Function	Description
monte_carlo	Runs a Monte Carlo simulation of a given model.
parameterize_1comp	Parameterizes the model 1compartment.
parameterize_3comp	Parameterizes the model 3compartment.
parameterize_pbtk	Parameterizes the model pbtk.
parameterize_schmitt	Parameterizes predict_partitioning_schmitt.
parameterize_steadystate	Parameterizes the model 3compartmentss, used in Wetmore *et al.* (2012) and Wetmore (2015).
predict_partitioning_schmitt	Predicts partition coefficients using Schmitt's method (Schmitt 2008b).
solve_1comp	Solves the model 1compartment.
solve_3comp	Solves the model 3compartment.
solve_pbtk	Solves the model pbtk.

Table 5: List of functions in the package – Part II. Models are described in Table 2. Parameters are defined in Table 1. Jarnac and SBML are external languages for systems biology models.