

## Dynamic analysis of metabolic networks for ethanol production in *Saccharomyces cerevisiae*

박창훈<sup>1</sup>, 원왕연<sup>1</sup>, 이광순<sup>1</sup>, 이진원<sup>1,2,\*</sup>  
<sup>1</sup>서강대학교; <sup>2</sup>서강대학교 바이오융합사업단  
(jinwonlee@sogang.ac.kr\*)

The data of enzymatic kinetic related to carbohydrate metabolic network of *Saccharomyces cerevisiae* are based on literature and web database. Kinetics of several specific enzymes that have particular impedance were also studied. In addition, the new enzyme kinetics from the literature, enables the experimenter to acquire more accurate design model which has higher resemblance with the actual cell metabolism.

MATLAB were used as a simulator. Newton method was mainly used to derivative calculation in MATLAB, and LSDOA(Livermore Solver of Ordinary Differential Equation) was mainly used to solve ODE(Ordinary Differential Equation) in MATLAB. The merit of data provided by MATLAB is that it is easy to read kinetics information of metabolites in timescale, and also the information of MCA(metabolic control analysis).

The key factor of ethanol production in *Saccharomyces cerevisiae* was studied by measuring the elasticity coefficient and parameter elasticity. In order to obtain the quantitative value of the parameter elasticity coefficients the euclidean norm which base on vector norm were used.