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Integrative compartmental model of carnitine and its derivatives

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Carnitine is a fundamental compound for humans. Mainly introduced via nutrition, but also synthetized in the body, this metabolite allows the transport of long-chain fatty acids in the mitochondria, where they can undergo β -oxidation. Lately, the attention on carnitine and acyl-carnitine, carnitine derivatives, has increased since it has been proposed that insulin resistance may be linked to incomplete fatty acid β-oxidation and the subsequent increase in acyl-carnitine species in different tissues.

Mathematical modelling can give us a quantitative understanding of specific rates in the carnitine metabolism, e.g. synthesis of carnitine derivatives . Therefore we contribute to the research on carnitine by building a compartmental model for carnitine and its derivatives. This model integrates knowledge about carnitine uptake and synthesis, carnitine distribution and expulsion, and carnitine role in the transport of long-chain fatty acids, therefore covering all the carnitine occurrences in the body. Additionally, the simultaneous comprehension of carnitine and its derivatives enables the model to highlight the role of carnitine concentration as a bottleneck in the transport of the long-chain fatty acids into the mitochondria.

Our model utilizes metabolome datasets publically available in the literature for validation.

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