

Pablo: clinical prototype software for automatic image segmentation of normal anatomical structures using medially based deformable models

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Purpose/Objective: Image segmentation is performed more often as a clinical procedure in radiation oncology than for all other medical specialties combined. Current practice is inherently inefficient and expensive because most methods in routine clinical practice are user-guided and require highly skilled, well trained users to produce results acceptable for 3D RTP. The development of automatic methods is compelled by needs to improve efficiency and contain costs, and to improve accuracy and reproducibility to steer user-guided planning decisions and inverse treatment planning algorithms consistently in the right direction. Moreover efficient, automatic segmentation can facilitate new technologies for localizing structures of interest in volume images acquired immediately prior to or during a treatment fraction. Pablo is prototype software that is being used in the clinical setting to investigate automatic 3D segmentation of normal anatomic structures from volume images using deformable models called m-reps.

Materials/Methods: The current Pablo prototype software requires minimal user interaction and provides rich image- and graphics-based visualizations to evaluate each stage of segmentation. M-reps, constructed as meshes of individual building blocks called medial atoms, are medially based, trainable, multifigure, multiscale deformable models that are particularly well suited for segmenting structures with variable but statistically predictable shapes such as normal anatomic structures. Segmentation using Pablo begins with interactive initialization with a mouse or other interactive device to position, pose and scale the m-rep model in the image data to roughly match the structure to be segmented. Fully automatic segmentation then follows a number of stages at successively smaller levels of scale, with the output of each stage forming the model for the next stage. The stages are 1) similarity transformation of the whole m-rep; 2) similarity-like transform of each protrusion or indentation figure; 3) iterative modification of the parameters of each medial atom; and 4) fine-scale surface refinement. The transformations and deformations at each stage are driven by optimizing an objective function that has a geometric typicality metric based on the statistical probabilities of transformations and deformations, and a model-to-image match metric based on the goodness of match of the currently deformed m-rep with the target image data. The general form of the objective function is the same at each stage but the analytic formulas are specific to each stage.

Results: Pablo is being used on CT and MR images in the clinical radiation oncology setting as a prototype system to evaluate the clinical acceptance of automatic segmentation and visualization tools and methodology, and to compare automatic segmentation results with conventional user-guided results. M-rep models have been constructed for a number of anatomical structures including the kidneys, rectum, prostate, bladder, pelvic bones, liver, brain ventricles, and hippocampus. At this stage of

investigation shape statistics are simulated using boundary displacement distances, and image match is based on an object-width proportional Gaussian-based template and a single training image. Because m-reps are computationally efficient, automatic segmentation is on the order of a fraction of a minute to several minutes per organ, depending on the complexity of the model, using a single 800 MHz CPU.

Conclusions: Pablo is easy to use and has been well accepted by physicists, dosimetrists, and radiation oncologists for clinical evaluation purposes. Results from formal and informal observer studies are being used to drive further development of Pablo tools and m-rep models for ultimate use in treatment planning. Pablo is available as an investigative tool to facilities involved in image processing research.

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