Abstract: A spatially distributed metabolic model of the liver in fasted, resting state

A spatially distributed model of the liver is proposed that describes the metabolic concentrations and reaction fluxes in the tissue and blood domains. The blood domain equations account for convection, axial dispersion, and blood/tissue transport. The tissue equations account for key metabolic reactions as well as blood/tissue transport. This model deals with spatial distribution via a railway construction, where different stations (tissue compartments) along the blood flow route are modeled by a metabolic pathway network. As the blood flows, the concentrations of the species transported into the tissue by the blood change according to the mass balance equations. This implies that transports vary in space, hence it is necessary to include a differential equation of second order. Discretizing the differential equation generates as many variables as points used in estimation. Therefore, the number of parameters required for model identification is quite large. A recently developed method of statistical Flux Balance Analyis is used to estimate these parameters. This approach is especially useful in this case, as it allows the use of a smoothness prior to account for the continuity of the spatially continuous parameters. Under a Bayesian framework, Gibbs and adaptive sampling algorithms are implemented in order to explore the posterior probability densities of the metabolic fluxes in the tissue, blood concentrations, and transports. The large number of parameters required the utilization of different adaptive sampling techniques, such as Adaptive Hit and Run (AHR) and Adaptive Metropolis Hastings (AM). We compare these algorithms for speed, accuracy and convergence.