study, influences of these two factors were examined by same numerical function. For the dead time loss correction, masking interval (\(=0.01\)) were set and for the background, constant term (B) were added to the original data.

Analysis of the effect of the sample size \(m\), the time scale interval \(\tau\) and the number of exponentials \(p\) on the variance of \(A_i\) and \(\alpha_i\) by numerical samples revealed the following results;

1. For a fixed sample size, there is an optimal time scale interval which increases with sample size.
2. For a fixed time scale interval, the variance of each parameter decreases with the sample size, but it converges to a certain level for a large sample size. (3) The allowable limit on \(\tau\) as the optimal time scale interval decreases with increases of the number of exponentials.

And the results of the numerical sample which were influenced by these factors were not so remarkably changed as above, but in all experiments, variance of \(A_i\) and \(\alpha_i\) were increased and for the background, variances were increased in the case of increase of constant(B).

The Effect of the Amount of RI Tracer Dosis on the Accuracy of Identification in Compartmental Analysis

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The so-called compartmental analysis offers the theoretical basis of tracer kinetic studies which have found wide practical applications in the nuclear medicine.

The observation of the tracer kinetic process at time \(t_i\) is generally represented by a sum of decaying exponentials.

\[
\langle n_j \rangle = \sum_{i=1}^{p} A_i \exp (-\alpha_i t_i)
\]

where \(p\) represents the number of compartments associated with the process. Thus the compartmental analysis is a method by which the number of compartments \(p\) as well as other pertinent parameters are determined.

In this report, we have studied theoretically the relationship between the amount of input tracer dose and the estimated variances of \(A_i\)'s and \(\alpha_i\)'s. Then we have tested the results by numerical examinations.

We suppose that the experimental data are taken at equally spaced interval of time and there are \(m\) independent observations \(n_1, n_2 \ldots n_m\) available.

Since the probability density of \(n_j\) is assumed to be Poissonian, the joint likelihood function \(L\) can be written as

\[
L = \exp \left( - \sum_{j=1}^{m} \langle n_j \rangle - \frac{\langle n_1 \rangle^{n_1} \langle n_2 \rangle^{n_2} \ldots \langle n_m \rangle^{n_m}}{n_1! n_2! \ldots n_m!} \right)
\]

The variances of \(A_i\)'s and \(\alpha_i\)'s were obtained in the following way.

Let \(V\) be the variance-covariance matrix of \(A_i\)'s and \(\alpha_i\)'s. Then \(V\) is larger than \(I^{-1}\) in the sense that \(V-I^{-1}\) is non negative definite. Here, (k,l) element of \(I\) is \(-E\left(\frac{\partial^2}{\partial \theta_k \partial \theta_l} \ln L\right)\) and \((\theta_1 \ldots \theta_p), (\theta_{p+1} \ldots \theta_{2p})\) are equivalent to \((A_1 \ldots A_p), (\alpha_1 \ldots \alpha_p))\).

Hence, diagonal elements of \(I^{-1}\) can be considered as the best unbiased estimator of the variances of \(A_i\)'s and \(\alpha_i\)'s.

These mathematical procedure revealed that the variances of \(A_i\)'s increase and those of \(\alpha_i\)'s decrease linearly according to the increase of the amount of RI dose. Then numerical examinations of identification by the maximum likelihood method have been carried out for several test functions with different RI doses. These experiments also demonstrated that the difficulty increases with the decrease of the amount of RI dose.