AbstractID: 11243 Title: Validation of an analytical 1D filtering of the dose distribution for the calculation of the expected PET distributions in proton therapy.

Purpose: A non-invasive method for verification of treatment delivery to ensure the high quality of proton therapy is offered by Positron Emission Tomography (PET), which takes advantage of the β+-activation produced via nuclear reactions between the protons and the nuclei of the tissue during irradiation,. Since dose distributions and measured PET images are correlated but not identical, a procedure to provide clinical feedback on the correct dose delivery and irradiation field position is necessary. This study aims to validate the measured activity patterns by means of activity distributions calculated using a novel and fast one-dimensional filtering model recently proposed. This way the actual dose delivery can be validated without reverting to Monte Carlo simulated PET distributions.

Method: We derived the analytical expressions of the filters by converting the dose into the specific isotope profiles along the penetration depth, for all the main reaction channels which yield positron emitters in biological tissue. For the application to inhomogeneous targets a dedicated MATLAB®-based code has been developed.

Results: The new filters were first applied to monoenergetic depth dose distributions at different beam energies and the results were validated against FLUKA-MC β^+ isotope distributions. All resulting distributions were found in agreement with the MC distributions, confirming filter independence from the proton beam energy. The filter functions were then applied to more realistic spread out Bragg peaks, simulated in simple inhomogeneous targets consisting of PMMA, lung and bone equivalent inserts.

C**onclusion**: Results have shown a fairly good agreement in terms of both 50% distal fall-off position (<1mm) and absolute value between simulated depth activity profiles and filter predictions (few percent), demonstrating how a proper filtering of the MC depth dose distribution can be used to predict in a simple and fast manner all the possible β^+ activations of an arbitrary target.