

Layered Synthetic Biomolecular Systems

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Decomposition in terms of original variables

Decompose the stoichiometry

$$S = S^1 + \dots + S^L$$

System dynamics:

$$\dot{x}(t) = Sv(x)$$

$$x(0) = x_0$$

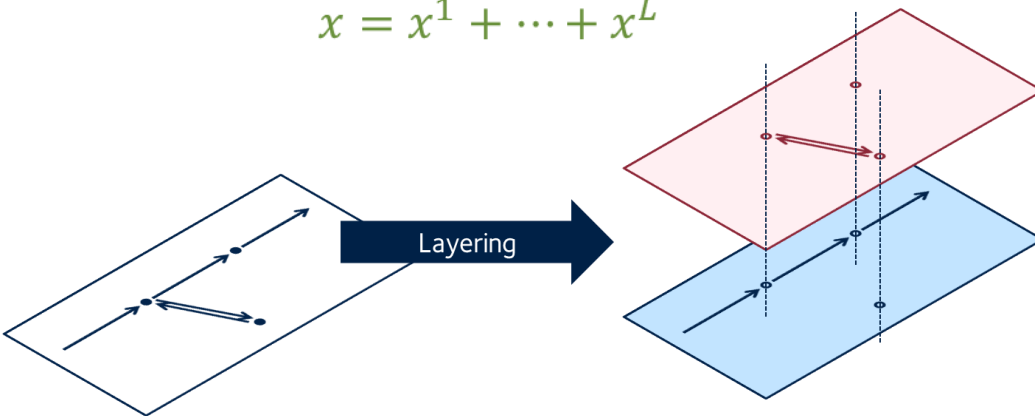
Layered dynamics:

$$\dot{x}^i(t) = S^i v(x^1 + \dots + x^L)$$

$$x^i(0) = x^i(0)$$

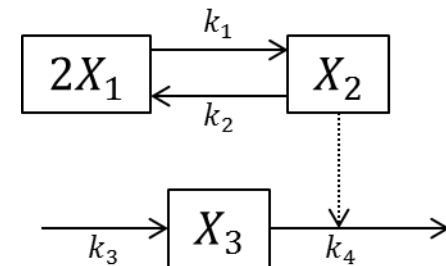
Recompose the layered states

$$x = x^1 + \dots + x^L$$



Biological Network ODE Model:

$$\dot{x} = Sv(x)$$



Concentration vector:

$$x = [x_1, x_2, x_3]^T$$

Flux vector:

$$v(x) = [k_1(x_1)^2, k_2x_2, k_3, k_4x_2x_3]^T$$

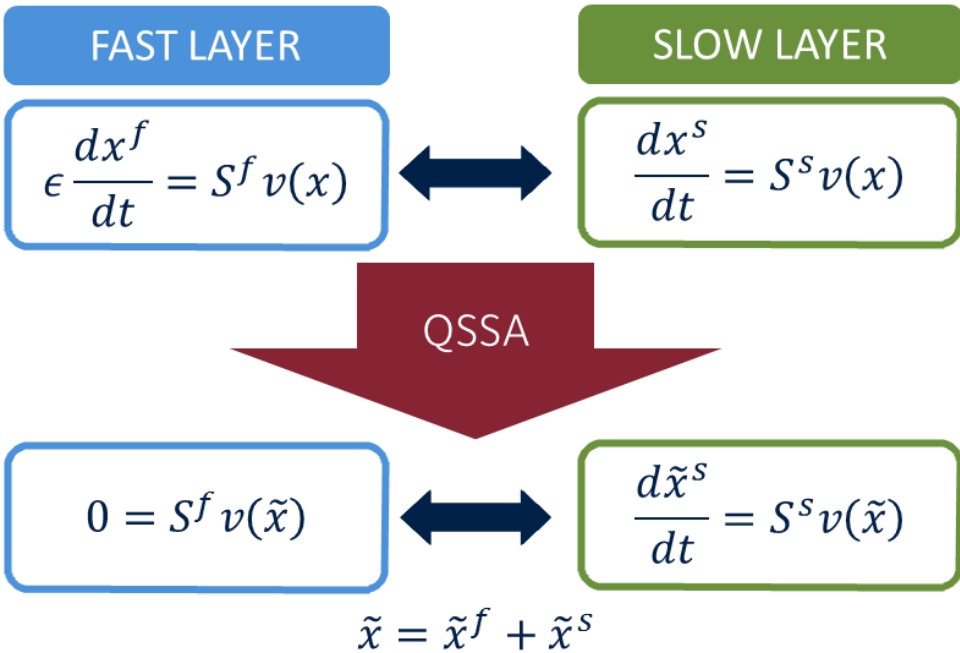
Stoichiometric matrix:

$$S = \begin{bmatrix} -2 & 2 & 0 & 0 \\ 1 & -1 & 0 & 0 \\ 0 & 0 & 1 & -1 \end{bmatrix}$$

Key question – how to decompose? Clearly this depends on the application. In the following example, reactions classed as fast or slow. Normally, singular perturbation requires transformation, but we can keep this system in its original variables by layered decomposition.

Layered Singular Perturbation

$$\dot{x} = \frac{1}{\epsilon} S^f v(x) + S^s v(x) \text{ with } \epsilon \ll 1$$



$$X_1 \overset{\sim 1/\epsilon}{\longleftrightarrow} X_2 \overset{\sim 1}{\longleftrightarrow} X_3$$

$$\dot{x} = \begin{bmatrix} -1 & 1 & 0 & 0 \\ 1 & -1 & -1 & 1 \\ 0 & 0 & 1 & -1 \end{bmatrix} \begin{bmatrix} k_1 x_1 / \epsilon \\ k_{-1} x_2 / \epsilon \\ k_2 x_2 \\ k_{-2} x_3 \end{bmatrix}$$

The diagram shows two planes representing the fast and slow manifolds. The fast manifold is a blue plane and the slow manifold is a green plane. They are separated by a vertical dashed line. Arrows indicate the direction of flow on each manifold. The matrices S^f and S^s are given as:

$$S^f = \begin{bmatrix} -1 & 1 & 0 & 0 \\ 1 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

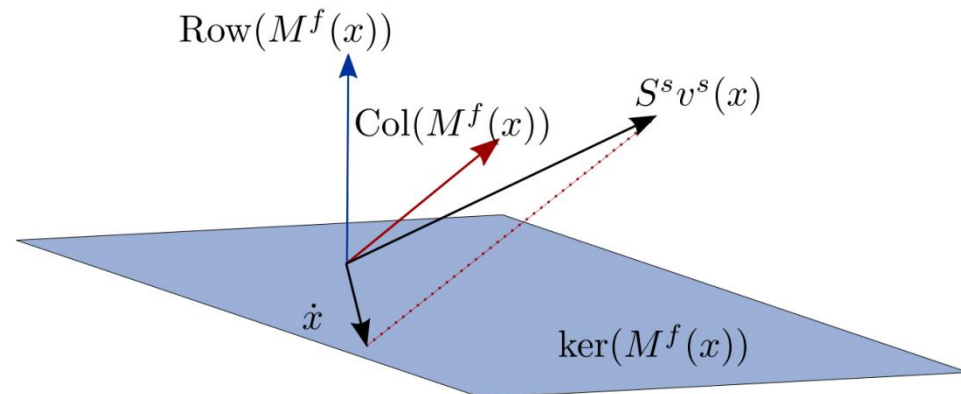
$$S^s = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 1 \\ 0 & 0 & 1 & -1 \end{bmatrix}$$

Original dynamics:

$$\dot{x} = \frac{1}{\epsilon} S^f v(x) + S^s v(x)$$

Approximated dynamics:

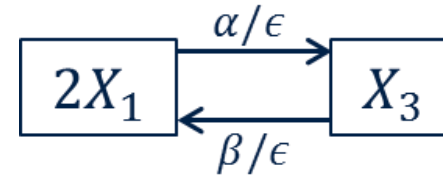
$$\dot{\tilde{x}} = \left(I + M^f(\tilde{x}) \right) S^s v(\tilde{x})$$



Dynamics under Nonlinear, Tuneable Constraints

Gene Module 1

$$\dot{x}_1 = \alpha_1 - \delta_1 x_1 + R_1(x)$$



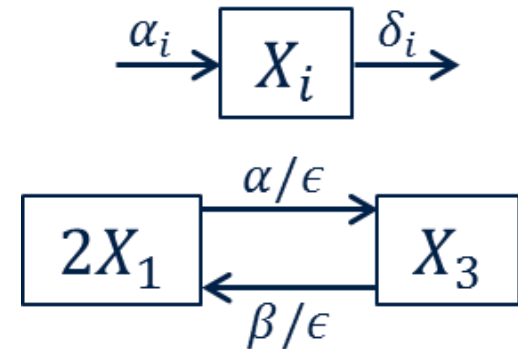
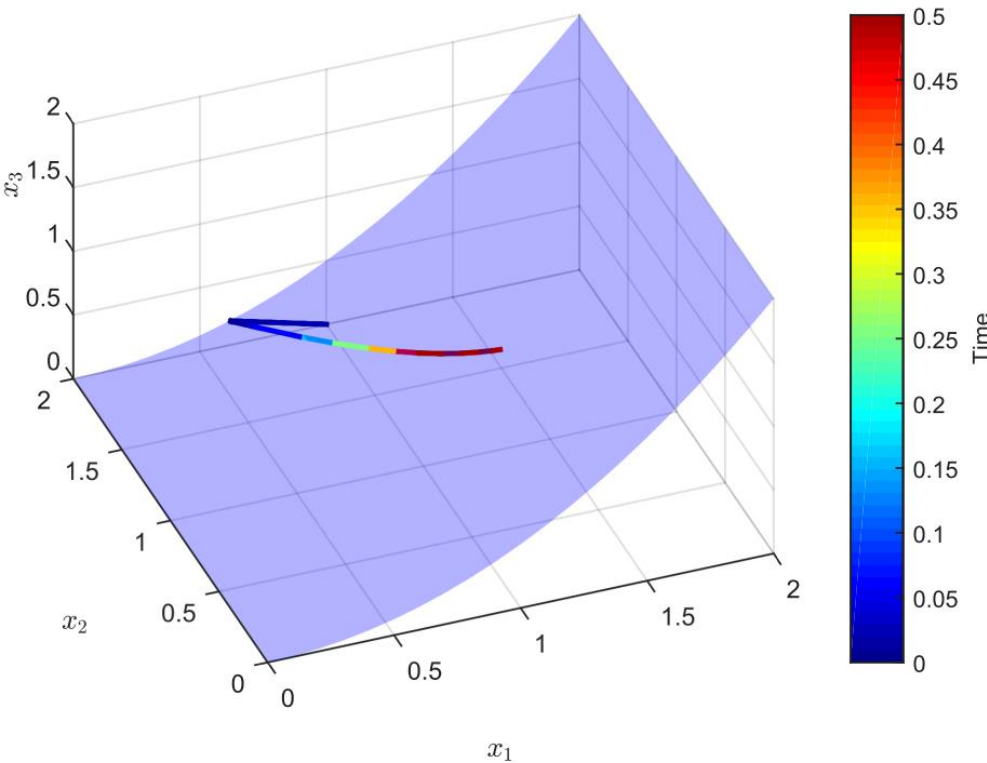
The genetic layer is designed by $R_i(x)$ while the fast PIN (i.e. nonlinear constraint) is tuned separately.

Gene Module 2

$$\dot{x}_2 = \alpha_2 - \delta_2 x_2 + R_2(x)$$

Gene Module 3

$$\dot{x}_3 = \alpha_3 - \delta_3 x_3 + R_3(x)$$



$$S = \begin{bmatrix} 1 & 0 & 0 & -2 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 \end{bmatrix}$$