Conclusion
SFOV 4D-CBCT images were found to improve visually when subjected to a simple streak correction. Improvements were likewise observed on quantitative measurements of gradients as well as on CBCT HU to CT HU comparisons, and did not degrade the overall HU levels of the image. With gpu-optimization the calculation time of the method can potentially be reduced to less than a minute which will make it usable for on-line IGRT.

EP-2140 A Bayesian mixture-model for ion identification and filter in particle imaging
C.A. Collins Fekete[1]
[1]*National Physical Laboratory, Chemical- Medical and Environmental Science, Teddington, United Kingdom*

Purpose or Objective
Proton imaging promises to produce accurate relative stopping power (RSP) maps crucial for particle therapy treatment planning. Yet, protons suffer from multiple Coulomb scattering that degrades the image spatial resolution. Less deflected-heavier ions have been suggested to reduce this problem. However, those ions produce secondary particles through nuclear interactions, which increase the detector noise. A Bayesian mixture-model (BMM) is developed to predict the most-likely particle related to each set of measurements produced by an event.
Material and Methods
In a mixture model, it is assumed that a given event can be drawn from one of N generating processes. In particle imaging, it is assumed that the detector's measurements for a single event are caused by either a primary or secondary particle generated from electromagnetic or nuclear processes. First, a likelihood model with loose parameters is constructed for each process. The indicator $q_i \in [0,N]$ is introduced to point the *i-th* measurement to a model. The likelihood of the measurement to origin from this process is then calculated from the chosen model. The BMM posterior is the product of this likelihood over all particles with a prior estimated from the expected ratio of primaries and secondaries. The set of indicators **q** is modified iteratively, while improving the models' parameters, to maximize the posterior. The optimal set indicates the most-likely particle attached to each event. The BMM is compared to the classical three-sigma clipping filter. To validate the BMM, helium ions are simulated (n=10^6,330 MeV/u) crossing an abdomen phantom.
Results
The three-sigma filter identifies correctly 51.2% real positive (RP) and 1.2% real negative (RN) measurements, giving a total of 52.3% true identifications. This filter lacks precision in rejecting secondary events. The proposed BMM identifies correctly 49.2% RP and 48.8% RN measurements, giving a total of 98.0% true identifications. In addition, the BMM correctly identifies 79.3% of the charged secondaries as protons, deuteron, tritium and ^{3}He.

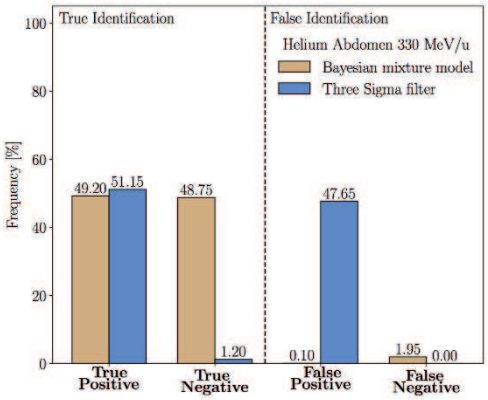

Figure 1: Fraction of the particles identified correctly and incorrectly when compared to their actual identity for both techniques (BMM and three-sigma filter). Helium ions (n=10^6, 330 MeV/u) were simulated through an abdomen anthropomorphic phantom to generate this figure.

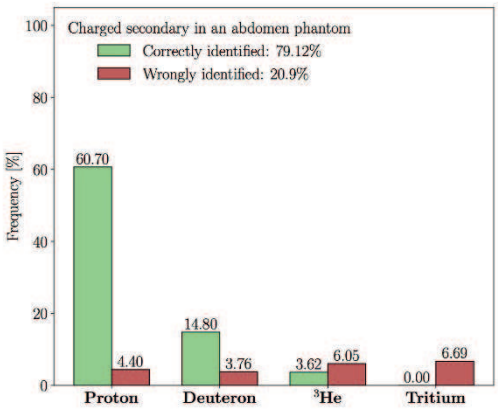

Figure 2: Percentage of the secondary particles correctly and incorrectly identified by the BMM technique against the particle type. Helium ions (n=10^6, 330 MeV/u) were simulated through an abdomen anthropomorphic phantom to generate this figure.
Conclusion
The higher rate of true identifications compared to the three-sigma method shows that the BMM is a prime candidate for filtering in helium imaging. This development opens the way for precise particle imaging, which is hypothesized to produce high accuracy/resolution RSP maps. Furthermore, the precise classification of charged secondaries is encouraging for future applications, *e.g.* nuclear fluence loss tomography.

EP-2141 Evaluation of 2D and 3D radiomics features extracted from CT images of oesophageal cancer patients
C. Piazzese[1], P. Whybra[1], R. Carrington[2], T. Crosby[2], J. Staffurth[2], K. Foley[3], E. Spezi[1]
[1]*Cardiff University, School of Engineering, Cardiff, United Kingdom*
[2]*Velindre Cancer Centre, Cardiff, United Kingdom*
[3]*Cardiff University, School of Medicine, Cardiff, United Kingdom*

Purpose or Objective
Radiomics is the practice of extracting large number of quantitative features from medical images and it can be used to inform decision support systems. Radiomic features can be computed by considering one tumour layer at a time in 2D or the whole tumour layers in 3D. Due to lower complexity and faster calculation, 2D

features can be easier to obtain, although 3D features can carry more information about the tumour. The aim of this work is to determine if there is a statistical significant difference between textural features extracted from a gross tumour volume (GTV) delineated in a 2D single CT section compared to the same features extracted from the GTV defined as a 3D volume.

Material and Methods

This study included 213 patients with staging CT from a clinical trial in oesophageal cancer[1]. For each patient, the GTV was delineated by an expert oncologist. The CT and structure data in DICOM RT format were imported and processed into the CERR software package[2] for all patients, and automatically processed using in-house developed data analytics software[3]. To test the features' stability, patients were randomly divided into three groups of 71 subjects each and a Kruskal-Wallis test was performed. Stable features were selected as the ones with similar distributions among groups. Unstable features were excluded from further analysis. The remaining corresponding stable features between the 2D and 3D groups were evaluated with a paired two-sided Wilcoxon signed rank test to assess for significant differences between 2D and 3D groups. A p-value of <0.05 was considered statistically significant.

Results

A total of 238 radiomics features (119 2D and 119 3D features, respectively) were computed from the analysed data. The Kruskal-Wallis test excluded 43 features (39 2D vs 43 3D). Among the 76 remaining corresponding stable features, 70 features showed a statistically significant difference between 2D and 3D groups. Six features showed no difference if computed in 2D or 3D. Figure 1 depicts a heat map of the 76 2D and 3D normalized features.

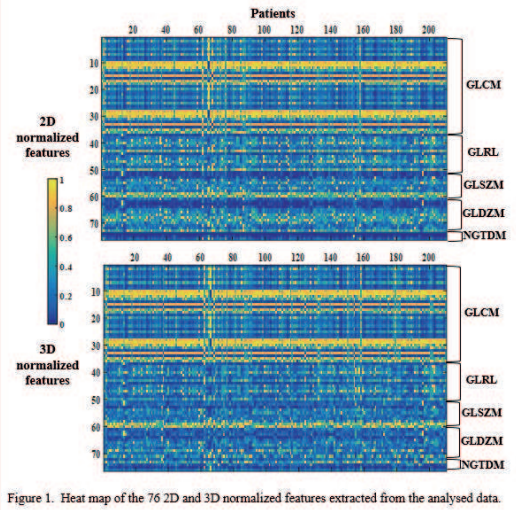

Figure 1. Heat map of the 76 2D and 3D normalized features extracted from the analysed data.

Conclusion

There are significant differences between features extracted from tumours in 2D and 3D. Consequently, prognostic information may vary depending on the method used to compute these features. Further work is needed to fully assess the impact of 2D and 3D texture feature extraction methods on the derivation of prognostic models.

References:

1. Hurt CN, Nixon LS, Griffiths GO, et al. SCOPE1: a randomised phase II/III multicentre clinical trial of definitive chemoradiation, with or without cetuximab, in carcinoma of the oesophagus. BMC Cancer. 2011 Oct 28;11:466.
2. Deasy JO, Blanco AI, Clark VH. CERR: a computational environment for radiotherapy research. Med Phys. 2003 May;30(5):979-85.
3. Gwynne S, Spezi E, Wills L, et al. Toward semi-automated assessment of target volume delineation in radiotherapy trials: the SCOPE 1 pretrial test case. Int J Radiat Oncol Biol Phys. 2012 Nov 15;84(4):1037-42.

EP-2142 Implementation of registration quality assurance

K. Anderle[1], T. Brandt[2], J. Wölfelschneider[2], C. Bert[2], C. Graeff[1]
[1]*GSI Helmholtz Centre for Heavy Ion Research, Biophysics, Darmstadt, Germany*
[2]*Universitätsklinikum Erlangen, Radiotherapy, Erlangen, Germany*

Purpose or Objective

A registration is nowadays commonly used in radiotherapy, most commonly to connect different image modalities. With a more precise deformable image registration (DIR) several new fields in radiotherapy arise, such as contour propagation, plan adaptation and time-resolved (4D) dose calculation. However, DIR is prone to errors and a rigorous quality assurance (QA) is required to implement DIR in clinical environment. We have developed an open-source software to provide a registration QA with several different measures.

Material and Methods

We have followed the guidelines of recently published AAPM task group report (Brock *et al.*, 2017), where 8 different measures are proposed to be verified during registration QA. As shown on Figure 1, there are several different inputs necessary to fulfill all 8 measures and the list doubles with forward and backward registration (fixed and moving images are reversed in registration) present. We have incorporated all measures as an extension in the open-source software Slicer 3D, called RegQA. The RegQA module combines existing Slicer 3D functionality (measure 1, 2 and 4), SlicerRT Segment Comparison module logic (measure 6), three custom designed command-line modules based on ITK (measure 3, 7 and 8) and custom design logic (measure 5). All inputs can be loaded manually or automatically, if the paths to files are specified. The user can export the result of DIR QA as a set of images and as a table with quantitative results from measures 5, 6, 7 and 8.

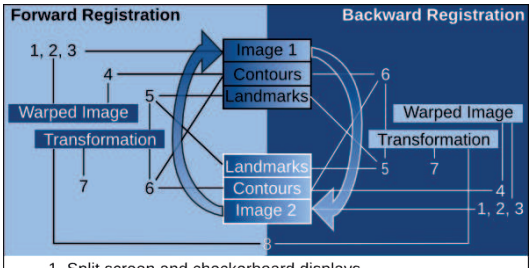

Figure 1 - Schematic presentation of 8 measures for registration quality assurance and the necessary inputs for each measure. Forward and backward registration correspond to reversed fixed and moving image in registration algorithm.

Results

Our software was validated on several CT-CT, CT-MRI and inter-4DCT DIR. The resulting DIR QA pointed out errors in either image acquisition or DIR results. A special efficiency was proven for the 4DCT DIR QA, where 10 4DCT phases, along with forward and backward registration resulted in a large number of different inputs (414 DIR). An automation process in our software enabled quantitative DIR QA on 414 different DIR with minimal