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# Regularised patient-specific stopping power calibration for proton therapy planning based on proton radiographic images

Accepted manuscript

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## Abstract

Proton transmission imaging has been proposed and investigated as imaging modality complementary to X-ray based techniques in proton beam therapy. In particular, it addresses the issue of range uncertainties due to the conversion of an X-ray patient computed tomography (CT) image expressed in Hounsfield Units (HU) to relative stopping power (RSP) needed as input to the treatment planning system. One approach to exploit a single proton radiographic projection is to perform a patient-specific calibration of the CT to RSP conversion curve by optimising the match between a measured and a numerically integrated proton radiography.

In this work, we develop the mathematical tools needed to perform such an optimisation in an efficient and robust way. Our main focus lies on set-ups which combine pencil beam scanning with a range telescope detector, although most of our methods can be employed in combination with other set-ups as well. Proton radiographies are simulated in Monte Carlo using an idealised detector and applying the same data processing chain used with experimental data. This approach allows us to have a ground truth CT-RSP curve to compare the optimisation results with.

Our results show that the parameters of the CT-RSP curve are strongly correlated when using a pencil beam based set-up, which leads to unrealistic variation in the optimised CT-RSP curves. To address this issue, we introduce a regularisation procedure which guarantees a plausible degree of smoothness in the optimised CT-RSP curves. We investigate three different methods to perform the numerical projection operation needed to generate a proton digitally reconstructed radiography. We find that the approximate and computationally faster method performs as well as the more accurate but more demanding method. We perform a Monte Carlo experiment based on a head and neck patient to evaluate the range accuracy achievable with the optimised CT-RSP curves and find an agreement with the ground truth expectation of better than 0.5%. Our results further indicate that the region in the patient in which the proton radiography is acquired does not necessarily have to correspond to the treatment volume to achieve this accuracy. This is important as the imaged region could be freely chosen, e.g. in order to spare organs at risk.

## 1 INTRODUCTION

Proton beam therapy offers high selectivity in dose deposition due to the protons' distinct depth dose profile, commonly referred to as Bragg curve. This feature potentially allows for high dose to the tumour while sparing healthy surrounding tissue (Durante & Paganetti 2016). To fully exploit this advantage, precise knowledge of the relative stopping power (RSP) of the patient tissue is needed to correctly predict the proton range in the treatment planning system (TPS), in the best case on the day of treatment.

48 Currently, proton treatment planning is performed based on X-ray computed tomography  
49 (CT) data typically acquired some days before the first delivered fraction. The X-ray CT  
50 is expressed in Hounsfield Unit (HU) and approximately converted to RSP (Schneider et al.  
51 2005). The uncertainties associated with the conversion process require additional safety margins  
52 around the contoured treatment volume (Jäkel et al. 2001, Paganetti 2012b). Proton radiography  
53 and proton CT have already been investigated a long time ago (West & Sherwood 1972, Koehler  
54 1968, Steward & Koehler 1973, Takada et al. 1988) and more recently been brought up in the  
55 context of proton beam therapy (Schneider & Pedroni 1995, Schulte et al. 2004). In analogy to  
56 X-ray based transmission imaging, protons are shot through the patient and an image is formed  
57 based on the residual energy or residual range measured by a suitable detector positioned behind  
58 the patient (Parodi 2014, Poludniowski et al. 2015, Johnson 2018). A full tomographic scan  
59 directly provides a volumetric RSP map of the patient and therefore bypasses any conversion.  
60 It could thereby allow for reduced safety margins (Arbor et al. 2015).

61 Schneider et al. (2005) proposed an approach based on a single proton radiography expressing  
62 the water equivalent thickness (WET) of the patient which is arguably easier to achieve in  
63 practice and exposes the patient to a lower dose than a full proton CT scan. The idea is not to  
64 circumvent the conversion, but to perform a patient-specific calibration of the CT-RSP curve  
65 by comparing a proton radiographic image with a proton digitally reconstructed radiography  
66 (pDRR). This optimised curve would then be used for the treatment planning instead of the  
67 clinical one.

68 More recently, the method has been studied in combination with two types of proton imaging  
69 set-ups. Doolan et al. (2015) used a single plane detector in double scattering beam delivery.  
70 In this case, the beam is gradually pulled back by a range modulator device while the pixel  
71 detector behind the patient records the signal created by many protons at once. On the other  
72 hand, in single proton tracking, the imaging set-up records information proton by proton and an  
73 estimate of individual proton trajectories through the patient can be derived, the so-called most  
74 likely path (Williams 2004, Schulte et al. 2008). Collins-Fekete et al. (2017) have investigated  
75 the patient-specific calibration in combination with this kind of system.

76 In this work, we consider a proton imaging set-up which combines pencil beam scanning  
77 with a range telescope (Rinaldi et al. 2013, 2014, Farace et al. 2016). It can be employed in clin-  
78 ical practice potentially using available quality assurance (QA) equipment and without further  
79 hardware modifications in the treatment room (Krah et al. 2018). It is therefore of interest to  
80 develop the mathematical tools necessary to perform a patient-specific CT-RSP calibration in  
81 combination with such a set-up. In particular, we develop a regularised optimisation procedure  
82 which, as it turns out, is necessary to obtain plausible calibration curves. We perform a Monte  
83 Carlo study to assess the accuracy and robustness of the proposed methods. Although we fo-  
84 cused on a specific kind of imaging system, most of our methods can be adapted and applied to  
85 other proton imaging set-ups as well.

## 86 2 MATERIALS AND METHODS

### 87 2.1 Patient specific calibration - general principle

88 The CT-RSP conversion curve is typically modelled as a series of linear segments parametrised by  
89 a set of parameter tuples  $(H_\alpha, R_\alpha)$ , as illustrated in the centre of figure 1 (Schneider et al. 1996,  
90 Taasti et al. 2018). The patient-specific calibration optimises the values of  $R_\alpha$  by minimising the  
91 difference between a pDRR and a measured proton radiography. A brute force implementation  
92 would start from an initial guess for the CT-RSP curve, convert a planning CT (expressed in  
93 Hounsfield Units [HU]) to a three-dimensional (3D) RSP map, project it to produce the pDRR,  
94 compare with the proton radiography (e.g., by calculating the mean squared difference), update  
95 the set of  $R_\alpha$  values, and iterate again. We will present a method to separate the projection  
96 operation from the actual optimisation step.

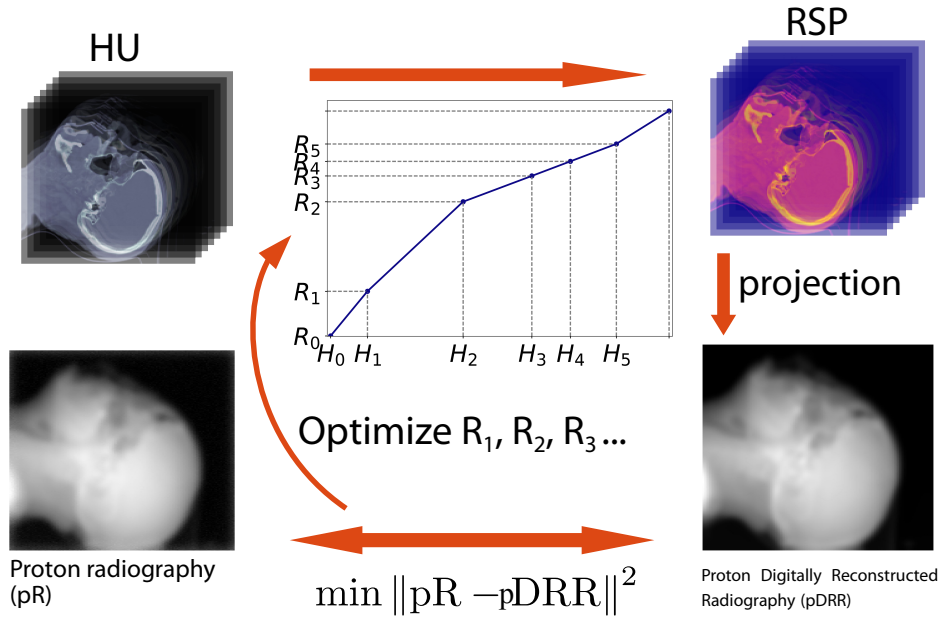


Figure 1: Optimisation scheme for the patient-specific CT-RSP calibration. The plot in the center is a schematic illustration of the CT-RSP curve defined as set of linear interpolations.

## 97 2.2 Framework of this study

98 Naturally, an important question to be asked would be: “How accurate does the patient-specific  
 99 calibration method reproduce the HU to RSP relation of the patient’s tissue?” Answering this  
 100 experimentally on the basis of phantom measurements would require precise knowledge of the  
 101 phantom’s spatial material distribution. For realistically complex anthropomorphic or animal  
 102 tissue phantoms, this information is difficult to have, although proton radiographic measure-  
 103 ments have been performed in phantoms of known material composition in some studies (Farace  
 104 et al. 2016, Wohlfahrt et al. 2018). Phantoms which are geometrically less complex than a  
 105 patient, on the other hand, might lead to unrealistic conclusions. For this reason, we remained  
 106 entirely within a Monte Carlo framework for our study where we could use a digital patient  
 107 model as ground truth. It was derived by converting a patient CT into RSP before importing  
 108 it into Monte Carlo (see section 2.4). The CT-RSP curve used for this conversion was therefore  
 109 the ground truth reference curve and we evaluated how well it was recovered by the optimisation  
 110 procedure. At no point do we attempt to directly compare the calibration outcome with some  
 111 clinical curve. This would require quantifying or modelling the typical discrepancies between  
 112 the true tissue properties and those predicted by a clinical curve, and it was not the scope of  
 113 this work.

## 114 2.3 Proton radiographies

115 We used *Fred*, a GPU-accelerated Monte Carlo code developed at University Rome La Sapienza,  
 116 to simulate proton radiographies. The code has been validated against other MC toolkits, Geant4  
 117 (Agostinelli et al. 2003, Allison et al. 2016) and FLUKA (Ferrari et al. 2005, Böhlen et al. 2014)),  
 118 as well as experimental data from the CNAO proton therapy facility in Italy (Schiavi et al. 2017,  
 119 ?) and, more recently, against measurements from the Krakow proton therapy facility (Garbacz  
 120 et al. 2019). Its advantage for our study was the high computation speed.

121 A patient CT image was imported into *Fred* and to each voxel, an elemental composition,  
 122 density, RSP, and radiation length was assigned as explained in section 2.4. No segmentation  
 123 into tissue compartments was performed.

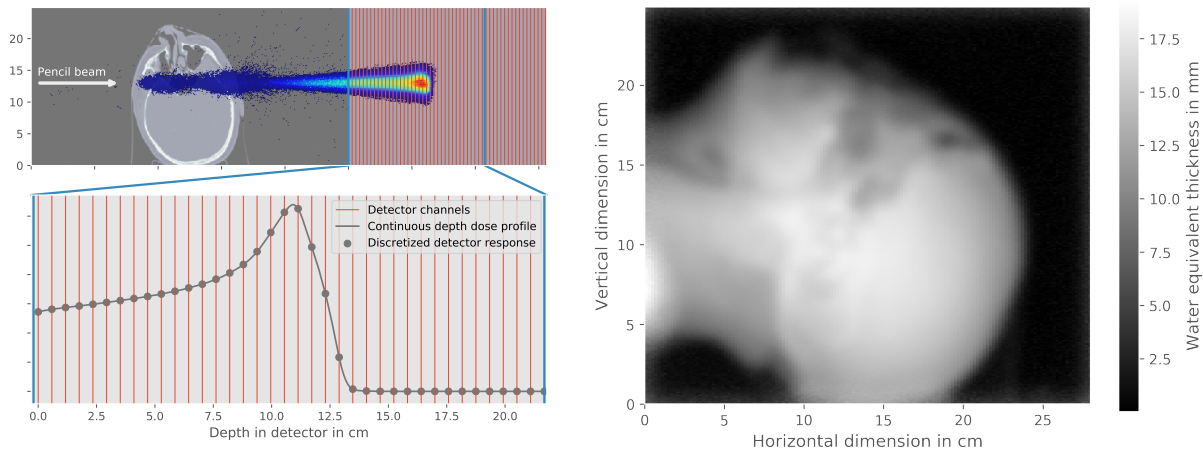


Figure 2: Left: Geometry used in Monte Carlo to simulate proton radiographies. The detector is idealised as solid block of water and the dose scored in 2.3 mm depth intervals. Right: Example of a simulated proton radiography.

124 We modelled the range telescope as a homogeneous box of water in which the integrated  
 125 depth dose profiles were scored in depth increments of 2.3 mm. The geometry used in *Fred*  
 126 is shown in figure 2 as well as a proton radiography of the patient used in this study.

127 The irradiation plan contained a two dimensional array of pencil beams with  $10^3$  protons  
 128 per spot and a beam energy of 200 MeV, i.e., high enough so that the protons fully traversed  
 129 the patient and partly penetrated the range telescope. For simplicity, we used a parallel beam  
 130 geometry and kept the beam axis aligned with the voxel grid. Furthermore, we chose the beam  
 131 spot positions to be centred on the voxel surfaces. The initial beam profile was assumed to be  
 132 a symmetric Gaussian distribution characterised by the full width at half maximum (FWHM)  
 133 parameter.

134 For each scanned beam spot, the range telescope recorded a (discretised) Bragg curve from  
 135 which the water equivalent thickness (WET) was determined using a data processing procedure  
 136 detailed in (Krah et al. 2018). From the list of beam spot coordinates and WET values, the  
 137 proton radiography was constructed as 2D image so that each spot corresponded to one pixel  
 138 in the proton radiography.

## 139 2.4 Conversion of CT to RSP, density, and elemental composition

140 *Fred* interpolates all parameters (density, RSP, radiation length, elemental composition) linearly  
 141 between the materials provided in a lookup table according to the CT number in each voxel, i.e.,  
 142 it treats each tissue as a composition of two out of the given set of reference materials. *Fred* uses  
 143 RSP, density, and radiation length to calculate electromagnetic energy loss and multiple Coulomb  
 144 scattering (MCS), and the elemental composition to obtain cross sections of nuclear interactions  
 145 (Schiavi et al. 2017). When simulating the proton radiographies, we used *Fred*'s default set  
 146 of materials reported in table 1 which is essentially table 4 in Schneider et al. (1996) with an  
 147 additional column containing the calculated radiation length  $X_0$ . Following the arguments in  
 148 Sec. 2.2, we defined the relationship between CT numbers and RSP in this table as ground  
 149 truth conversion curve. Some materials in the table refer to tissues which do not appear in a  
 150 patient head and which would be disregarded when using the table in a TPS. For the purpose of  
 151 providing a ground truth information, we kept them to have a relatively granular lookup table  
 152 in the simulation.

153 We built an additional reference lookup table (table 2) using the material compositions and  
 154 HU intervals reported in table 6 in Schneider et al. (2000). The density was determined using

Table 1: Material table from Schneider et al. (1996) used to simulate the proton radiographies. It contains the CT-RSP relationship which we used as ground truth knowledge.

	Elemental fraction in %													$\rho$ [g/cm <sup>3</sup> ]	CT No. [HU]	RSP	$X_0$ [cm]
	O	C	H	N	Ca	P	Na	Mg	S	Cl	K	Fe	I				
Air	23.5	0	0	76.5	0	0	0	0	0	0	0	0	0	0.0012	-1000	0.001062	30862.6
Lung infl.	74.9	10.5	10.3	3.1	0	0.2	0.2	0	0.3	0.3	0.2	0	0	0.26	-741	0.257998	140.478
Adip. tissue	27.8	59.8	11.4	0.7	0	0	0.1	0	0.1	0.1	0	0	0	0.95	-70	0.978975	43.3744
Yellow marrow	23.1	64.4	11.5	0.7	0	0	0.1	0	0.1	0.1	0	0	0	0.98	-42	1.01303	42.5351
Water	88.81	0	11.19	0	0	0	0	0	0	0	0	0	0	1	0	1	36.0823
Breast	52.7	33.2	10.6	3	0	0.1	0.1	0	0.2	0.1	0	0	0	1.02	3	1.02898	37.8775
Red marrow	43.9	41.4	10.5	3.4	0	0.1	0	0	0.2	0.2	0.2	0.1	0	1.03	14	1.04102	38.0317
GI tract	75.1	11.5	10.6	2.2	0	0.1	0.1	0	0.1	0.2	0.1	0	0	1.03	23	1.02804	35.7108
Lymph	83.2	4.1	10.8	1.1	0	0	0.3	0	0.1	0.4	0	0	0	1.03	28	1.02701	35.1365
Testis	69.4	16.9	10.6	2.2	0	0.2	0.2	0	0.1	0.2	0.2	0	0	1.04	32	1.04104	35.7064
Brain	71.2	14.5	10.7	2.2	0	0.4	0.2	0	0.2	0.3	0.3	0	0	1.04	37	1.04	35.3985
Thyroid	74.5	11.9	10.4	2.4	0	0.1	0.2	0	0.1	0.2	0.1	0	0.1	1.05	40	1.04496	34.9107
Muscle	71	14.3	10.2	3.4	0	0.2	0.1	0	0.3	0.1	0.4	0	0	1.05	42	1.04401	35.0533
Kidney	72.4	13.2	10.3	3	0.1	0.2	0.2	0	0.2	0.2	0.2	0	0	1.05	43	1.04496	34.9957
Lung defl.	74.9	10.5	10.3	3.1	0	0.2	0.2	0	0.3	0.3	0.2	0	0	1.05	44	1.04401	34.785
Ovary	76.8	9.3	10.5	2.4	0	0.2	0.2	0	0.2	0.2	0.2	0	0	1.05	45	1.04601	34.7622
Eye lens	64.6	19.5	9.6	5.7	0	0.1	0.1	0	0.3	0.1	0	0	0	1.07	50	1.06005	34.9361
Liver	71.6	13.9	10.2	3	0	0.3	0.2	0	0.3	0.2	0.3	0	0	1.06	53	1.05396	34.6543
Spleen	74.1	11.3	10.3	3.2	0	0.3	0.1	0	0.2	0.2	0.3	0	0	1.06	54	1.05396	34.5251
Heart	74.5	11	10.2	3.3	0	0.1	0.1	0	0.2	0.3	0.2	0.1	0	1.06	55	1.053	34.5819
Skin	64.5	20.4	10	4.2	0	0.1	0.2	0	0.2	0.3	0.1	0	0	1.09	75	1.08401	34.2994
Cartilage	74.4	9.9	9.6	2.2	0	2.2	0.5	0	0.9	0.3	0	0	0	1.1	98	1.08097	32.4815
Skel. spong.	36.7	40.4	8.5	2.8	7.4	3.4	0.1	0.1	0.2	0.2	0.1	0.1	0	1.18	260	1.15605	29.3503
Skel. sacrum	43.8	30.2	7.4	3.7	9.8	4.5	0	0.1	0.2	0.1	0.1	0.1	0	1.29	413	1.23801	25.3857
Vert. col. (D6,L3)	43.7	28.7	7	3.8	11.1	5.1	0	0.1	0.2	0.1	0.1	0.1	0	1.33	477	1.26696	24.0933
Femur	36.8	34.5	7	2.8	12.9	5.5	0.1	0.1	0.2	0.1	0	0	0	1.33	499	1.26895	23.8711
Ribs (2nd, 6th)	43.6	26.3	6.4	3.9	13.1	6	0.1	0.1	0.3	0.1	0.1	0	0	1.41	595	1.32907	22.0085
Vert. col. (C4)	43.6	26.1	6.3	3.9	13.3	6.1	0.1	0.1	0.3	0.1	0.1	0.1	0	1.42	609	1.33693	21.7318
Humerus	36.9	31.4	6	3.1	15.2	7	0.1	0.1	0.2	0	0	0	0	1.46	683	1.37006	20.8816
Ribs (10th)	43.4	23.5	5.6	4	15.6	7.2	0.1	0.1	0.3	0.1	0.1	0	0	1.52	763	1.41299	19.6246
Cranium	43.5	21.2	5	4	17.6	8.1	0.1	0.2	0.3	0	0	0	0	1.61	903	1.48007	17.9969
Mandible	43.5	19.9	4.6	4.1	18.7	8.6	0.1	0.2	0.3	0	0	0	0	1.68	1006	1.53401	16.9642
Cortical bone	43.5	15.5	3.4	4.2	22.5	10.3	0.1	0.2	0.3	0	0	0	0	1.92	1376	1.71398	14.0583

155 the fit shown in their figure 9. The stopping power and radiation length values were calculated  
156 based on the elemental composition exploiting Geant4’s functionality (Agostinelli et al. 2003).  
157 We used this table for some of the presented results to determine the regulariser weights (see  
158 section 2.10.1).

## 159 2.5 Notations

160 Throughout the paper, we will use the lower case variables  $h$  and  $r$  to refer to the HU and RSP  
161 values in the voxels, respectively. We use  $i, j, k$  as voxel indices and, by convention, associate  $k$   
162 with the beam axis. With  $P$ , we refer to the proton radiography and with  $D$  to the pDRR. Both,  
163  $P$  and  $D$ , share the same pixel indices denoted as  $i_p$  and  $j_p$ . It is sometimes convenient to combine  
164 the two indices  $i_p, j_p$  into a single index  $l$  so that, e.g.,  $P_l$  denotes the vector of pixels in the  
165 proton radiography. The  $N$  interval limits of the CT-RSP conversion curve are given as capital  
166 letter variables  $R_\alpha$  and  $H_\alpha$  with the Greek index enumerating the parametrisation intervals (see  
167 figure 1). We use the  $\vec{\cdot}$  symbol to indicate vector notation, e.g.  $\vec{R} = (R_0, R_1 \dots, R_N)$ .

## 168 2.6 Remapping of CT image

169 We exploit the piecewise linear character of the CT-RSP conversion curve to remap the CT  
170 numbers [in HU] in the CT image onto a set of coefficients. This allows us to state the optimi-  
171 sation as a linear minimisation problem. Let  $h$  be the HU value in one voxel of the patient CT  
172 image. Its conversion to  $r$  depends on a parameter tuple  $(H_\alpha, R_\alpha)$  if and only if  $h$  lies in the HU  
173 intervals left or right of  $H_\alpha$ , i.e.,  $h \in (H_{\alpha-1}, H_{\alpha+1})$ . Specifically,  $r$  is the linear barycentric in-  
174 terpolation between the parameter pair  $(R_\alpha, R_{\alpha+1})$  if  $h \in (H_\alpha, H_{\alpha+1})$  and between  $(R_{\alpha-1}, R_\alpha)$ ,  
175 if  $h \in (H_{\alpha-1}, H_\alpha)$ .

176 This motivates the definition of a vector  $\vec{w}$  whose components  $w_\alpha$  are calculated in the  
177 following way:

Table 2: Lookup table according to Schneider et al. (2000) with additional columns containing RSP (at 200 MeV) and radiation length  $X_0$ .

O	C	H	N	Elemental fraction in %								$\rho$ [g/cm <sup>3</sup> ]	CT No. [HU]	RSP	$X_0$ [cm]	
				Ca	P	Na	Mg	S	Cl	K	Ar					
23.2	0	0	75.5	0	0	0	0	0	0	0	0	1.3	0.000605	-1050	0.000537909	60521.5
74.9	10.5	10.3	3.1	0	0.2	0.2	0	0.3	0.3	0.2	0	0	0.052695	-950	0.0529346	693.293
19.8	68.1	11.6	0.2	0	0	0.1	0	0.1	0.1	0	0	0	0.907347	-120	0.934753	46.3824
30.8	56.7	11.3	0.9	0	0	0.1	0	0.1	0.1	0	0	0	0.943934	-82	0.967335	43.3455
41.1	45.8	11	1.5	0	0.1	0.1	0	0.2	0.2	0	0	0	0.97083	-52	0.989457	40.9452
50.9	35.6	10.8	2.2	0	0.1	0	0	0.2	0.2	0	0	0	0.997725	-22	1.01295	38.9291
57.8	28.4	10.6	2.6	0	0.1	0	0	0.2	0.2	0.1	0	0	1.02462	8	1.03652	37.2415
72.3	13.4	10.3	3	0	0.2	0.2	0	0.2	0.2	0.2	0	0	1.03056	19	1.0359	35.7234
62.2	20.7	9.4	6.2	0	0	0.6	0	0.6	0.3	0	0	0	1.09681	80	1.09214	34.0022
35.5	45.5	9.5	2.5	4.5	2.1	0.1	0	0.1	0.1	0.1	0	0	1.08746	120	1.0832	33.8555
36.3	42.3	8.9	2.7	6.4	3	0.1	0	0.1	0.1	0.1	0	0	1.13485	200	1.11908	31.2418
37.2	39.1	8.2	2.9	8.3	3.9	0.1	0	0.1	0.1	0.1	0	0	1.19409	300	1.16414	28.6198
38	36.1	7.6	3	10.1	4.7	0.1	0.1	0.2	0.1	0	0	0	1.25333	400	1.20957	26.3764
38.7	33.5	7.1	3.2	11.7	5.4	0.1	0.1	0.2	0	0	0	0	1.31257	500	1.25601	24.5068
39.4	31	6.6	3.3	13.2	6.1	0.1	0.1	0.2	0	0	0	0	1.37181	600	1.30145	22.8421
40	28.7	6.1	3.5	14.6	6.7	0.1	0.1	0.2	0	0	0	0	1.43104	700	1.34623	21.3871
40.5	26.5	5.6	3.6	15.9	7.3	0.1	0.2	0.3	0	0	0	0	1.49028	800	1.38998	20.0717
41.1	24.6	5.2	3.7	17	7.8	0.1	0.2	0.3	0	0	0	0	1.54952	900	1.43531	18.9582
41.6	22.7	4.9	3.8	18.1	8.3	0.1	0.2	0.3	0	0	0	0	1.60876	1000	1.4818	17.9454
42	21	4.5	3.9	19.2	8.8	0.1	0.2	0.3	0	0	0	0	1.668	1100	1.52574	17.0139
42.5	19.4	4.2	4	20.1	9.2	0.1	0.2	0.3	0	0	0	0	1.72724	1200	1.57143	16.2022
42.9	17.9	3.9	4.1	21	9.6	0.1	0.2	0.3	0	0	0	0	1.78648	1300	1.61658	15.4529
43.2	16.5	3.6	4.2	21.9	10	0.1	0.2	0.3	0	0	0	0	1.84572	1400	1.66118	14.7594
43.5	15.5	3.4	4.2	22.5	10.3	0.1	0.2	0.3	0	0	0	0	1.90496	1500	1.7082	14.1711

$$\begin{aligned}
 w_\alpha(h) &\equiv \frac{h - H_{\alpha-1}}{H_\alpha - H_{\alpha-1}} \Omega_\alpha(h) + \frac{H_{\alpha+1} - h}{H_{\alpha+1} - H_\alpha} \Omega_{\alpha+1}(h) \\
 w_0(h) &= \frac{H_1 - h}{H_1 - H_0} \Omega_{\alpha=1}(h) \\
 w_N(h) &= \frac{h - H_{N-1}}{H_N - H_{N-1}} \Omega_{\alpha=N}(h)
 \end{aligned} \tag{1}$$

178 with

$$\Omega_\alpha(h) = \begin{cases} 1 & \text{for } H_{\alpha-1} \leq h < H_\alpha \\ 0 & \text{otherwise.} \end{cases} \tag{2}$$

179 The value of  $w_\alpha$  thus quantifies how much  $r$  depends on the corresponding parameter  $R_\alpha$ .  
 180 Note that most components of the vector  $\vec{w}$  are zero except for two (or one if  $h$  lies exactly on  
 181 an interval boundary) and that the sum over all  $w_\alpha$  is always one. The RSP value  $r$  is obtained  
 182 by contracting  $\vec{w}$  with the vector  $\vec{R}$  containing the parameters  $R_\alpha$  of the conversion curve:

$$r = \sum_{\alpha=0}^N w_\alpha R_\alpha = \vec{w} \cdot \vec{R}. \tag{3}$$

183 When applying the piecewise barycentric interpolation to all voxels in the CT image, the  
 184 three dimensional HU matrix,  $h_{ijk}$ , is mapped onto a four dimensional coefficient matrix  $w_{ijk,\alpha}$ .  
 185 In accordance with equation 3, the 3D RSP map is:

$$r_{ijk} = \sum_{\alpha=0}^N w_{ijk,\alpha} R_\alpha = \vec{w}_{ijk} \cdot \vec{R} \tag{4}$$

## 186 2.7 Proton digitally reconstructed radiography

187 The pDRR is obtained by projecting the RSP map along lines corresponding to the pencil beams  
 188 used to acquire the proton radiography. We do not consider projection directions oblique to the  
 189 CT grid in this work (see section 2.3). Denoting with  $\text{proj}_k$  the projection operation along axis

190  $k$ , the pDRR is calculated as

$$D_{i_p j_p} = \text{proj}_{k, i_p j_p}(r_{ijk}) = \text{proj}_{k, i_p j_p} \left( \sum_{\alpha=0}^N w_{ijk, \alpha} R_{\alpha} \right) = \sum_{\alpha=0}^N \text{proj}_{k, i_p j_p}(w_{ijk, \alpha}) R_{\alpha} = \sum_{\alpha=0}^N A_{i_p j_p, \alpha} R_{\alpha} \quad (5)$$

191 with

$$A_{i_p j_p, \alpha} = \text{proj}_{k, i_p j_p}(w_{ijk, \alpha}). \quad (6)$$

192 The projection operation is wrapped into the matrix  $A$  because it only acts on the coefficients  
 193  $w_{ijk}$ , but not on the parameters  $R_{\alpha}$ , and may therefore be interchanged with the contraction over  
 194 the  $\vec{R}$  vector. For an ideal pencil beam with FWHM=0 and neglecting scattering, the projection  
 195 is simply the sum along  $k$  multiplied by the voxel size  $s$ , i.e.,  $A_{i_p, j_p, \alpha} = s \sum_k w_{i=i_p, j=j_p, k, \alpha}$ . A  
 196 more realistic projection operation must at least take into account the beam size and possibly  
 197 the effect of scattering. In this work, we investigated the following three projection models:  
 198 (1) Gaussian beam without scattering, (2) Gaussian beam with material and depth dependent  
 199 scattering, and (3) Monte Carlo based projection.

### 200 2.7.1 Gaussian beam without scattering

201 In this model, the beam is described by a Gaussian transverse profile characterised by the  
 202 FWHM, which is 5-10 mm for clinical proton beams at the energies used for proton imaging  
 203 ( $\approx 200$  MeV). The effect of scattering within the patient is neglected and the beam profile is  
 204 considered to be constant in depth and independent of the pencil beam position. Mathematically,  
 205 this corresponds to a convolution with a shift invariant Gaussian kernel  $G_{i_p - i, j_p - j}$  in the plane  
 206 orthogonal to the proton beam. The matrix  $A_{i_p, j_p, \alpha}$  is then calculated as

$$A_{i_p, j_p, \alpha} = s \sum_k \sum_{i, j} G_{i_p - i, j_p - j} w_{ijk, \alpha} = s \sum_{i, j} G_{i_p - i, j_p - j} \sum_k w_{ijk, \alpha}. \quad (7)$$

207 The convolution needs to be performed only once after summing along  $k$ , making the implemen-  
 208 tation computationally inexpensive.

### 209 2.7.2 Gaussian beam model with scattering

210 This more realistic projection model takes into account the effect of scattering which leads to  
 211 a gradual widening of the proton beam with depth. The most important contribution is due  
 212 to MCS, i.e., a succession of many small angle deflections as a proton propagates through the  
 213 medium. We take as depth dependent beam size a combination of the initial beam size and the  
 214 contribution due to MCS in the medium,

$$\sigma_{\text{beam}}(z_k) = \sqrt{\sigma_{\text{init}}^2 + \sigma_{\text{mcs}}^2(z_k)}, \quad (8)$$

215 because the Gaussian pencil beam can approximately be thought of as a weighted superposition  
 216 of many pin-like pencil beams, each of which undergoes MCS. We denote with  $z_k$  the depth of  
 217 the slices in the CT voxel grid along the beam axis.

218 We used a discretised version of the analytical formulae from (Lynch & Dahl 1991) and  
 219 (Gottschalk et al. 1993) to calculate  $\sigma_{\text{mcs}}^2$  as a function  $z_k$ :

$$\sigma_{\text{mcs}}^2(z_k) = \Omega_0^2 \left[ 1 + 0.038 \ln \left( \frac{z_k}{X_0} \right) \right] s \sum_{k'=0}^k \frac{z_{k'}^2}{\beta^2(z_{k'}) p^2(z_{k'}) X_0(z_{k'})}, \quad (9)$$

220 with  $\Omega_0 = 13.6$  MeV and  $s$  the voxel size. The radiation length  $X_0$  depends on the type  
 221 of material and parametrises the amount of MCS the protons suffer while traversing it. In  
 222 a heterogeneous medium like a patient, it depends on the three dimensional position within



the patient volume. The terms  $\beta$  and  $p$  are the proton’s velocity relative to the speed of light,  $\beta = v/c$ , and its momentum, respectively. They relate to the proton energy as  $\beta p = (E^2 + 2E E_p)/(E + E_p)c$ , where  $E_p$  is the proton’s rest mass, and decrease as a proton continuously slows down while traversing the patient.

Evaluating equation 9 requires some prior knowledge about the material composition within the patient which we obtained by converting the patient CT to an RSP and  $X_0$  map through the default tables implemented in *Fred*. Alternatively, one could perform a first optimisation of the CT-RSP curve using the Gaussian model without scattering, use the result to evaluate equation 9, and optimise the CT-RSP curve again, this time using the Gaussian beam model with scattering.

We make the following approximations to be able to sum along the beam axis  $z$  only in equation 9. For a given pencil beam, we determine the mean radiation length the protons encounter in each slice of the CT volume by calculating the weighted average value of  $X_0$  around the beam center  $(i_p, j_p)$  in the  $(i, j)$  plane at depth  $z_k$ . We use a two dimensional Gaussian weighting kernel with a standard deviation reflecting the beam spot size. This yields the depth dependent term  $X_0(z_k)$  in equation 9. Similarly, we calculate the water equivalent thickness  $z_{\text{WET}}$  that the protons belonging to a given pencil beam have traversed on average when penetrating the patient up to some geometric depth  $z_k$ . We then use the expression  $E(z_{\text{WET}}) = ((R - z_{\text{WET}})/\chi)^{1/\xi}$  from Bortfeld & Schlegel (1996) to calculate the average proton energy in depth  $z_k$ . In this formula,  $R$  refers to the proton range in water and  $\chi$  and  $\xi$  are fit constants.

We determine the approximate beam size for each pencil beam  $(i_p, j_p)$  and in all CT slices  $k$  as explained above to build a space variant Gaussian convolution kernel  $G_{i_p j_p; i j}(z_k)$  of width  $\sigma_{\text{beam}, i_p j_p}(z_k)$ . The matrix  $A_{i_p j_p, \alpha}$  is calculated as

$$A_{i_p j_p, \alpha} = s \sum_k \sum_{i, j} G_{i_p j_p; i j}(z_k) w_{i j k, \alpha}. \quad (10)$$

Fast Fourier transform based convolution algorithms cannot be used here because the kernel is shift variant. Instead, the multiplication and summation operations in equation 10 must be executed explicitly for all HU intervals  $\alpha$ . We therefore implemented equation 10 on an Nvidia Titan X GPU card using the OpenCL library. This helped lowering the computation time from several hours per projection down to about 15 sec.

### 2.7.3 Monte Carlo based projection

We used Monte Carlo to perform the projection in equation 5 to avoid the approximations inherent in the analytical beam model and to include the effect of nuclear interactions on the proton trajectories. To this end, we implemented a dedicated plugin to *Fred* which iterates through the following scheme: Initially, the patient CT is loaded and the components of the matrix  $\omega_{i j k, \alpha}$  are calculated. The pencil beams are defined and arranged in the same way as in the proton radiography simulation (see Sec. 2.3). The protons are then transported across the patient CT volume using the physics models of the MC code. After each transport step (before traversing into a new voxel the latest), the coefficient vector  $\vec{w}$  is extracted from the current voxel and multiplied by the step length projected onto the beam axis  $z$ . This information is cumulated along the entire trajectory and for all protons within one pencil beam. The result is the integrated coefficient vector  $\vec{w}$  associated with one pencil beam and repeating the procedure over the entire array of pencil beams yields the matrix  $A_{i_p j_p, \alpha}$ .

If the number of protons per pencil beam remained constant across the patient volume, the integrated coefficient vector would simply be normalised by this number. In reality, the number of protons fluctuates as a function of depth because (1) secondary protons are created through inelastic scattering or knock-on elastic collisions, (2) protons stop inside the patient because they lose a large fraction of their energy in a nuclear interaction, and (3) some protons are

270 scattered at large Rutherford-like angles and exit the patient laterally without fully traversing  
 271 it. Our plugin accounts for these effects by applying a depth dependent normalisation and only  
 272 includes protons which would have reached the detector. In the current implementation of *Fred*,  
 273 the plugin can only be executed in a single thread on a CPU which makes the computation time  
 274 much longer (order of hours) than for the analytical projection model.

## 275 2.8 Linear minimisation problem

276 Henceforth, we use a single index  $l$  for the pixels in the proton radiography (see section 2.5).  
 277 We define the data attachment term of the cost function as

$$E_{\text{data}}(\vec{R}) = \sum_l \left( P_l - \sum_{\alpha=0}^N A_{l\alpha} R_\alpha \right)^2 = \|\vec{P} - A\vec{R}\|^2 \quad \text{with} \quad A_{l\alpha} = \text{proj}_k(w_{lk,\alpha}), \quad (11)$$

278 where  $\|\cdot\|^2$  refers to the  $\ell$  norm. We have introduced compact matrix/vector notation on the  
 279 right hand side.

280 The optimal parameters of the CT-RSP conversion (denoted with the  $\hat{\cdot}$  symbol) curve are the  
 281 components of the vector  $\hat{\vec{R}}$  which minimises the objective function, i.e.,

$$\hat{\vec{R}} = \text{argmin} \left\{ E(\vec{R}) \right\}. \quad (12)$$

282 Note that the HU intervals  $H_\alpha$  are implicitly encoded in the matrix  $A$  and not subject  
 283 to optimisation, i.e. the parameters  $\hat{\vec{R}}$  are optimal for a given discretisation of the CT-RSP  
 284 curve. Optimising  $H_\alpha$  and  $R_\alpha$  alongside each other would mean to optimise both  $A$  and  $\vec{R}$   
 285 in equation 11 - a much harder problem to solve, if solvable at all. In practice, the intervals  
 286  $H_\alpha$  can be chosen to yield a desired degree of granularity (e.g. smaller intervals in soft tissue  
 287 region, fewer in bone region), or in accordance with a clinical calibration curve already in use  
 288 in the facility. In this work, we used the same intervals as in the ground truth curve except for  
 289 one dedicated test where different intervals were used in the optimization than in the proton  
 290 radiography simulation (figure 4 in section 3.1).

## 291 2.9 Parameter correlation coefficients

292 The minimisation problem in equation 12 is mathematically well posed if matrix  $A$  has full rank,  
 293 or, in practical terms, if there are at least as many pixels in the proton radiography as there  
 294 are  $R_\alpha$  parameters to be optimised. Even if this criterion is met, the optimised CT-RSP curve  
 295 would not be plausible from a physics point of view in many cases, as we will show in section 3.1.  
 296 The reason is the following: The WET value encoded in a single pixel of the pDRR results from  
 297 a summation of RSP values in many voxels along and around the proton beam (see section 2.7).  
 298 Increasing the value of a parameter  $R_\alpha$  increases the RSP in some of the contributing voxels and  
 299 consequently the average WET. At the same time, lowering the value of another parameter  $R_{\alpha'}$   
 300 tends to lower the WET value. Therefore, the  $R$  parameters are expected to be correlated. We  
 301 also note that neighboring  $R_\alpha$  parameters are in any case anti-correlated because the CT-RSP  
 302 curve interpolates linearly between them and is continuous by construction. The correlation  
 303 coefficient of the parameters  $R_\alpha$  can be determined from the covariance matrix of the cost function  
 304 as follows:

$$\rho_{\alpha\alpha'} = \frac{\text{Cov}_{\alpha\alpha'}}{\sqrt{\text{Cov}_{\alpha\alpha} \text{Cov}_{\alpha'\alpha'}}} \quad \text{with} \quad \text{Cov}_{\alpha\alpha'} = (A^T A)^{-1}_{\alpha\alpha'}. \quad (13)$$

305 The coefficient values always lie within the  $[-1, 1]$  interval and  $\rho_{\alpha\alpha} = 1$  by construction.

## 2.10 Regularised optimisation

As we will show in the results, correlation among the parameters  $R_\alpha$  would lead to unrealistic optimised CT-RSP curves. Therefore, we introduce a regularisation term in the cost function to control the variation of the CT-RSP curve. It penalises the intrinsic variation of the patient-specific CT-RSP curve. We define

$$E_{\text{reg}} = \sum_{\alpha=\alpha_0}^{\alpha_M} (d_{\alpha+1} - d_\alpha)^2, \quad (14)$$

with the discrete derivative  $d_\alpha$  of the curve calculated as

$$d_\alpha = \frac{R_\alpha - R_{\alpha-1}}{H_\alpha - H_{\alpha-1}}. \quad (15)$$

The regularisation may be applied to a subset of HU intervals only (see section 2.10.1) and  $\alpha_0$  and  $\alpha_M$  refer to the first and last of them, respectively.

Equation 14 can be written as matrix equation,

$$E_{\text{reg}} = \sum_{\alpha=\alpha_0}^{\alpha_M} (A_{\alpha'\alpha}^{\text{reg}} R_\alpha)^2 = \|A^{\text{reg}} \vec{R}\|^2, \quad (16)$$

where the matrix components are given as

$$A_{\alpha'\alpha}^{\text{reg}} = \frac{1}{H_{\alpha+1} - H_{\alpha-1}} (\delta_{\alpha',\alpha-1} - 2\delta_{\alpha',\alpha} + \delta_{\alpha',\alpha+1}), \quad \text{with } \delta_{\alpha',\alpha} = \begin{cases} 1 & \text{for } \alpha' = \alpha \\ 0 & \text{otherwise.} \end{cases} \quad (17)$$

### 2.10.1 Regularised cost function

The conversion curve is expected to be rather smooth and monotonic in the regions  $\text{HU} < -100$  and  $\text{HU} > 100$ , but should be allowed to fluctuate slightly in the region of soft tissue, i.e.,  $-100 < \text{HU} < 100$  (Schneider et al. 2000). For this reason, we applied the regularisation separately to the three intervals.

The regularised cost function is the sum of the data term (equation 11) and three regulariser terms (equation 16). It takes the form

$$E(\vec{R}) = E_{\text{data}} + \gamma_{\text{air}} E_{\text{reg,air}} + \gamma_{\text{soft}} E_{\text{reg,soft}} + \gamma_{\text{bone}} E_{\text{reg,bone}}. \quad (18)$$

We have used the extra subscripts “air”, “soft”, and “bone” as short hand notation to refer to the three distinct HU regions of the conversion curve subject to the regularisation, with the indices  $\alpha_0$  and  $\alpha_M$  in equation 16 chosen appropriately to confine the selected HU intervals. We used the python package *scipy.linalg.lstsq* to minimise the cost function, which is based on singular value decomposition.

The  $\gamma$  factors set the relative weight of the regularisers compared to the data term and their value should be chosen such that the optimised curve contains a plausible level of smoothness.

We adopted the following method to automatically select the weights  $\gamma$ : Starting with an initial guess, we ran the optimisation and then calculated the magnitude of each regulariser term once for the optimised CT-RSP curve and once for a reference curve. We increased the respective weight  $\gamma$ , if the regulariser term of the optimised curve was greater than that of the reference curve, and lowered it in the opposite case. This procedure was repeated iteratively until all regulariser terms of the optimised and reference curve corresponded to within a few percent. In this way, the optimised CT-RSP curve had a comparable amount of variation as the reference.

The reference curve should be chosen (or constructed) such that it includes a level of RSP variation which is thought to be necessary to reflect the tissue variability within one patient.

340 The relative weights need to be set for each optimisation because the data term to which they  
341 refer is linked to a specific proton radiography (and the choice of a region-of-interest - see  
342 section 2.12). Note also that the regulariser does not force the absolute RSP values of the  
343 optimised and reference curves to resemble each other, but only their degree of smoothness.  
344 Therefore, optimised RSP may still vary strongly among patients even in the case of a very  
345 smooth reference curve which suppresses RSP variation within one patient. In this work, we  
346 used the ground truth CT-RSP curve as reference to fix the regulariser weights, except for  
347 figure 4.

### 348 **2.11 Assessment of range accuracy**

349 The patient-specific CT-RSP calibration optimises the parameters  $R_\alpha$  by minimising the differ-  
350 ence between predicted and measured average residual range for a field of pencil beams which  
351 fully penetrate the patient. From the treatment point of view, it is of interest to estimate how  
352 accurately the optimised curve predicts the range of lower energy protons stopping inside the  
353 patient.

354 To quantify the range accuracy which would be obtained with an optimised CT-RSP curve,  
355 we performed the following kind of Monte Carlo experiment. We defined a volume inside the  
356 patient's head and built an irradiation plan containing 10,000 pencil beams with randomised  
357 positions and beam energies. The positions were constrained by the lateral extension of the  
358 volume and the energy was chosen so that the pencil beams would penetrate the patient at  
359 least 20% of its total water equivalent thickness at that point and at most 80%. We scored the  
360 integrated depth dose profiles individually for all pencil beams. The same plan was simulated  
361 twice: once using the ground truth CT-RSP curve (see sections 2.2 and 2.3) to convert the patient  
362 CT to RSP and once using the optimised one. In this way, we obtained 10,000 pairs of integrated  
363 depth dose profiles. From each of them, we estimated the proton range by determining the water  
364 equivalent depth in which the distal edge decayed below 80 % of the peak value (Paganetti 2012a).  
365 The profiles were linearly interpolated to reach subvoxel resolution. We built histograms out of  
366 the 10,000 range differences and determined the mean value as estimate for the range accuracy.

367 We note that for certain pencil beams directed towards complex structures (e.g. nose and  
368 air cavities), the 80% distal fall-off technique may suffer from range mixing and therefore lead  
369 to additional variation of the range differences. Manual inspection of a random subsample of  
370 profiles led us to conclude that such cases are rare enough not to compromise the results in  
371 terms of average range accuracy in the Monte Carlo experiment.

### 372 **2.12 Region of interest in the proton radiography**

373 To perform the CT-RSP curve optimisation, it suffices to acquire a proton radiography of a  
374 region of interest of the patient instead of, e.g., the entire head to perform the patient-specific  
375 calibration as long as the image contains a sufficient amount of pixels. The region could for  
376 example be chosen such to reduce the dose given to healthy tissue. To investigate how much  
377 the optimised CT-RSP curve depends on such a choice, we simulated nine proton radiographies  
378 capturing differently positioned (but equally sized) rectangular areas (shown in figure 9) and  
379 calculated an optimised CT-RSP curve for each of them.

380 In practice, the region imaged by the proton radiography could be selected in accordance  
381 with the treatment volume or, instead, be placed so that the imaged volume does not correspond  
382 to the treated one, e.g. to avoid giving dose to an organ at risk distal to the treatment volume  
383 during image acquisition. We performed the Monte Carlo experiment (see section 2.11) to  
384 investigate whether this would have an impact on the range accuracy. Specifically, we selected  
385 a region of interest,  $\text{ROI}_{\text{exp}}$ , and defined the randomised irradiation plans so that the lateral  
386 coordinates of all pencil beams lay within it. We used the CT-RSP curve previously optimised  
387 based on another (or the same) region of interest proton radiography,  $\text{ROI}_{\text{opti}}$ , as look up table

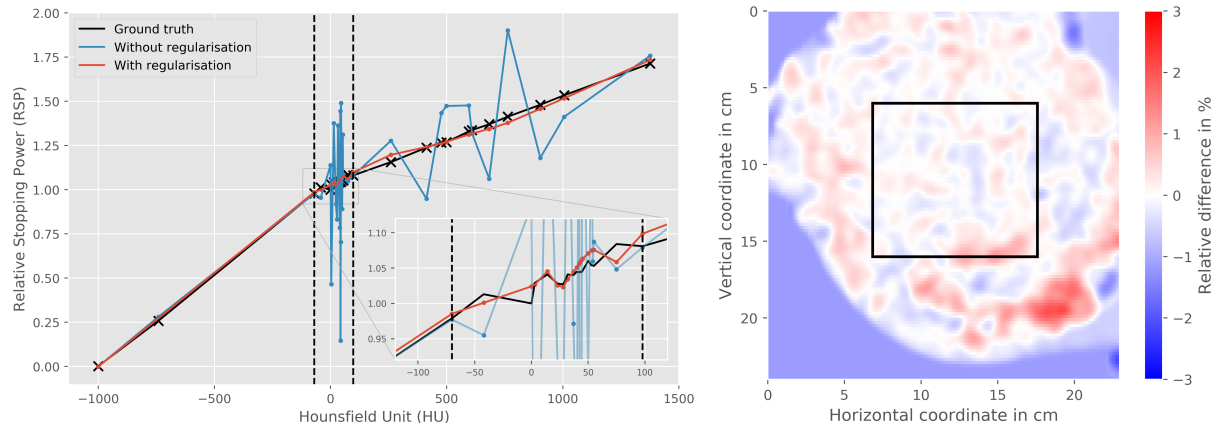


Figure 3: Left: Optimised CT-RSP curves obtained without (blue) and with (red) regulariser applied. The black curve is the ground truth reference used to simulate the proton radiography. The two dashed vertical lines indicate the three separately regularised HU regions “air”, “soft tissue”, and “bone” (see section 2.10.1). Right: Relative difference between the DRRs calculated using the regularised and non-regularised CT-RSP curves, respectively.

388 in the Monte Carlo. We then determined the range accuracy as explained in section 2.11 for  
 389 each pair ( $\text{ROI}_{\text{exp}}$ ,  $\text{ROI}_{\text{opti}}$ ).

### 390 3 RESULTS

#### 391 3.1 Regularisation

392 In figure 3 left, we show a patient-specific CT-RSP with and without regularisation used in the  
 393 optimisation process. The proton radiography was simulated with an 8 mm FWHM beam and  
 394 we used a rectangular region of interest indicated as black box in the right panel containing  
 395 5500 pixels. The projection was performed using the Gaussian beam model with scattering (see  
 396 section 2.7.2). The patient-specific calibration curve contained 33  $(H_\alpha, R_\alpha)$  pairs to be optimised.  
 397 It is evident that the variation in the non-regularised curve is unacceptable, while it is kept at  
 398 a plausible level when employing regularisation. The right panel shows the relative difference  
 399 between two pDRR images: one calculated using the regularised CT-RSP curve and the other  
 400 one using the non-regularised version. The two DRRs agree to better than 3% although the  
 401 two conversion curves themselves differ by much more. This underlines that the non-regularised  
 402 solution, despite its unrealistic variation, does indeed optimise the residual range similarly well  
 403 as the regularised one.

404 The left panel of figure 4 shows optimised calibration curves for which the regulariser weights  
 405  $\gamma$  in equation 18 were determined based on two different reference CT-RSP relationships (see  
 406 section 2.4). The regulariser terms have consequently enforced a degree of smoothness in the  
 407 optimised curves similar to each reference curve. At the same time, both optimised curves  
 408 approximately recovered the RSP values of the ground truth curve. This demonstrates that  
 409 the regulariser does not affect absolute RSP, but only the RSP variability within the curve (see  
 410 section 2.10.1).

411 The right panel shows optimised CT-RSP curves for which different HU intervals were used.  
 412 The five HU thresholds in the yellow curve were  $[-1000, -100, 0, 100, 1376]$ . The  $\gamma$  weights  
 413 were determined based on the dashed reference curve and consequently the optimised curves are  
 414 smoother than the ground truth curve. It is interesting to note that the yellow curve does not  
 415 exhibit any unrealistic variation despite the fact that no regularisation was applied.

416 The patient-specific calibration curves shown in figure 5 are based on proton radiographies

### 3. RESULTS

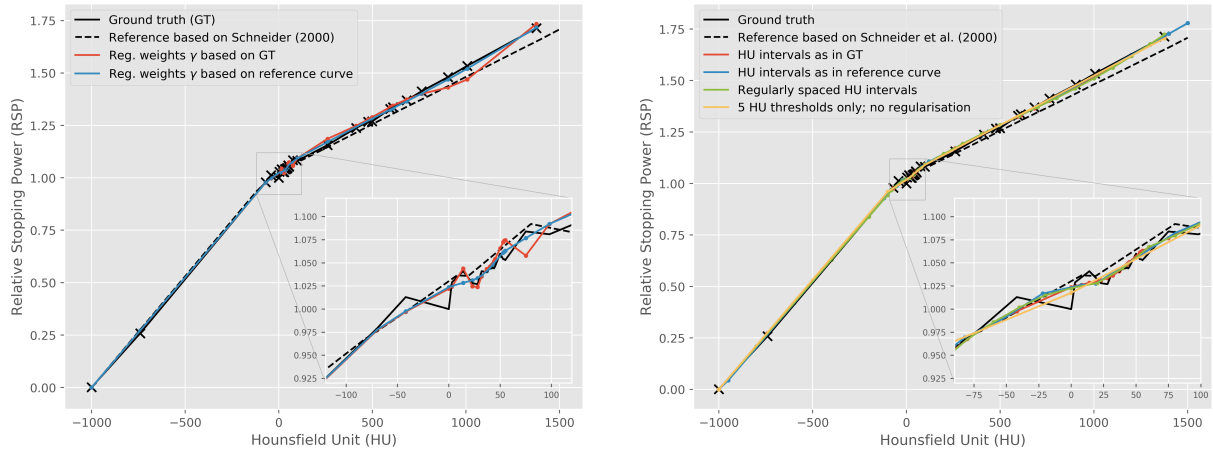


Figure 4: Left: Optimised CT-RSP curves using two different reference curves to determine the regulariser weights  $\gamma$ . Right: Optimised CT-RSP curves using different HU-intervals for the parameterisation. The regulariser weights  $\gamma$  were determined in accordance with the smoothness of the reference curve based on (Schneider et al. 2000) (see section 2.4). For the curve with five HU thresholds only, these were placed at HU=-1000, -100, 0, 100, 1376. No regularisation was applied to this curve.

417 simulated with different beam sizes, where “pin like” means FWHM=0 mm. We used the Gaus-  
 418 sian beam model with scattering to perform the projection of the pDRR. The optimisation was  
 419 regularised as explained in section 2.10. No regularisation was used for the green curve. The  
 420 lower panel shows the relative difference in percent between the ground truth CT-RSP and the  
 421 optimised ones. We have omitted the data point for  $HU = -1000$  because dividing by a very  
 422 small ground truth RSP value (0.012) makes the relative difference large and meaningless.

423 Figure 6 illustrates the parameter correlation matrix  $\rho_{\alpha\alpha'}$  (equation 13) for three different  
 424 beam sizes. We have used the Gaussian beam model with scattering (see section 2.7.2) to  
 425 calculate the pDRR. The central diagonal contains values of 1 by construction, while the two  
 426 diagonals off-set to the left and right are close to -1 because  $R_\alpha$  parameters of neighbouring HU  
 427 intervals of the conversions curve tend to be anti-correlated. Non-zero correlation coefficients  
 428 further away from the central diagonal occur because RSP information from many voxels is  
 429 mixed during the projection operation (see section 2.9). Indeed, they are much more prominent  
 430 in the left panel corresponding to an 8 mm FWHM beam than in the right panel, which refers  
 431 to a pin-like beam.

432 In figure 7, we present optimised calibration curves obtained from proton radiographies simu-  
 433 lated with different scattering processes activated. The lower panel shows the relative difference  
 434 in percent between optimised and ground truth CT-RSP curves. “Full physics” includes all  
 435 processes currently available in *Fred*, i.e., MCS and nuclear elastic and inelastic scattering; for  
 436 “No nuclear”, only MCS was included; and “no nuclear, no MCS” corresponds to a pure con-  
 437 tinuous slowing down simulation in which protons travel on straight lines through the voxel  
 438 geometry. Energy loss and straggling was left at default settings in all cases. The Gaussian  
 439 beam model with scattering was used to calculate the pDRR except for “no nuclear, no MCS”  
 440 where the Gaussian beam model without scattering was employed. The FWHM=8 mm curves  
 441 were regularised (see section 2.10), while the pin-like curves were not.

442 Figure 8 left shows optimised CT-RSP curves obtained with the three projection models  
 443 (see section 2.7). In all cases, the proton radiography was simulated with 8 mm FWHM pencil  
 444 beams and the optimisation was regularised. The Monte Carlo projection (see section 2.7.3)  
 445 was performed with 1000 protons per pencil beam. The right panel shows the relative difference  
 446 between the pDRR obtained with the Gaussian projection model with scattering and the Monte  
 447 Carlo projection.

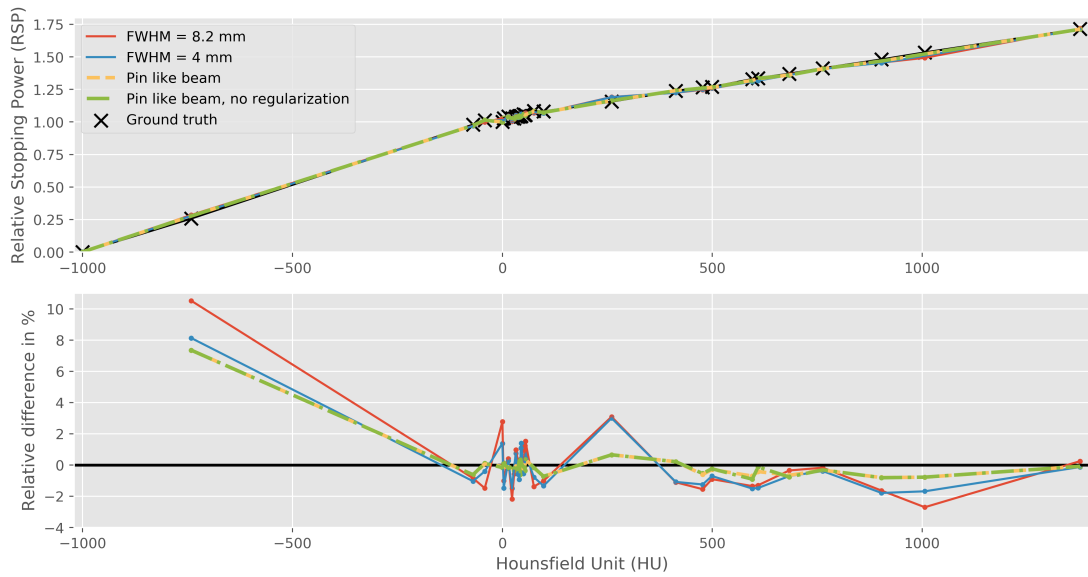


Figure 5: CT-RSP curves obtained from proton radiographies simulated with different beam sizes. The lower panel shows the relative difference in percent between the optimised and the ground truth CT-RSP curve.

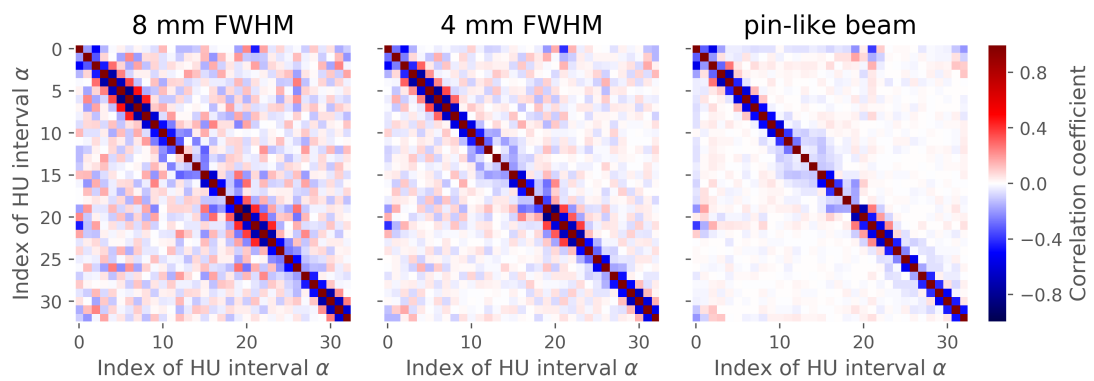


Figure 6: Visualisation of the parameter correlation matrix  $\rho_{\alpha\alpha'}$  (equation 13) for three different beam sizes.

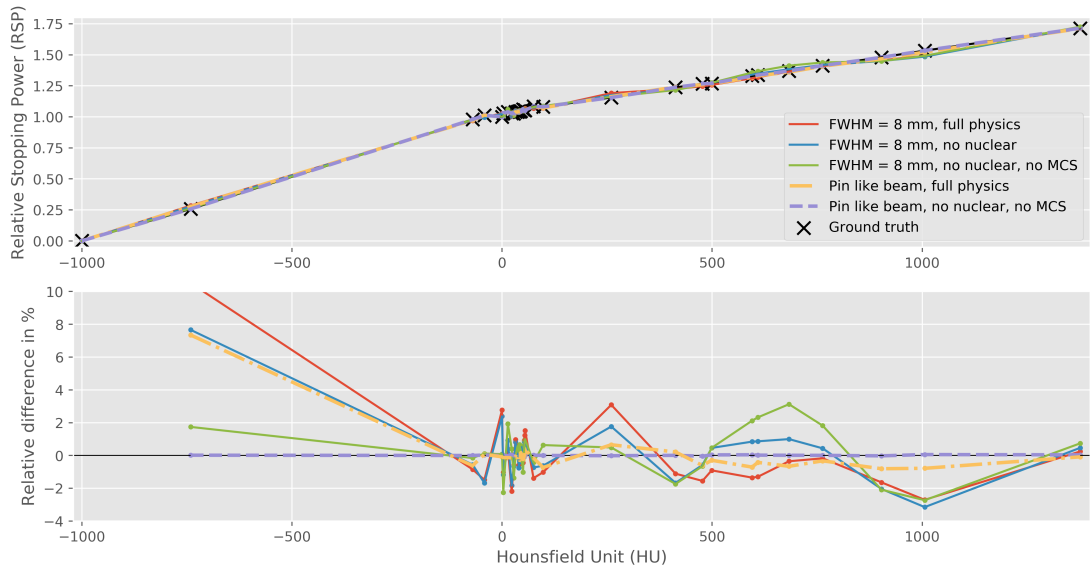


Figure 7: CT-RSP curves obtained from proton radiographies simulated with different physics processes activated. The lower panel shows the relative difference in percent between the optimised and the ground truth CT-RSP curve.

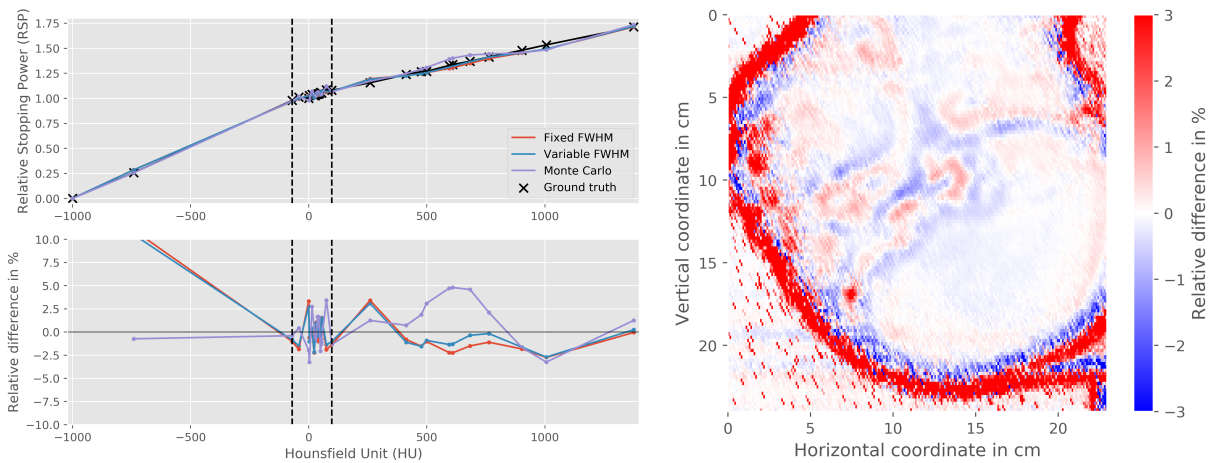


Figure 8: Left: CT-RSP curves obtained using three different projection models (see section 2.7). The lower panel shows the relative difference in percent between the optimised and the ground truth CT-RSP curve. Right: Relative difference between pDRR images obtained with the Gaussian projection model with scattering and the Monte Carlo based projection.



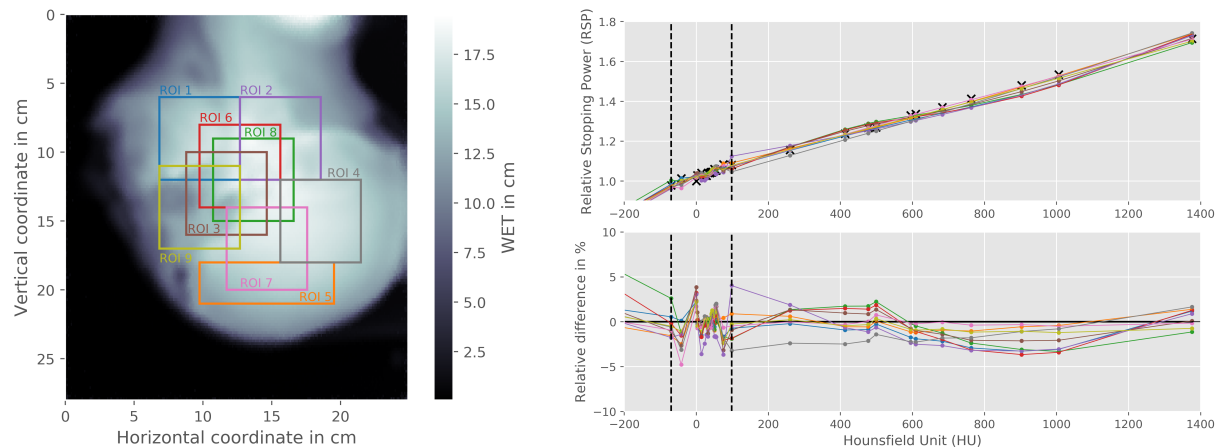


Figure 9: Left: regions of interest in the proton radiography used for the optimisation. Right: Optimised CT-RSP obtained using these regions of interest.

### 3.2 Range accuracy and region of interest

In the figure 9, we show optimised CT-RSP curves (right panel) using the different regions of interest in the proton radiography illustrated in the left panel. Colours in all panels match. The optimisation was performed using the Gaussian projection model with scatter (see section 2.7.2) and employing the regularisation separately in three HU regions (see section 2.10.1). The curves vary by a few percent among each other, but deviate no more than 4% from the ground truth curve. There appears to be some systematic under estimation in the range above 800 HU associated with bony tissue.

Figure 10 presents the results of the Monte Carlo range experiment explained in section 2.11. The upper left panel shows an example distribution of range differences obtained from 10,000 pencil beams. The blue distribution refers to the difference between predicted and true range of the pencil beams when using an optimised CT-RSP. The mean relative range difference quantifies the overall average range accuracy while the RMSE is indicative of the range precision. The yellow distribution was generated by repeating the Monte Carlo experiment twice, both times with the same ground truth curve, and it reflects the intrinsic range variations due to statistics in the depth dose profiles.

The upper right panel of figure 10 shows the mean relative range difference obtained when performing the Monte Carlo experiment in a region of interest,  $\text{ROI}_{\text{exp}}$ , while optimising the CT-RSP curve based on another,  $\text{ROI}_{\text{opti}}$  (see section 2.12). The diagonal elements in the graphic correspond to the case when the imaged area corresponds to the treated volume. On the other hand, for combinations such as  $\text{ROI}_{\text{exp}} = 1$  and  $\text{ROI}_{\text{opti}} = 4$  (see figure 9, left), there is no overlap between the imaged and the treated volume. The lower panels show the RMSE for the control experiment (left) and the optimised vs. ground truth runs (right). The fact that the RMSE tends to be slightly higher when the Monte Carlo experiment was performed in a relatively heterogeneous region (e.g. ROI 9) is in line with the remark in section 2.11 concerning the robustness of the 80% fall-off test. Overall, the RMSE associated with the optimised CT-RSP curves is less than 0.3% higher than the RMSE in the control run.

Figure 11 shows the mean relative range accuracy and the RMSE (as error bars) resulting from the Monte Carlo experiment using the optimised CT-RSP curves based on DRRs calculated with the three beam models (see section 2.7). We performed both, the optimisation and the Monte Carlo experiment, in the same nine regions of interest shown in the left panel of figure 9. The RMSE is only slightly larger than the RMSE of the control run (ground truth vs. ground truth; not shown), i.e. it is mainly due to Monte Carlo statistics and variation of the range retrieved by means of the 80% fall-off criterion (see section 2.11). Overall, the Gaussian beam

### 3. RESULTS

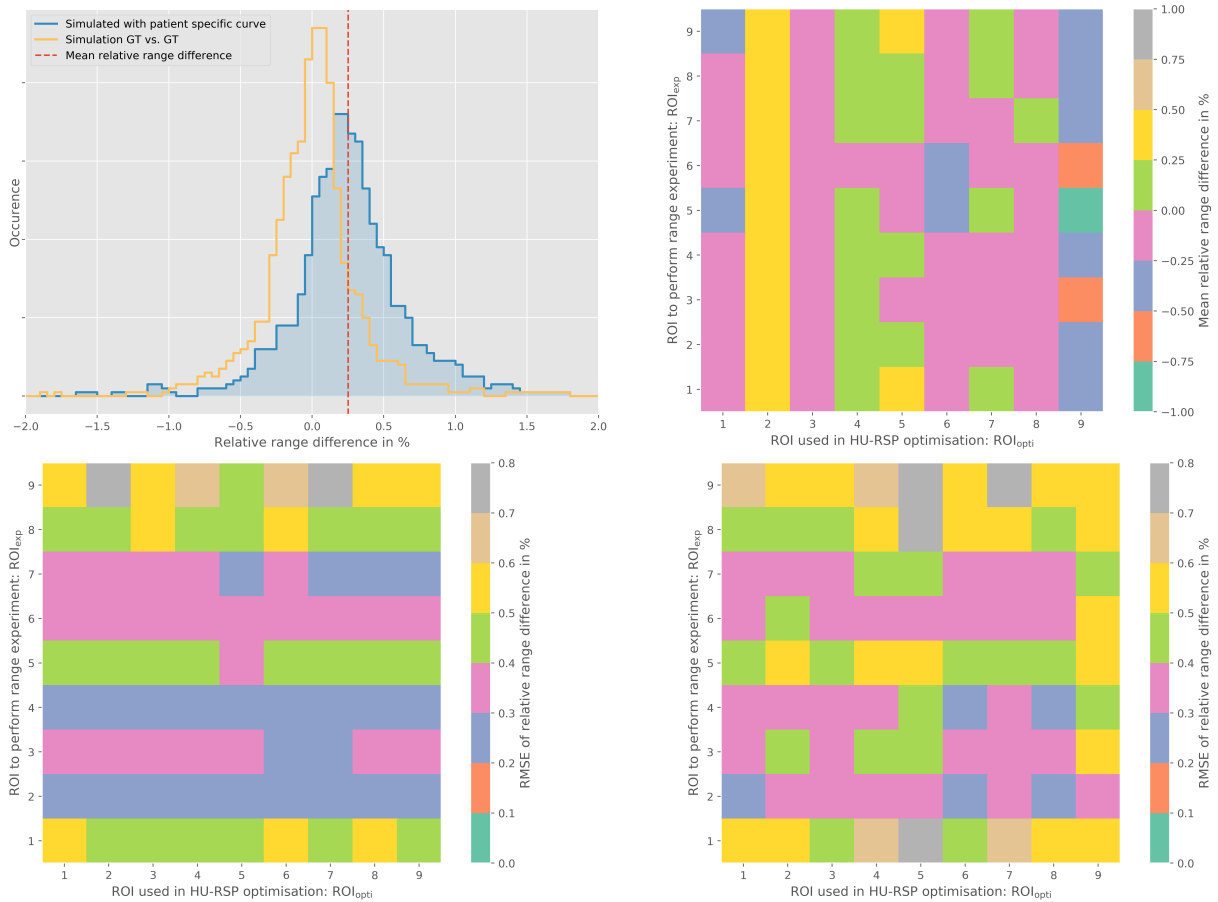


Figure 10: Upper left: example distribution of relative range differences obtained from the Monte Carlo experiment (see section 2.11). Upper right: Mean relative range difference between true and predicted range using different regions of interest for the optimisation and the Monte Carlo experiment (see section 2.11). Lower panels: RMSE in control experiment (left) and between true and predicted range (right).

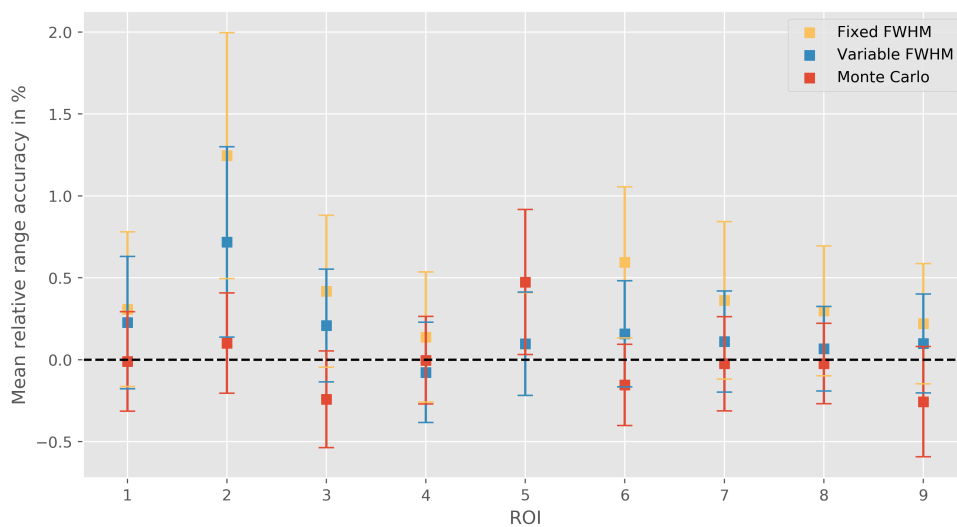


Figure 11: Mean relative range accuracy obtained in the Monte Carlo experiment (see section 2.11). The CT-RSP curves were optimised for the nine regions of interest shown in figure 9 left and using DRRs calculated with three different beam models (see section 2.7).

482 model with fixed beam size seems to introduce a slight overestimation of the proton range. The  
483 other two beam models, on average, reproduce the ground truth range faithfully to within 0.2-  
484 0.5%. Whether or not the minimal positive bias observed with the variable FWHM model is  
485 statistically significant appears difficult to establish based on the nine data points.

## 486 4 DISCUSSION

487 In the presented work, we introduced methods for the patient-specific calibration of the CT-RSP  
488 conversion curve based on proton radiography, with a special regard to proton imaging set-ups  
489 which combine pencil beam scanning with a position-insensitive range telescope. Our results  
490 demonstrate that the optimisation of a piecewise linear conversion curve needs to be regularised  
491 because it otherwise leads to unrealistic variations in the optimised curve. The advantage of a  
492 quadratic norm is that the regulariser terms can be easily combined with the data attachment  
493 term keeping the optimisation computationally very feasible. With the proposed procedure  
494 to select the relative weights of the regulariser terms, the variation in the optimised curve  
495 corresponds to that observed in the stoichiometric curve used as reference.

496 Our results show that the main reason for the need to regularise the cost function is linked  
497 to the correlation among the parameters  $R_\alpha$  of the CT-RSP conversion curve, which in turn is  
498 strongly influenced by the beam size (figure 6). In a wider phantom than the one considered in  
499 this work, scattering becomes more important leading to increased correlation and potentially  
500 poorer optimisation results unless more strongly regularised. In case of a pin-like pencil beam, for  
501 example, the non-regularised optimisation yielded almost the same result as the regularised one  
502 (figure 5). This explains why Collins-Fekete et al. (2017), who investigated the patient-specific  
503 CT-RSP calibration based on proton radiographies acquired with single tracking set-ups, did  
504 not encounter similar problems: the integration in their case is performed along an estimate of  
505 individual proton trajectories with very thin uncertainty envelopes around them and the degree  
506 of parameter correlation is expected to be even smaller than with a pin-like pencil beam in our  
507 case. On the other hand, the set-up used by Doolan et al. (2015) detects many protons at the  
508 same time, as in our case, yet delivered in a passive field rather than by pencil beam scanning.  
509 Parameter correlation is therefore expected to be even stronger because the effective beam size  
510 is larger. The authors did not report any variation in the optimised CT-RSP curves, such as  
511 seen in figure 3, although they did not regularise the optimisation. The reason is probably that  
512 they overrode HU values to a single value in each organ making the phantom geometry much  
513 more homogeneous. They furthermore excluded heterogeneous regions prone to range mixing.  
514 We remark that such a region-wise homogenous RSP map might potentially over-simplify the  
515 patient geometry.

516 We note that the way of parametrising the CT-RSP curve has an impact on the correlation  
517 between parameters and thus on the need to regularise the optimisation. Figure 4 shows that no  
518 regularisation might be required when using relatively few HU intervals. On the other hand, the  
519 CT-RSP curve has then less granularity to resolve intra-patient tissue variability. In practice, a  
520 reasonable option would be to choose the HU intervals in accordance with the parametrisation of  
521 the clinical lookup table, possibly with some additional intervals for more granularity. The way  
522 of interpolating between HU intervals is also expected to affect the optimisation outcome. In  
523 our case, neighbouring  $R_\alpha$  values are intrinsically anti-correlated because the linear segments are  
524 assumed to form a continuous conversion curve. This is seen from the negative entries below and  
525 above the diagonal of the correlation matrix in figure 6. Alternative parametrisations include  
526 a piecewise linear interpolation without the constraint of continuity at the intervals boundaries  
527 or a piecewise constant conversion curve which assigns the same RSP value to all voxels whose  
528 HU values fall in the same interval. In the latter case, the  $R_\alpha$  parameters would be correlated  
529 only through the projection operation and consequently less variation would be expected in  
530 the optimised conversion curve even without regularisation. We remark that such a piecewise

constant conversion curve assigns the same RSP value to all voxels whose HU values fall in the same interval and is therefore similar to segmenting the CT image into homogeneous material regions as in (Doolan et al. 2015). Investigating the impact of different kinds of interpolation was beyond the scope of this work.

Among the three projection models used in our work, the Monte Carlo based one (section 2.7.3) takes the scattering processes into account most accurately through the physics models implemented in the code. In line with this, differences between the pDRR obtained with the Gaussian projection model with scattering and the Monte Carlo projection are mainly visible in heterogeneous regions and along the outer perimeter of the patient’s head (figure 8, right) where proton scattering has the greatest impact on the projected image. In the left panel of figure 8, the resulting optimised CT-RSP curve differs from the one obtained with the analytical beam model in its shape, but both lie within 3-5% of the ground truth curve. In terms of range accuracy (figure 11), our results suggest that the simple Gaussian beam model with a fixed beam size might lead to an overestimation of up to about 1%. The other two models reproduce the ground truth range expectation to 0.2-0.5% accuracy on average. Among the two, the Monte Carlo beam model seems to be slightly preferable over the variable FWHM Gaussian model, although we cannot deduce whether this observation is statistically significant. At the moment, the latter is much faster ( $< 1$  min) to calculate thanks to our GPU implementation compared to the former (order of hours) which currently runs on single CPU only, although these technical issues could be improved in the future.

Remapping the HU values  $h$  in the CT voxels to coefficient vectors  $\vec{w}$  (section 2.6) allowed us to separate the projection operation from the actual optimisation. This is particularly useful when using a cost function that requires iterative minimisation. We emphasise that the remapping can be used with proton radiographies acquired by any kind of set-up. For example, when using a single tracking proton scanner (Collins-Fekete et al. 2017), the projection operation to construct the pDRR (section 2.7) would be performed by integrating the  $w_{ijk,\alpha}$  matrices along the estimated most likely path of every detected proton.

In our Monte Carlo experiment, the range accuracy achievable with patient-specific conversion curves optimised using the methods presented here was well below 1%. Whether or not the imaged region-of-interest is chosen in accordance with the treated volume did not systematically impact the range accuracy. This statement only refers to the optimisation process itself and does not take into account possible local variability in the tissue composition.

We chose to perform our study entirely in Monte Carlo because it allowed us to define a ground truth CT-RSP conversion curve. This approach is idealised in one regard: In reality, no one-to-one correspondence exists between the HU and RSP of the patient tissue. Our ground truth scenario is therefore an approximation because we generate the RSP map through a one-to-one conversion process. Studying the impact of the tissue composition on range accuracy could be achieved by modelling the expected tissue variation (Yang et al. 2010, Möhler et al. 2016, Wohlfahrt et al. 2017) and perturbing the converted RSP value in each voxel. We emphasise that this was not the scope of this work. It should also be noted that the patient-specific CT-RSP calibration based on proton radiography cannot solve the issue of tissue variability within one patient because it intrinsically relies on a conversion curve. Only a full volumetric proton CT image would provide a voxel-wise RSP value and thereby circumvent the conversion process.

## 5 CONCLUSION

We developed a series of methods to perform a patient-specific calibration of the HU to RSP conversion curve based on proton radiography. We introduced a regulariser term in the cost function and showed that this is necessary to avoid unrealistic variation in the optimised curve. The main reason is the correlation between the parameters of the piecewise linearly interpolated CT-RSP curve and the effect is more pronounced with larger beam size. We performed Monte

580 Carlo experiments and obtained a range accuracy of better than 0.5%. Our results further in-  
581 dicate that from the point of view of the optimisation procedure, no systematic loss of range  
582 accuracy is probably to be expected if the imaged region of the patient does not correspond to  
583 the treatment volume. This work underlines that it is possible to perform a patient-specific cal-  
584 ibration of the CT-RSP conversion curve on the basis of a single proton radiographic projection  
585 acquired with a detector typically available in a treatment facility.

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