Human Brain Mapping 2007 Print

Abstract Number: 337 Submitted By: Bjarni Bodvarsson
Last Modified: January 7 2007

Estimation of time activity curves from positron emission tomography with NMF and Bootstrap.

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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 [4]. A vascular input TAC can be estimated using non-negative matrix factorization (NMF) [1] [2]. The scaling of the estimated TAC is found by making assumptions on the mixing matrix in the NMF model.

To estimate how precise the estimated curve are, a resampling scheme called Bootstrap[3] is applied to the NMF estimated TACs. The Bootstrap gives error bars on the curves and this can be used to validate the precision of the solution. Correlation with the sampled TAC is used to estimate the number of components in the NMF.

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 Arterial and venous blood samples were withdrawn automatically and manually and counted in an external coincidence counter.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.

V=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[2].

The Bootstrap resampling scheme randomly chooses n voxels with replacement from **V** (n being number of voxels in **V**). This is done 10 times and thereby error bars can be generated. Since the ordering of the components in **H** is random when using NMF, correlation is used to get the same ordering of the components in the 10 runs.

Since the absolute scale of the estimated components is unknown a rescaling method is proposed to be able to use the estimated TAC in actual modeling. The rescaling is possible since assumptions on **W** can be made. Since **W** describes the parts of each component in each voxel, it can be assumed that the parts must sum to one in all voxels, if the model is a

good approximation of the data in **V**. A further assumption is made namely that the vascular component must sum to 5% of the total brain volume.

Results

In figure 1 the comparison between the estimated vascular TAC and the arterial sampled TAC from the arm is shown. They are very similar although the estimated curve has a higher peak. This might be because the sampling is in the arm and not in the brain. The estimated TAC is mostly venous, which can be seen in figure 3 and in [2].

The correlations between the estimated and sampled TAC are shown in figure 2. It can be seen that using 3 components gives the highest correlation.

Conclusion

NMF together with the Bootstrap resampling scheme is an effective way of estimating cerebral input curves. The assumptions on the **W** matrix seem to hold since the result scaling is correct.

References

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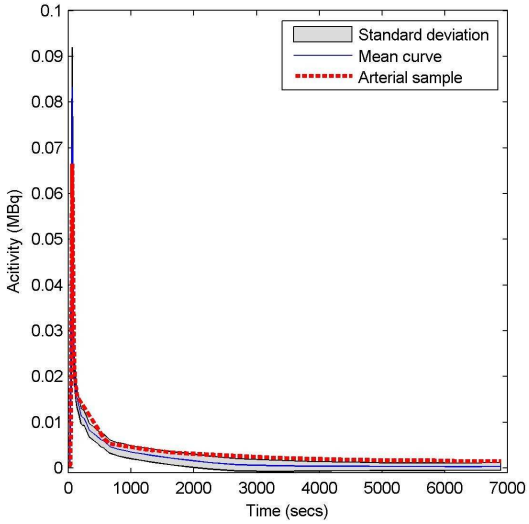

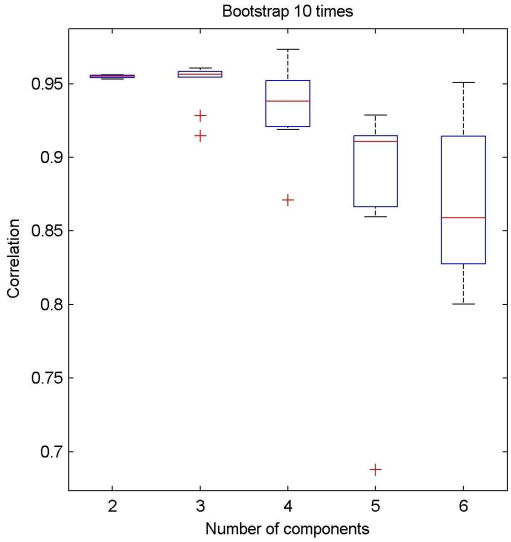

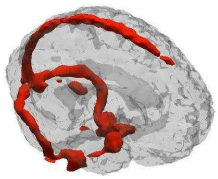

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