Function	Description
`add_chemtable`	Adds chemical data for HTTK analysis.
`available_rblood2plasma`	Retrieves $R_{blood2plasma}$ (measured preferred over predicted)).
`calc_analytic_css`	Calculates C_{ss} and blood concentrations for the four models used in the package from infusion dosing at a constant rate.
`calc_css`	Calculates the maximum and average steady state concentrations along with the day steady state is reached.
`calc_elimination_rate`	Calculates k_{elim} for a one compartment model due to the liver and kidneys, dividing the total clearance by V_{dist}.
`calc_hepatic_clearance`	Calculates the hepatic clearance for a well-stirred model or other type if specified (Ito and Houston 2004).
`calc_mc_css`	Calculates C_{ss} using Monte Carlo simulation, defaulting to HTTK-Pop simulator (Ring *et al.* 2017).
`calc_mc_oral_equiv`	Calculates an oral equivalent dose using C_{ss} from `calc_mc_css`.
`calc_rblood2plasma`	Calculates the blood:plasma chemical concentration ratio.
`calc_stats`	Calculates the area under the curve, mean, and peak values for the blood or plasma concentration of either a specified chemical or all chemicals for a given simulation.
`calc_total_clearance`	Calculates the total clearance rate for a one compartment model where clearance is equal to the sum of the well-stirred metabolism by the liver and glomerular filtration in the kidneys.
`calc_vdist`	Calculates the one compartment volume of distribution.
`export_pbtk_jarnac`	Exports the model pbtk to Jarnac (Sauro and Fell 2000).
`export_pbtk_sbml`	Exports the model pbtk to SBML (Hucka *et al.* 2003).
`get_cheminfo`	Provides a list of CAS numbers along with compound names, logP, pKa, molecular weight, Cl_{int} and its p value, and f_{ub} if specified for chemicals with sufficient data for a given model.
`get_httk_params`	Converts table generated by `httkpop_generate` to the corresponding table of httk model parameters.
`get_rblood2plasma`	Retrieves *in vivo* $R_{blood2plasma}$.
`get_wetmore_cheminfo`	Provides the names and CAS numbers of chemicals with information from Wetmore *et al.* (2012), Wetmore *et al.* (2013), and Wetmore (2015).
`get_wetmore_css`	Retrieves C_{ss} as a result of oral infusion dosing from Wetmore *et al.* (2012), Wetmore *et al.* (2013), and Wetmore (2015).
`get_wetmore_oral_equiv`	Calculates an oral equivalent dose using C_{ss} from Wetmore *et al.* (2012), Wetmore *et al.* (2013), and Wetmore (2015).
`httkpop_generate`	Generates a virtual population.
`lump_tissues`	Lumps tissue flows, volumes, and input partition coefficients based on specified grouping.

Table 4: List of functions in the package – Part I. Models are described in Table 2. Parameters are defined in Table 1. Jarnac and SBML are external languages for systems biology models.