Modeling Transit Compartments with Multiple Doses in Phoenix NLME

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Objective

Savic et al. [1] give a closed-form computation to model absorptive delay through multiple transit compartments, where the number of compartments is a parameter to be estimated. It works for single delta-function inputs sufficiently separated in time. It is desirable to model such absorption in a way that easily handles arbitrary dosing sequences and steady-state determination. This scheme has been incorporated in the Phoenix Modeling Language (PML) as a statement. The fragments below illustrate a first-order model with time-lag and a corresponding transit compartment model:

Simple tlag model:

 $\frac{\text{deriv}(\text{ Aa} = -\text{Aa}*\text{Ka})}{\text{dosepoint}(\text{ Aa}, \frac{\text{tlag}}{\text{tlag}} = \text{mtt})}$ $\frac{\text{deriv}(\text{ A1} = \text{Aa}*\text{Ka} - \text{A1}*\text{Ke})}{\text{deriv}(\text{ A1} = \text{Aa}*\text{Ka} - \text{A1}*\text{Ke})}$

Transit compartment model:

transit(Aa, mtt, n, out = -Aa*Ka)
dosepoint(Aa)
deriv(A1 = Aa*Ka - A1*Ke)

Methods

It is typical to model absorption delay by a simple time lag, but a useful alternative is to model the delay as a sequence of transit compartments terminating in an absorption compartment. Following Savic et al. [1], a closed form expression for the flow rate into the absorption compartment is given by:

$$\frac{dA_a}{dt} = Dose F k_{tr} \frac{(k_{tr} t)^n}{\Gamma(n+1)} e^{-k_{tr} t}$$
(1)

Where k_{tr} is given in terms of the number of transit stages *n*, and the mean transit time *mtt*:

$$k_{tr} = \frac{n+1}{mtt} \tag{2}$$

This formulation has the advantage that *n* can vary between individuals, and it need not be an integer. However, it has a difficulty that it cannot be used easily with multiple doses unless they are separated by a washout interval. An alternative is to use a sequence of compartments modeled with differential equations, and deliver the dose to an upstream compartment chosen by *n*. If *n* is not an integer, an approximation is to linearly interpolate between the final two transit compartments, as in this diagram, where A_x is an extra compartment: In both models, the lag time and mean transit time are represented by *mtt*. In the transit model there is an additional parameter *n*, where $maxn > n \ge 0$, representing the number of transitions minus one. (*maxn* can be specified by an optional argument, default 50.) *n* functions as a sigmoidicity parameter, analogous to the Hill parameter in a sigmoid Emax model. A simple example is shown below.

🔡 OneSubjectTransit.W	orkflow.New Project (Out of Date)
Window	
Setup Results Verif Main (One Subject) Model Dosing Parameters Parameters Parameters.Mapping Random Effects	Apply 1 test() { 2 transit(A1, mtt, ntr, out = -A1*Ke) 3 dosepoint(A1) 4 C = A1 / V 5 stparm(V = tvV) fixef(tvV = c(, 0.44,)) 6 stparm(Ke = tvKe) fixef(tvKe = c(, 0.7,)) 7 stparm(mtt = tvmtt) fixef(tvmtt = c(0,1,)) 8 stparm(ntr = tvntr) fixef(tvntr = c(0,1,)) 9 error(CEps = 0.542233) 10 observe(CObs = C + CEps)
Population? C Time: 1111 I tvV 1111 I tvKe 1111 I tvKe 1111 I tvmtt 1111	Seneral Parameters Input Options Initial Estimates Run Options № ↓ ▶ IIII / 0.46 x 2.5 IIII / 0.66 x 2- IIII / 0.72 x 15-



and where f = n - [n], and doses are delivered to compartment $A_{[n]}$. However, it is not particularly accurate for non-integer n because it is piecewise linear w.r.t. n and equation (1) is a smooth curve. An alternative is to perform logarithmic interpolation as in this diagram:



Logarithmic interpolation has smaller errors than linear interpolation. Furthermore, the errors are proportional, not a function of time, and they can be exactly corrected by the following function:



Discussion

The advantage of the interpolated transit model is that it can handle arbitrary dosing sequences, including steady-state. A disadvantage is that the size of *n* is limited, because it effectively creates a vector differential equation of size *maxn*, creating a performance cost.

References

[1] R. M. Savic, D. M. Jonker, T. Kerbusch, M. O. Karlsson,
"Implementation of a transit compartmental model for describing drug absorption in pharmacokinetic studies", J. of
Pharmacokinetics and Pharmacodynamics (2007) 34:711-726

$$C(n) = \frac{\Gamma([n] + 1)}{\Gamma(n + 1)} ([n] + 1)^{f}$$

whose graph is as follows:

Interpolation correction factor vs. N



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