AUTOMATIC PATIENT ALIGNMENT IN SIX DEGREES OF FREEDOM FOR PARTICLE BEAM TREATMENT

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1. Purpose

Modern particle beam treatment methods allow highly accurate application of the treatment dose onto diseased tissue, so that accuracies in the sub millimeter domain are feasible. However, the accuracy is limited by initial patient alignment inaccuracies in the treatment device, causing aberrations of the location of the planned radiation target relative to the particle beam. Strategies like tracking of external markers or fixation of the patient's body do not suffice the requirement of high set-up precision and are not applicable for many anatomical regions.

To overcome this problem, our approach uses high-resolution slices of a planning CT and two X-ray images acquired from within the treatment device. The X-ray images are acquired seconds before the treatment takes place, using high-resolution digital radiographic equipment mounted in the radiation gantry.

Automatic comparison of the X-ray images with the reference data from the CT allows calculating a full six degrees of freedom displacement for the patient. The calculated misalignment is used to derive an appropriate alignment correction for the patient support equipment, so that an accurate treatment position can be achieved by application of the automatically computed correction vector, with low user interaction. A last comparison of X-rays with the patient in the corrected position can now be conducted to verify the patient's final alignment for the treatment.

2. Methods

Our automatic alignment procedure is conducted in several single steps. To be able to compare the CT data to the X-ray images the CT volume is first projected virtually into the geometric planes of the X-ray detectors. Therefore we use an optimized ray-tracing algorithm.

In the next step two separate image registrations are performed. We use a Mutual Information approach for the comparison of each X-ray image with the respective volume projection. Downhill Simplex minimization of the negative Mutual Information results in two sets of transformations, which consist of two shifts and one in-plane rotation.

The last step is to combine the respective 2D transformations to one single 3D transformation in patient space. This is done by back projection of the transformed coordinate systems defined in the X-ray image spaces. During the back projection the consistency of the transformations is evaluated and serves as an indicator for the correctness of the final alignment correction.

Because changing the patients alignment means rearrangement of the image contents, we use a first alignment correction, to re-project the CT volume into the imager spaces and repeat the correction procedure iteratively, assuming a new, corrected patient alignment for each iteration.

As for most imager configurations the roll rotation axis of the patient support is parallel to both X-ray image Y-axes, no roll alignment correction can be obtained by pure 2D registrations. To overcome this drawback another correction step is carried out optionally, where the best fitting volume projection for different roll angles is determined by evaluation of the combined Mutual Information of the CT volume projections and the X-ray images.

To offer a solution for all cases, where insufficient image data obstructs the automatic procedure, a semi-automatic positioning is provided.

3. Results

Accuracy and performance tests have been conducted using several CT datasets with at most 0.8 mm slice distance. Anatomical phantoms of a human skull, thorax and pelvis have been used.

The best results could be achieved for the human skull, where misalignments of up to 10.0 mm and 10.0° could be corrected with an accuracy of at most ±0.4 mm and ±0.2°. The presented methods were able to perform the alignment correction on a high end PC within 15 seconds without and within 40 seconds with correction of the patient roll angle. For the thorax data, we obtained accuracies of at most ±0.6 mm and for the pelvis, about ±0.8 mm could be achieved. For the skull and the thorax region, the alignment correction could be determined successfully in all test cases.

Because of dense bone structures in case of the pelvis area, disadvantageous X-ray energies and acquisition angles can easily lead to X-ray images that cannot be used for a proper alignment correction. In these cases the algorithm indicated automatically that the underlying image data does not suffice the requirement for precise alignment calculation. Our semi-automatic correction procedure provides a solution for those cases.

4. Conclusions

The presented methods allow very accurate and reliable alignment correction with low time consumption and low user interaction. The automatic alignment correction can be conducted in much less time than a manual alignment correction and fewer X-ray acquisitions are needed. The X-ray dose applied onto patients can be reduced and lowering the initial patient alignment efforts can increase the throughput of patients in modern therapy centers.