An exploration of the prognostic utility of shortened dynamic imaging protocols for PET-FDG scans

Qi Wu, Finbarr O'Sullivan, Mark Muzi and David A. Mankoff

***Abstract*—Standard whole-body clinical fluoro-deoxyglucose (FDG)-PET scans typically involve imaging for around 15 minutes about 60 minutes after tracer injection. The scan duration is often the critical constraint limiting patient through-put. Scans taken long after tracer injection restrict the ability to assess vascular and perfusion information that might be revealed by the early pattern of tracer uptake. On the other hand, early scanning may compromise the recovery of the late time uptake (SUV) which in many contexts has well established prognostic value. In this study, we explore the potential for short-duration dynamic scans, acquired immediately after tracer injection, to recover information that can predict late-stage uptake of FDG. The work involves re-analysis of existing series of dynamic brain and breast tumour imaging data to simulate the type of information that would arise from early and late scanning. Using a collection of machine learning techniques (including random forests, neural networks, gradient boosting), we find that short-duration clinical protocols, soon after the tracer injection, show significant potential to recover the late stage FDG flux information.**

I. Introduction

POSITRON emission tomography scanning is an important tool for cancer diagnosis and treatment planning. As the next generation of PET total-body scanners[1] will have full coverage of a subject's blood pools, they may offer potential to refine the acquisition of clinical scan data in order to extract more detailed kinetic information. Hence it is of interest to examine if earlier scanning would allow recovery of more detailed kinetic parameters and provide enhanced prognostic benefits relative to the late scan SUVs. In order to examine this, we undertook a study to evaluate the value of the kinetic information that might be recovered from short dynamic scans, acquired immediately after the FDG tracer injection.

II. Materials and Methods

We consider data from a brain tumor study reported by Spence et al.[8] and a locally advanced breast cancer (LABC) study reported by Mankoff et al.[3]. The brain set consisted of 14 patients (6 Male, 8 Female) aged between 30 to 65 with malignant Glioma had dynamic PET-FDG scans 2 weeks prior to standard radiation treatment. The scan duration was typically 90 minutes with a few patients images for 70 minutes or less. All brain studies had frequent arterial sampling. In the Mankoff et al. study, 53 female LABC patients aged between 32 to 76 underwent ^{15}O-water and ^{18}F-FDG PET imaging before neo-adjuvant chemotherapy and surgery. Image-based AIF recovered from a region of interest of left ventricle[7]. Full image data were resampled to simulate the series that might result from shorter duration imaging sessions. Series corresponding to the first 15 minutes only and 0-30 minutes for both brain and breast data.

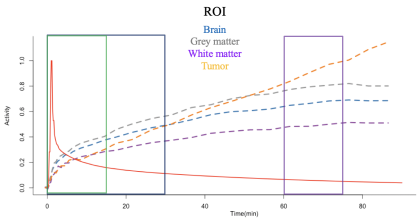

Fig. 1: Resampled PET-FDG scan data in the brain tumour series: first 15 minutes(green), 0-30 minutes(navy) and clinical setting 60-75 minutes(purple). A similar resampling approach was used for the breast series.

A. Mixture Analysis and Residue Mapping

Raw dynamic scan data were processed, using a mixture analysis[5, 6], to recover voxel-level metabolic variables - see Figure 2. The basis of this is as follows: The total tissue concentration, $C_T(t)$ is expressed as a convolution between the tissue response(Residue) and the arterial input function, $c.f.$ Meier and Zierler[4].

$$C_T(t) = K \int_0^t R(t-s) C_P(s) ds = R \otimes C_P(t) \qquad (1)$$

where $C_T(t)$ is the concentration of radio-labeled tracer in a tissue region, measured as activity per unit volume (KBq/cm3). $C_P(t)$ is the time-course of the tracer the arterial blood as activity per millilitre(ml) of blood; R is the tissue residue function - this can be regarded as a life-table for tracer atoms in a tissue region. Using mixture model[5] and a non-parametric approach to residue analysis[6] we can map the residue for each voxel. From the residue we evaluate Vascular flow and volume (K_B,V_B), distribution flow and volume (K_D,V_D), flux (K_i), overall flow (K_1) and extraction (Ext=K_i/K_1). Each metabolic variable represents a metabolic feature extracted from the Residue. So we converted the dynamic image data to a set of 3-D metabolic images on the voxel bases. The metabolic mapping process is applied to the full dynamic scan and also to the shorter 0-15 minute and 0-30 minute scans. Our further analysis are based on these datasets - metabolic feature variables.

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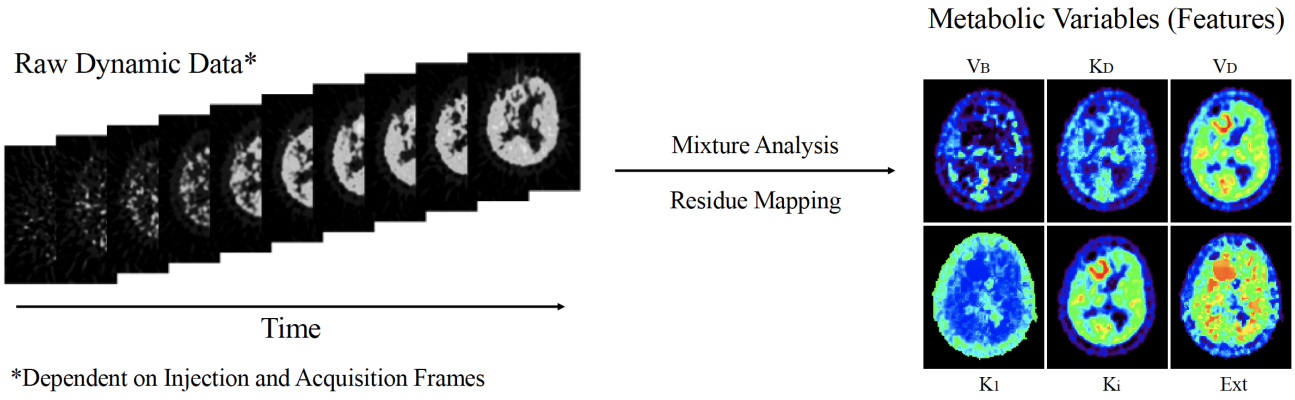

Fig. 2: Concepts of converting dynamic image data to a set of 3-D metabolic images

B. Machine Learning Methods Applied to Voxel-Level Data in the Metabolic Parameter Domain

A range of machine learning (ML) techniques[2] [multiple linear regression, Generalized additive models(GAM), random forests, Neural networks(NN) and Gradient Boosting Machines(GBM)] were used to construct Voxel-level predictions of flux derived from the full dynamic data using the metabolic variables recovered from analysis of shorter duration scans. We selected a sample of patients as a training set and separate patient for testing. Within training sets, random samples of voxels were used, this was to reduce impact of spatial autocorrelation within images. Model selection used standard training and test-set schemes for tuning.

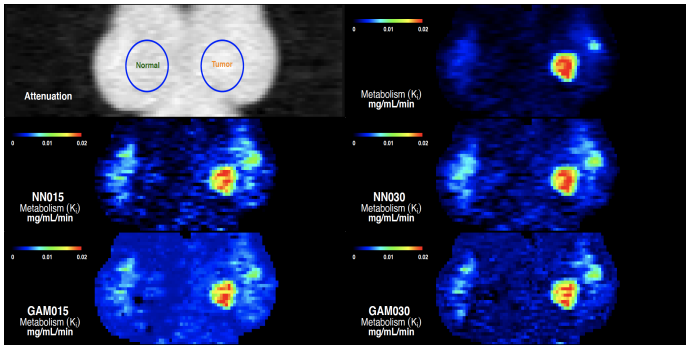

Fig. 3: Sample voxel-level mapping of the FDG flux (acquired from the full dynamic data) using on shorter scan metabolic information and a range of ML techniques results in breast tumor study

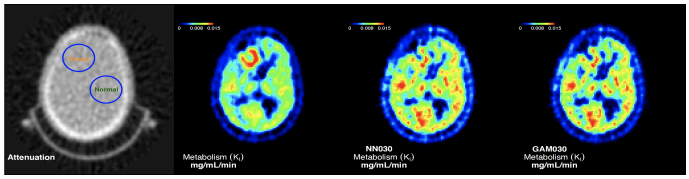

Fig. 4: Sample voxel-level mapping of the FDG flux (acquired from the full dynamic data) using on shorter scan metabolic information and a range of ML techniques results in brain tumor study

III. Results

Figure 3 shows the result of the analysis of data from breast cancer subject. We used Neural network and Generalized additive model to train the model with flux required from full dynamic scan as response variable and several kinetic parameters recovered from shorter duration scans, corresponding to first 15 minutes and first 30 minutes. And use separate patient's dynamic PET data for validation. Lower four images give the estimated flux image. The tumor region can be easily identified on these images and 30 minutes early scan can also shows the tumor characteristics which could has prognostic value in treatment planning. Similar result for brain tumor datasets shows in Figure 4. Results for the brain tumor data are less good but a more refined implementation that incorporates information about the specific range of tissues involved and different types of tumor may enhance performance.

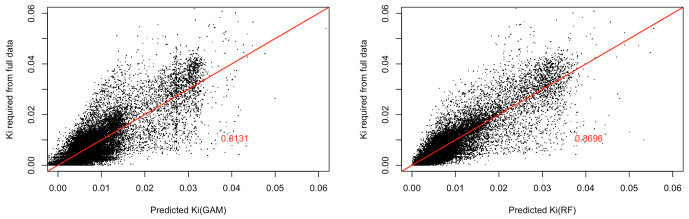

Fig. 5: Sample voxel-level comparisons between true and predicted flux based on generalized additive models and random forests.

IV. Conclusion

Voxel level results are mixed with much better performance in the breast cancer setting. Overall results from this series are promising and merit more detailed evaluation. This work is underway.

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