Lengauer, Thomas. (ed.) Bioinformatics - From Genomes to Therapies

2007. 1732 pages with 355 figures 134 in color and 56 tables. Hardcover. ISBN: 978-3-527-31278-8 (Wiley-VCH, Weinheim)

Supplementary Material & Errata

Figures 1 and 6 of Chapter 20 "Modeling and Simulating Metabolic Networks" by Stefan Schuster and David Fell were accidentally printed in black and white. Colour versions are available below:



Figure 1 Part of sugar metabolism in various cell types. Abbreviations of metabolite names used in the text: F6P, fructose-6-phosphate; Gluc, glucose; G6P, glucose-6-phosphate, GSH/GSSG, reduced and oxidized forms of glutathione, respectively; Pyr, pyruvate. Red, hexokinase; green, phosphoglucoisomerase; orange, phosphofructokinase; blue (brown), reactions of oxidative (nonoxidative) pentose phosphate pathway.







Figure 6 Scheme of the TCA cycle and gluconeogenesis. Thick arrows represent fluxes that are double as high as through the other reactions. Dashed arrows represent unused enzymes. Abbreviations of metabolites: AcCoA, acetyl-coenzyme A; Cit, citrate; Fum, fumarate; Gly, glyoxylate; IsoCit, isocitrate; OG, oxoglutarate; Oxac, oxaloacetate; PEP, phosphoenolpyruvate; Mal, malate; Pyr, pyruvate; Succ, succinate; SucCoA, succinyl coenzyme A. (A) Situation in mammals. A pathway from acetyl-CoA to glucose seems to exist (solid arrows).

However, Oxac is not stoichiometrically balanced at steady state. (B) Situation in plants and many bacteria, where the TCA cycle involves the glyoxylate shunt, consisting of isocitrate lyase (IcI) and malate synthase (Mas). This allows conversion of acetyl-CoA into glucose at steady state (pathway in blue). (C) Classical TCA cycle (red); pathway of glucose catabolism alternative to the classical TCA cycle (green).

Further material to be added soon.