Correction of the limited spatial resolution of ionization chambers by iterative deconvolution

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Introduction

The volume effect of ionization chamber is attributed to the finite spatial extension of its sensitive volume which gives rise to a spatial averaging effect, characterized by the chamber's line spread function. The lateral and longitudinal line spread functions of cylindrical ionization chambers, as well as of flat chambers and of the single chambers of two 2D ionization chamber arrays have been characterized by Gaussian distributions (Looe *et al* 2012). The lateral and longitudinal line spread functions of each investigated chamber can be parameterized by the standard deviations σ_{lat} and σ_{long} respectively. Using this knowledge of the line spread functions, the true dose profile can be recovered from the ionization chamber's measurement distorted by its volume effect through deconvolution. In this work, we will describe some methodical aspects of a numerical deconvolution method developed to correct the measured dose profile. These comprise the description of the iterative algorithm and a method of iterative smoothing to be applied before deconvolution.

Materials and Methods

The iteration rule

The measured transverse signal profile M(x) of a photon beam is regarded as the convolution product of the true dose profile D(x) and the ionization chamber's line spread function K(x):

$$M(x) = \int_{-\infty}^{+\infty} D(\xi) K(x - \xi) d\xi , \qquad (1)$$

where $K(x-\xi)$ is described by a normalized Gaussian distribution:

$$K(x-\xi) = \frac{1}{\sqrt{2\pi\sigma}} \exp\left[-\frac{(x-\xi)^2}{2\sigma^2}\right].$$
 (2)

The deconvolution is performed using an iterative method (van Cittert 1931) already applied previously in medical physics (e.g. Skarsgard *et al* 1961, Feist *et al* 1968, Looe *et al* 2010, 2011). The iteration process, whose iterative steps are counted as 1, 2, 3, ... n, n+1, n+2, ..., consists in the generation of a sequence of approximations $D^{n}(x)$ by which the true dose

profile D(x) is stepwise approximated. The *first step* of the "iteration rule" is that the n-th approximation $D^n(x)$ is numerically convolved with the line spread function, yielding the corresponding approximated measured function $M^n(x)$:

$$M^{n}(x) = \sum_{i=1}^{k} D^{n}(x_{i}) K(x - x_{i}), \qquad (3)$$

where k is the total number of measured points. The only modification from eq. (1) is that the discrete values x_i are now replacing the continuous variable x. In the *second step* of the "iteration rule", the next approximation $D^{n+1}(x)$ is derived from $D^n(x)$ and the difference between the actually measured profile value M(x) and the approximated profile $M^n(x)$ resulting from eq. (3):

$$D^{n+1}(x) = D^{n}(x) + M(x) - M^{n}(x).$$
(4)

The iteration is started by assuming $D^{1}(x) = M(x)$.

In order to suppress the influence of the noise superposed to the measured profile upon the deconvolved result, it is essential to implement a criterion for the termination of the iteration. The iteration loop is terminated using the χ^2 -test, i.e. by computing the sum of the squares of the relative deviations of all stepwise approximated values $M^n(x)$ from the originally measured values M(x), allowing a relative deviation of 1% for each x value considered. Thus the iteration termination criterion is:

$$\sum_{x=1}^{k} \left[\frac{M(x) - M^{n}(x)}{M(x)} \right]^{2} < k \cdot 0.0001.$$
(5)

Noise suppression by iterative smoothing

In some cases, it may be necessary to perform data smoothing prior to the deconvolution, because the iteration rule, eq. (4), shows that any noise, superposed to the measured function M(x), will be amplified in the iteration process. In this work, we have applied a method of smoothing (Morrison 1963, Dromey and Morisson 1970, 1971), which has several advantages over Fourier smoothing performed by truncating or suppressing high frequency components in the original signal (Morrison 1963, Ioup and Thomas 1967, Dromey and Morisson 1970, 1971, Ioup et al 1983). According to this smoothing method, the data measured in the presence of noise can be rewritten as:

$$M(x) = D(x) * K(x) + n(x).$$
 (6)

The noise n(x) can be made up of two different components: compatible and incompatible noise (Morrison 1963). The incompatible part of the noise is responsible for the failure in the

deconvolution result, as the deconvolution process will amplify its magnitude. The incompatibility is expressed as:

$$n_{\rm incomp}(x) * K(x) = 0.$$
⁽⁷⁾

The smoothing process, aiming at a smoothed function $M_s(x)$ where the subscript *s* stands for smoothed data, involves the removal of this incompatible component of noise. It is started with:

$$M_{s}^{1}(x) = M(x) * K(x), \qquad (8)$$

where K(x) is the same convolution kernel as used in the iterative deconvolution. Eq. (8) means that the measured profile is first broadened by convolution with K(x), whereby the incompatible noise is removed. In the successive iteration steps, the original signal profile is restored:

$$M_{s}^{n+1}(x) = M_{s}^{n}(x) + \left[M(x) - M_{s}^{n}(x)\right] * K(x).$$
⁽⁹⁾

The iterative smoothing is terminated using a similar χ^2 -criterion as in the iterative deconvolution:

$$\sum_{x=1}^{k} \left[\frac{M_{\rm s}^{\rm n+1}(x) - M_{\rm s}^{\rm n}(x)}{M_{\rm s}^{\rm n}(x)} \right]^2 < k \cdot 0.0001.$$
⁽¹⁰⁾

Unlike conventional averaging methods, the profile is not further broadened due to the smoothing process (Morisson 1963). For measurement data that is only slightly affected by statistical noise, the noise removal can be omitted and the iterative process can be terminated either by using the χ^2 -test (eq. (5)) or by limiting the number of iterations allowed.

Results

Deconvolution of dose profiles

Examples for the measurement of transverse dose profiles of photon beams with ionization chambers and for the performance of the iterative deconvolution are given in Figures 1 and 2. For known true dose profiles D(x) (open symbols), the signal profiles measured with the PTW 31010 and IBA CC08 chambers, M(x), are presented by dashed lines, and the results of the deconvolution (full lines) are compared to the true dose profiles. The true dose profiles had before been obtained by deconvolving the signal profiles measured with the Si diode with its line spread function ($\sigma_{\text{Diode}} = 0.30 \text{ mm}$) (Looe *et al* 2012). The standard deviations of the Gaussian convolution kernels used in the deconvolutions are stated in the figures (Looe *et al* 2012). Good agreement between the true dose profile and the deconvolved dose profiles is obtained.



Figure 1: Full lines: Dose profiles, obtained by iterative reconstruction from the signal profiles (dashed lines) measured using the PTW 31010 Semiflex chamber at 2 cm (left panels) and 4 cm (right panels) field width in 6 MV (upper panels) and 15 MV (lower panels) photon beams. The true dose profiles (open symbols) were obtained by deconvolving the Si diode measured signal profiles with its line spread function ($\sigma_{\text{Diode}} = 0.30$ mm). All dose profiles are normalized at dose maximum. Only one half profile is presented for 4 cm field width for better visibility.



Figure 2: Full lines: Dose profiles, obtained by iterative reconstruction from the signal profiles (dashed lines) measured using the IBA CC08 chamber at 2 cm (left panels) and 4 cm (right panels) field width in 6 MV (upper panels) and 15 MV (lower panels) photon beams. The true dose profiles (open symbols) were obtained by deconvolving the Si diode measured signal profiles with its line spread function ($\sigma_{\text{Diode}} = 0.30$ mm). All dose profiles are normalized at dose maximum. Only one half profile is presented for 4 cm field width for better visibility.

For the examples in Figures 1 and 2 the number of iterations needed for the deconvolution was 5 or 6. Additional "smoothing iterations", as described above, were also carried out prior to the deconvolution, but in the cases shown in Figures 1 and 2 practically the same results were obtained without smoothing if the deconvolution was terminated after 3 iterations.

Discussion

The iterative deconvolution method has been earlier applied to one-dimensional (Looe *et al* 2010) and two-dimensional problems (Looe *et al* 2011) in radiation therapy. The deconvolution algorithm is not limited to narrow photon beams but can be equally applied to large fields and irregular dose profiles. The flexibility and robustness of this iterative algorithm is advantageous for clinical applications, where a general solution is preferable that requires minimal user interactions. Dose profiles such as those measured in conjunction with machine commissioning can be deconvolved in order to improve the beam models in treatment planning systems (TPS). The accurate description of the dose-fall-off region has significant implications on the accuracy of the dose calculation model in TPS, especially in IMRT and stereotactic radiosurgery, where a large number of small fields are superpositioned to form the desired dose distribution. However, it should be noted that dose profiles should always be scanned with the narrower dimension of the ionization chamber in the scanning direction in order to minimize the influence of the volume effect, avoiding low-pass filtering of the measured profile as far as possible. Limitations of the iterative reconstruction algorithm exist, and methods to overcome these will be reported soon.

Conclusions

We show that by deconvolution, the influence of a chamber's line spread function upon the measured dose profile can be eliminated. An iterative smoothing algorithm to be used in conjunction with the iterative deconvolution is also presented. The combination of these two methods results in a robust approach to deconvolve clinical photon beam dose profiles measured with ionization chambers.

References

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