Exercise NUC #2 – Quantitative PET Data Analysis

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Task 2.1

In this task, we consider the two tissue compartments (C_e, C_m) and treat the blood/plasma compartment (C_p) separately. So we should take rate of constants (k_2, k_3, k_4) into consideration

Initial condition $\begin{cases} C_e(0) = k_1 & \text{(input)} \\ C_m(0) = 0 \end{cases}$

$$\begin{cases} \frac{dC_e(t)}{dt} = -k_2 \cdot C_e(t) - k_3 C_e(t) + k_4 C_m(t) \approx -(k_2+k_3) C_e(t) \\ \frac{dC_m(t)}{dt} = k_3 C_e(t) - k_4 C_m(t) \approx k_3 C_e(t) \end{cases}$$

$$\Rightarrow \begin{cases} C_e(t) = k_1 e^{-(k_2+k_3)t} \\ C_m(t) = \frac{-k_1 k_3}{k_2+k_3} e^{-(k_2+k_3)t} + \frac{k_1 k_3}{k_2+k_3} \end{cases}$$

Task 2.2

Using dsolve function in MATLAB to solve the differential equations and obtain the impulse response functions of the extracellular compartment $C_e(t)$ and the metabolized compartment $C_m(t)$.

$h\_C_e(t)$:

```
h_ce =

  function_handle with value:

    @(k1,k2,k3,t)k1.*exp(-t.*(k2+k3))
```

$h\_C_m(t)$:

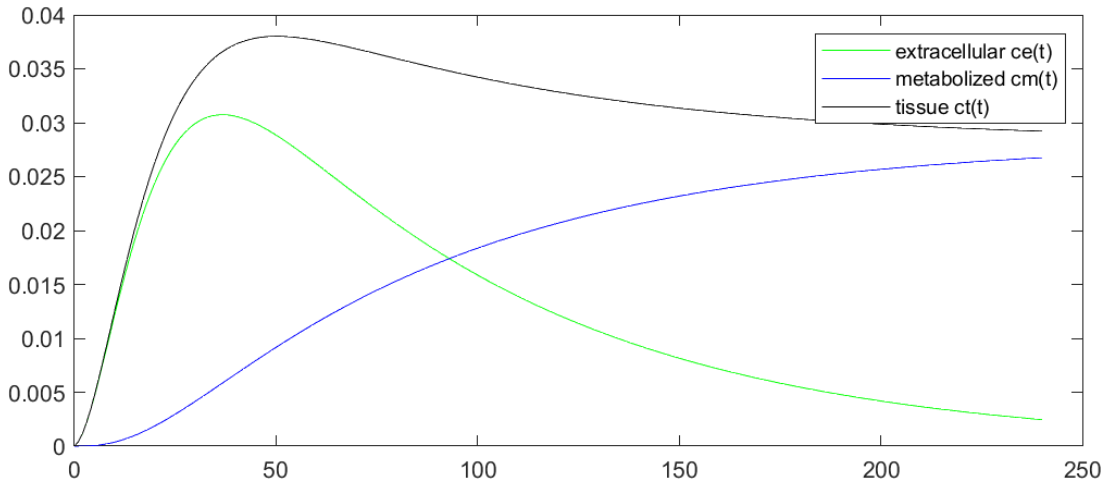
```
h_cm =

  function_handle with value:

    @(k1,k2,k3,t)(k1.*k3)./(k2+k3)-(k1.*k3.*exp(-t.*(k2+k3)))./(k2+k3)
```

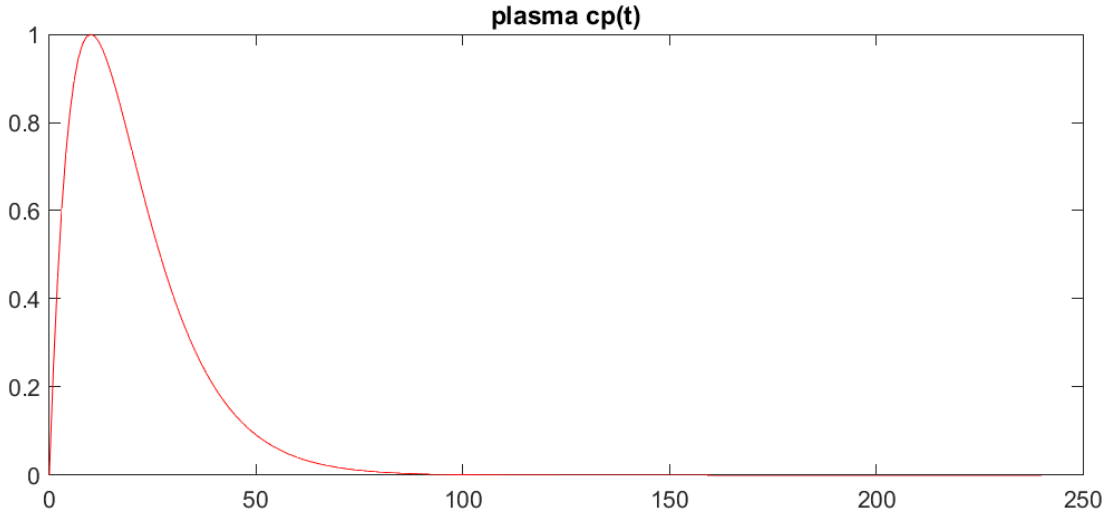
These results are compatible with the results derived in Task 2.1.

Set the following values: $k_1 = 0.1min^{-1}$, $k_2 = 0.3min^{-1}$, $k_3 = 0.5min^{-1}$. Implement convolution of the impulse response functions with the input curve $C_p(t)$.



In this task, we assume that the rate constant k_4 to be 0. This is based on the fact that it is relatively easier for radiotracers to combine with receptors rather than disassociation. And the concentration of ^{18}F-FDG-6-P is low and increases slowly during the reaction process. In this way, we have $k_3 \gg k_4$ and we can ignore the influence of k_4.

Task 2.3

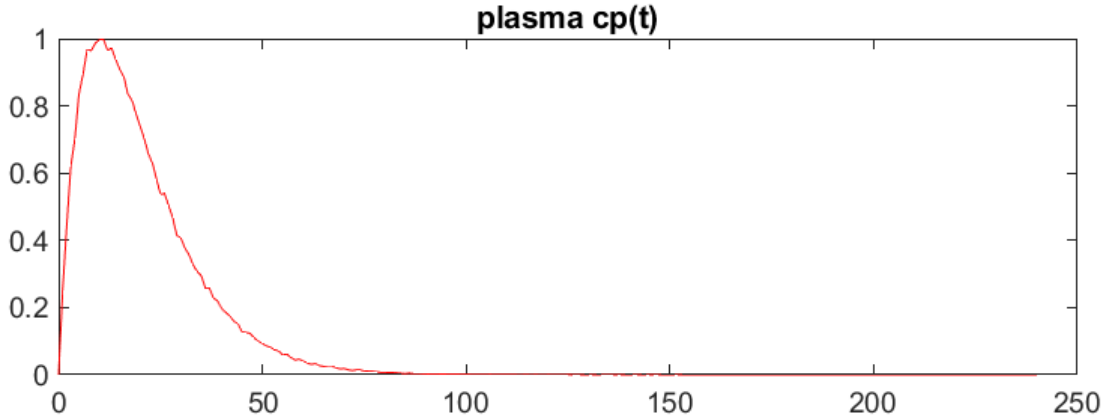


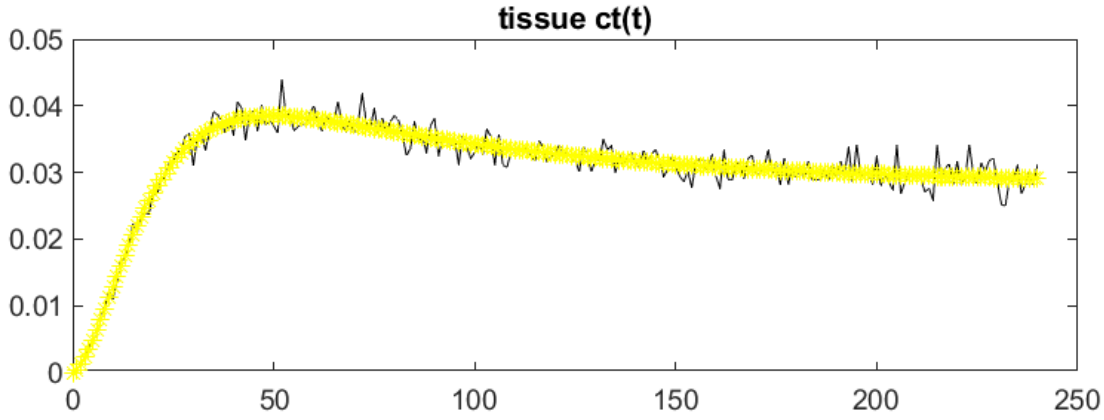
To obtain a peak SNR=100 of the blood plasma signal, we can use the definition of SNR and the noise distribution (following the Poisson distribution) to calculate the photon counts.

$$SNR = \frac{mean(N)}{std(N)} = \sqrt{N} = 100$$

The result turns out that the maximum photon counts should be 100 in order to obtain a peak SNR of 100, which also corresponds to the peak of blood plasma concentration which has a value of 1. So the conversion factor should be 10000.

Set the initial value of rate constants (k_1, k_2, k_3) as (0.01, 0.01, 0.01). Implement the nonlinear fitting.





Fitting results of rate constants for 10 repetitions:

3x10 double

	1	2	3	4	5	6	7	8	9	10
1	0.1022	0.0998	0.1012	0.0994	0.1014	0.1009	0.0984	0.1009	0.0997	0.1000
2	0.3340	0.3170	0.3094	0.2705	0.3239	0.3016	0.2700	0.3076	0.2943	0.3172
3	0.5113	0.5574	0.4782	0.4271	0.5493	0.4976	0.4498	0.4855	0.4916	0.5456

Mean:

```
Mean  [k1 k2 k3]: 0.100392 0.304557 0.499322
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Standard deviation:

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StDev [k1 k2 k3]: 0.001120 0.021223 0.042844
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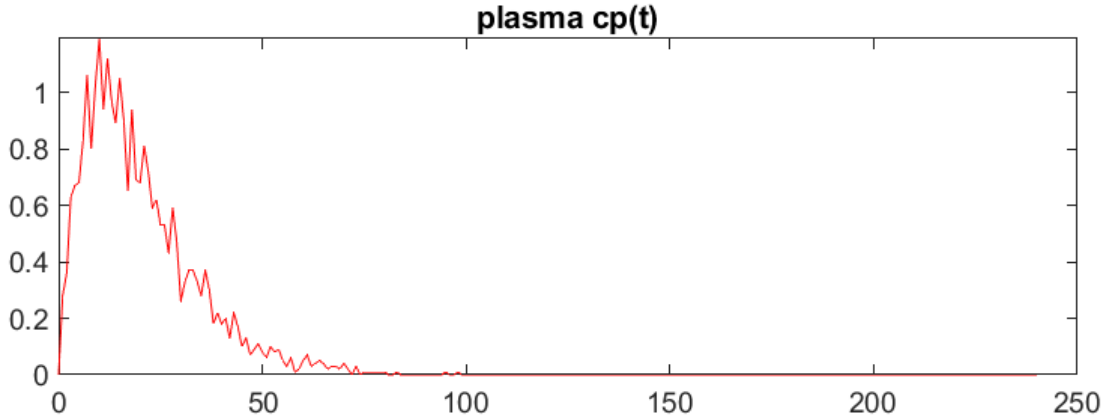
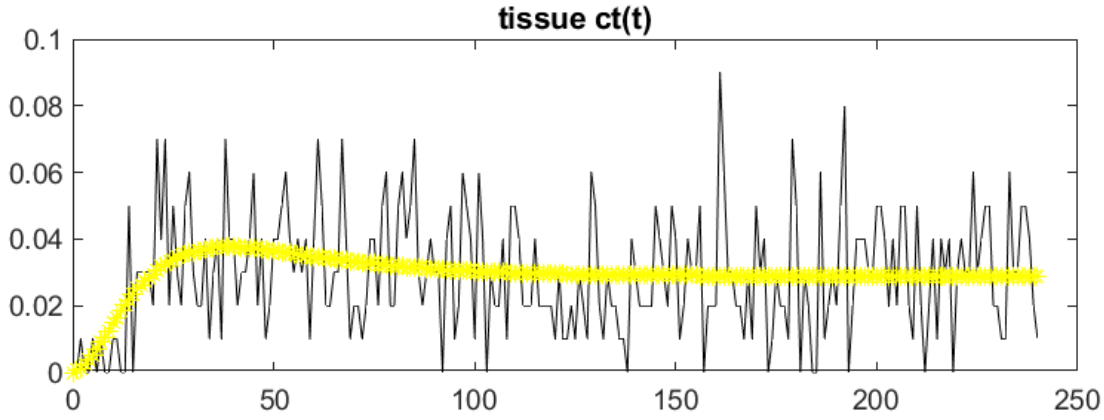
Reduce the SNR by 10 and repeat the experiments.





Fitting results of rate constants for 10 repetitions:

3x10 double

	1	2	3	4	5	6	7	8	9	10
1	0.1251	0.0977	0.1061	0.0813	0.0926	0.1333	0.1240	0.1005	0.1222	0.0859
2	1.1482	0.6098	0.4538	0.1821	0.2386	1.1106	1.7385	0.3296	0.6698	0.0123
3	1.1888	1.2077	0.6157	0.6093	0.3484	1.2430	2.6382	0.3890	0.5717	-1.0621

Mean:

```
Mean  [k1 k2 k3]: 0.106881 0.649339 0.774980
```

Standard deviation:

```
StDev [k1 k2 k3]: 0.018207 0.535736 0.933883
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According to the results of different SNRs, we can find that the mean of fitted rate constants will become more deviated from the actual value. And the standard deviation will increase. In this way, we should use PET data with higher SNR to obtain more convincible rate constants. One way to do this is to increase the scan time to count more photons.