A NOVEL TECHNIQUE FOR MODEL REDUCTION OF BIOCHEMICAL REACTION NETWORKS

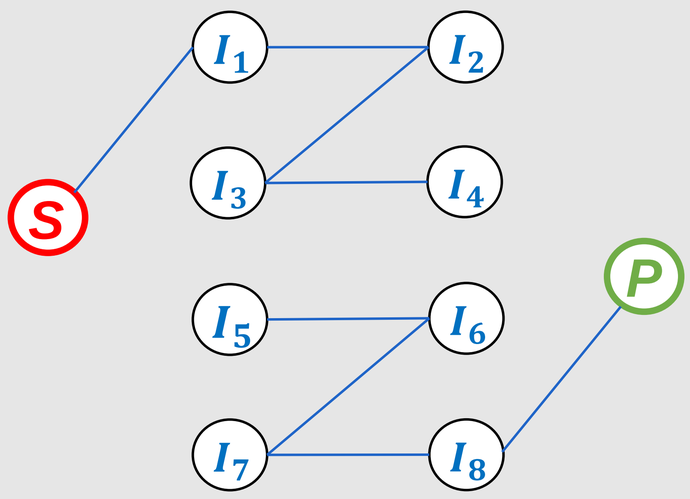
Manvel Gasparyan, Arnout Van Messem, Shodhan Rao

Ghent University Global Campus, Center for Biotech Data Science

INTRODUCTION

THE BALANCE LAWS

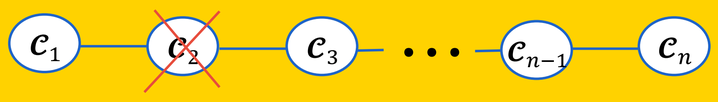
$$\dot{x} = S\vartheta(x)$$



Biochemical reaction network containing
10 complexes
8 reversible reactions
2 linkage classes

Rao Method [1]

Selecting complexes to be deleted from a single linkage classes in such a way that the behavior remains close to the original one



Computing the Schur complement of the weighted Laplacian matrix

Reducing Models

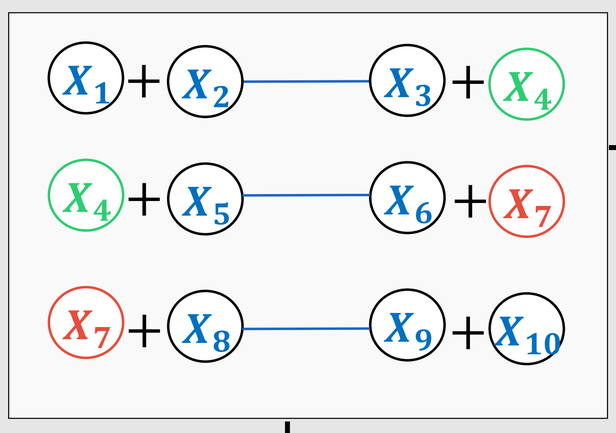
- Extremely huge number of variables
- Identifying parameters is enormously hard
- Requires large experimental datasets
- Not all of the species' concentrations can be measured

Necessity of Reducing Models →
- Less parameters
- Preserving the original behavior

Reduced Network After Deleting c_2

- Remaining reaction fluxes are the same as the original
- Less variables and parameters

NEW APPROACH FOR MODEL REDUCTION OF BIOCHEMICAL REACTION NETWORKS



Balance Laws

$$\dot{x}_1 = -\vartheta_1 \qquad \dot{x}_2 = -\vartheta_1$$
$$\dot{x}_3 = \vartheta_1 \qquad \dot{x}_4 = \vartheta_1 - \vartheta_2$$
$$\dot{x}_5 = -\vartheta_2 \qquad \dot{x}_6 = \vartheta_2$$
$$\dot{x}_7 = \vartheta_2 - \vartheta_3 \qquad \dot{x}_8 = -\vartheta_3$$
$$\dot{x}_9 = \vartheta_3 \qquad \dot{x}_{10} = \vartheta_3$$

Law of the Mass Action Kinetics

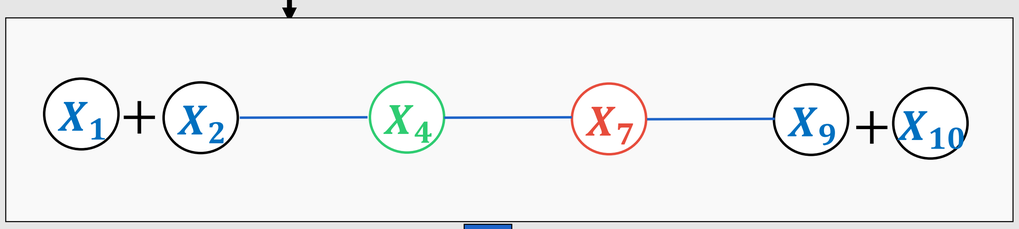
$$\vartheta_1(x) = k_1 x_1 x_2 - k_{-1} x_3 x_4$$
$$\vartheta_2(x) = k_2 x_4 x_5 - k_{-2} x_6 x_7$$
$$\vartheta_3(x) = k_3 x_7 x_8 - k_{-3} x_9 x_{10}$$

Conservation Laws

$$x_3 = C_1 - x_1$$
$$x_5 = C_2 + x_2 + x_4$$
$$x_6 = C_3 + x_7 + x_9$$
$$x_8 = C_4 - x_{10}$$

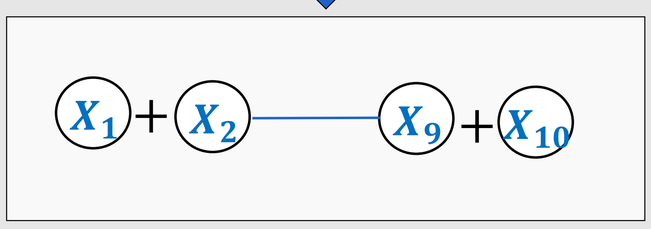
Reducing reaction network using the conservation laws obtained from the balance laws

Reaction fluxes after rewriting the network



$$\bar{\vartheta}_1(x) = k_1 x_1 x_2 + k_{-1} x_1 x_4 - k_{-1} C_1 x_4$$
$$\bar{\vartheta}_2(x) = k_2 x_2 x_4 - k_{-2} x_7 x_9 + k_2 x_4^2 - k_{-2} x_7^2 + C_2 k_2 x_4 - C_3 k_{-2} x_7$$
$$\bar{\vartheta}_3(x) = C_4 k_3 x_7 - k_3 x_7 x_{10} - k_{-3} x_9 x_{10}$$

Deleting the intermediate complexes X_4 and X_7 using the Rao method [1]



Remark

Substitution of x_3, x_5, x_6 and x_8 in the expression of the vector ϑ allows us to rewrite the model as a single linkage class.

[1] Rao S., van der Dchaft A., Eunen K. V., Bakker B., and Jayawardhana B., "A model reduction method for biochemical reaction networks", BMC Systems Biology, 2014, 8, 1--17.

Contact

manvel.gasparyan@ghent.ac.kr

Ghent University Global Campus

@ugentkorea

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