

An Interpretation of Transit Compartment Pharmacodynamic **Models As Lifespan Based Indirect Response Models**

Wojciech Krzyzanski

Department of Pharmaceutical Sciences, University at Buffalo, State University New York

Objectives

Transit compartments (TC) models are used to describe pharmacodynamic responses that involve drug action on cells undergoing differentiation and maturation [1-3]. Such PD systems can also be described by lifespan based indirect response (LIDR) models [4]. Our objectives were to determine the lifespan distribution for which the LIDR model coincides with the TC model, to show that if the number of transit compartments n increases to infinity, then the TC model approaches the basic LIDR model with the point lifespan distribution centered at the mean lifespan TR, and to propose a new class of LIDR models for agents acting on the cell lifespan distribution.

Methods

The TC model consists of a series of compartments P_1, \ldots, P_n connected with each other by first-order processes in a catenary manner as shown in Fig. 1. A compartment P_i represents a subset of cells of a mean age i $T_{R'}n$, since the mean transit time through each compartment is T_R/n, if TR denotes the mean cell lifespan. It is assumed that cells are produced at a time dependent zero-order rate $k_{in}(t)$, and the drug affects the transit rates between the compartments. The drug effect is described by a function E(t).

PK/PD Model



$$R=P_1+P_2+...+P_n$$

Fig. 1. Schematic representation of TC model (upper) and basic LIDR model (lower). In both models cells are produced at a zero-order rate that can be affected by drug $k_{ij}(t)$. The transfer rates between the transit compartments are first-order constants n/T_g where n is the number of compartments and T_g is the total mean transit time through all compartments. The cell elimination for the lifespan indirect response model is determined by their time dependent lifespan distribution (t_i). Drug affects both n/T_g and (t_i) via mechanism described by the effect function E(t). The sum of the transit compartments P_1 , P_2 , ..., P_s can be described by a lifespan driven indirect response R.

TC Model

LIDR Model

 $\frac{\mathrm{dR}}{\mathrm{dt}} = k_{\mathrm{in}}(t) - \int_{0}^{\infty} k_{\mathrm{in}}(t-\tau)\ell(t-\tau,\tau)\mathrm{d}\tau$

 $\mathbf{R}(0) = \mathbf{R}_0 = \mathbf{k}_{\mathrm{in0}} \cdot \mathbf{T}_{\mathrm{R}}$

king = cell production rate at steady-state

$$\begin{split} \frac{dP_1}{dt} &= k_{in}(t) - \frac{n}{T_R} E(t) P_1 \qquad P_1(0) = \frac{R_0}{n} \\ \frac{dP_i}{dt} &= \frac{n}{T} E(t) (P_{i-1} - P_i) \qquad P_1(0) = \frac{R_0}{n} \qquad i = 2, ..., n \end{split}$$

E(t) = drug effect function. R₀ = number of cells in all compartments at steady-state

Baseline conditions: k

$$\mathbf{k}_{in}(t) = \mathbf{k}_{in0}$$
 $\mathbf{E}(t) = 1$ for $t \le 0$
 $\mathbf{R}_0 = \mathbf{k}_{in0} \cdot \mathbf{T}_{\mathbf{R}}$

Drug effect

 $k_{in}(t) = k_{in0} \left(1 + \frac{S_{max}C(t)}{SC_{x0} + C(t)} \right), E(t) \equiv 1$ Stimulation of kine: Stimulation of n/T_R:

 $E(t) = 1 + \frac{S_{max}C(t)}{SC_{50} + C(t)} \ , \qquad k_{in}(t) \equiv k_{in0}$

$$\begin{split} Inhibition ~of ~n/T_R & E(t) = 1 - \frac{I_{max}C(t)}{IC_{50} + C(t)} ~,~ k_{in}(t) {=} k_{in0} \\ I_{max} = maximal ~drug ~effect. \\ IC_{50} = drug ~plasma ~concentration eliciting 50% ~of the \end{split}$$

maximum effect.

Inhibition of kin₀: $k_{in}(t) = k_{in0} \left(1 - \frac{I_{max}C(t)}{IC + C(t)} \right)$, $E(t) \equiv 1$

 $S_{max} = maximal \mbox{ drug effect}. \\ SC_{50} = \mbox{ drug plasma concentration eliciting 50% of the}$ maximum effect

Results

Solution to TC model:

$$P_{1}(t) = \frac{R_{0}}{n} + \frac{1}{(i-1)!} \left(\frac{n}{T_{R}}\right)^{i-1} \int_{0}^{t} \left(k_{m}(\tau) - \frac{R_{0}}{T_{R}} E(\tau)\right) \left(\int_{\tau}^{t} E(z) dz\right)^{i-1} exp\left(-\frac{n}{T_{R}}\int_{\tau}^{t} E(z) dz\right) dt$$
Lifespan distribution for LIDR model:

$$\ell_{n}(t,\tau) = \left(\frac{n}{T_{R}}\right)^{n} \frac{E(t+\tau)}{(n-1)!} \left(\int_{\tau}^{t+\tau} E(z) dz\right)^{n-1} exp\left(-\frac{n}{T_{R}}\int_{\tau}^{t+\tau} E(z) dz\right)$$
Stimulation of kin₀ (E(t)=1)
Inhibition of n/T_R (k_{in}(t)=k_{in0})
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Fig. 2. Simulated profiles of the p.d.f. $\gamma_n(\tau)$ for n = 1, 2, ..., 10, 20, ..., 100. The $T_R = 24$. Each curve has a unique peak at $\tau_n = (1-1/n)T_n$.







s for TC m ading to the monoexponential pharmacokinetic function C(t) Fig. 3. Respo =Dose/V-exp(- k_{el} t) for n = 1, 2, 3, 4, 5, 10, 20, 100. The bold curves represent solutions of LIDR model R_a(t). The parameter values used for simulations were Dose = 10000, V = 3, k_{el} = 0.3, k_{in} = R₀/T_R, R_0 = 100, T_R = 24, I_{max} = S_{max} = 1, and IC₅₀ = 0.3, k_{el} $SC_{50} = 100$



Fig. 4. Respo ase time courses for TC models corresponding to the monoexponential pharmacokinetic function C(t) =Dose/V-exp(k_{ef} t) for n = 1, 2, 3, 4, 5, 10, 20, 100. The bold curves represent solutions of LIDR model R_{e} (t). The param values used for simulations were as in Fig. 3.

 Table L. Percent difference between the transit compartment response Rn and a limit lifespan based indirect response R_n for

 four models. The difference was evaluated at indicated R_n peak times: $[R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_n(T_{peak})-R_$

	n	Stimulation of	Inhibition of	Stimulation of	Inhibition of
		k_{in0} $T_{peak} = 24$	k_{in0} $T_{peak} = 24$	n/T_R $T_{peak} = 13.7$	n/T_R $T_{peak} = 35.8$
Ī	1	49.8	96.4	39.8	60.0
	2	39.5	80.3	29.7	55.9
	3	35.5	64.3	26.7	53.9
	4	31.4	52.2	21.1	51.8
	5	29.3	36.1	18.7	49.8
	10	23.2	32.1	14.1	47.8
	20	17.0	26.5	9.4	43.7
	100	6.8	16.1	4.6	35.5

Conclusions

TC models can be considered as LIDR models with the gamma lifespan distribution.

· If the number of compartments increases and the mean lifespan is constant, then the TC

models approach a basic LIDR model with a point lifespan distribution.

• TC models with the number of TCs between 5 and 20 provide a good approximation of the basic LIDR model.

References

[1] Harker LA, Roskos LK, Marzec UM, Carter LA, Cherry JK, Sundell B, Cheung EN, Terry D, Sheridan W, Effects of ent factor on pl akaryocyte growth and development facts an volunteers. Blood 95:2514-22 (2000). ction, platelet life span, and pl telet function in healthy

human volunteers. Blood 95:2314-22 (2000). [2] Hamren B, Bjook E, Sunzel M, Karlsson MO. Models for plasma glucoseHbA1c, and hemoglobin interrelationships in patients with type 2 diabetes following tesagilturar treatment. Clim. Pharmacol. & Ther. 84:28-235 (2008). [3] Friberg LE, Alo C, Karlsson MO. Mcchanistic models for myleosuppression. Interst New Drugs 21:183-194 (2003). [4] Karzyamski W, Woo S, Juako WJ, Pharmacokyn-Bmarnocdyn astron Edit for agents that alter production of natural cells with various distributions of Hiespans. J Pharmacokyn-Bmarnocdyn. 33:125-165 (2006).

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