

Using an autoencoder to determine the input function for dynamic PET data in the presence of radiometabolites

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Previously, we have demonstrated that an estimate of the arterial input function can be found from dynamic positron emission tomography (PET) data using a machine learning tool called an autoencoder. [1] Our initial study made use of an inflammation tracer ([¹⁸F]LW223) which is not greatly influenced by radiometabolites. [2] This means that an input function estimate derived from the image data without further correction has some hope of being accurate.

Here we focus on the synaptic density tracer [¹⁸F]SynVesT-1 and pre-clinical studies of rodent models. For this radiotracer initially, 100% of the radioactivity is associated with the tracer, however as the scan progresses an increasing proportion of the radioactivity originates from radiometabolites. [3] We use the autoencoder to decompose the dynamic signals from the PET data into three characteristic components. We associate the component with the earliest peak with the input function. Finally, we re-train the autoencoder while constraining the input function to be similar to a population curve. This provides the estimate of the input function which we then use to analyse time activity curves from different tissues. [1]

Microparameters characteristic of different tissues were obtained using a linearisation approach due to Ito (Figure 1) which produces values for K1 (rate of entry of tracer from blood to tissue) and VT (the volume of distribution). [4] Estimating K1 relies on the earliest part of the input function. This part of the curve is least influenced by radiometabolites; we find good agreement between our K1 values and those derived using invasive blood sampling and radiometabolite correction. By contrast, VT is much more dependent on the later parts of the curve which are most corrupted. Unsurprisingly we were unable to capture reasonable values without taking account of radiometabolites.

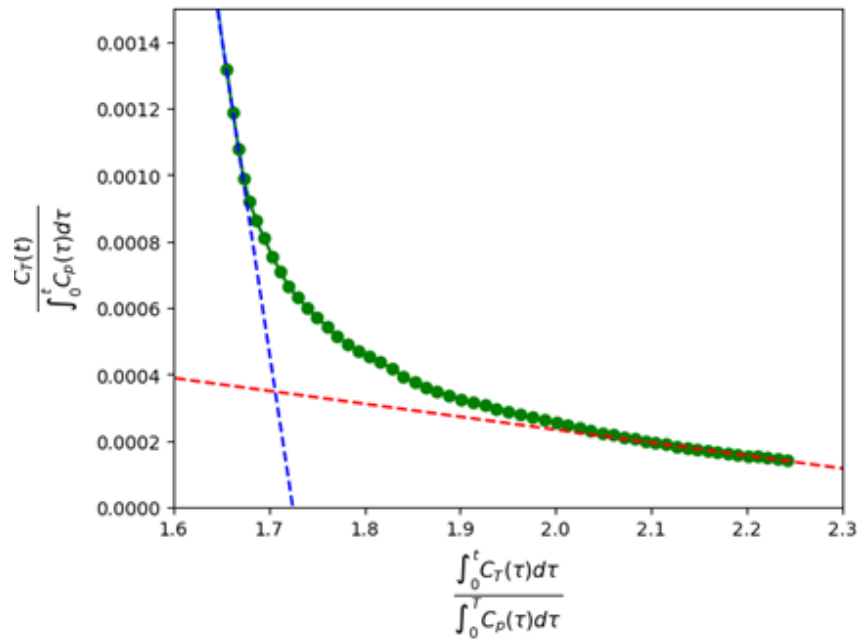


Figure. 1 Time activity curves for individual tissues $C_T(t)$ were used together with our estimate of the input curve $C_P(t)$ to determine values for the microparameters K_1 and V_T .

References:

- (1) A. von Kietzel et al. "An autoencoder for non-invasive arterial input function estimation in pre-clinical dynamic PET imaging" IEEE Nuclear Science Symposium (2024).
- (2) M. G. MacAskill et al. "Quantification of Macrophage-Driven Inflammation During Myocardial Infarction with ^{18}F -LW223, a Novel TSPO Radiotracer with Binding Independent of the rs6971 Human Polymorphism" J. Nucl. Med. **62**, 536 (2021).
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- (4) H. Ito et al. "A new graphic plot analysis for determination of neuroreceptor binding in positron emission tomography studies" NeuroImage **49**, 578 (2010).