (NRMSE) across the iterations.

biomass. Finally, a strong perturbation (1 order of magnitude) resulted in an average change of 0.2385 mmol h⁻¹ gDW⁻¹ in the flux rates, 2.0696 mmol h⁻¹ gDW⁻¹ for acetate, and 0.044 h⁻¹ for biomass. We would like to remark that γ can be assigned individually for each reaction where information on the translation rate, codon usage, or post-translational modifications is available.

3.2. Bacterial Flux Responses and Pathway Cross-Correlations. With the objective to maximize both biomass and acetate production, as shown in Figure 3, the *E. coli* strains

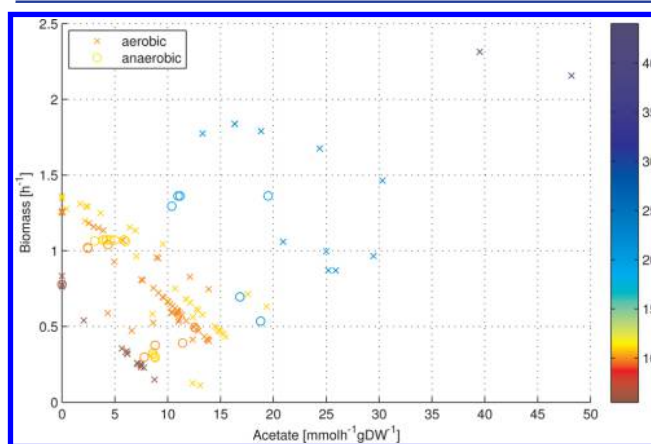


Figure 3. Through augmented FBA, all 466 gene expression profiles are mapped to the acetate-biomass objective space. Each point contains 2583 reaction flux rates, whereas only acetate and biomass are shown, representing the objectives of the bilevel linear program. The color bar shows the glucose uptake rate [mmol h⁻¹ gDW⁻¹]. Interestingly, the *E. coli* grown under some conditions with a 10 mmol h⁻¹ gDW⁻¹ of glucose uptake rate is able to produce more biomass and acetate than the strains grown on higher glucose. The pathway-based Bayesian analysis is performed on the flux rates in the four conditions based on the two criteria of oxygen and glucose.

grown under conditions with a 10 mmol h⁻¹ gDW⁻¹ of glucose uptake rate produce more biomass and acetate than the strains in lower glucose. Under aerobic conditions, the maximum biomass is 2.31 h⁻¹ with 39.52 mmol h⁻¹ gDW⁻¹ of acetate, while the maximum acetate reached is 48.20 mmol h⁻¹ gDW⁻¹ with a biomass of 2.16 h⁻¹. Under anaerobic conditions and low glucose, the maximum biomass is 1.04 h⁻¹ (with 4.36 mmol h⁻¹ gDW⁻¹ of acetate production). Under anaerobic conditions and high glucose, the *E. coli* is able to produce only 1.36 h⁻¹ of biomass, with a maximum of 19.50 mmol h⁻¹ gDW⁻¹ of acetate. The full table with the experimental conditions and the values of acetate and biomass are in the Supporting Information. We are interested in investigating the underlying mechanisms under different oxygen conditions and glucose uptake rates (high/low

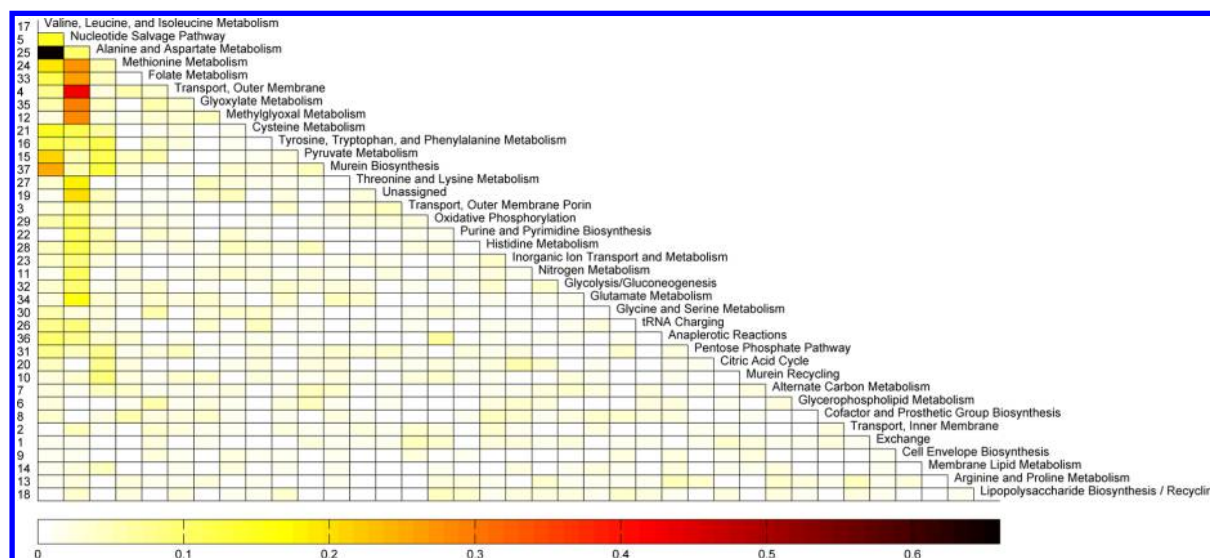


Figure 4. Pathway correlation matrix derived from Φ , an output of the Bayesian factor modeling. On the y axis, we report the pathway identifiers (PID) that correspond to their pathway names labeled on the diagonal. The color bar shows the correlation between pathways computed with the Bayesian factor modeling. These values suggest the strength of pathway cross-correlations underlying the bacterial response through flux rates in both steady-state and time-course experiments.

glucose environments with a threshold of $10 \text{ mmol h}^{-1} \text{ gDW}^{-1}$).

The Bayesian factor modeling with GMRF allows us to extract the behaviors of *E. coli* in response to a variety of experimental conditions and cross-correlations between pathways. Since we assume that the pathway cross-correlations represent a static, intrinsic property of *E. coli*, the model computes the cross-correlations as a global factor that is shared by individual conditions and over time. Figure 4 illustrates the sparse network of inferred cross-correlations between metabolic pathways. It is remarkable that the nucleotide pathway (PID:5) acts as a central hub of the cross-correlation network and is involved with multiple pathways. The strongest correlation is the cross-correlation between the alanine and aspartate metabolism pathway (PID:25) and the pivot pathway of another small community pertaining to the valine, leucine, and isoleucine metabolism (PID:17). A recent review of amino acids and their functions shows that alanine is the primary amino acid in gluconeogenesis and that valine can be used directly to synthesize glutamine and alanine.²⁷

Interestingly, there is a modest link between these two clusters, PID:5 and PID:17, with correlation ≈ 0.15 (top 3% in the correlation matrix) by a transcription factor called leucine-responsive regulatory protein (Lrp).²⁸ This link plays an important role depending on the availability of oxygen over time, which we will discuss in the next section. Table 1 shows the average responsiveness degree of the most responsive pathways to different oxygen and glucose conditions. While the nucleotide pathway is important under anaerobic conditions on low glucose, the valine, leucine, and isoleucine metabolism pathway and the alanine and aspartate metabolism pathway both exhibit a key role under aerobic conditions on high glucose, highlighting a pathway cross-correlation between them (Figure 4).

3.3. Flux Rate Progression and Temporal Pathway Activation. Not only do the *E. coli* strains respond to the environment differently from condition to condition within the same time frame but also their temporal behaviors progress over time in a different way. In order to perform a dynamical

Table 1. Average Responsiveness of the Most Responsive Pathways under Aerobic and Anaerobic Conditions of High and Low Glucose^a

PID	pathway name	high glucose		low glucose	
		aerobic	anaerobic	aerobic	anaerobic
5	Nucleotide salvage	0.0865	0.0965	0.1366	0.1714
17	Valine, leucine, and isoleucine metabolism	0.2219	0.2147	0.1974	0.1590
25	Alanine and aspartate metabolism	0.1544	0.1487	0.1285	0.1076

^aPID:5 is important under anaerobic conditions on low glucose, whereas PID:17 and PID:25 both exhibit a key role under aerobic conditions on high glucose, highlighting a pathway cross-correlation between them.

analysis of pathway activation, we consider the gene expression profiles of 41 time-course experiments after the exposure to stimuli or under stress conditions.

Figure 5 shows the acetate secretion/assimilation and the growth rate as a result of the metabolic regulation system of *E. coli* in response to the changing environment. We also compare the Euclidean distance covered by each of the 41 conditions from the start to the end of the observations (four time steps). The fluctuations in acetate production depend on the balance between pyruvate fermentation to acetate and Krebs cycle. Interestingly, the most remarkable fluctuations are those caused by the presence of ampicillin, norfloxacin, and spectinomycin, antibiotics used to treat a number of bacterial infections. This result confirms that under specific conditions some antibiotics can have a high impact on the metabolism and physiology of *E. coli*, whereas others (e.g., kanamycin) have no effect (for instance, due to the development of antimicrobial resistance). These metabolic transitions confirm well-known experimental results on the acetate switch during growth under different conditions and on the inverse relation between growth rate and acetate secretion.^{29,30} The global response of the biomass to a changing environment can be explained also as a separated response of two subpopulations reacting at different speeds to the environmental change.³¹

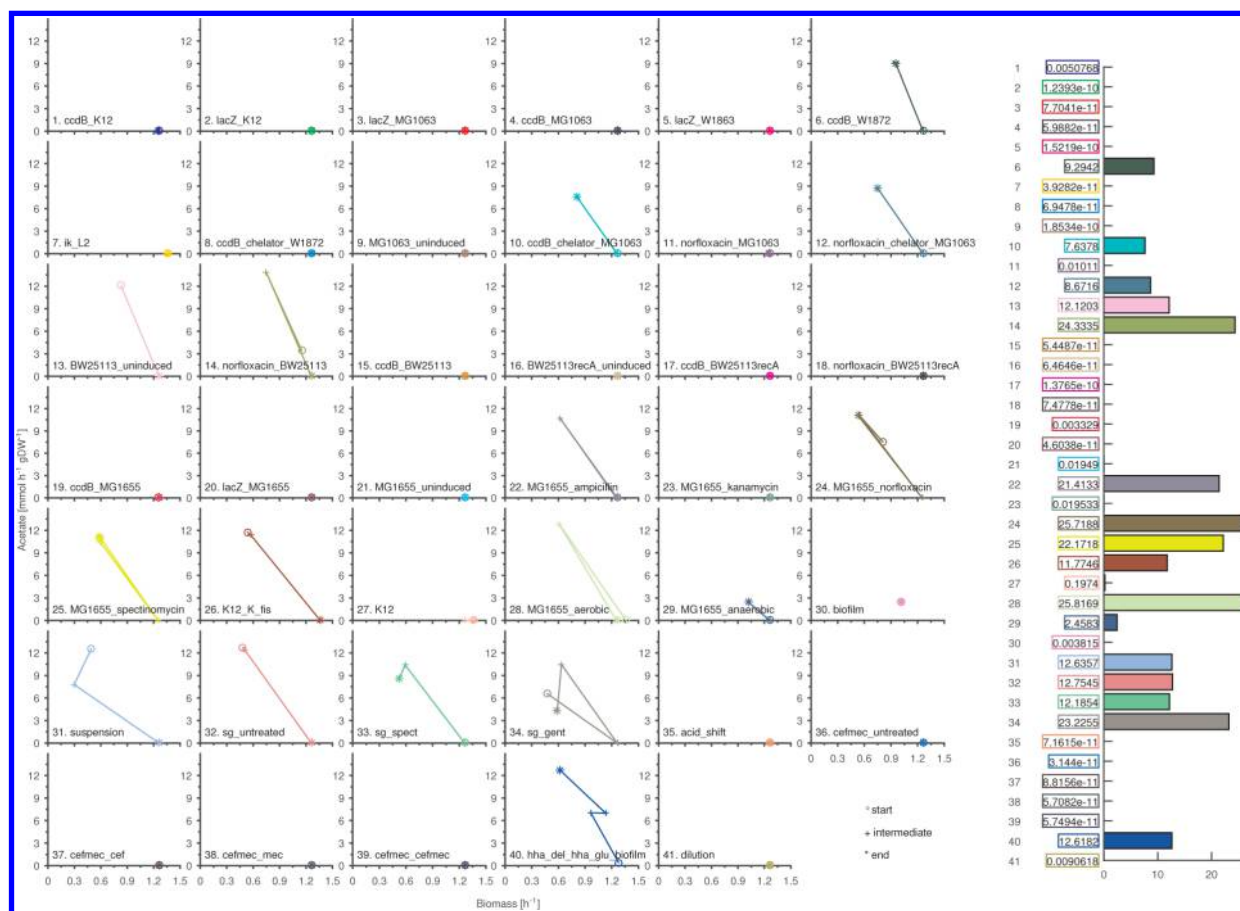


Figure 5. Acetate production/assimilation and biomass produced by *Escherichia coli* under 41 different environmental conditions. We used a set of 164 expression arrays consisting of 41 conditions with four measurements each. Growth conditions include pH changes, antibiotics, genetic perturbations, heat shock, different growth media, carbon source, and oxygen and glucose concentrations (see Supporting Information for further details). Some conditions show quick metabolic rearrangement during growth, whereas under other conditions, the bacterium metabolism remains stable. In the right panel, we show the Euclidean distance covered by each of the 41 conditions in the biomass-acetate space during the four time steps. The conditions whose bars are not shown have a negligible (less than 10^{-9}) distance covered in the acetate-biomass space during the four time steps.

Pathway activation shows an apparent progress over time under the aerobic condition shown in Figure 6a, whereas the anaerobic activation is more static (Figure 6b). As expected, the nucleotide salvage pathway (PID:5) highly responds to the environment where oxygen was present, whereas the valine, leucine, and isoleucine metabolism pathway (PID:17) and alanine and aspartate metabolism (PID:25) are less active. In contrast, all of these pathways are active in response to low-oxygen environments and maintain their activity over time. These results support the inferred cross-correlation between two communities of PID:5 and PID:17 linked by the transcription factor called leucine-responsive regulatory protein (Lrp),²⁸ which is designated as a global transcription factor in *E. coli*.³² A recent experiment confirmed that the activity of Lrp decreases as aerobiosis increases.³³ This may explain the mechanism of the inactive PID:17 after the exposure to oxygen.

In addition, we observed that the cysteine metabolism pathway (PID:21) was activated under the anaerobic condition and lasted for three time steps before it was deactivated in the last time point. The case of cysteine has long been studied in bacteria: although cysteine residues of FNR, another global transcription factor in *E. coli*,³² are alkylated with iodoacetate under permeabilized aerobic or anaerobic conditions, the process takes 50 min in anaerobic bacteria and 6 min in

aerobic bacteria.³⁴ Thus, we could not observe that the cysteine metabolism was active at any time steps after 6 min in aerobic bacteria, but we could observe the activation of the cysteine pathway at the first three time frames within the first 50 min under anaerobic conditions.

Different levels of glucose uptake also change pathway activities over time, as shown in Figure 6c,d. At the early stage of glucose prevalence, the methylglyoxal metabolism pathway (PID:12) was activated, unlike when the bacterium was starved of glucose. Methylglyoxal (MG) is usually synthesized under conditions with low phosphate and high dihydroxyacetone phosphate (DHAP), an environment that occurs most frequently under high-glucose settings.³⁵ A recent experiment confirmed that the increase of glucose uptake rates results in the temporary excretion of methylglyoxal synthase (MgsA).^{36,37} As MG accumulation will lead to cell death, *E. coli* requires a mechanism for MG degradation.³⁷ The detoxification of methylglyoxal includes the conversion MG to S-lactoyl glutathione and then to D-lactate by glyoxalase enzymes I and II.³⁷ This procedure has also been presented to be the predominant MG detoxification system in *E. coli*.^{37,38} This exposition also endorses our discovery about the modest correlation (≈ 0.05) between the methylglyoxal metabolism pathway (PID:12) and the glyoxalase metabolism pathway

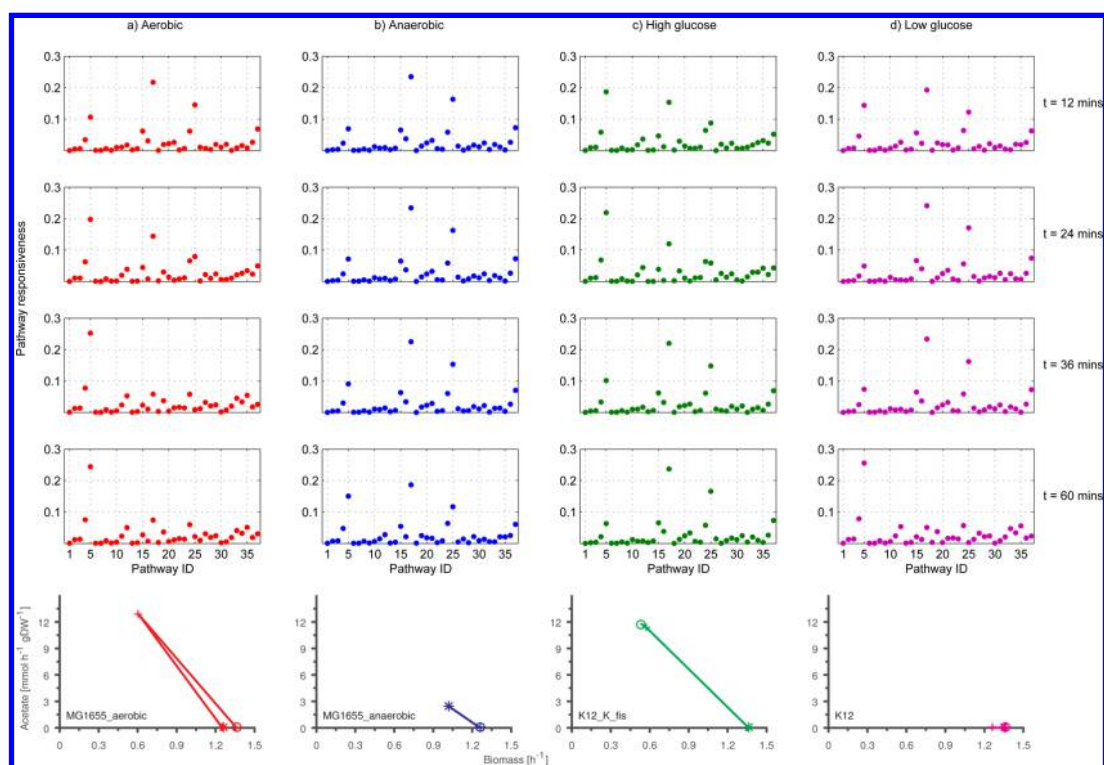


Figure 6. Pathway responsiveness in four conditions: (a) aerobic, (b) anaerobic, (c) high glucose, and (d) low glucose at four time steps. We performed the Bayesian factor modeling on the time-course flux rate responses sharing the same underlying cross-correlations. As a result, pathway responsiveness indicates how much a pathway is likely to be responsive to a given condition at a given time. The pathway responsiveness plots provide us the comprehensive interpretation of the *E. coli* progression of phenotypic behavior in response to each condition, as shown in the plots at the bottom. Specifically, conditions with large variations in the biomass and acetate production are also likely to cause large variation in the pathway responsiveness.

(PID:35), which appears at the top 10% of the inferred sparse cross-correlation network.

3.4. Conclusions. As a result of many recent research efforts to elucidate the relation between genotype and phenotype, we currently have models for a better understanding of the individual components, but we arguably have a less clear picture of the interactions between the biological components that result in a given phenotype.¹⁰ We still have, moreover, limited knowledge about how to use these models to predict a phenotypic response to a changing environmental condition, due to the lack of comprehensive data across different conditions and accurate training processes performed on the models.³⁹ Probabilistic, sometimes rare interactions between molecules and metabolic activation depend on external conditions and may change over time. These interactions and active components give rise to important effects in the bacterial physiology, such as nonlinear activation of toggle switches or master regulators.

When a particular bacterial phenotype has to be achieved, some pathways are required to respond more than others. Our idea is to analyze a compendium of experimental conditions to investigate the combinations of pathway activation that will allow the bacterium to mimic the behavior of the desired phenotype. In order to map the environmental changes to the *E. coli*, we started from the most recent genome-scale metabolic reconstruction,²⁰ and we used bilevel flux-balance analysis to modify the constraints on the metabolic fluxes according to the gene expression profile associated with each condition. Each environmental condition is converted into a flux profile and mapped to a single point in a bidimensional objective space,

therefore translating dynamic genetic activities into dynamic reactions fluxes. (In this article, we focused on the acetate-biomass space, but the methodology is readily applicable to any multidimensional space by extending bilevel FBA to many-level FBA.)

At this step, thousands of reaction flux rates for each experimental condition would need a lot of expertise and manual work for their interpretation. We therefore summarized the reaction fluxes by developing a Bayesian factor model able to identify the *pathway responsiveness*, representing the responsive degree of each pathway under each environmental condition. Our method is also able to achieve a systematic prediction of *E. coli* metabolic pathway responses to time-varying signals. The Bayesian factor model simultaneously elucidates all of the pathway–pathway interactions (pathway cross-correlations), which are also the underlying process behind the pathway activation at each time step. While the activation of some metabolic pathways is kept at the same level, other pathways fluctuate as part of the global response to the fluctuating environment.

While the cross-correlations are considered an intrinsic property of the *E. coli* metabolic network, and thus being computed globally, the degrees of responsiveness depend on the particular environmental conditions at each time step. This characterizes the temporal progression of pathway activation, throughout the time series, in response to given stimuli. Instead of considering a single condition at a time, performing the analysis across all conditions provides insights into pathway connectivity and pathway islands that rarely coactivate with others. Pathway activation profiles allow different conditions in

which the *E. coli* responds similarly to be clustered. This is also advantageous for discovering alternative antibiotic treatments by replacing stimuli with different chemicals.⁴⁰ Many interesting applications can be implemented from the particular pathway cross-correlations predicted from a set of environmental experiments. For instance, they facilitate the prediction of bacterial behaviors in specific situations involving reciprocal action or influence between different organisms, e.g., the interaction between bacteria and plants in mycorrhiza or sepsis and health conditions (e.g., gut microbiota). Our results can also help to shed light on why different conditions can show the same response in a given multiobjective output space. Finally, assessing the pathway correlations with our framework can indicate an *operating distance* between pathways, thus enhancing the current knowledge of the metabolic network and providing foundations of methodological value for analyzing multiomic data.

■ ASSOCIATED CONTENT

● Supporting Information

Table S1: Flux rates obtained as output of the augmented FBA for the 466 experimental conditions. Table S2: Pathway cross-correlations inferred by the Bayesian factor model. Table S3: Pathway responsiveness to the 466 experimental conditions and the 41 conditions at four time steps, resulted from the Bayesian factor modeling; Code S1: MATLAB source code. The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/sb5003407.

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Notes

The authors declare no competing financial interest.

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