



Technical notes

Rotation effects on the target-volume margin determination

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ABSTRACT

Rotational setup errors are usually neglected in most clinical centers. An analytical formula is developed to determine the extra margin between clinical target volume (CTV) and planning target volume (PTV) to account for setup errors. The proposed formula corrects for both translational and rotational setup errors and then incorporated into margin determination for PTV.

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Introduction

It is well known that setup errors during treatment compromise the precision of radiation treatment. To improve the accuracy of patient positioning during treatment, On Board Imager (OBI) system has been developed and commonly used in present clinical centers [1]. Though six degrees of freedom (DOF) registration of cone-beam CT (CBCT) and planning CT can determine translational and rotational setup errors [2] in practice conventional couches do not allow rotational corrections. Therefore six DOF couch has been introduced to radiation clinics [3]. However, six DOF couches are not widely installed due to the various reasons including high cost.

In practice, most setup adjustments are applied to only translational shifts and rotational positioning errors are routinely disregarded throughout the patient's treatment. It is known that clinical target volume (CTV) to planning target volume (PTV) margin is determined by setup errors and possible motion during the treatment [4–10]. The margin should account for both translation and rotation setup uncertainties. The correction of translation setup will lead to a reduction of the margin and thereby spare more normal tissues. However, the oversight rotation error should result in a relatively larger margin. It was found that those rotation errors might cause dosimetric errors during clinical treatments

[11]. Thus, it is interesting to derive an analytical formula to estimate the extra margin in the planning stage.

There are two purposes of this paper: (1) to derive the setup error distribution for a group of patients; and (2) to estimate the maximum setup error from rotations for each tumor size.

Methods

In this section we will: (1) derive the setup error distribution for a group of patients; (2) estimate the maximum setup error from rotation for each tumor. In our derivation, we only consider rigid-body registration.

For a patient setup, one must register the patient's CBCT images to the patient's planning CT images. For two rigid-body registrations, two things are needed for consideration: translation and rotation. In the following sections, we will discuss the registration of two brain tumors. The procedure we present here holds the truth when we register bones or other rigid structures.

Both tumors have N voxels in both the CT image and CBCT image. The CT image has a coordinate $\vec{x}_i (i = 1, \dots, N)$ and CBCT image has another coordinate $\vec{y}_i (i = 1, \dots, N)$. Without rotation, only translation is left for registration. Therefore, one tries to find the minimum difference between the tumors in the CBCT and CT images. In other words, we try to find a vector \vec{A} such that:

$$I = \sum_{i=1}^N (\vec{x}_i - \vec{y}_i - \vec{A})^2 \quad (1)$$

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is minimal. One can easily find that the solution of this equation is:

$$\vec{A} = \frac{1}{N} \sum_{i=1}^N \vec{x}_i - \frac{1}{N} \sum_{i=1}^N \vec{y}_i = \vec{x}_{CM} - \vec{y}_{CM} \quad (2)$$

Notice that we have used $\vec{x}_{CM} = \frac{1}{N} \sum_{i=1}^N \vec{x}_i$ and $\vec{y}_{CM} = \frac{1}{N} \sum_{i=1}^N \vec{y}_i$ to represent the center of mass (CM) of the tumors in the CT and CBCT images. Eq. (2) means that we translate the CM of tumor of CBCT to that of CT. However, rotation always exists so it needs to be included in our registration. Suppose the rotation matrix is R , then we try to match the CBCT image to the CT image by translation and rotation. Thus, we try to minimize:

$$I = \sum_{i=1}^N \left((\vec{x}_i - \vec{x}_{CM} - R(\vec{y}_i - \vec{y}_{CM}))^2 \right) \quad (3)$$

One can determine the rotation matrix or R from Eq. (3). However, we will not discuss the method to determine R here. Instead, we will discuss the mismatch between those two tumors with this known rotation matrix. The above can be understood in the following way: For a rigid-body registration, one needs to first match the CM of the tumor (ROI) in the CT image with the CM of tumor in the CBCT image. After that, one can rotate the CBCT image to match the shape of tumor in the CT image. Using the traditional three Euler angles—roll (θ), pitch (ψ), and yaw (ϕ)—the rotation matrix can be expressed as (pitch-roll-yaw):

$$R = \begin{pmatrix} 1 & 0 & 0 \\ 0 & \cos \psi & \sin \psi \\ 0 & -\sin \psi & \cos \psi \end{pmatrix} \begin{pmatrix} \cos \theta & 0 & -\sin \theta \\ 0 & 1 & 0 \\ \sin \theta & 0 & \cos \theta \end{pmatrix} \times \begin{pmatrix} \cos \phi & \sin \phi & 0 \\ -\sin \phi & \cos \phi & 0 \\ 0 & 0 & 1 \end{pmatrix} \quad (4)$$

It is well known that the final rotation matrix depends on the order of multiplication [12,13]. Using the first-order approximation, (i.e., $\sin(\theta) \approx \theta$ and $\cos \theta \approx 1$, with the same approximation for roll and yaw) and ignoring second-order terms and cross-product terms, we have:

$$R = \begin{pmatrix} 1 & \phi & -\theta \\ \phi & 1 & \psi \\ \theta & \psi & 1 \end{pmatrix} \quad (5)$$

Its inverse (ignoring the second-order terms) is:

$$R^{-1} = R^T = \begin{pmatrix} 1 & -\phi & \theta \\ \phi & 1 & -\psi \\ -\theta & \psi & 1 \end{pmatrix} \quad (6)$$

when the rotation setup error is around $2^\circ = 0.0349$ radian, it can be easily verified that the error introduced by this approximation used above is of the order of 0.000007 for the $\sin(x)$ function and 0.0006 for the $\cos(x)$ function. Eq. (5) is a first order approximation to rotation matrix. It is independent of the order of the multiplications. We have calculated all rotation matrices for different order of multiplications. We have found that when pitch, roll, and yaw are $<5^\circ$, the maximum difference between the approximation and exact solution is 0.0084. Therefore, the small angle approximation is sufficient and accurate enough for practical clinical applications. Nevertheless, we encourage our readers to check the rightness of this approximation for their own data.

Unfortunately, 6-DOF couches are not available in many clinical centers that most of us do not apply couch rotation in our clinical practices. Therefore, even if we can match the CM of the CBCT

image to that of the CT image, we will still have residual setup errors left for tumor points. After matching the CM of the tumor in the CBCT image with the CM of the tumor in the CT image (e.g., the isocenter of the linac), the corresponding tumor points in the CBCT image are $\vec{y}_i = R^T \vec{x}_i$. Therefore, the residual setup error from rotation for point \vec{x}_i can be defined as:

$$\vec{V}_{\vec{x}_i}^R = R^T \vec{x}_i - \vec{x}_i = \begin{pmatrix} 0 & -\phi & \theta \\ \phi & 0 & -\psi \\ -\theta & \psi & 0 \end{pmatrix} \vec{x}_i \quad (7)$$

Here $\vec{V}_{\vec{x}_i}^R = (V_{\vec{x}_{i1}}^R, V_{\vec{x}_{i2}}^R, V_{\vec{x}_{i3}}^R)^T$ is a vector. Ideally, we try to identify a CTV-PTV margin large enough to cover all those residual setup errors. Thus, we will try to find the maximum value of the residual setup errors for all points. This, of course, will depend on the shape of tumor and is specific to the patient. One can always use an ellipsoid function to fit each tumor:

$$\frac{x_{i1}^2}{a^2} + \frac{x_{i2}^2}{b^2} + \frac{x_{i3}^2}{c^2} = 1 \quad (8)$$

Here (1,2,3) refers to the x , y and z components in the patient coordinate system. One can easily rewrite this equation by using the following format:

$$\begin{aligned} x_{i1} &= a \cos \beta \cos \lambda \\ x_{i2} &= b \cos \beta \sin \lambda \\ x_{i3} &= c \sin \beta \end{aligned} \quad (9)$$

With

$$-\frac{\pi}{2} \leq \beta \leq \frac{\pi}{2} \quad -\pi \leq \lambda \leq \pi$$

It is easily checked from Eq. (7) that:

$$\vec{V}_{\vec{x}_i}^R = \begin{pmatrix} -x_{i2}\phi + x_{i3}\theta \\ x_{i1}\phi - x_{i3}\psi \\ -x_{i1}\theta + x_{i2}\psi \end{pmatrix} \quad (10)$$

Bringing Eq. (9) into Eq. (10), one has (the first row):

$$V_{\vec{x}_{i1}}^R = -x_{i2}\phi + x_{i3}\theta = -b\phi \cos \beta \sin \lambda + c\theta \sin \beta \quad (11)$$

By taking $\frac{\partial V_{\vec{x}_{i1}}^R}{\partial \beta} = 0$ and $\frac{\partial V_{\vec{x}_{i1}}^R}{\partial \lambda} = 0$, we have following two equations:

$$b\phi \sin \beta \sin \lambda + c\theta \cos \beta = 0 \quad (12)$$

and

$$b\phi \cos \beta \cos \lambda = 0 \quad (13)$$

Using the solutions of Eq. (12) and Eq. (13) and brought them into Eq. (11), we found that the maximum residual setup error for the x component is $\pm \sqrt{b^2\phi^2 + c^2\theta^2}$. Repeating that process for the y and z components, we have found that the maximum residual setup errors in the x - y - z components are:

$$\begin{aligned} &\pm \sqrt{b^2\phi^2 + c^2\theta^2} \quad x \text{ component} \\ &\pm \sqrt{a^2\phi^2 + c^2\psi^2} \quad y \text{ component} \\ &\pm \sqrt{a^2\theta^2 + b^2\psi^2} \quad z \text{ component} \end{aligned} \quad (14)$$

Here the rotation angles are measured in radian. Therefore, as long as we can expand our CTV to include these maximum setup errors, we can cover the whole tumor. For typical setup errors $\theta \leq 1^\circ$, $\phi \leq 1^\circ$, and $\psi \leq 1^\circ$, one can use Eq. (14) to calculate the

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