Reconstruction of the carbon metabolism by batch cultures of E. coli strains on variable carbon sources

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E-Cell is a concept of constructing virtual cells on computers. This can be established by the reconstruction and analysis of metabolic and regulatory networks of target cells.

To establish the metabolic network of the target cell, a lot of data about growth and metabolites of the target cell is needed. Escherichia coli is the most widely used prokaryotic system for the synthesis of heterologous proteins. So in silico experiments using E-Cell can be save the time and cost in production of heterologous proteins by Escherichia coli. For in silico experiments, the carbon metabolic network of Escherichia coli is established. Besides glucose central carbon metabolic pathway of Escherichia coli already known, the information about the metabolism of variable carbon sources is needed. In this study, batch fermentations by E.coli XL1-Blue, K12 and BL21 were examined on several carbon sources (glucose, glycerol, acetate, lactate, gluconate and oleic acid) to get the metabolic data.

References

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