# Automated Functional Analysis in Dynamic Medical Imaging

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**Abstract**. Dynamic medical imaging is concerned with acquisition and analysis of a sequence of images of the same region of a body during time. In nuclear medicine, each pixel of an image is the sum of particles coming from an applied radioactive tracer from the body in a specific time-interval. Hence, each observed image is a superposition of an unknown number of underlaying organ images. The aim of functional analysis is to separate the images of biologic organs and related time-activity curves from the sequence of images.

The mathematical model of each image is

$$\mathbf{d}_t = \sum_{k=1}^{r} \mathbf{a}_k x_{t,k} + \mathbf{e}_t, \quad t = 1, \ldots, T \tag{1}$$

where $r$ is the expected number of organs or structures, $T$ is number of images in the sequence, $\mathbf{d}_t$ is a vectorized measured image in time $t$, $\mathbf{a}_k$ is an image of $k$th organ, $\mathbf{x}_k$ is a time-activity vector of $k$th organ, and $\mathbf{e}_t$ is an error vector in time $t$.

The model (1) is known as the factor analysis model with potentially infinitely many solutions. In clinical practice, the space of solutions is manually restricted to the biological ones. The sequence is analyzed using manual-based region of interest, where active regions are manually selected by experienced physician for further analysis. Several semi-automated methods of analysis are available [1]; however, a manual intervention is still necessary. The objective of our work is to restrict the space of solutions of model (1) to those with biological meaning using general mathematical assumptions. We extend the factor analysis model as follows: (i) we model the fact that the image of organ affects only small number of pixels of the whole image [2] and (ii) we incorporate the model of fluid transport in the body into the model of time-activity curves [3].

First, the model of factor analysis, (1), assumes that each factor covers the whole image which is evidently incorrect. We propose incorporation of indicator $i_{i,j}$ to each pixel of organ image, $\mathbf{a}_j$. Then, $a_{i,j} = 0$ if $i_{i,j} = 0$ and $a_{i,j} > 0$ if $i_{i,j} = 1$. This innovation supports small but important structures in the sequence.

Second, we use the biologic assumption that each time-activity curve is a convolution of blood, $\mathbf{b}$, and organ-restricted kernel, $\mathbf{u}_j$, [4], such as

$$\mathbf{x}_j = \mathbf{b} * \mathbf{u}_j, \tag{2}$$

where symbol $*$ denotes convolution.

Following the Bayesian approach, the strictness of previous assumptions is relaxed using probabilistic modeling. We seek parameters of posterior densities represents images and

time-activity curves of biological structures. Since exact solution of the proposed models is intractable, we propose to use an approximate solution using the Variational Bayes Method [5]. The method leads to a set of implicit equations which must be solved iteratively.

The proposed algorithms are tested on medical sequences from renal scintigraphy, see Fig. 1. Both algorithms are capable to provide comparable or better results than state of the art algorithms. Moreover, our approach is the step to full automation in dynamic medical analysis.

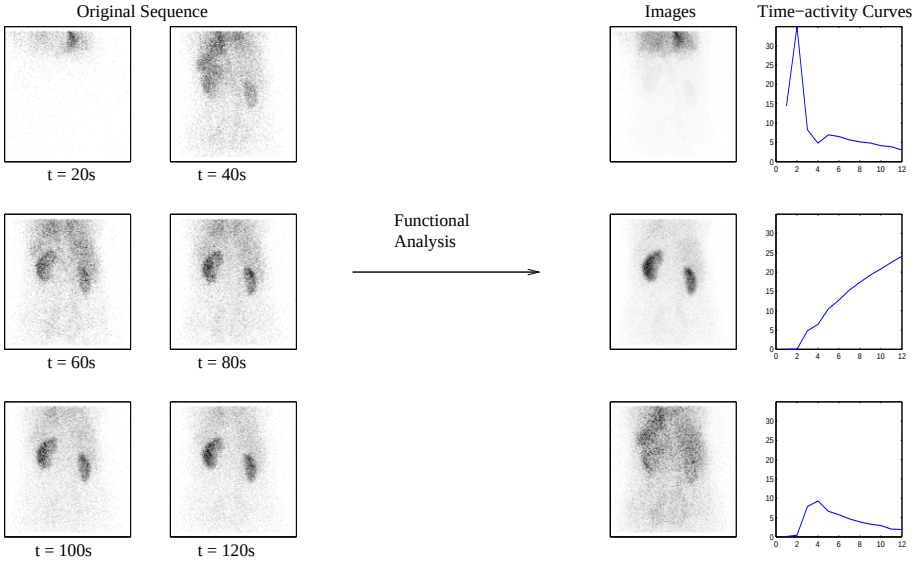


Figure 1: Example of functional analysis in renal scintigraphy.

**Literatura:**


[1] Lawson, R.S., Application of mathematical methods in dynamic nuclear medicine studies, Physics in medicine and biology (1999),

[2] Šmídl, V. and Tichý, O., Automatic Regions of Interest in Factor Analysis for Dynamic Medical Imaging, in 2012 IEEE International Symposium on Biomedical Imaging (ISBI), IEEE (2012)

[3] Šmídl, V. and Tichý, O. and Šámal, M., Factor Analysis Of Scintigraphic Image Sequences With Integrated Convolution Model Of Factor Curves, in Proceedings of the second international conference on Computational Bioscience, IASTED (2011),

[4] A. Kuruc, J. Caldicott, and S. Treves, Improved Deconvolution Technique for the Calculation of Renal Retention Functions, Comp. and Biomed. Res., vol. 15, no. 1, pp. 46-56, (1982),

[5] Šmídl, V. and Quinn, A., The Variational Bayes Method in Signal Processing, Springer (2006),