

## ABSTRACT

A novel, efficient, robust, feature-based algorithm is presented for intramodality and multimodality medical image registration. The algorithm achieves subpixel (0.4 mm) and pixel (0.8 mm) accuracy for intramodality and multimodality imaging respectively. It is based on a branch-and-bound strategy proposed by Mount et al., and is relatively insensitive to outliers, typically generated by feature extraction. The feature extraction uses classical edge detection algorithms to extract feature points from bony anatomy. An 82% reduction in computation time was achieved by introducing a new measure: gradient weighted partial Hausdorff measure. Further computational improvements were achieved by using: (i) an initial estimate of the registration using stochastic hill climbing as a local optimization technique in the branch-and-bound algorithm; (ii) a distance based priority, and (iii) multiresolution feature extraction. This algorithm is applied to patient positioning in cranial radiotherapy. The test imaging consisted of digitally reconstructed radiographs (DRRs), which are 2D projections of 3D computed tomography (CT) data acquired with kilovoltage x-rays, 2D portal images acquired with an electronic portal imaging device (EPID) and megavoltage x-rays. Image registration software based on this algorithm produced a registration between DRR and EPID images in approximately 2.5 seconds based on 1400 feature points using a 1.4 GHz processor.

## WEIGHTED HAUSDORFF MEASURE

Given two point sets  $A$  and  $B$ , the Hausdorff distance from  $A$  to  $B$  is defined as

$$H(A, B) = \max_{a \in A} \min_{b \in B} d(a, b),$$

where  $d(a, b)$  is any distance metric between two points. We refer to this distance as *unweighted*.

We present a robust measure that uses the gradient of the point in the source image. Note that stronger edges correspond to higher gradients, and in x-ray imaging, with the exception of tissue-air interfaces, higher edges typically correspond to bony anatomy, which typically has higher gradient values than tissue-air interfaces. Generally, one has more confidence in using bony anatomy as features for determining patient position because it is nondeformable, and the major bones are generally rigid with respect to each other. Thus a bias is introduced towards using "stronger" points to compute the Hausdorff distance. The mathematical formulation is as follows:

$$H(A, B) = \max_{a \in A} w_a \min_{b \in B} (1 - w_a) d(a, b),$$

where

$$w_p = \nabla I_A(p) = \frac{\partial I_A(p)}{\partial x} + \frac{\partial I_A(p)}{\partial y}$$

is the weight of point  $p$ , and  $I_A$  is the image from which the point set  $A$  was extracted. As shown later, this weighted measure improves the efficiency considerably. Henceforth, for brevity, we will refer to the gradient weighted partial Hausdorff distance as *weighted Hausdorff distance*.

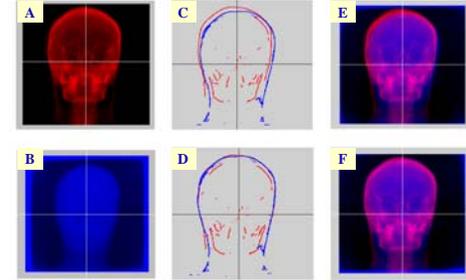
## REGISTRATION ALGORITHM

The algorithm presented here first requires the computation of feature-points extracted from the image.

In our approach, these feature points correspond to the bony anatomy of the patient.

It is not necessary to have a unique one-to-one correspondence between the two sets, or equal number of points.

The matching algorithm takes two extracted point sets and finds the transformation that maps the two extracted point sets as close as possible.



[A] DRR Image. [B] EPID Image. [C] Point sets before registration [D] Aligned point sets. [E] Overlapped EPID and DRR images before registration. [F] Overlapped images following image registration.

## MATCHING ALGORITHM

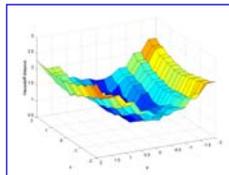
The Feature Matching Algorithm takes two sets of points as input and finds the transformation that maps the target set as close as possible to the reference set.

- Domain:** The domain consists of two sets of points in  $\mathbb{R}^2$ ; the origin corresponds to the radiation center of the image.
- Search Space:** The search space, or the space of transformations is  $\mathbb{R}^3$  for rigid transformations
- Search Method:** A branch-and-bound algorithm was used. The search space was divided into cells. Upper and lower bounds for the best transformation was calculated for each cell and was used to decide whether or not to discard the cell.
- Similarity Metric:** The weighted Hausdorff was used to evaluate the quality of a matching.

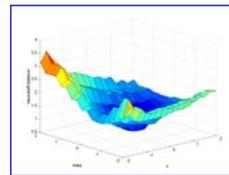
## ATTRACTOR FOR WEIGHTED HAUSDORFF

The behavior of the weighted Hausdorff under perturbations is presented below. The weighted Hausdorff increases noticeably after small perturbations. As the three graphics below suggest, subpixel perturbations were successfully detected. The graphs show a nice bell shaped surface with a correct minimum value for a perturbation  $\Delta = 0$ .

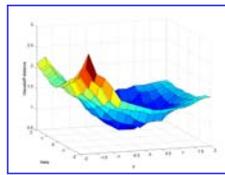
A. Perturbations in X and Y



A. Perturbations in  $\theta$  and X



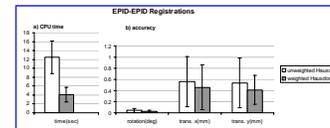
A. Perturbations in  $\theta$  and Y



Given a reference image  $A$  and a target image  $B$ , the best transformation  $t$  is found. A rigid transformation  $t'$  is created by adding a perturbation to  $t$  such that,  $t' = t + \Delta$ , where  $\Delta$  is a vector that represents the perturbation in  $\theta$ ,  $x$  and  $y$ . The perturbations were between  $[-2, 2]$  mm for translation on  $x$  and  $y$  and  $[-2, 2]$  deg for rotations with increments of 0.25 for rotations and translations

## ACCURACY AND SPEED

For the EPID-EPID registration, the average CPU time was 4.1 sec. The mean error was 0.46 mm for translations and 0.03 deg for rotations. For the EPID-DRR case, the mean error was 0.79 mm for translations and 0.51 deg for rotations.



Given a reference image  $A$  and a rigid transform  $t$ , the target image  $B$  was produced by applying  $t$  to  $A$ , i.e.  $B = t(A)$ . Feature extraction generates two point sets  $P_A$  and  $P_B$ . These point sets are used as input to the feature matching algorithm that produces a matching  $t_p$ . The differences between  $t'$  and  $t_p$  ( $\Delta\theta$ ,  $\Delta x$  and  $\Delta y$ ) are recorded. The process was run 1000 times. The point sets sizes were close to 1400.

## CONCLUSIONS

- A new point-based algorithm for **intra- and inter-modal image registration** has been developed.
- The matching algorithm uses the **weighted Hausdorff measure** for matching point sets.
- It is **robust** (unaffected by limited number of outliers)
- It is **accurate** -- subpixel and pixel accuracy for intramodal and multimodal registration respectively.
- It is **fast** -- matching times under 30 seconds for point sets with size larger than 8000.
- The attractor analysis shows that the Hausdorff distance is a **good inter-modal similarity measure**.