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Segmentation in Quantitative Dynamic Nuclear Medicine: The Insufficiency of AAPM's TG-211

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INTRODUCTION

- Quantitative Dynamic Nuclear Medicine (QDNM) is used to track the movement of radiopharmaceuticals in regions of an organism (Maguire).
- By its functional nature, it can be difficult to properly segment an image, on account of physiological and metabolic displacements of the radiopharmaceutical compound.
- Purely manual segmentations is too user-dependant (Fahey).

AIM

- The aim of this project is to raise the technical difficulties present in the segmentation schemes for QDNM.
- TG-211 of the AAPM highlights static segmentation schemes for nuclear medicine images (Hatt). **These techniques are not sufficient in a dynamic context**.
- Two dynamic aspects between timeframes are not taken into account:
  - Metabolic movements of the radiopharmaceutical;
  - Physiological movements between timeframes.

METHOD

Two experimental setups were used to obtain QDNM data:

- A dynamic fantom injected with FDG was imaged for 60 minutes with 60 timeframes of 60 seconds. Died FDG was flowing from one compartment to another. For some acquisitions, an oscillatory motion was integrated.
- Rats were injected with F[18]-fluoropyridine Candesartan and were imaged for 60 minutes, with 12 x 10s, 3 x 60s, and 11 x 300s timeframes.

Three segmentation schemes were applied for each dynamic acquisitions, according to the classification of the AAPM-211: statistics-based, gradient-based, and filling-based segmentations.

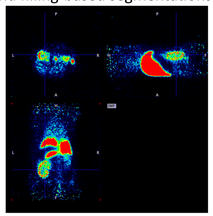

Figure 1: Three cuts of a rat injected with a radipharmaceutical compound. The cross is located on the left kidney.

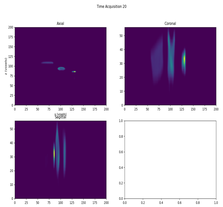

Figure 2: Three cuts of the phantom, where each compartment flows into the next. The compartment of interest is between two others.

ANALYSIS

The segmentations were applied on a single timeframe and were kept for the whole QDNM acquisition; the process was repeated for each timeframe.

The goal was to segment one of the compartment of the fantom and the left kidney of the rats.

The segmentations were first classified by manual observation: those that gave a valid shape were kept, whereas the others were discarded.

Two categories of analysis were done, on the resulting Time-Activity Curves (TACs) and on the segmentations themselves.

Analysis of the TACs (posteriori/backward):

1. To estimate an uncertainty on each TACs, each segmentation was shifted by one (1) voxel along each of the cardinal axes;
2. A TAC was computed for each of these shift, i.e. a **shifted TAC**;
3. The resulting curve used (Figure 3 top) was computed from the mean and standard deviation of all shifted TACs.

Analysis of the Segmentation (priori/forward):

1. Each volume of the segmentation were compared with each other using the Sørensen-Dice similarity coefficient:

$$D(A,B) = \frac{2|A \cap B|}{|A| + |B|},$$

where A and B are the segmentation and $|.|$ is the cardinality of that segmentation, i.e. its volume; $\cap$ is the intersection of the two sets.

2. The Sørensen-Dice coefficients were plotted for all valid segmentations, to compare the segmented volume (Figure 3 bottom).

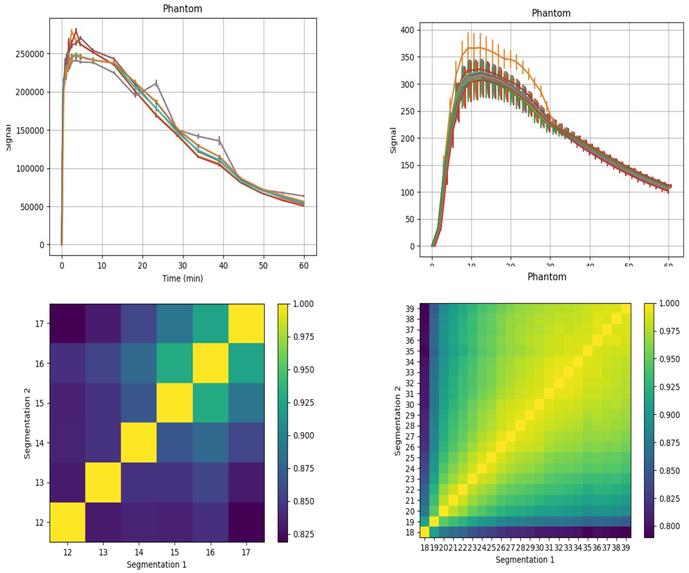

Figure 3: TACs (top) and Sørensen-Dice coefficients (bottom) for the various segmentations on a rat (left) and a fantom (right).
The illustrated results were obtained for a statistical segmentation, based on an ICM; the same hyperparameters were used for all timeframes.
Each axis of the bottom images represent a segmentation based on a specific timeframe. Each entry is thus the Sørensen-Dice coefficient between these two segmentations.

RESULTS

The relationship between the Sørensen-Dice coefficients and the TACs is not obvious. For some acquisitions, the coefficients were high and the TACs were statistically similar, whereas, in other cases, the coefficients were also high, but the TACs were dissimilar; in some other cases, low coefficients led to either poor or good overlapping of the TACs and their uncertainties. **The Sørensen-Dice coefficients are thus a necessary component for the quality of the segmentation, but they are not sufficient.**

Concerning the behaviour of the TACs

- In general, the **TACs with their uncertainties overlap for the phantoms**;
- In general, the **TACs with their uncertainties don't overlap for the rats**.

Thus, the presence of a movement within the subject implies varying segmentations;

These varying segmentations have a significant impact on the TACs and, thus, the transfer coefficients that could be extracted for pharmacokinetic purposes.

NEXT STEPS

- Repeat the acquisitions on the phantoms, but with varying movements, with faster or lower oscillatory motions.
- Estimate the uncertainties on individual TACs by shifting them differently, ideally based on the known movement of the subject.
- Develop a method to segment dynamic images reliably.

CONCLUSIONS

The process of segmentation plays an important role in quantitative dynamic nuclear medicine imaging.

Manual segmentation is not enough, since there is a high dependency on the user and between them.

By using a static segmentation as described by the Task Group 211 of the AAPM, the results are not consistent, depending on which timeframe is used as a reference.

This leads to the need to revisit the methods used to segment images in QDNM, either by integrating experimental uncertainties on the TACs or by determining a valid dynamic segmentation method.

Such an endeavour would allow for more precise and accurate TACs, which would, in turn, allow for better subsequent analysis, such as in pharmacokinetics.

REFERENCES

- Canny, J. *A Computational Approach to Edge Detection.* IEEE Transactions on Pattern Analysis and Machine Intelligence 8(6). 1986.
- Diaz, A.M.A. et al. *Evaluation of the High Affinity of [18F]fluoropyridine- candesartan in rats for PET imaging of renal AT1 receptors.* Nuclear Medicine and Biology, 96-7. 2021.
- Fahey, F. et al. *Variability in PET quantitation within a multicenter consortium*. Med. Phys. 37(7). 2010.
- Hatt, M. *Classification and evaluation strategies of auto-segmentation approaches for PET: Report of AAPM Task Group No. 211.* Med. Phys. 44(6). 2017.
- Lortie, M. et al. *Analysis of [11C]methyl-candesartan kinetics in the rat kidney for the assessment of angiotensin II type I receptor density in vivo with PET*.
- Nuclear Medicine and Biology 40(2). 2013.
  Maguire, R.P. et al. *PET Pharmacokinetic Course*. Montreal Neurological
- Institute: Montréal. 2003.
- Meikle, S.R. et al. *Quantitative PET in the 2020s: A Roadmap.* Phys. Med.
- Biol. in press. 2020.

ACKNOWLEDGEMENTS

This research was conducted as part of the activities of the TransMedTech Institute, thanks in part to the financial support of the Apogee Canada Research Excellence Fund and the Fonds de Recherche du Québec.

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