BJR

Received: 25 April 2013 | Revised: 20 August 2013 | Accepted: 27 August 2013

doi: 10.1259/bjr.20130238

Cite this article as:
Sarkar B, Manikandan A, Nandy M, Gossman MS, Sureka CS, Ray A, et al. A mathematical approach to beam matching. Br J Radiol 2013;86: 20130238.

FULL PAPER

A mathematical approach to beam matching

[1]B SARKAR, MS, Dip. RP, [2]A MANIKANDAN, MS, Dip. RP, [3]M NANDY, PhD, [4,5]M S GOSSMAN, MS, DABR, [6]C S SUREKA, PhD, [7]A RAY, MB BS, MD and [8]N SUJATHA, MS, Dip. RP

[1]Department of Radiation Oncology, Medical Physics Division, Advance Medicare and Research Institute Cancer Centre, Kolkata, West Bengal, India
[2]Department of Radiation Oncology, Medical Physics Division, Inlaks and Budhrani Hospital, Pune, Maharastra, India
[3]Chemical Science Division, Saha Institute of Nuclear Physics, Kolkata, West Bengal, India
[4]Regulation Directive Medical Physics® LLC, Flatwoods, KY, USA
[5]Medical Physics Section, Tri-State Regional Cancer Center, Ashland, KY, USA
[6]Department of Medical Physics, School of Physical Sciences, Bharathiar University, Coimbatore, Tamil Nadu, India
[7]Department of Radiation Oncology, Nilratan Sircar Medical College and Hospitals, Kolkata, India
[8]Department of Radiation Oncology, Guntur Medical College, Guntur, Andhra Pradesh, India

Address correspondence to: Mr B Sarkar
E-mail: *biplabphy@gmail.com*

Parts of this work were presented at the 2011 Joint Meeting of the American Association of Physicists in Medicine (AAPM) and the Canadian Organization of Medical Physicists (COMP), 31 July–4 August, Vancouver, Canada. The idea was published in a 300-word abstract with a different title. The abstract can be found here: http://www.aapm.org/meetings/2011AM/PRAbs.asp?mid=59&aid=15623

Objective: This report provides the mathematical commissioning instructions for the evaluation of beam matching between two different linear accelerators.
Methods: Test packages were first obtained including an open beam profile, a wedge beam profile and a depth–dose curve, each from a 10×10 cm^2 beam. From these plots, a spatial error (SE) and a percentage dose error were introduced to form new plots. These three test package curves and the associated error curves were then differentiated in space with respect to dose for a first and second derivative to determine the slope and curvature of each data set. The derivatives, also known as bandwidths, were analysed to determine the level of acceptability for the beam matching test described in this study.
Results: The open and wedged beam profiles and depth–dose curve in the build-up region were determined to match within 1% dose error and 1-mm SE at 71.4% and 70.8% for of all points, respectively. For the depth–dose analysis specifically, beam matching was achieved for 96.8% of all points at 1%/1 mm beyond the depth of maximum dose.
Conclusion: To quantify the beam matching procedure in any clinic, the user needs to merely generate test packages from their reference linear accelerator. It then follows that if the bandwidths are smooth and continuous across the profile and depth, there is greater likelihood of beam matching. Differentiated spatial and percentage variation analysis is appropriate, ideal and accurate for this commissioning process.
Advances in knowledge: We report a mathematically rigorous formulation for the qualitative evaluation of beam matching between linear accelerators.

Radiotherapy centres with more than one linear accelerator of the same make, model and multileaf collimator (MLC) often desire "beam matching" for immediate interchange of patients between these accelerators, without having to replan, in the event that one machine is not functioning properly. A high level of similarity between beam profiles, depth–dose curves and other properties from two similar accelerators signifies beam matching. Beam matching can be defined as a methodology that needs to be performed between two or more linear accelerators to ensure the equivalence of dose delivery. A linear accelerator is characterised by numerous electrical, mechanical and dosimetric parameters. Proper evaluation of the dosimetric and the mechanical parameters is crucial for precision and accuracy in treatment delivery to patients. Some parameters relating to dose include the output factor, depth–dose, profile, energy and dose rate. Electromechanical parameters consist of the gantry, collimator and couch isocenters, MLC positional accuracy, MLC speed, jaw positional accuracy, gantry speed, etc. [1]. It is possible that many of these parameters will be close in value between those for an existing accelerator and a newly installed one to within some specified tolerance limit. However, the method for beam matching is not well described for commissioning

purposes. The only study that describes the problem in a quantitative manner is from Hrbacek et al [2]. The vendor-defined criteria for beam matching are insufficient to ensure the *interchangeability* of the beams [2–4]. Other investigators described the problem in a more qualitative way [5–8]. There is no task group report that clearly indicates the acceptability criteria of two or more matched beams. Here, we describe the test package required for necessary and adequate testing as well as the process by which comparisons should be objectively made.

It is important to understand that instead of measuring the full set of dosimetric data for the test accelerator, comparison of only a limited set of baseline measurements between the reference linear accelerator and the test linear accelerator is required for dosimetric fidelity cross-check between them. If the reference beam and test beam are found to be in agreement within a specified tolerance limit, no further profile and depth–dose measurement for the new machine are required. Therefore, beam matching leads to a considerable reduction in the dosimetric workload [2]. Matched linear accelerators may then be represented by a common set of data used in the treatment planning system.

Accelerator manufacturers, such as Varian Medical Systems, Inc. (Palo Alto, CA) and Elekta (Stockholm, Sweden), offer beam matching for X-rays. Varian's specific criterion requires the depth of maximum dose (d_{max}) along the central axis as well as the beam energy specification to match within ± 1.5 mm of the nominal specified value between machines. The relative dose at a depth of 10 cm should also match within ± 1%. For profile matching, the dose at d_{max} and at a depth of 10 cm is required to be in agreement within ±1% and ±2%, respectively, in the flat region for field sizes larger than $10\times10\,cm^2$. Elekta's specified criterion is nearly the same. However, an assignment for d_{max} to specify the matching criteria for energy and beam flatness is disregarded. Only a 10-cm-depth specification is needed. Further, profile matching is only averaged over an arbitrary 1-cm region in the flat region of the profile [3,4]. Neither manufacturer has any specific criteria for output factor matching or profile penumbra matching. Match criteria is entirely based on a single field size and at only one or two depths of interest. Such limited criteria are insufficient to ensure the interchangeability of linear accelerators in clinical practice.

The quantitative evaluation of the dose distribution must be much less generous. This is one of the single most attributable causes of intensity-modulated radiotherapy (IMRT) delivery quality assurance failures for patients who are required to be switched to a different machine after completing treatment planning for a particular linear accelerator. To elaborate this point, we consider IMRT quality assurance. The integral dose given from a beam passing through segmented fields must be evaluated for accuracy in any dynamic plan [2]. As encountered by many investigators, a systematic error is observable in energy fluence comparisons of the computerised plan and the actual delivery when the MLC motion is not identical [2,5–8]. The same difficulty arises when the therapy is planned on one machine and delivered on another that is not acceptably matched.

The best methodology available at present for a quantitative evaluation of the dose distribution for beam matching is based on the gamma index (γ), distance to agreement or percentage dose difference criteria [2,9,10]. Each of these methods has disadvantages. They are sensitive to normalisation and do not accentuate the dose gradient [11]. However, all beam matching methodologies described are based on an one-dimensional gamma analysis and have the same characteristic demerit of not appreciating the dose gradient [2,9–11]. It is noteworthy that prior published literature examined only Varian accelerators. [2,5–8]. No prior study has yet been reported for Elekta linear accelerators.

To address the deficiencies of beam matching methods commonly used at present, a new mathematical technique for the evaluation of dosimetric parameters is proposed in this report. The intent of this study is to demonstrate how to evaluate quantitatively a beam from a new accelerator that was manufactured to match an existing linear accelerator beam having the same energy. We emphasise the importance of beam match accuracy by demonstrating how to apply this method uniformly for all beam energies, whether the emission is bremsstrahlung X-rays or electrons, and to any accelerator model.

MATERIALS AND METHODS

Accelerator and software

The machines evaluated are identical to Elekta Model Precise linear accelerators. Before proceeding for dosimetric beam matching, all electromechanical parameters of both the linear accelerators were verified using the TG-142 [1] protocol. The vendor-defined "fine beam matching" (also referred to as "factory matching") was conducted at the Elekta factory. The reference accelerator was installed 5 years before the delivery of this new machine. The machine to be installed was purchased to include a beam matching for 6-MV X-rays. In carrying out beam matching quality assurance test as part of the customer acceptance test by the manufacturers, it was found that the dose difference between the two machines for the flat region of the open beam profile was slightly higher than 2% (2.04%) [3]. Although this result does not strictly conform to the beam matching criterion specified by the manufacturer, the machine was accepted as beam matched, considering the mismatch as statistically insignificant. Moreover, because we planned to develop our own methodology with necessary tweaking on profile and depth–dose curves, vendor-specified criteria were taken only as initial values. Our beam matching requirements must also be satisfied. In this need, it was necessary to calibrate the machine for absolute dose as stipulated in standard documents in medical physics; AAPM TG-51 or International Atomic Energy Agency Technical Report Series 398 (IAEA TRS-398) [12,13]. Immediately following this, profile and depth–dose measurements were completed as recommended by AAPM TG-106 [14]. All relative measurements were taken in 1-mm increments with a PTW (Freiburg, Germany) dosimetry system, then exported from the scanning software to a spreadsheet. All the depth–dose curves and profiles were compared in absolute dose values ($cGy\,MU^{-1}$) to avoid any ambiguity in normalisation [5]. Acceptability of the new linear accelerator, with respect to beam matching with the

reference linear accelerator, was evaluated in the Nucletron (an Elekta company) Model Plato Sunrise treatment planning system.

The high gradient penumbra region of the profile curve can be expressed in terms of a gauss error function for one side and a complementary error function on the contralateral side [9]. However, these two error functions cannot be feasibly combined to express the complete profile. A similar problem exists for the depth–dose curve. There is no simple fit for the increase in the depth of maximum dose that adequately follows the declination in dose beyond that point [15,16]. Owing to the inability in obtaining these data in an analytical form, numerical differentiation is required. Scanning data now present in spreadsheet software were operated on with simple calculus tools in OriginLab (Northampton, MA) Model Microcal Origin v. 6.0 mathematical software. It is this first derivative that defines the slope of the fitted profile or curve, whereas the second derivative represents the curvature. First and second derivatives together are ideally suited to discern any variance between the new beam and the existing beam.

Profile beam matching method

The profile is expressed in terms of the dose (D) per monitor unit (MU) with units cGy MU^{-1}. The first derivative denoted $D' = \mathrm{d}D/\mathrm{d}x$ is the rate of change of energy deposition in space or the slope of the curve. The second derivative termed $D'' = \mathrm{d}^2D/\mathrm{d}x^2$ indicates the rate of change of slope or termed as curvature. For a dose profile curve, the first and the second derivatives are important to highlight the sharpness in the rise and fall of the penumbra region. There are two regions of the profile curve and its derivates that are of main interest; the derivative significant area (DSA) and the derivative insignificant area (DIA). Figure 1 illustrates half of the 10×10 cm^2 open profile for a 6 MV beam, including the first derivative and second derivative in space. The nature of the other half of the profile is complementary. For critical visualisation, the profile curve was plotted on a $\log_{10}$ scale, whereas the derivatives are shown on a linear scale. Venselaar et al [17] indicated that dose differences in the penumbral region may be as high as 40% and predominates all other profile variations [9]. Therefore, it is only necessary to evaluate ΔD in the DIA region and to critically judge $\Delta D'$ and $\Delta D''$ in the DSA region. Although $\Delta D'$ is insignificant in the DIA region, it can be compared to estimate the local fluctuation of the test profiles against reference profiles, as has been done here additionally for the reader.

We considered the open wedged profile and percentage depth dose (PDD) for a 10×10 cm^2 field from the reference machine as standard curve. A percentage dose error (%DE) and spatial error (SE) were then introduced to the standard curves. The errors chosen included a 1%, 2% and 3% dose error, a 1-, 2- and 3-mm SE as well as a mixed error (%DE and SE) of 1%/1 mm, 2%/2 mm and 3%/3 mm. The first and second derivatives of the standard curves and error-introduced curves were then computed. Finally, the dose differences (ΔD), first derivative differences ($\Delta D'$) and second derivative differences ($\Delta D''$) were calculated between each set of standard curve and error curve. These bandwidth values in the test package, expressed as ΔD_{BW}, ΔD_{BW} and $\Delta D''_{BW}$, were over both sides of the central axis.

While evaluating beam matching characteristics quantitatively, between the reference and test linear accelerators, a set of similar values for dose and derivative difference were defined for the reference accelerator. These values denoted as ΔD_{BM}, $\Delta D'_{BM}$ and $\Delta D''_{BM}$ were compared against the ceiling values of the test package (ΔD_{BW}, $\Delta D'_{BW}$ and $\Delta D''_{BW}$). Tables 1 and 2 demonstrate the results for the open profile and wedged profile, respectively.

Depth–dose beam matching method

The depth–dose curve monotonically increases from the surface to the depth of maximum dose and then monotonically decreases as a function of depth at an exponential rate. The portion of the depth–dose curve beyond d_{max} has a simple and nearly constant

Figure 1. Half of a standard profile and its first and second derivatives in space; the profile (cGy MU^{-1}) plotted on a $\log_{10}$ scale; first and second derivatives are shown in a linear scale; the derivative significant area (DSA) and derivative insignificant area (DIA) are indicated (the contralateral side of the curve not shown exists complimentary to this side).

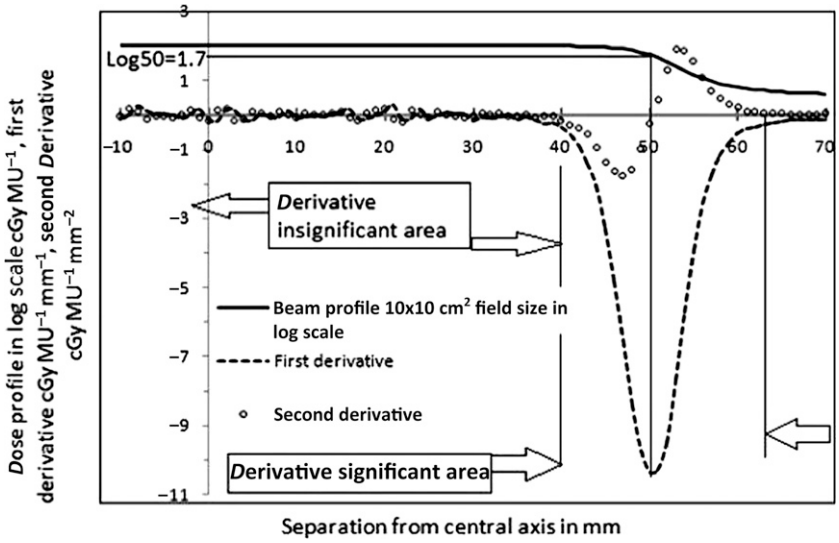


Table 1. Test package for open photon profile with induced errors tabulated according to their respective bandwidth value in ascending order—ΔD_{BW} (cGy MU^{-1}), $\Delta D'_{BW}$ (cGy MU^{-1}mm^{-1}) and $\Delta D''_{BW}$ (cGy MU^{-1}mm^{-2}) are dose, first and second derivative differences, respectively

Induced error	Rise/fall average BW: $\Delta D'_{BW}$	Induced error	Rise/fall average BW: $\Delta D''_{BW}$	Induced error	Plateau average BW: ΔD_{BW}	Induced error	Plateau BW: $\Delta D'_{BW}$
1%	0.11	1%	0.04	1%	0.02	1%	0.00
2%	0.21	2%	0.15	2%	0.04	2%	0.00
3%	0.31	3%	0.11	3%	0.05	3%	0.00
1%/1 mm	3.83	1%/1 mm	1.37	1 mm	0.85	1 mm	0.70
1 mm	3.84	1 mm	1.37	1%/1 mm	0.87	1%/1 mm	0.74
2 mm	7.25	2%/2 mm	2.55	2%/2 mm	1.23	2 mm	0.76
2%/2 mm	7.28	2 mm	2.60	2 mm	1.46	2%/2 mm	0.77
3 mm	10.36	3%/3 mm	3.58	3%/3 mm	1.54	3%/3 mm	0.78
3%/3 mm	10.55	3 mm	3.62	3 mm	2.02	3 mm	0.79

BW, bandwidth.

slope. It then follows that the highest variations of the first and second derivatives is obtained in the build-up region since small spatial dose variation yields minimal derivatives beyond that point. Hence, for the depth–dose curve $\Delta D'$ and $\Delta D''$ were compared up to the depth d_{max}. The second derivative becomes insignificant beyond d_{max}. Therefore, only the ΔD was compared downstream from that point. An identical set of errors were introduced as described for the profile curves in Profile beam matching method section to obtain the bandwidth values ΔD_{BW}, $\Delta D'_{BW}$ and $\Delta D''_{BW}$ for the test package. The bandwidths were then compared with the test package ceiling values. The test package table for depth–dose beam matching was not enumerated, but rather pictorially presented.

RESULTS

Profile beam matching analysis—open fields

Comparison of the dose profiles of the reference and test machines showed that the plateau region of the two curves is matched for lower %DE/SE values than that for the penumbra region. This observation is in agreement with our hypothesis that beam matching for the entire dose profile curve cannot be ensured using a single number [2]. We deduced appropriate criteria by dividing the profile curve in these two regions separately. Open field results are shown in Table 3. Here, the "rise" and "fall" refer to the penumbra regions for $x<0$ and $x>0$, respectively. All results were within the specified limits of the introduced error, except for the $\Delta D''$ values for 40×40 cm^2 field

Table 2. Test package for wedge profile with induced errors tabulated according to their respective bandwidth values in ascending order—ΔD_{BW}, ΔD_{BW} (cGy MU^{-1}), $\Delta D'_{BW}$ (cGy MU^{-1}mm^{-1}) and $\Delta D''_{BW}$ (cGy MU^{-1}mm^{-2}) are dose, first and second derivative differences, respectively

Wedge thick end			Constant slope region				Wedge thin end		
Induced error	Thick end BW: $\Delta D'_{BW}$	Thick end BW: $\Delta D''_{BW}$	Induced error	Constant slope BW: ΔD_{BW}	Induced error	Constant slope BW: $\Delta D'_{BW}$	Induced error	Thin end BW: $\Delta D'_{BW}$	Thin end BW: $\Delta D''_{BW}$
1%	0.02	0.01	1%	0.13	1%	0.00	1%	0.04	0.02
2%	0.03	0.01	1 mm	0.24	2%	0.00	2%	0.08	0.03
3%	0.05	0.02	2%	0.27	3%	0.00	3%	0.12	0.05
1 mm	0.69	0.34	1%/1 mm	0.28	1 mm	0.14	1%/1 mm	1.77	0.83
1%/1 mm	0.69	0.34	2 mm	0.39	3 mm	0.14	1 mm	1.78	0.83
2 mm	1.32	0.62	3%	0.40	1%/1 mm	0.14	2 mm	3.38	1.44
2%/2 mm	1.32	0.63	2%/2 mm	0.42	3%/3 mm	0.14	2%/2 mm	3.38	1.46
3 mm	1.80	0.74	3%/3 mm	0.42	2 mm	0.19	3 mm	4.62	1.88
3%/3 mm	1.88	0.77	3 mm	0.48	2%/2 mm	0.19	3%/3 mm	4.70	1.91

BW, bandwidth.

Table 3. Open field beam matching result showing the dose difference ΔD_{BM} (cGy MU^{-1}), first $\Delta D'_{BM}$ (cGy MU^{-1} mm^{-1}) and second derivative difference $\Delta D''_{BM}$ (cGy MU^{-1} mm^{-2}) for different square field sizes and evaluated with respect to the ceiling value of bandwidths obtained from Table 1

Field size (cm^2)	Direction and depth	Rise BW: $\Delta D'_{BM}$	Below $\Delta D'_{BW}$[a]	Rise BW: $\Delta D''_{BM}$	Below $\Delta D''_{BW}$[a]	Constant slope BW: ΔD_{BM}	Below ΔD_{BW}[a]	Constant slope BW: $\Delta D'_{BM}$	Below ΔD_{BW}[a]	Fall BW: $\Delta D'_{BM}$	Below ΔD_{BW}[a]	Fall BW: $\Delta D''_{BM}$	Below $\Delta D''_{BW}$[a]
5×5	x-d_{max}	0.97	1%/1 mm	0.35	1%/1 mm	1.13	2%/2 mm	0.23	1 mm	0.46	1%/ 1 mm	0.27	1%/1 mm
10×10	y-d_{max}	2.18	1%/1 mm	1.05	1%/1 mm	0.05	3%	0.56	1 mm	1.28	1%/ 1 mm	0.87	1%/1 mm
15×15	y-d_{max}	1.54	1%/1 mm	0.84	1%/1 mm	1.71	3 mm	0.44	1 mm	0.98	1%/ 1 mm	0.64	1%/1 mm
20×20	y-d_{max}	2.29	1%/1 mm	0.88	1%/1 mm	1.17	2 mm	0.31	1 mm	2.46	1%/ 1 mm	0.89	1%/1 mm
25×25	x-d_{max}	3.86	1%/1 mm	1.58	2%/2 mm	1.95	3 mm	0.51	1 mm	2.57	1%/ 1 mm	0.96	1%/1 mm
30×30	y-100 mm	0.38	1%/1 mm	0.30	1%/1 mm	1.94	3%	0.41	1 mm	2.68	1%/ 1 mm	1.09	1%/1 mm
40×40	y-d_{max}	6.34	2 mm	4.87	*	0.05	3%	0.56	1 mm	6.84	2 mm	2.90	3%/3 mm

BM, beam matching; BW, bandwidth.
[a]From Table 1.

Table 4. Wedge field beam matching results detailing the dose difference ΔD_{BM} (cGy MU^{-1}), first derivative $\Delta D'_{BM}$ (cGy MU^{-1} mm^{-1}) and second derivative differences $\Delta D''_{BM}$ (cGy MU^{-1} mm^{-2}) for different square wedged fields evaluated with respect to the ceiling value of bandwidths obtained from Table 2

Field size (cm^2)	Direction and depth	Thick end				Constant slope region				Thin end			
		Thick end BW: $\Delta D'_{BM}$	Below $\Delta D'_{BW}$[a]	Thick end BW: $\Delta D''_{BM}$	Below $\Delta D''_{BW}$[a]	Constant slope region BW: ΔD_{BM}	Below ΔD_{BW}[a]	Constant slope region BW: $\Delta D'_{BM}$	Below $\Delta D'_{BW}$[a]	Thin end BW: $\Delta D'_{BM}$	Below $\Delta D'_{BW}$[a]	Thin end BW: $\Delta D''_{BM}$	Below $\Delta D''_{BW}$[a]
10×10	y-W-d_{max}	0.15	3 mm	0.130	1 mm	0.42	2%/2 mm	0.13	1 mm	0.74	1%/1 mm	0.43	1%/1 mm
30×30	y-W-d_{max}	0.11	2 mm	0.053	1 mm	0.37	2 mm	0.16	2 mm	0.61	1%/1 mm	0.33	1%/1 mm
30×30	y-W-10 cm	0.07	1 mm	0.043	1 mm	0.33	2 mm	0.09	1 mm	0.54	1%/1 mm	0.30	1%/1 mm
10×10	y-W-10 cm	0.10	1 mm	0.068	1 mm	0.32	2 mm	0.12	1 mm	0.76	1%/1 mm	0.44	1%/1 mm

BM, beam matching; BW, bandwidth.
[a]From Table 2.

size profile at d_{max} depth. The $\Delta D''$ value obtained in this case was beyond any ceiling value, giving rise to the speculation that the beam scan should be repeated for validity. This was intentionally provided for the reader to observe where a failure might exist.

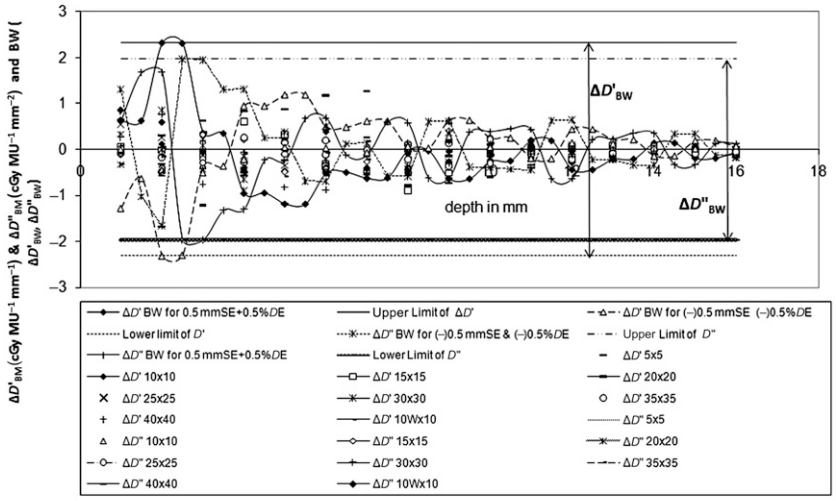
Our overall assessment of the open profile analysis was that 71.4% of all the segments for ΔD_{BM}, $\Delta D'_{BM}$ and $\Delta D''_{BM}$ (30 out of 42) matched within a bandwidth of 1%/1 mm. The dose difference (ΔD_{BM}) in the constant slope region matched within a maximum value of 3%. However, the slope difference ($\Delta D'_{BM}$) for all the tested field sizes matched within 1 mm in that same region. With the point-to-point dose variation between the reference and test profiles being relatively high, the difference in the rate of spatial dose deposition (slope difference) was quite low. In the DSA region, both $\Delta D'_{BM}$ and $\Delta D''_{BM}$ matched within 1%/1 mm.

For a better understanding, Table 3 demonstrates the beam matching results (ΔD_{BM}, $\Delta D'_{BM}$ and $\Delta D''_{BM}$) for a 10×10 cm^2 field size at a depth of d_{max}, and their respective bandwidths (ΔD_{BW}, $\Delta D'_{BW}$ and $\Delta D''_{BW}$) that matched. The first derivative difference ($\Delta D'_{BM}$) and dose difference (ΔD_{BM}) in the plateau region matched within 3% for ΔD_{BW} and within 1 mm for $\Delta D'_{BW}$. The first derivative difference matched within 1 mm in the plateau region and 1 mm in the fall/rise region. The second derivative difference ($\Delta D''_{BM}$) matched within 1%/1 mm for all data.

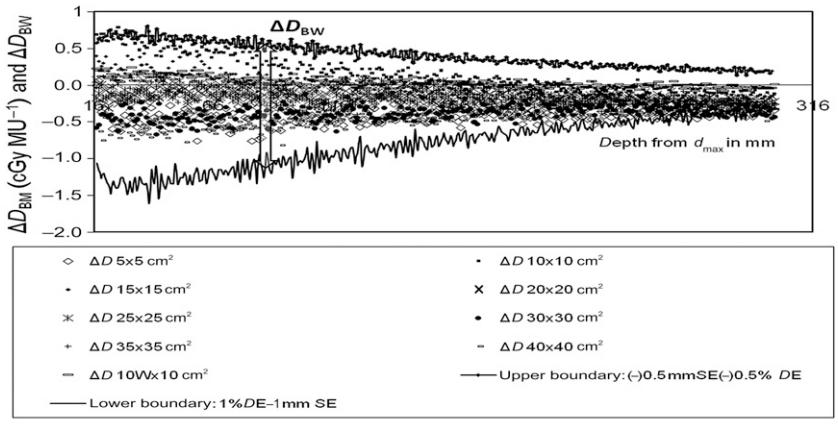
Profile beam matching analysis—wedged fields

Results of beam matching analysis for two wedged fields at two different depths (total four) are shown in Table 4. Only the radial scan is demonstrated for these wedged data. For transverse scan across the wedge, the employed methodology is the same as demonstrated in case of open field. The terminology changes according to the wedge geometry; the wedge profile curves were

Figure 2. (a) $\Delta D'_{BM}$ (cGy MU^{-1} mm^{-1}) and $\Delta D''_{BM}$ (cGy MU^{-1} mm^{-2}) values of the depth–dose curve in the build-up region, $\Delta D'_{BM}$ and $\Delta D''_{BM}$ for different square open field sizes from 5×5 cm^2 to 40×40 cm^2 and including a 10×10 cm^2 wedged field matching within a bandwidth ($\Delta D'_{BW}$ and $\Delta D''_{BW}$) of 1%/1 mm. (b) Difference (ΔD_{BM}) in depth–dose between the reference and test linear accelerators beyond the depth of maximum dose: 96.8% points of ΔD_{BM} for different square fields match within a bandwidth (ΔD_{BW}) of 1.5%/1.5 mm.



(a)



(b)

subdivided according to the thick and thin end of the wedge, and the mid-portion was analysed as a constant slope region (not plateau). For these matching curves, 70.8% (17 out of 24) profile segments match well within the 1%/1 mm in the bandwidth.

Depth–dose beam matching analysis

The results of depth–dose comparison are demonstrated in Figure 2a,b. Each of the first derivative bandwidths $\Delta D'_{BM}$ and second derivative bandwidths $\Delta D''_{BM}$ was compared from the surface up to d_{max}. For depths greater than d_{max} up to 300 mm, the dose difference ΔD_{BM} was compared only. The slope of the depth–dose curve was constant beyond d_{max}. $\Delta D'_{BM}$ and $\Delta D''_{BM}$ were insignificant in this region and were within 2% of that for the reference curve. Up to the depth of d_{max}, the $\Delta D'_{BM}$ and $\Delta D''_{BM}$ curves matched within 1%/1 mm, while beyond d_{max}, the ΔD_{BM} curve matched within 1.5%/1.5 mm. This is indicated in Figure 2b, where it is observed that 96.8% points (274 out of 283) fit within a window formed by an upper boundary of 0.5%/0.5 mm and a lower boundary of −1%/−1 mm. Only 3.2% of all points were found to fall outside the specified bandwidth. The output difference between the test and reference linear accelerators was found to match within a window of −0.2% to 0.7%.

DISCUSSION

In this work, a methodology has been developed for quantitative evaluation of beam matching between two linear accelerators and demonstrated for Elekta machines. This method has two advantages over prior published works on beam matching using a gamma index. Firstly, Low and Dempsey [10] described that the method of gamma index (γ) does not appreciate the dose gradient [11]. It then follows that any unacceptable dose gradient may be overlooked by that methodology as demonstrated by Hrbacek et al [2] based on the γ index. The beam matching methodology presented in this work is free from this difficulty, because it considers dose profile matching in the high gradient region. Secondly, as indicated in Figure 2b, ΔD_{BM} is negatively influenced about the y=0 boundary. This effect is accentuated when comparing the dose differences of depth–dose curves. For most of the field sizes considered in this work, the test depth–doses had higher values than the reference curves for the existing accelerator. This results in negative values for ΔD_{BM}. To accommodate these findings, the upper boundary was taken as 0.5%/0.5 mm and the lower boundary taken as −1%/−1 mm. This is an interesting feature that cannot be identified or corrected for by the γ analysis method, since γ indices can only yield positive [2,9] results.

For an Elekta linear accelerator, the beam profile is steered by adjusting the transverse magnetic field induced by two pairs of inductor coils 1R–1T (at the origin of the waveguide) and 2R–2T (at the end of the waveguide where the electron beam is rotated by 270°). For a fixed beam geometry shaped by beam limiting devices like jaws and/or an MLC, the shape of the profile is adjusted by changing the 2R–2T coil current. The 1R–1T coil current changes in proportion with the 2R–2T coil current and cannot be adjusted independently. The change in the coil currents changes the transverse magnetic field and consequently the trajectory and spatial spread of the accelerated electron beam. Similarly for a depth–dose curve adjustment, the penetration characteristic corresponds to the beam energy, which is governed by the bending coil current. Adjustment of the 2R–2T coil current or the bending coil current may change the shape of dose profile curves or depth–dose curves for field sizes other than that used during tweaking. Thus, after the 2R–2T coil current is adjusted, we recommend that scanning of all profile curves and depth–dose curves be repeated before implementation of the final beam matching procedure in the commissioning process.

CONCLUSIONS

We have described a new method for quantitative evaluation of beam matching between two linear accelerators and demonstrated its application for two factory-matched Elekta linear accelerators. Our results show that there is good agreement of the dosimetric characteristics of two beams of these machines. More than 70% of the open and wedge profile points and 98% of the depth–dose curve points matched within a 1%/1-mm window. It can be shown that using a simple calculation for 6-MV beam energy, a 1% error in depth–dose leads to a mere 1.7% of treatment delivery error. This is well within the tolerance level recommended in the International Commission on Radiation Units and Measurements 24 (ICRU-24) report [18]. These findings prove that the present method is a more reliable one for beam matching analysis between two linear accelerators. The manufacturer defined criteria for beam matching is often too generous and should be evaluated as detailed here. It is possible that the interchange of one patient's plan between two machines will not result in an identical treatment if dose-gradient matching is not taken into account.

For open and wedge beam profile gradient matching, we recommend that the $\Delta D'$ and $\Delta D''$ be kept within 1%/1 mm. For plateau matching, we recommend a ceiling of 2%/2 mm. For depth–dose curve matching, $\Delta D'$ and $\Delta D''$ in the build-up region should lie within 1%/1 mm and with ΔD should be within 1.5%/1.5 mm for all depths at 95% agreement. The technique described in this work for the quantitative evaluation of beam matching using first-order and second-order derivatives is a generalised method. The method is applicable for all energies of both X-ray and electrons and can be used for other linear accelerators without restriction. We recommend that users generate their own test packages (for the bandwidth values) using the demonstrated methodology from their reference linear accelerator rather than from any manufacturer-provided golden beam data set.

ACKNOWLEDGMENTS

All authors would like to sincerely thank Senior Medical Physicist Dr Sateesh Prasad of the National Centre for Cancer Care and Research, Hamad Medical Corporation, Doha, Qatar, for his suggestion and comments. We also sincerely thank Mr CSN Rao, Mr Dilip Kumar and Mr Nilendu Saha of Elekta Medical System (India) and Mr Gopinathan Chandrasekaran of Varian (India) for their technical inputs.

REFERENCES

1. Klein EE, Hanley J, Bayouth J, Yin FF, Simon W, Dresser S, et al. Task Group 142, American Association of Physicists in Medicine. Quality assurance of medical accelerators. Med Phys 2009;36: 4197–211.
2. Hrbacek J, Depuydt T, Nulens A, Swinnen A, Van den Heuvel F. Quantitative evaluation of a beam-matching procedure using one-dimensional gamma analysis. Med Phys 2007; 34:2917–27.
3. Specification clinical beam matching streamlined QA and treatment flexibility. Palo Alto, CA: Varian Medical Systems, Inc.; 2004.
4. Precise Treatment System, customer acceptance tests, part no. 4513370187004. Stockholm, Sweden: Elekta Oncology System limited, Elekta UK; 2003.
5. Sjöström D, Bjelkengren U, Ottosson W, Behrens CF. Beam-matching concept for medical linear accelerators. Acta Oncol 2009; 48:192–200. doi: 10.1080/02841860802258794
6. Fontenla DP, Napoli JJ, Chui CS. Beam characteristics of a new model of 6-MV linear accelerator. Med Phys 1992;19:343–9.
7. Marshall MG. Matching the 6-MV photon beam characteristics of two dissimilar linear accelerators. Med Phys 1993;20:1743–6.
8. Watts RJ. Comparative measurements on a series of accelerators by the same vendor. Med Phys 1999;26:2581–5.
9. Low DA, Harms WB, Mutic S, Purdy JA. Technique for the quantitative evaluation of dose distributions. Med Phys 1998;25:656–61.
10. Low DA, Dempsey JF. Evaluation of the gamma dose distribution comparison method. Med Phys 2003;30:2455–64.
11. Li H, Dong L, Zhang L, Yang JN, Gillin MT, Zhu XR. Toward better understanding of the gamma index: investigation of parameter with surface based distance method. Med Phys 2011; 38:6730–41. doi: 10.1118/1.3659707
12. Almond PR, Biggs PJ, Coursey BM, Hanson WF, Huq MS, Nath R, et al. AAPM's TG-51 protocol for clinical reference dosimetry of high-energy photon and electron beams. Med Phys 1999;26:1847–70.
13. International Atomic Energy Agency. Absorbed dose determination in external beam radiotherapy: an international code of practice for dosimetry based on standards of absorbed dose to water. IAEA Technical Report 398. Vienna, Austria: International Atomic Energy; 2000.
14. Das IJ, Cheng CW, Watts RJ, Ahnesjö A, Gibbons J, Li XA, et al. Accelerator beam data commissioning equipment and procedures: report of the TG-106 of the Therapy Physics Committee of the AAPM. Med Phys 2008;35: 4186–215.
15. Pal S, Muthukrishnan G, Ravisankar R, Sharma RP, Ghosh AM. Estimation of percentage depth-dose distributions for therapeutic machine. Radiat Phys Chem 2002;65:589–94.
16. Godin M, Galiano E. The development and experimental evaluation of simple analytical model for TPR in the build-up region of megavoltage photon beams. Med Phys 2012; 39:257–62. doi: 10.1118/1.3669489
17. Venselaar J, Welleweerd H, Mijnheer B. Tolerances for the accuracy of photon beam dose calculations of treatment planning systems. Radiother Oncol 2001;60:191–201.
18. ICRU Report 24. Determination of absorbed dose in a patient irradiated by beams of X- or gamma rays in radiotherapy procedures. Washington, DC: International Commission on Radiation Units and Measurements; 1976.