

Project: BMBF SysCompart
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Description:

The work package 9 within the BMBF funded joint research project SysCompart focuses on the quantitative evaluation of the compartmentalization of metabolic pathways. The focus is set on the spatial separation between cytosolic and mitochondrial sub-networks of the central metabolism.

For this purpose, the spatial distribution of mitochondria within the cell and of key enzyme complexes within the mitochondrial matrix is determined using confocal (Fig 1, 2) and STED microscopy (WP 5). The obtained geometries are combined with a previously developed model of the mitochondrial pyruvate dehydrogenase complex that has been extended with respect to regulation by reversible phosphorylation and exogenous co-factors (Fig. 1, Zeng et al., 2002). The combined spatiotemporally resolved model is implemented in VirtualCell (Moraru et al., 2008; National Resource for Cell Analysis and Modeling (NRCAM) - University of Connecticut Health Center).

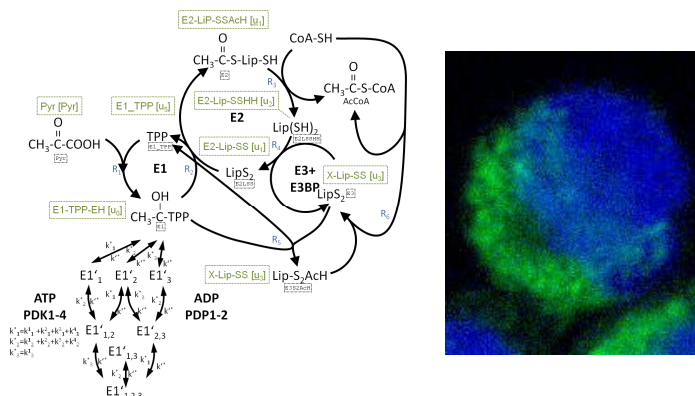


Fig. 1: Left: Reaction graph of the mitochondrial pyruvate dehydrogenase complex (PDC). Right: Confocal image (axial slice) of stained CHO cell.

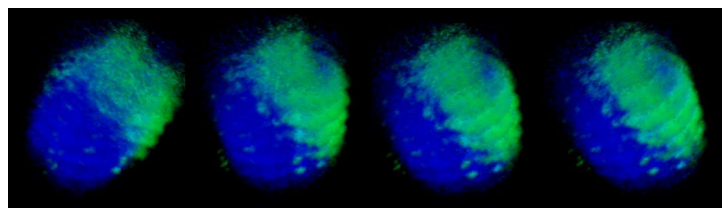


Fig. 2: Three-dimensional distribution of mitochondria (green) in cultured CHO cells. Nuclei are stained blue.

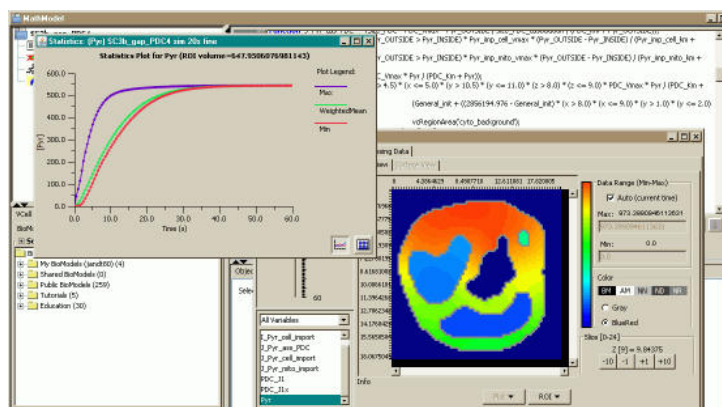


Fig. 3: Implementation in Virtual Cell.

References:

- Zeng AP, Modak J, and Deckwer W. 2002. Nonlinear dynamics of eucaryotic pyruvate dehydrogenase multienzyme complex: decarboxylation rate, oscillations, and multiplicity. *Biotechnol Prog*, 18(6):1265 – 1276.
- Moraru II, Schaff JC, Slepchenko BM, Blinov M, Morgan F, Lakshminarayana A, Gao F, Li Y, and Loew LM. 2008. The virtual cell modeling and simulation software environment. *IET Syst Biol* 2(5):352 – 362.

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