# Extraction of time activity curves from positron emission tomography: K-means clustering or Non-negative matrix factorization.

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## Objective

Measurement of the cerebral input function in terms of the arterial plasma input time activity curve (TAC) is required for assessment and validation of the quantification of receptor binding parameters on the basis of dynamic positron emission tomography (PET) images and kinetic models [1]. Alternative non-invasive methods for estimation of the input function have been described based on cluster analysis [1], based on linear decomposition methods such as independent component analysis (ICA) [2, 3], and by non-negative matrix factorization (NMF) of the signals in a region of interest [4]. The linear decomposition methods are preferred because they do not assume that voxels are dominated by the vascular signal, where the NMF method is attractive because of the relative straightforward estimation procedure. Furthermore, the NMF method is attractive because it - in contrast to the ICA methods - does not assume a specific form of the spatial distribution.

In this study the NMF method is used to extract the input function without the use of a set of predefined regions of interest (ROI) and the results are subsequently compared to the results from K-means clustering used in [1].

## Methods

Five healthy subjects were investigated with dynamic PET-scanning after rapid intravenous 18F-altanserin bolus injection. Arterial and venous blood samples were withdrawn automatically and manually and counted in an external coincidence counter.

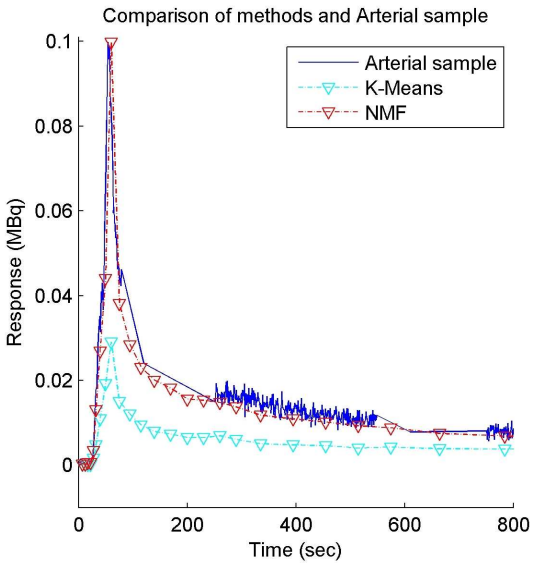
The non-negative matrix factorization describes the matrix **V**, as a linear combination of the factors **W** and **H**. All elements in **V**, **W** and **H** are non-negative.

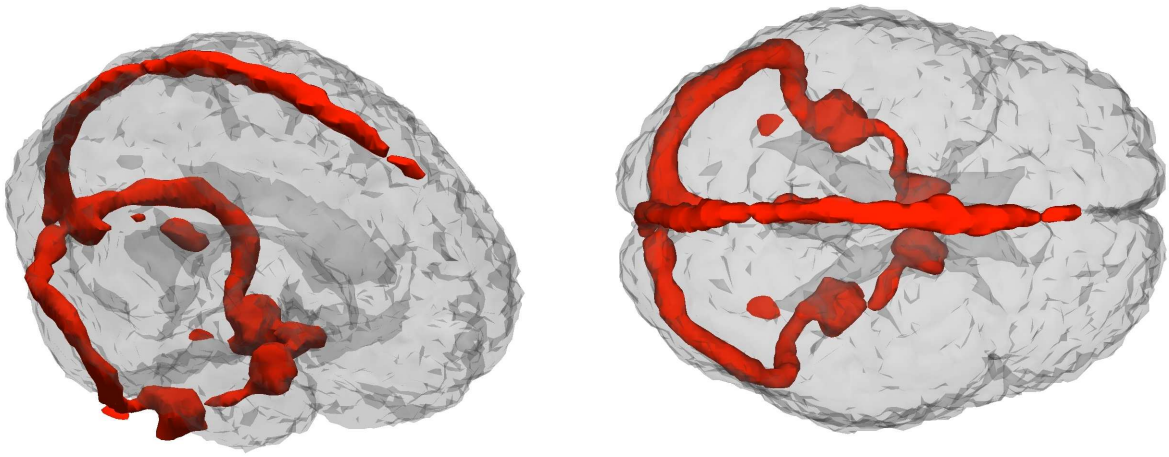
$$\mathbf{V}=\mathbf{WH}$$

This can be applied to the problem at hand of extracting TACs; **V** being the dynamic PET image, **W** is the mixing matrix, and **H** contains the basis TACs.

## Results

Figure 1 shows the outcome of the NMF approach in comparison to the measured arterial blood samples. It is clearly seen that the peak in the blood curve as identified by NMF is higher than the one found by clustering. In addition, it matches well with the sampled blood TAC.



The reason for the reduced amplitude of the clustering TAC is that it represents the average of voxel TACs some of which are only partly vascular, while the enhanced signal in the NMF TAC is due to the deconvolution of the signal from each voxel into different components.

To visualize and validate the results the spatial information from the vascular source is used to generate a 3D image (figure 2) by thresholding the column of the vascular component of the **H** matrix. Figure 2 demonstrates that the vascular TAC found by the NMF is spatially located corresponding to the larger cerebral veins.

**Conclusion**

For these data, NMF is excellent for extraction of TACs in PET data without using a predefined ROI for the analysis. For this particular set of data the NMF method is superior to the K-means clustering approach.

**References**

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***Category:*** *Imaging Techniques*