



# Simulating Plant Metabolic Pathways with Enzyme-Kinetic Models using Semi-Analytical Method



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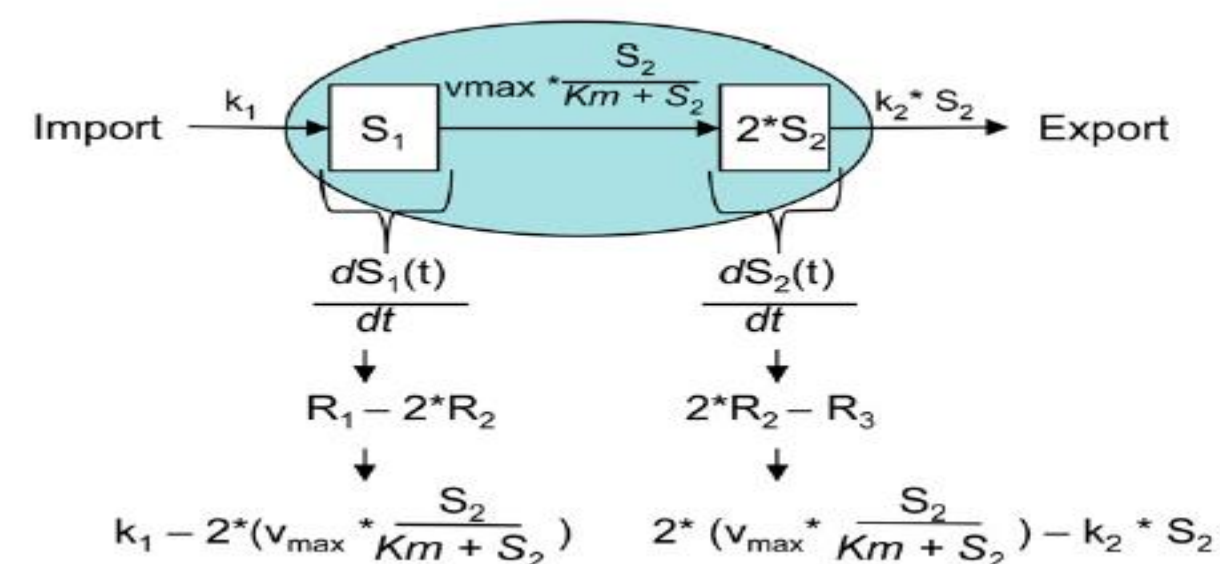
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## Introduction

The biotechnology potential is increasing exponentially with identification of plants, isolation of novel compounds and their pathways and the molecular and biochemical characterization of cellular components.



**Figure 1.0:** Schematic of the Differential equation for the change in metabolite concentrations,  $S_1$  is the substrate and  $S_2$  is the product (Schallau and Junker, 2010)

The Differential Transform Method (DTM) is an iterative procedure for obtaining analytic Taylor series solutions of differential equations.

This study describe for the first time an analytical solution to plant metabolic pathway with enzyme kinetic models using DTM

## Abstract

**Background:** Plant metabolites are exploited for biotechnological, biomaterial and recently nanomedicine applications. The dynamics of plant metabolic networks are predominated by the activities of enzymes. These enzymes regulates metabolic pathway via a concerted interplay of many biochemical reactions necessary to sustain life. Differential mathematical modeling of metabolic pathway is often closely associated with changes in metabolite concentrations that are described by enzyme kinetic rate laws, such as the Michaelis-Menten equation.

**Materials and Methods:** metabolic pathway with enzyme kinetic model was adopted and Differential Transform Spectra was formulated, solved with Mathematica® Software

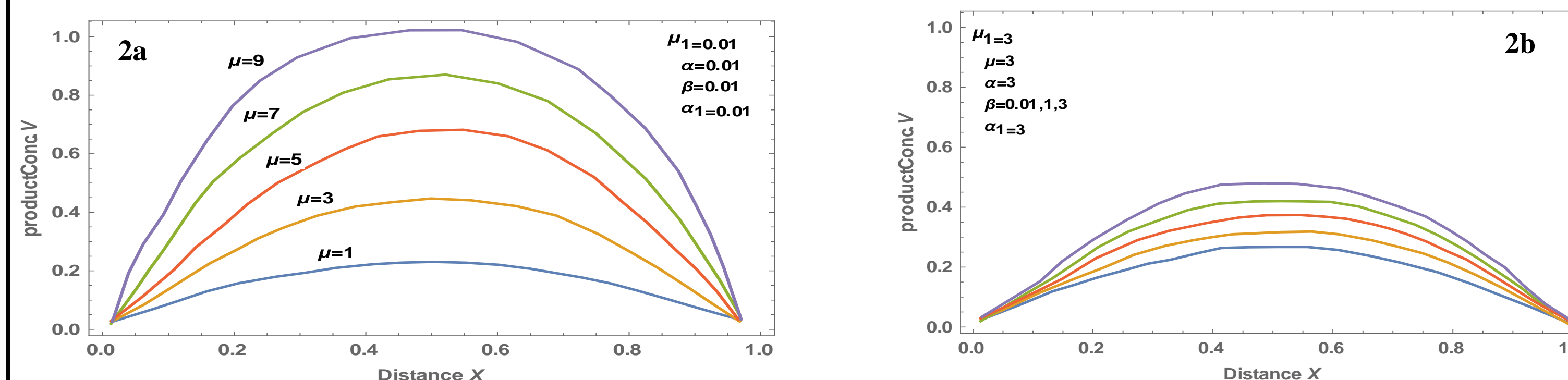
**Results and Conclusion:** This study reveals analytical solutions for the models of the concentration of substrate and product using differential transformation method (DTM) for all values of reaction-diffusion parameters. It is hoped that the simulation results will be useful for improving the productivity of meaningful plant metabolites for medicinal and industrial use.

**Keywords:** Plant Metabolic Pathways, Enzymes, Mathematical Modeling, Differential Transformation Method, Simulation

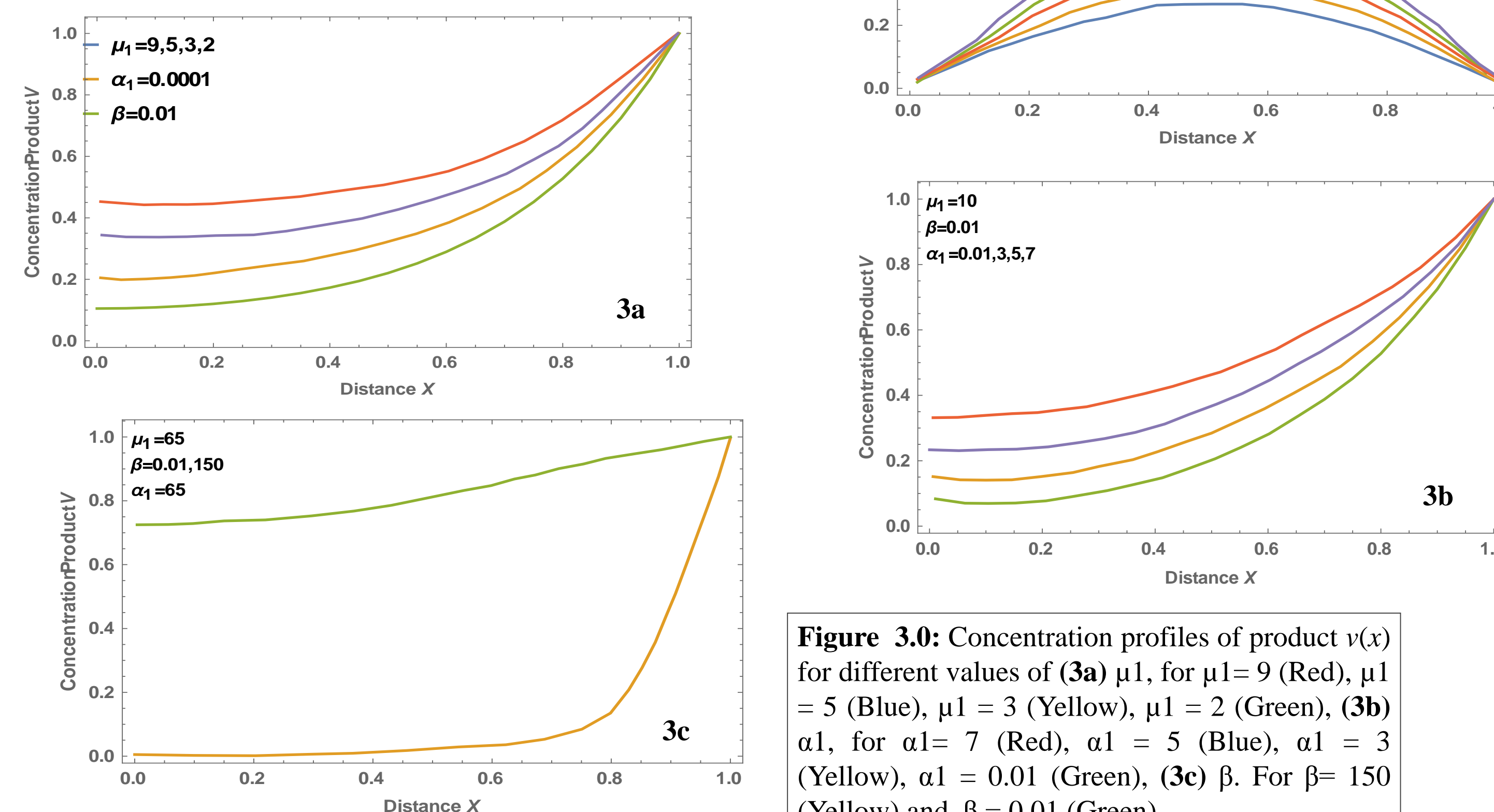
## Results & Discussion

The DTM spectra is given as :  $(h+2)U[h+2] = -\mu + \frac{\alpha V[h]}{1+\beta V[h]}$  (9),  $(h+2)V[h+2] = +\mu_1 V - \frac{\alpha_1 V[h]}{1+\beta V[h]}$  (10)

Mathematica® Software (Wolfram Inc. USA) was used to solve the DTM spectra and run simulation.



**Figure 2.0:** Concentration profiles of substrate  $u(x)$ , for different values of (2a)  $\mu$  (2b)  $\beta$ , for  $\beta = 7$  (Dark blue),  $\beta = 5$  (Green),  $\beta = 3$  (Red),  $\beta = 1$  (Yellow),  $\beta = 0.01$  (Light Blue) and (2c)  $\beta$ , for  $\beta = 7$  (Dark blue),  $\beta = 5$  (Green),  $\beta = 3$  (Red),  $\beta = 10$  (Yellow),  $\beta = 100$  (Light Blue).



**Figure 3.0:** Concentration profiles of product  $v(x)$  for different values of (3a)  $\mu_1$ , for  $\mu_1 = 9$  (Red),  $\mu_1 = 5$  (Blue),  $\mu_1 = 3$  (Yellow),  $\mu_1 = 2$  (Green), (3b)  $\alpha_1$ , for  $\alpha_1 = 7$  (Red),  $\alpha_1 = 5$  (Blue),  $\alpha_1 = 3$  (Yellow),  $\alpha_1 = 0.01$  (Green), (3c)  $\beta$ . For  $\beta = 150$  (Yellow) and  $\beta = 0.01$  (Green).

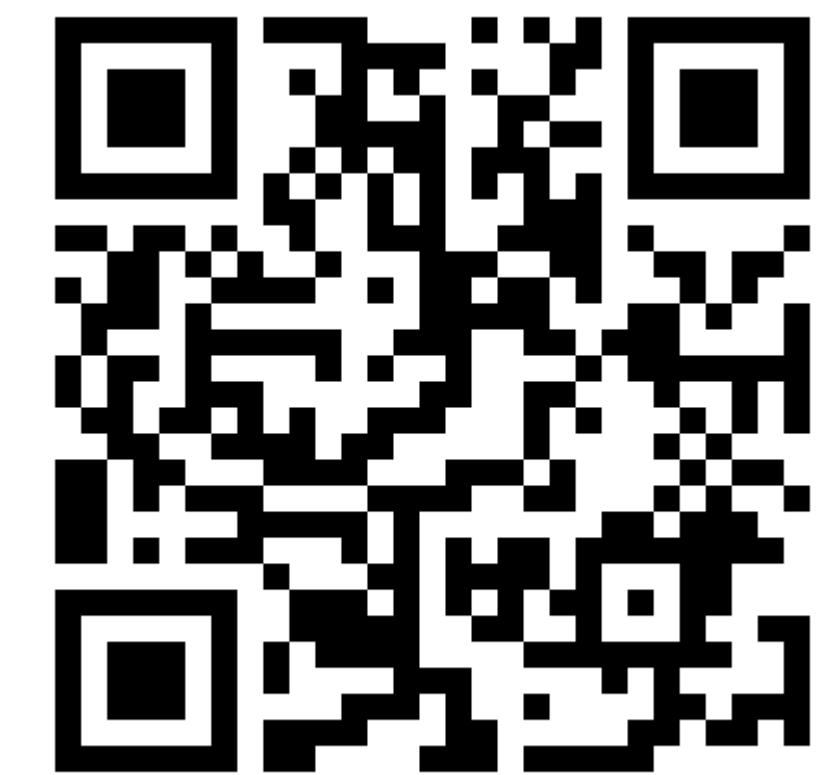
## Conclusion

In this study, the space dependent and time independent, non-linear reaction/diffusion equation has been formulated and solved analytically.

An approximate analytical expression for the concentration of substrate and product are obtained by using the Differential Transformation method. The DTM was used in a direct way without using linearization, perturbation or restrictive assumptions.

The primary result of this work is simple approximate calculation of concentration for all possible values of parameters.

We conclude that the DTM can be easily extended to find the solution of all other non-linear reaction diffusion equations in metabolic modelling for various complex boundary conditions.



## Materials and Methods

### Mathematical Formulation of the Problems

Plant metabolic pathway with enzyme-kinetic models equation was adopted from Rajendran and Deena, 2015. Where  $S$  and  $P$  are the concentrations of the two metabolites, in equations (1), (2), (3) and (4).  $R_1, R_2, R_3, D_s, D_p, V_{max}, K_M, K_p$ , and  $K_2$  are all embedding parameters.

$$D_s \frac{d^2 S_1}{dX^2} + R_1 - 2R_2 = D_s \frac{d^2 S_2}{dX^2} + k_1 - 2 \left( V_{max} \frac{S_2}{K_M + S_2} \right) = 0 \quad (1)$$

$$D_p \frac{d^2 S_2}{dX^2} + 2R_2 - R_3 = D_p \frac{d^2 S_2}{dX^2} + 2 \left( V_{max} \frac{S_2}{K_M + S_2} \right) - k_2 S_2 = 0 \quad (2)$$

$$\text{and } D_s \frac{d^2 S}{dX^2} + k_1 - 2V_{max} \frac{P}{K_M + P} = 0 \quad (3)$$

$$D_p \frac{d^2 P}{dX^2} + 2V_{max} \frac{P}{K_M + P} - k_2 P = 0 \quad (4)$$

$$\text{initial and boundary conditions: } X=0: S=0, \frac{dP}{dX} = 0 \quad (5)$$

$$X=L: S=0, P=P_0 \quad (6)$$

Equations (3) and (4) are expressed as the dimensionless forms in (7) and (8) respectively, where  $\alpha, \alpha_1$  and  $\beta$  are the saturation parameters,  $x$  is the dimensionless distance,  $m_1 = \mu_1$  and  $m = \mu$  are diffusion parameters,  $u$  and  $v$  are the dimensionless concentration.

$$\frac{d^2 u}{dx^2} + m - \frac{\alpha v}{1 + \beta v} = 0 \quad (7), \quad \frac{d^2 v}{dx^2} - m_1 v + \frac{\alpha_1 v}{1 + \beta v} = 0 \quad (8)$$

## References

1. Abdul-Monim Batiha and Belal Batiha (2011) "Differential Transformation Method for a Reliable Treatment of the Nonlinear Biochemical Reaction Model" *Advanced Studies in Biology*, Vol. 3, no. 8, 355 - 360
2. Rajendran L, Deena N (2015) Simulating Plant Metabolic Pathways with Enzyme-Kinetic Models Using a New Approach to Homotopy Perturbation Method. *J Material Sci Eng 4*: 167
3. Rohwer JM (2012) Kinetic modeling of plant metabolic pathways. Oxford University Press, Oxford.
4. Schallau K, Junker BH (2010) "Simulating Plant Metabolic Pathways with Enzyme-Kinetic Models", *Plant Physiology* 152: 1763-1771.

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