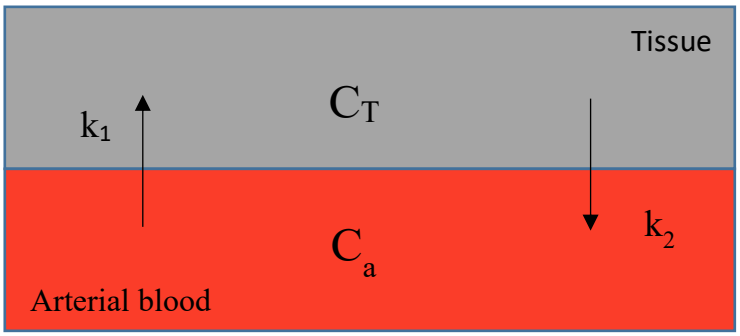
## Tracer Kinetic Modeling of PET Data—Logan Plots

Consider a simple two-compartment model of tracer exchange between arterial and tissue pools:




The tracer concentration in the arterial blood is $C_a$ and in the tissue compartment it is $C_T$. The transfer of tracer between compartments is dictated by the rate constants $k_1$ and $k_2$:

$$\frac{dC_T}{dt} = k_1 C_a(t) - k_2 C_T(t) \tag{1.1}$$

In the steady state, we have

$$\frac{dC_T}{dt} = 0 = k_1 C_a(t) - k_2 C_T(t)$$
$$k_1 C_a = k_2 C_T$$
$$C_T = \left(\frac{k_1}{k_2}\right) \cdot C_a$$

The term in parentheses equals the partition coefficient, $\lambda_T$, by definition (see the *Tracer Perfusion* lecture slides--the partition coefficient is the volume of blood that contains the same quantity of tracer as 1 mL of tissue). Hence,

$$\lambda_T = \frac{k_1}{k_2} \tag{1.2}$$

Integrating (1.1) over time and assuming that the initial tracer concentration in the tissue is zero, $C_T(0) = 0$, we have

$$C_T(t) = k_1 \int_0^t C_a(t')dt' - k_2 \int_0^t C_T(t')dt' \tag{1.3}$$

Dividing through by $k_2 \cdot C_T(t)$, we have

$$\frac{1}{k_2} = \frac{k_1}{k_2} \cdot \frac{\int_0^t C_a(t')\,dt'}{C_T(t)} - \frac{\int_0^t C_T(t')\,dt'}{C_T(t)}$$

or

$$\frac{\int_0^t C_T(t')\,dt'}{C_T(t)} = \lambda_T \cdot \frac{\int_0^t C_a(t')\,dt'}{C_T(t)} - \frac{1}{k_2} \tag{1.4}$$

To use this relation, we need information on $C_a(t)$, either from direct blood sampling or some other method. Suppose that some region of the brain is known to lack binding sites for the tracer—this region can be used as a reference tissue with only nonspecific uptake of the tracer. Writing (1.3) for the reference region,

$$C_R(t) = k_1 \int_0^t C_a(t')dt' - k_2 \int_0^t C_R(t')dt'$$

or

$$\begin{aligned} \int_0^t C_a(t')dt' &= \frac{k_2}{k_1} \cdot \int_0^t C_R(t')dt' + \frac{1}{k_1} \cdot C_R(t) \\ &= \frac{1}{\lambda_R} \cdot \left\{ \int_0^t C_R(t')\,dt' + \frac{C_R(t)}{k_2} \right\} \end{aligned} \tag{1.5}$$

where $\lambda_R$ has been used to denote the partition coefficient for the reference tissue (i.e., $k_1$ and $k_2$ are tissue-specific). Substituting this relation into (1.4) eliminates the arterial concentration:

$$\frac{\int_0^t C_T(t')\,dt'}{C_T(t)} = \frac{\lambda_T}{\lambda_R} \cdot \frac{\int_0^t C_R(t')\,dt' + C_R(t)/k_{2R}}{C_T(t)} - \frac{1}{k_{2T}} \tag{1.6}$$

where the $k_2$ values for the respective tissues have been explicitly labeled.

At some time following the tracer injection, the concentrations will approach their steady state values and

$$\frac{C_R(t)}{C_T(t)} \simeq const.$$

in which case (1.6) can be written as

$$\frac{\int_0^t C_T(t')\,dt'}{C_T(t)} \simeq \frac{\lambda_T}{\lambda_R} \cdot \frac{\int_0^t C_R(t')\,dt'}{C_T(t)} + b \tag{1.7}$$

where $b$ is a constant. Defining

$$y \equiv \frac{\int_0^t C_T(t')\,dt'}{C_T(t)} \quad , \quad x \equiv \frac{\int_0^t C_R(t')\,dt'}{C_T(t)} \tag{1.8}$$

(1.7) becomes

$$y \simeq \frac{\lambda_T}{\lambda_R} \cdot x + b$$

and the slope of the line is (very nearly) the distribution volume ratio (DVR) for the two regions. The plot of $y$ versus $x$ is called a 'Logan Plot.'

In a PET image, pixel intensity is proportional to the tissue tracer concentration. A time-series of images yields the time course of tracer concentration at each pixel position. In a time-series of $N$ images, $N$ pairs of $(x, y)$ values can be calculated using (1.8). Fitting the linear part (i.e., points for long times) of the $y$ vs. $x$ curve gives the DVR at each pixel position. The DVR map calculated from Logan plots reflects the relative concentration of tracer targets as a function of position in the image plane.

Source

M. Wernick and J. Aarsvold. Emission Tomography: The Fundamentals of PET and SPECT. Academic Press (2004).