Optimal Microsampling design non parameteric analysis

library(Pkdesign)  
paramList <- list()  
paramList$pkParameters <- getParameters( getExamplePkModel() )

## Pharmacokinetic model

# For debugging  
knitr::kable( paramList$pkParameters , eval = TRUE )

|  |  |  |  |
| --- | --- | --- | --- |
| parameter | value | coeffVariation | explanation |
| F | 1.00 | 0.0 | bioavailability |
| volumePlasma | 10.00 | 0.2 | volume of the central compartment (plasma) |
| Cld | 15.00 | 0.2 | distribution parameter between central and peripheral Compartment expressed in volume per time unit |
| volumeTissue | 15.00 | 0.2 | volume of the peripheral compartment (tissue) |
| VmaxAbsorption | 5.00 | 0.2 | maximum absorption rate ( absolute rate is rate per dose x dose) |
| kappaMMAbsorption | 2.50 | 0.2 | Michaelis-Menten constant for absorption |
| KaConstant | NA | 0.2 | constant absorption rate per unit of dose (overrides Michealis-Menten kinetics) |
| VmaxClearance | 30.00 | 0.2 | maximum clearance rate (absolute rate is rate per concentration x |
| kappaMMClearance | 0.25 | 0.2 | concentration) |
| ClConstant | NA | 0.2 | constant clearance rate ( overrides Michealis-Menten kinetics ) |

### Input parameters

### Model kinetics

## Settings

## Optimal design

### Time points

### Scheme