AUTOMATIC METHOD FOR TUMOR SEGMENTATION FROM 3-POINTS DYNAMIC PET ACQUISITIONS

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Abstract

A novel technique to segment tumor voxels in 3-points dynamic positron emission tomography (PET) scans is here presented. This algorithm allows the **identification of tumoral cells in dynamic FDG-PET scans** thanks to their peculiar anaerobic metabolism experienced over time.
The proposed tool has been preliminarily tested on a small dataset showing **promising performance** as compared to the state of the art in terms of both accuracy and classification errors.

Background

Glycolysis can be used as an excellent marker in the detection of cancer cells; FDG-PET - in which the concentrations of the tracer indicate a glucose uptake in the imaged area - turns to be a good tool in detecting tumoral masses.
In images obtained by PET acquisitions the intensity of a voxel represents local concentration of the tracer.
Dynamic PET: Tracer activity is measured in different time windows, resulting in a *time activity curve* (TAC) for each voxel. The shape of the TACs, usually found by sample interpolation, conveys tissue specific biochemical properties over time and carries precious information on the amount and rate of tracer flux and accumulation.

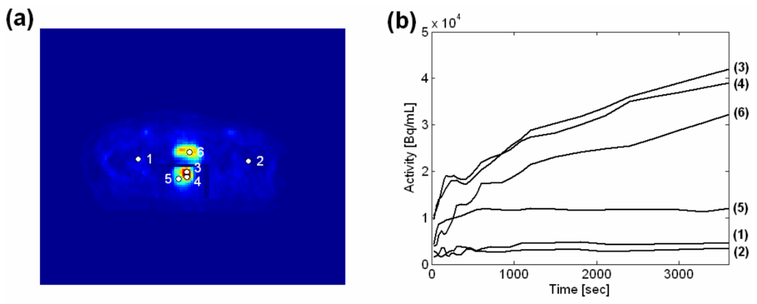
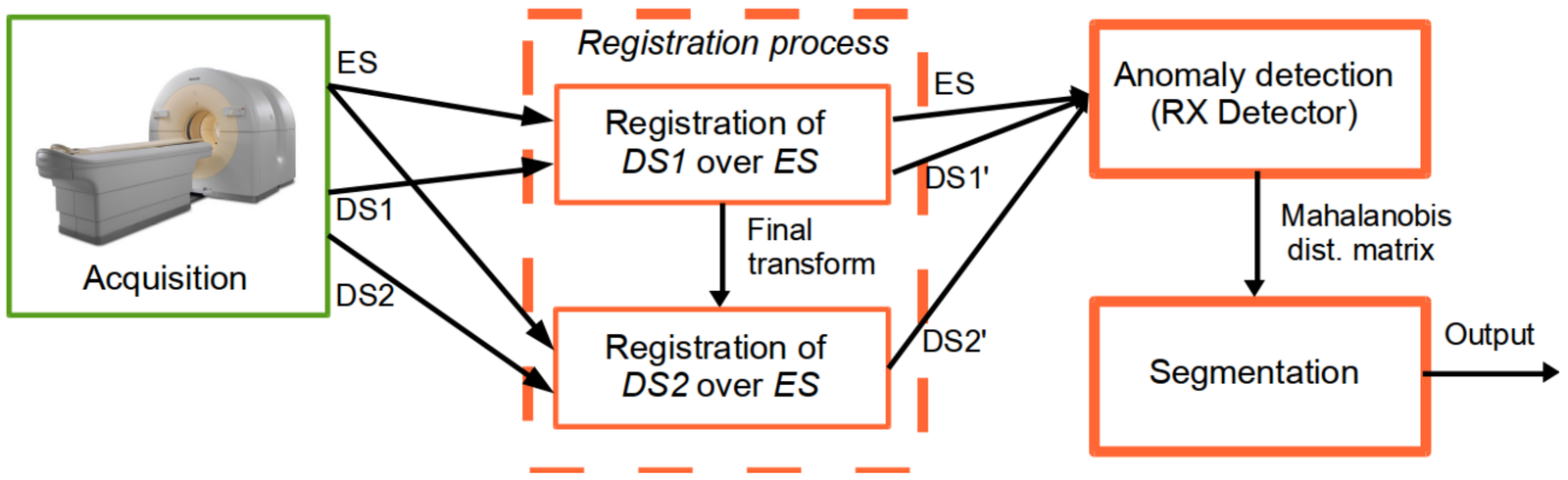


Image courtesy of [1]

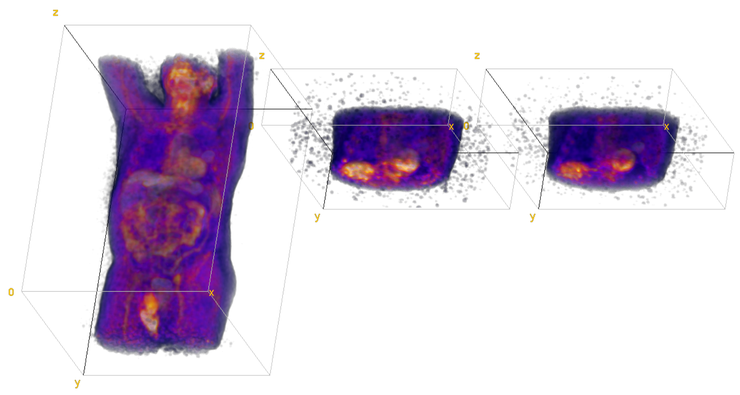
The proposed method



Registration

$DS1$ and $DS2$ are reconstructed from the same scan $\rightarrow$ the transformations leading to registration of $DS1$ and $DS2$ are expected to be very similar.
We first register $DS1$; then, the final transformation obtained on $DS1$ is provided as an initial estimate for $DS2$ registration.

Half the number of iterations required to register $DS2$



RX Detector

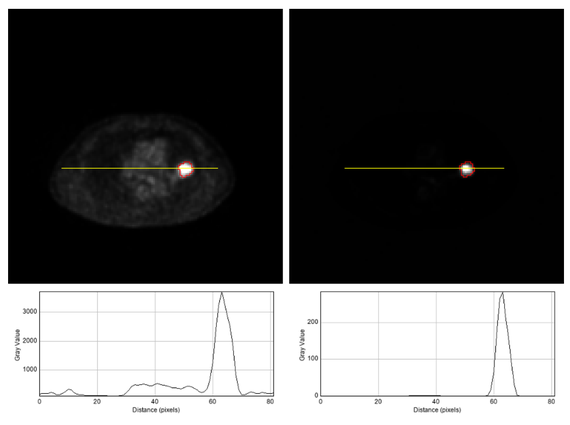
$$\widehat{C} = \frac{1}{N} \sum_{i=1}^{N} (x_i - M)(x_i - M)^T$$

where $x_i = (x_{i,ES}, x_{i,DS1'}, x_{i,DS2'})$ is the row vector representing the representing the 3 SUV values of the i-th voxel, N is the total number of voxels and $M = (\mu_{ES}, \mu_{DS1'}, \mu_{DS2'})$ is the average value of the 3 components.
To segment:

$$\delta_{RX}(x_i) = (x_i - M)^T \widehat{C}^{-1} (x_i - M) > \eta$$

where η is a proper decision threshold. δ_{RX} is also known as Mahalanobis distance [2].
We propose to detect the tumor voxels setting η adaptively as a function of the δ_{RX} dynamic range.
We set $\eta = P \cdot \max(\delta_{RX})$ with $P \leq 1$.

Experimental validation



-	SOI		Volumes (ml)		
n.	**RX**	**Thresh.**	**RX**	**Thresh.**	**ROI**
1	0.569	0.659	7.808	9.856	19.648
2	0.564	0.416	12.032	13.568	15.680
3	0.377	0.029	24.512	248.128	11.136
4	0.674	0.000	11.072	3.136	6.592
5	0.628	0.000	11.072	3.136	7.872
6	0.433	0.514	2.816	6.976	7.232
Mean	0.541	0.270	11.552	47.467	11.360
Std Dev	0.114	0.295	7.197	98.386	5.279

References

[1] M. H. M. Janssen et al., "Tumor Delineation Based on Time-Activity Curve Differences Assessed With Dynamic Fluorodeoxyglucose Positron Emission Tomography-Computed Tomography in Rectal Cancer Patients," Int. J. Radiat. Oncol. Biol. Phys., vol. 73, no. 2, pp. 456-465, 2009.

[2] P. C. Mahalanobis, "On the generalized distance in statistics," presented at the National Institute of Sciences of India, Calcutta, India, 1936, vol. 2, pp. 49-55.

Conclusions

The proposed approach leverages on the well known RX Detector, applied for the first time to this domain, to look for anomalies in 3points TAC.
RX Detector effectively improves the quality of the segmentation by significantly enhancing contrast between tumor region and background.
Future validation of the method should be performed.