

LTSI

A tensor-based population value decomposition to explain rectal toxicity after prostate cancer radiotherapy

Juan David Ospina^{1,2,4} Frédéric Commandeur^{1,2} Richard Ríos^{1,2,4} Gaël Dréan^{1,2}
 Juan Carlos Correa⁴ Antoine Simon^{1,2} Pascal Haigron^{1,2} Renaud de Crevoisier^{1,2,3}
 Oscar Acosta^{1,2}

¹INSERM, U 1099, Rennes, F-35000, France

²Université de Rennes 1, LTSI, F-35000, France

³Centre Eugène Marquis, Département de Radiothérapie

⁴Universidad Nacional de Colombia, Sede Medellín, Colombia
 jdospina@unal.edu.co



Context and Objectives

In radiotherapy (RT) of prostate cancer:

- The goal of radiotherapy is to deliver high doses of radiation to the tumour whereas sparing the neighbouring organs (rectum and bladder).
- The side-effects must be minimized in order to ensure the patients' life quality.
- The prediction of side-effects is classically carried out using the dose-volume histograms, which lack spatial accuracy, and the normal tissue complication probability models.

The goal is to analyze the dose distribution across a population to detect patterns correlated to rectal bleeding after prostate cancer radiotherapy.

We propose a **population value decomposition** method that is applied to non-rigidly registered 3D dose distributions. Our method is a generalization of a 2D population value decomposition technique [1]. The differences between patients presenting or not a side-effect are assessed:

- Using a component-wise t-test like in VBM [2] in a transformed space;
- The normality assumptions are verified;
- The typical dose of each group is reconstructed allowing for the computation of the difference of dose amongst the two groups.

Population value decomposition (PVD)

Population model

- We have N 3D images (one for each patient), \mathbf{Y}_i , $i = 1, \dots, n$, spatially aligned. Each image can be classified either in one group, G_1 (side-effect), or its complement, G_2 (non side-effect).
- For each image we compute the High Order Singular Value Decomposition (HOSVD) [3] to obtain: $\mathbf{Y}_i = \mathbf{V}_i \times_1 \mathbf{S}_i^1 \times_2 \mathbf{S}_i^2 \times_3 \mathbf{S}_i^3$, where \mathbf{V}_i is the core tensor and $\mathbf{S}_i^1, \mathbf{S}_i^2$ and \mathbf{S}_i^3 are the corresponding factor matrices.
- Create 3 matrices $\mathbf{S}^k = [\mathbf{S}_1^k | \dots | \mathbf{S}_N^k]$, $k = 1, \dots, 3$.
- Perform a PCA over each \mathbf{S}^k to obtain the projection matrices \mathbf{P}^k such as $\mathbf{S}^k = \mathbf{P}^k (\mathbf{P}^k)^T \mathbf{S}^k$, $k = 1, \dots, 3$.
- Express each individual's image as $\mathbf{Y}_i = \mathbf{A}_i \times_1 \mathbf{P}^1 \times_2 \mathbf{P}^2 \times_3 \mathbf{P}^3$, where $\mathbf{A}_i = \mathbf{V}_i \times_1 (\mathbf{P}^1)^T \mathbf{S}_i^1 \times_2 (\mathbf{P}^2)^T \mathbf{S}_i^2 \times_3 (\mathbf{P}^3)^T \mathbf{S}_i^3$.

Compression

This technique allows for data compression:

- At the individual's level each image can be expressed as $\mathbf{Y}_i \approx \hat{\mathbf{V}}_i \times_1 \mathbf{S}_{L_1}^1 \times_2 \mathbf{S}_{L_2}^2 \times_3 \mathbf{S}_{L_3}^3$, where $\mathbf{S}_{L_i}^k$ is a matrix consisting of the first L_i^k columns of \mathbf{S}_i^k , and $\hat{\mathbf{V}}_i \in \mathbb{R}^{L_1^1 \times L_2^2 \times L_3^3}$ is the truncated core tensor.
- At the population level the \mathbf{P}^k matrices can be truncated by taking only the first Q_k columns leading to the reduced matrix \mathbf{P}^{Q_k} . The same reduction is possible when the PCA is carried out on $\mathbf{S}^{L_k} = [\mathbf{S}_{L_1}^k | \dots | \mathbf{S}_{L_N}^k]$.

Group comparison

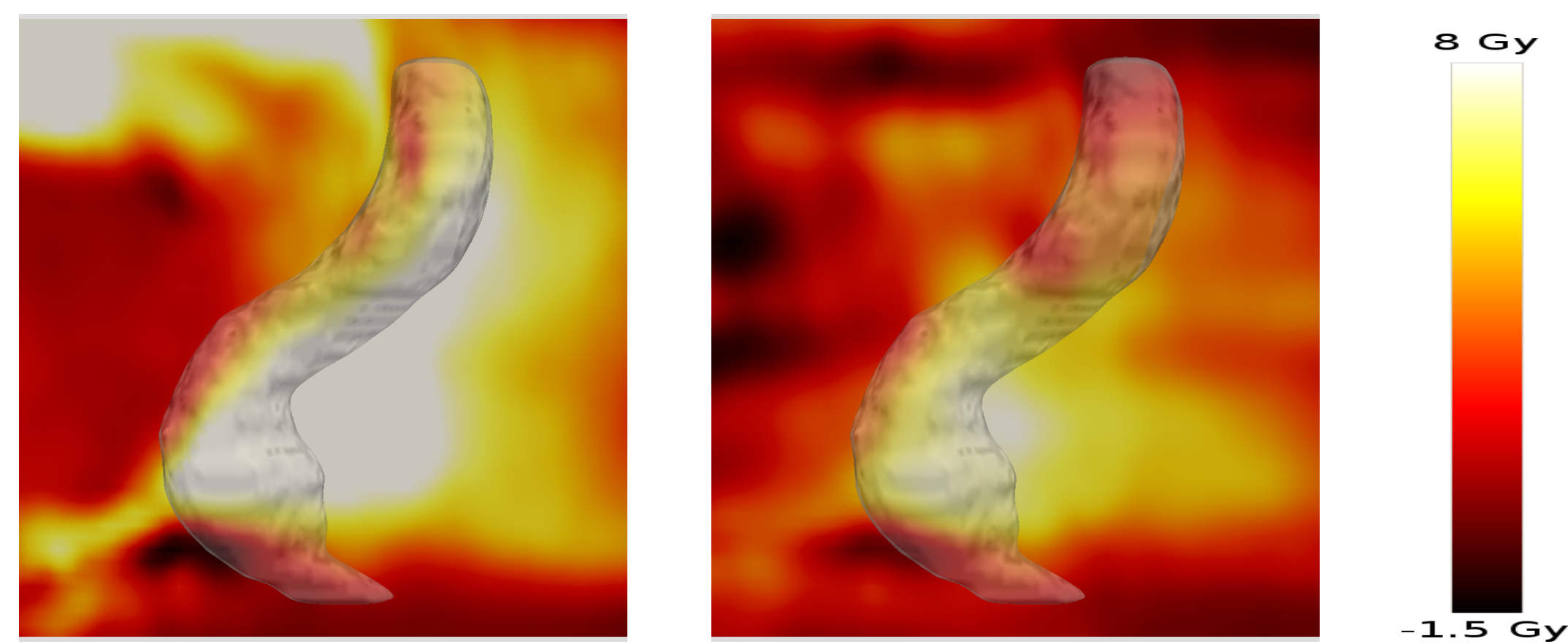
- Two-sample t-tests are used component-wise over the components of the average core tensors of groups G_1 and G_2 , namely $\mathbf{A}^{(G_1)}$ and $\mathbf{A}^{(G_2)}$.
- The typical image for each group can be written as $\mathbf{Y}^{(G_j)} = \mathbf{A}^{(G_j)} \times_1 \mathbf{P}^{Q_1} \times_2 \mathbf{P}^{Q_2} \times_3 \mathbf{P}^{Q_3}$, $j = 1, 2$, where each component of $\mathbf{A}^{(G_j)}$ is computed as the average of the core tensors of all individuals if no statistical difference is accepted for that component or as the average of only the individuals belonging to the group if a statistical difference is accepted.

Experiments and Results

Experiment set up:

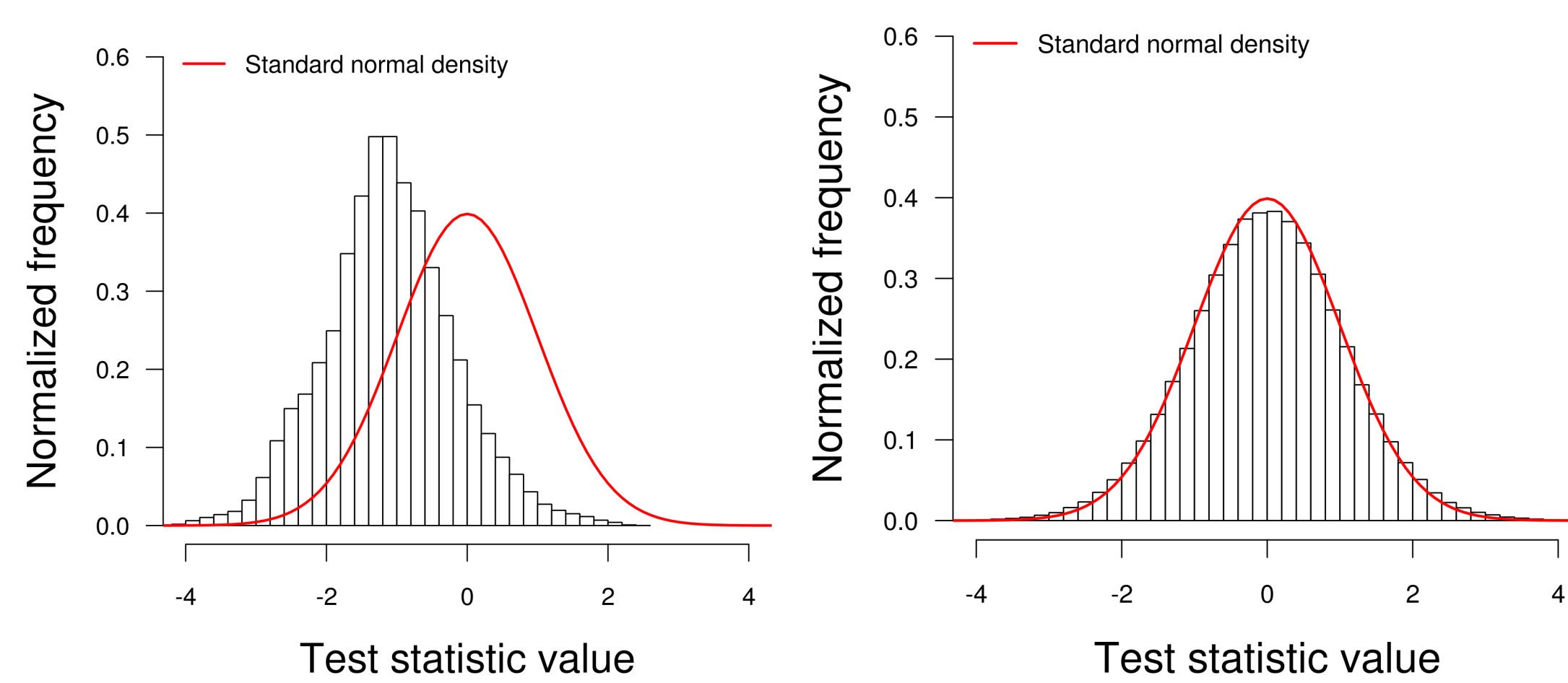
- In our study 63 (12 bleeders) patients treated for localized prostate cancer with IMRT were included from a randomised study [4].
- The clinical endpoint was 2-year rectal bleeding grade ≥ 1 (CTCAE version 3.0).
- Patients' planned CTs were non-rigidly registered into a single coordinate system by combining the CTs and organs delineations with the demons algorithm [5], and then the obtained transformations were applied to the dose distributions.

- Each patient's dose was decomposed using the HOSVD **without compression**.
- Figure (a) shows the simple difference of the means (in Gy) of the bleeding and nonbleeding patients on the rectum template. A "typical" core tensor for each group was calculated. Then the difference in dose between the two groups were computed (figure (b)).
- The histogram of the test statistics in the native aligned image space is presented in figure (c) and in the core tensor space in figure (d).



(a) Simple difference of means (Gy).

(b) Tensor-based PVD difference of means (Gy).



(c) Native space test statistic histogram. (d) Tensor-based test statistic histogram.

Conclusions and future work

- The proposed methodology can be applied to high order data ($\geq 3D$).
- The method can be used to find dose patterns correlated with other side-effects following RT.
- In many cases, the direct application of the t-test on the registered dose images is not advised as normality assumption is rejected.
- The method can be applied to any population of 3D images previously spatially normalized.
- The effect of compression in population analysis using PVD is ongoing research.

References

- [1] Ciprian M Crainiceanu et al. "Population Value Decomposition, a Framework for the Analysis of Image Populations". In: *Journal of the American Statistical Association* 106.495 (2011), pp. 775–790.
- [2] K.J. Friston et al. "Statistical parametric maps in functional imaging: a general linear approach". In: *Human brain mapping* 2.4 (1994), pp. 189–210.
- [3] Lieven De Lathauwer et al. "A multilinear singular value decomposition". In: *SIAM J. Matrix Anal. Appl* 21 (2000), pp. 1253–1278.
- [4] Véronique Beckendorf et al. "70 Gy Versus 80 Gy in Localized Prostate Cancer: 5-Year Results of GETUG 06 Randomized Trial". In: *International Journal of Radiation Oncology*Biophysics* 80.4 (2011), pp. 1056–1063.
- [5] Jean-Philippe Thirion. "Image matching as a diffusion process: an analogy with Maxwell's demons". In: *Medical image analysis* 2.3 (1998), pp. 243–260.