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## Objective

The aim was to assess a *denoising* [1] and *deconvolution* [2] technique based on Legendre polynomials compared to matrix deconvolution on dynamic  $^{18}\text{F}$ -FDG renal scintigraphy of healthy patients for split function (SF) and mean transit time (MTT) measurement.

## Method

The study was carried out and compared to the data of 24 patients from an Austrian study (BKG) [3] who underwent examinations with  $^{99\text{m}}\text{Tc}$ -MAG<sub>3</sub> and  $^{18}\text{F}$ -FDG (PET/MRI). Due to corruption issues in some data used in the published article, post-publication measurements were provided (pv). We have been warned that post-publication data were treated differently. The smoothing method switched from Bezier to Savitzky-Golay, and the deconvolution from matrix-based (with Tikhonov Regularization) to Richardson-Lucy method. A comparison of the split function and MTT of the published and pv data against our method was performed.

## Results

We had a good agreement only for the MAG<sub>3</sub> SF of pv data. However the correlation found in the original study between the split functions obtained on the MAG<sub>3</sub> and the  $^{18}\text{F}$ -FDG was lost. For MTT, the correlation was very good with the pv measurements for the MAG<sub>3</sub> and  $^{18}\text{F}$ -FDG (Figure 1). Bias of the Bland-Altman analysis of MTT for MAG<sub>3</sub> versus  $^{18}\text{F}$ -FDG are summarized in Table 1. Partial data (16 patients only due to data loss) were fully reprocessed for both MAG<sub>3</sub> and  $^{18}\text{F}$ -FDG studies using our Legendre-based methods. MAG<sub>3</sub> data were also processed using Hermes software.

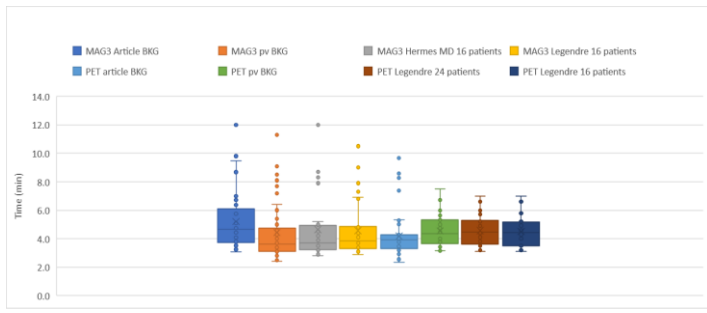


Figure 1: Box-plot comparison of the MTT MAG<sub>3</sub> from article and provided values against Hermes and Legendre method measurement on partial data. The MTT  $^{18}\text{F}$ -FDG spread comparison for article, Legendre deconvolution on all provided curves and partial data.

Table 1: summary of the Bland-Altman MTT comparisons:

			Bias (min)	SD (min)
MTT <sub>MAG3</sub>	vs	MTT <sub>FDG</sub> BKG both from article	1.1	1.7
MTT <sub>MAG3</sub>	vs	MTT <sub>FDG</sub> BKG both from pv	-0.11	1.9
MTT <sub>MAG3</sub> BKG pv	vs	MTT <sub>FDG</sub> LG	-0.14	1.8
MTT <sub>MAG3</sub>	vs	MTT <sub>FDG</sub> LG (partial)	0.05	1.9
MTT <sub>FDG</sub> LG	vs	MTT <sub>FDG</sub> BKG	-0.04	0.5

## Conclusion

The methods used for the BKG published and post-published processing were quite complex and required adaptation of the fitting parameters for each examination. Our method did *not require any specific adjustment*, the same algorithm was applied to all data. In addition, the denoising and deconvolution processes based on Legendre polynomials were *fully automated*.

## References

[1] Destine M, Seret A. Legendre Polynomials: A fully automatic method for noise reduction in  $^{99\text{m}}\text{Tc}$ -mercaptoacetyltriglycine renogram analysis. J Nucl Med Technol 2020;48:346-353.  
 [2] Destine M, Hanin FX, Mathieu I, Willemart B, Seret A. Deconvolution of Tc- $^{99\text{m}}$ -Mercaptoacetyltriglycine Renograms with the Concomitant Use of a Sparse Legendre Polynomial Representation and the Moore-Penrose Pseudo-inverse. Mol Imaging Radionucl Ther. 2022 Feb 2;31(1):7-15. doi: 10.4274/mirt.galenos.2021.17363.  
 [3] Geist BK et al. Assessment of the kidney function parameters split function, mean transit time, and outflow efficiency using dynamic FDG-PET/MRI in healthy subjects. Eur J Hybrid Imaging. 2019 Feb 15;3(1):3. doi: 10.1186/s41824-019-0051-9.