MMCTP: a radiotherapy research environment for Monte Carlo and patient-specific treatment planning

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NOTE

MMCTP: a radiotherapy research environment for Monte Carlo and patient-specific treatment planning

A Alexander, F DeBlois, G Stroian, K Al-Yahya, E Heath and J Seuntjens

McGill Medical Physics Unit, Montreal General Hospital L5-113, 1650 avenue Cedar, Montreal, Quebec H3G 1A4, Canada

E-mail: andrew@medphys.mcgill.ca

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Abstract

Radiotherapy research lacks a flexible computational research environment for Monte Carlo (MC) and patient-specific treatment planning. The purpose of this study was to develop a flexible software package on low-cost hardware with the aim of integrating new patient-specific treatment planning with MC dose calculations suitable for large-scale prospective and retrospective treatment planning studies. We designed the software package 'McGill Monte Carlo treatment planning' (MMCTP) for the research development of MC and patient-specific treatment planning. The MMCTP design consists of a graphical user interface (GUI), which runs on a simple workstation connected through standard secure-shell protocol to a cluster for lengthy MC calculations. Treatment planning information (e.g., images, structures, beam geometry properties and dose distributions) is converted into a convenient MMCTP local file storage format designated, the McGill RT format. MMCTP features include (a) DICOM_RT, RTOG and CADPlan CART format imports; (b) 2D and 3D visualization views for images, structure contours, and dose distributions; (c) contouring tools; (d) DVH analysis, and dose matrix comparison tools; (e) external beam editing; (f) MC transport calculation from beam source to patient geometry for photon and electron beams. The MC input files, which are prepared from the beam geometry properties and patient information (e.g., images and structure contours), are uploaded and run on a cluster using shell commands controlled from the MMCTP GUI. The visualization, dose matrix operation and DVH tools offer extensive options for plan analysis and comparison between MC plans and plans imported from commercial treatment planning systems. The MMCTP GUI provides a flexible research platform for the development of patient-specific MC treatment planning for photon and electron external beam radiation therapy. The impact of this tool lies in the fact that it allows for systematic, platform-independent, large-scale MC treatment

planning for different treatment sites. Patient recalculations were performed to validate the software and ensure proper functionality.

(Some figures in this article are in colour only in the electronic version)

1. Introduction

The impact of improvements in dose calculation algorithms needs to be established using realistic treatment plans, and comparisons of these plans must be made using a common platform. Clinical impact of treatment plan evaluation and comparisons with different treatment planning systems using commercial software is often not reproducible since these packages use their own plan evaluation algorithms such as DVH and data storage format. Results between packages are typically not reproducible and these platform-dependent effects could lead to inconsistent results between researchers. Inconsistency amongst researchers may be partially due to the lack of a widely available graphical data analysis and programming environment which could be used to read, review, and compare dose, contours and image data from a wide range of clinical and academic planning systems (Deasy *et al* 2003). For further research and to establish large-scale retrospective studies, there is a need for an accessible software platform that combines different forms of treatment planning and analysis tools with ease. Two software environments, CERR (Deasy *et al* 2003) and MINERVA (Lehmann *et al* 2005) were designed for radiotherapy research. However, these software environments require additional (commercial) packages to be installed, use interpreted and slow language tools, lack MC capabilities or are not easily available.

We describe a radiotherapy research environment for MC and patient-specific treatment planning, 'McGill Monte Carlo treatment planning' (MMCTP), to facilitate comparison of MC dose calculations and the evaluation of treatment plans from different platforms. MMCTP provides a flexible software environment to integrate MC planning and to support the development of new treatment modalities. The aim of this project is to build a patient-specific treatment planning system, with (1) MC treatment planning (external beam electron and photon planning), (2) the use of multi-modality and multi-instance imaging, and (3) analysis tools for plan evaluation and studies of outcome correlations.

2. Materials and methods

2.1. Programming environment

The MMCTP platform was designed using REALBasic® (RealSoftware Inc., Austin, Texas). REALBasic® compiles on Macintosh, Windows and Linux operating systems and includes built-in 3D graphics tools for visualization effects. It is a rapid application development environment (RAD) meaning that one can quickly design applications and GUIs with full fledge object oriented programming (OOP) offering great flexibility for programming changes.

2.2. Monte Carlo software

There are many MC codes available for radiation transport simulations. In this work, we have interfaced MMCTP with BEAMnrc (Rogers *et al* 1995) and the voxel Monte Carlo code XVMC (Kawrakow *et al* 1996, Kawrakow and Fippel 2000). These codes are used in succession to calculate patient dose. BEAMnrc simulates the particle phase space data at

Table 1. MMCTP version 1, features.

Features	Summary
Import formats	DICOM_RT, RTOG, CADPlan CART
Export formats	RTOG
Visualization options	2D axial, sagittal or coronal view for images, contours and dose distributions. 3D beam's eye view and room's eye view for images, contours, and beam geometry settings (e.g., jaws, MLC, couch, table and gantry rotation)
Treatment planning	Add and delete external beams, edit beam properties (e.g., treatment unit, energy, jaw settings and MLC leafs) Structure contouring and editing tools
Monte Carlo	Generation of input files and simulation submission for BEAMnrc and XVMC
Dose analysis	DVH calculator and dose distribution operations (e.g., addition, subtraction, multiplication and division of dose distributions)

70 cm from the source while XVMC transports the simulated phase-space file through the patient geometry to calculate patient dose. The patient geometry is defined within the XVMC density matrix (DMX) file. The DMX voxel densities may be assigned either by manual input through assigning a density value to a structure volume or through an algorithm which assigns densities based on CT numbers, as shown by Constantinou *et al* (1992). The dose distribution uncertainty is an important detail in treatment planning. This is no more apparent than in the stochastic nature of MC dose distributions where the uncertainty is closely related to the number of histories. BEAMnrc and XVMC report the statistical uncertainty upon completion of each simulation.

All MC codes including BEAMnrc and XVMC require commissioning before one can trust the simulation results. The commissioning process for BEAMnrc includes tweaking of the virtual linac configurations and adjusting the source energy within the BEAMnrc input files so that the dose calculations under controlled conditions are in agreement with measurements (Chetty and Seuntjens 2006).

2.3. MMCTP features

MMCTP version 1 features are summarized in table 1. The MMCTP design consists of a GUI, which runs on a simple workstation connected through standard secure-shell protocols to a cluster for lengthy MC calculations. As the local station controls the shell, this strategy enables the use of an off-site cluster that does not require specific software (e.g., daemons, etc) to be installed. In addition, the design allows for anonymous patient information on the calculation cluster and a minimal amount of data interchanged between calculation cluster and workstation.

2.4. MMCTP validation steps

MMCTP validation involved DVH verifications, measurement comparisons and patient dose recalculations to check the consistency of coordinate transformations and the implementation of beam settings (e.g., wedge orientations, etc). DVH testing included DVH comparisons with

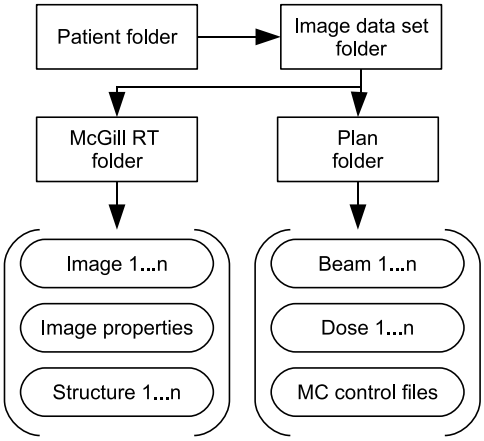


Figure 1. McGill RT file structure, folders and files. The image data set includes one McGill RT folder for the image and structure files and one or more plan folders for the various plans associated with an image data set. Plan folders contain beam geometry files, Monte Carlo control files and dose distribution files.

commercial treatment planning systems and DVH calculations of simplistic dose distributions for which the DVH was manually calculated for comparison. Patient recalculations under simplified conditions (e.g., heterogeneous patient density replaced by homogeneous water density) and comparison of the MMCTP dose distribution against dose distributions from conventional planning systems verified many consistency features.

3. MMCTP development

The initial programming task was to develop an organized object class structure to store treatment planning information within memory. The RTOG format, a well-documented and widely available radiotherapy archiving mechanism, was used as a model to base the REALbasic® objects. This not only helps us to organize the variables but also ensures native reading and writing to RTOG. In addition, new MMCTP programmers will benefit from a simple RTOG object-based GUI.

3.1. McGill RT characteristics

While the RTOG format provides a convenient object class, it does not provide a flexible file storage format. A new file format 'McGill RT' was introduced for saving patient plans on the workstation as an internal format. The file system resembles the RTOG format but includes efficiency improvements. The RTOG format was designed for exporting and importing patient plans and thus, there is no simple method for saving small changes. The McGill RT format, on the other hand, was developed to minimize redundant information and minimize the number of files edited to save changes. Figure 1 shows a schematic diagram of the McGill RT file format. McGill RT format uses a specific organization of folders containing files which are either binary or text. Images and dose distributions are stored as binary files while structures and beam information are stored as text files. The file structure of the McGill RT format contains a main McGill folder, under which folders for each patient are located. The patient folders are titled with the patient name and ID number. Within a patient's folder there can be multiple

image sets (CT, magnetic resonance imaging (MRI), ultrasound (US)) and each set has its own folder. Under each image set, there are folders for multiple plans as well as a folder for the images and structures. The plan folders store beams, doses and MC control files. The McGill RT file storage format is flexible enough to allow for future adaptation to include image data sets such as, image fusion between MRI, US, positron emission tomography (PET), CT and time phased computed tomography (4D CT). The McGill RT format should not be considered as yet another radiotherapy storage format. The MMCTP design uses McGill RT as an internal format, but also includes export functions to standard radiotherapy formats such as RTOG.

3.1.1. Image files. These files are stored individually under the McGill RT folder and define the image set for a MMCTP patient. The image data files are binary files containing the slice position and pixel data. In order to properly read these files, there is an image properties text file which stores the image dimension size, the bytes per pixel value and the (X, Y) origin of the patient coordinate system. Generally, the (X, Y) origin of the patient coordinate system is at the center of the image. Additional parameters to the properties file are required for the future implementation of MRI, US, PET or 4D data sets.

3.1.2. Structure files. These files contain a sequence of three-dimensional coordinates which define a volume of interest including target volumes and organs at risk. Coordinates are defined on each CT image slice. Within a given slice, a structure may consist of one or more segments where each segment is a sequence of at least four points which define a closed curve. Structure files are found under the McGill RT folder since they are associated with the image files. Each structure file contains a header section followed by the structure coordinates. The header information contains the structure name and colour while the structure coordinates points are arranged in order per slice number. Coordinate points are written relative to the patient coordinate system.

3.1.3. Plans. Patient plans are assigned folders within an image set folder. The files found within a patient plan folder include beam files, dose distribution files and MC control files.

3.1.4. Beam geometry files. These files contain the information defining an external radiation beam. These include various properties such as treatment unit, beam energy, beam applicators, number of monitor units (MU), number of fractions, aperture type, wedge angle and orientation, collimator gantry and couch angle, isocenter distance, isocenter coordinates (x, y, z) and X, Y jaw positions. The MLC leaf positions are not included within the beam file. Instead, there is a MLC file which contains the MLC fields for all beams of a plan.

3.1.5. Dose distribution files. These files store a matrix of dose values at one or more points throughout a volume. The format allows for a regularly spaced grid in which a two-dimensional array of points is defined on one or more evenly spaced parallel planes. This format permits the computation of dose on a two-dimensional array of points on each CT image plane. The coordinate system for the array of dose points is defined with the patient coordinate system. Within one plane, a two-dimensional array of points is defined with the x, y position of the top left-hand corner point, the number of points in x, y and the grid spacing in x, y. Each axial plane is identified with its z position, which normally corresponds to an axial CT image.

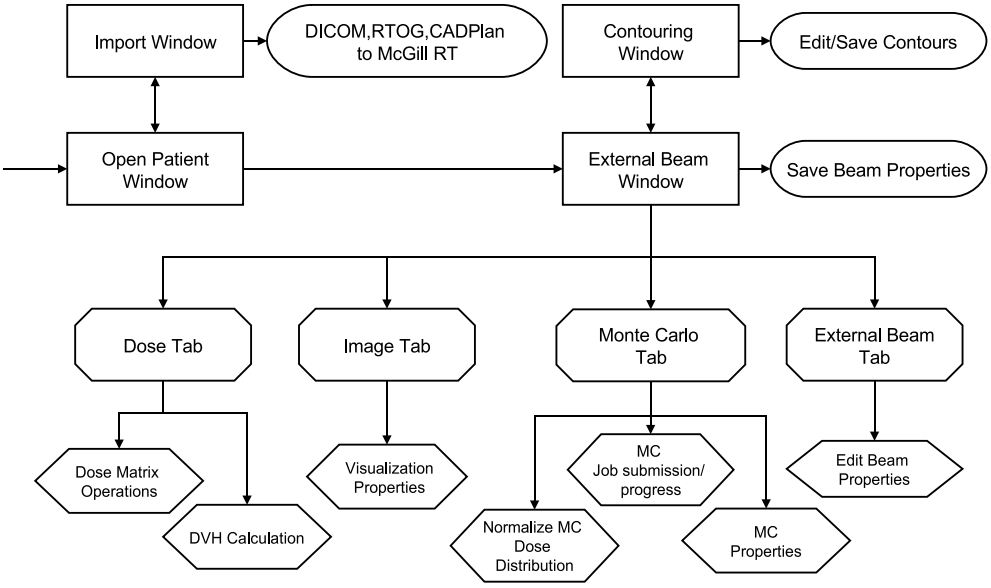


Figure 2. MMCTP flow chart. MMCTP opens with the open patient window; the user may then navigate to the main program windows for importing, contouring or external beam editing. The tab menu groups MMCTP features into common categories.

3.1.6. Monte Carlo control files. These files store specific properties and the simulation progress for each MC simulation. The BEAMnrc properties file stores the number of initial particles, job split number and the simulation status. The XVMC properties file records the DMX settings, the XVMC calibration dose and the simulation progress for each beam. The DMX settings describe the specific properties of the DMX file since there are a few ways to generate the DMX file, either from CT numbers or assigning density values based on structure volumes or using a combination of both methods.

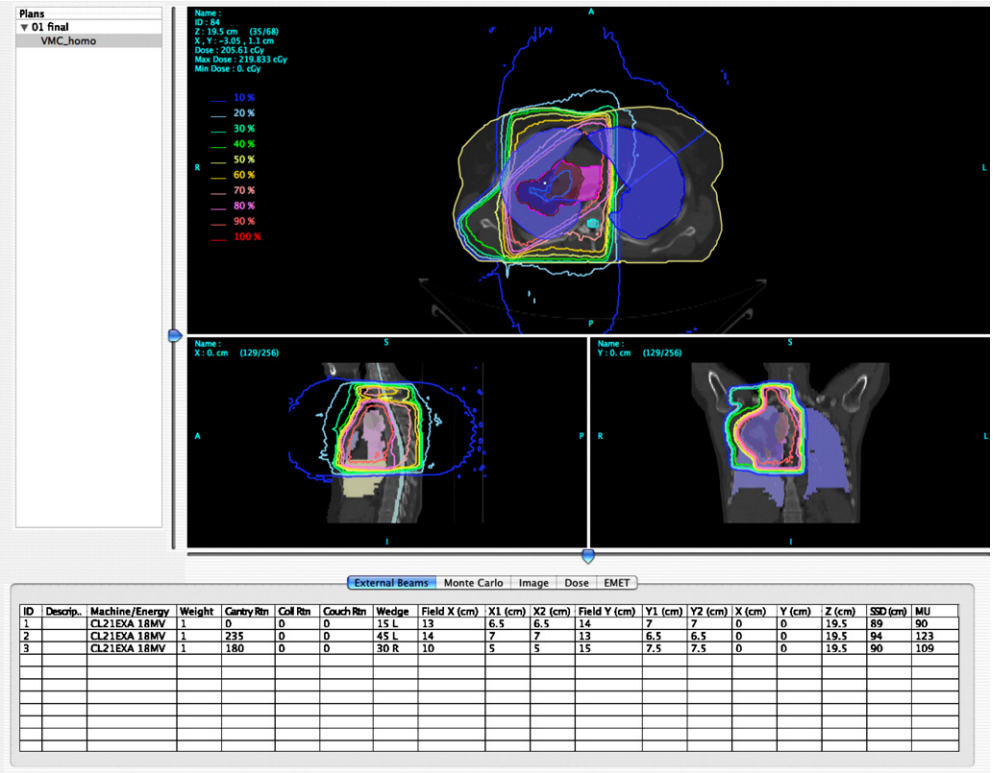
3.2. MMCTP description

MMCTP comprises individual task windows and a main program window which is subdivided into tabs. A flow chart of MMCTP windows and tabs is shown in figure 2.

3.2.1. The external beam window. It is the main program window which opens after one loads a patient. The window as shown in figure 3 comprises a list-box, three graphic canvases and a tab menu. The list-box displays the patient plans and available dose distributions associated with each plan. The three canvases display images, contours and dose distributions where each canvas can display three views: axial, sagittal or coronal. The tab menu splits the bottom portion of the beam window into four sections: external beams, Monte Carlo, image and dose.

The external beam tab lists the beams associated with a plan within a list-box. The list-box also displays various beam properties for each beam. Most of these properties are editable within the list-box. There is also a beam properties window which allows access to all the beam properties. A right click on the list-box allows the user to add or delete a beam.

The image tab lists various canvas display options. These options include window and level adjustments, scale settings, contour display options, colour-wash dose distribution options, isodose lines, display image and display cross-hairs. The contours and colour-wash



ID	Descrip.	Machine/Energy	Weight	Gantry Rtn	Coll Rtn	Couch Rtn	Wedge	Field X (cm)	X1 (cm)	X2 (cm)	Field Y (cm)	Y1 (cm)	Y2 (cm)	X (cm)	Y (cm)	Z (cm)	SSD (cm)	MU
1		CL21EXA 18MV	1	0	0	0	15 L	13	6.5	6.5	14	7	7	0	0	19.5	89	90
2		CL21EXA 18MV	1	235	0	0	45 L	14	7	7	13	6.5	6.5	0	0	19.5	94	123
3		CL21EXA 18MV	1	180	0	0	30 R	10	5	5	15	7.5	7.5	0	0	19.5	90	109

Figure 3. The external beam window showing patient plans on the left, three canvas views for axial, sagittal and coronal display and the tab menu. The external beam tab is selected which displays a properties list-box of the external beams for the selected plan.

dose distribution options include a transparency setting to view overlapping objects. Contour options include the structure colour and check boxes to fill in the area and or show the edges.

The Monte Carlo tab handles the simulation properties for BEAMnrc and XVMC. Simulations are run on a remote cluster using a shell terminal which requires properties such as login IP, user name and password. MMCTP periodically checks the status of the simulation for both BEAMnrc and XVMC. Once a simulation is complete, the shell sends commands to add phase-space files or download dose distribution files. A second sub-tab menu separates the BEAMnrc and XVMC properties. The BEAMnrc tab includes BEAMnrc simulation properties, a run button and a simulation progress list-box. The BEAMnrc properties include the job split number and the number of initial particles. The run button generates the BEAMnrc input file, uploads the input file to the cluster and submits the job to the queue. The XVMC tab includes the DMX generation setting, XVMC normalization properties, run button and a progress list-box. The DMX generation settings define how the patient geometry will be modeled within XVMC. DMX generation settings include an option to generate the density values either from CT numbers (e.g., using a CT to density calibration curve) or assigning density values based on structure volumes or using a combination of both methods. Changes to these settings are saved within the XVMC properties file. If there are significant artifacts in the CT data set (patients with dental fillings or prostheses), one may choose to omit the CT images with artifacts. In this action, the CT to density algorithm will average over the omitted CT images. Alternatively, one may assign density values based on structure volumes

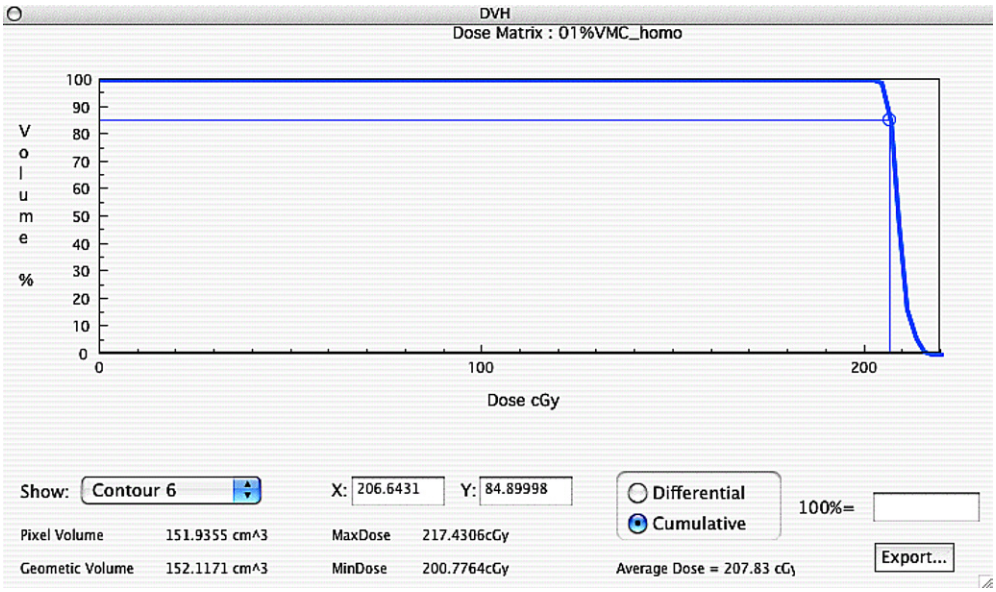


Figure 4. MMCTP DVHs are displayed as differential or cumulative within the DVH window. The window includes a summary of the contour volume, maximum and minimum dose, as well as an option to show multiple or single DVH graphs.

to deal with artifacts. The DMX file and XVMC input files are automatically generated and uploaded to the cluster. After the simulation is complete, the XVMC dose distribution files are downloaded to the workstation. Once all XVMC simulations are complete (one dose distribution per beam), MMCTP normalizes and adds the dose distribution file(s) to generate one McGill RT dose file. The XVMC normalization property includes the energy-specific calibration value, which is used to properly normalize the MC dose distribution into dose per monitor unit. The uncertainty of the normalized dose distribution is spatially dependent and as such requires careful analysis of the voxel uncertainties. Uncertainties for each voxel will eventually be available within MMCTP, although, the current version of MMCTP does not make use of the XVMC uncertainties to generate an uncertainty map of the normalized dose distribution.

In general, a three-field plan with MLC and wedged fields will take about 30 h of CPU time on a single 1.8 GHz 64 bit AMD processor. With the use of a cluster, the total CPU time remains the same but the CPU time on the individual nodes is significantly decreased depending on the number of nodes. Within MMCTP, BEAMnrc and XVMC simulations are run using a comfortably high number of histories to ensure a low statistical uncertainty. This approach is inefficient and undesirable since the goal of MCTP is to simulate a dose distribution to a specific uncertainty (Kawrakow 2000). Future versions will attempt to use statistical uncertainty as the cutoff point for simulations.

The dose tab It contains the DVH calculator and the dose comparison tools. DVHs are calculated and stored in memory for all contours and can be viewed in differential or cumulative mode. Once calculated, DVHs are displayed in the DVH window, as shown in figure 4. The dose comparison tools allow the addition, subtraction, multiplication and division of two dose distributions. The second dose distribution may be replaced with a constant. This operation generates a new dose distribution based on the selected operation. The newly generated dose distribution is automatically saved under the appropriate plan folder. Currently, MMCTP

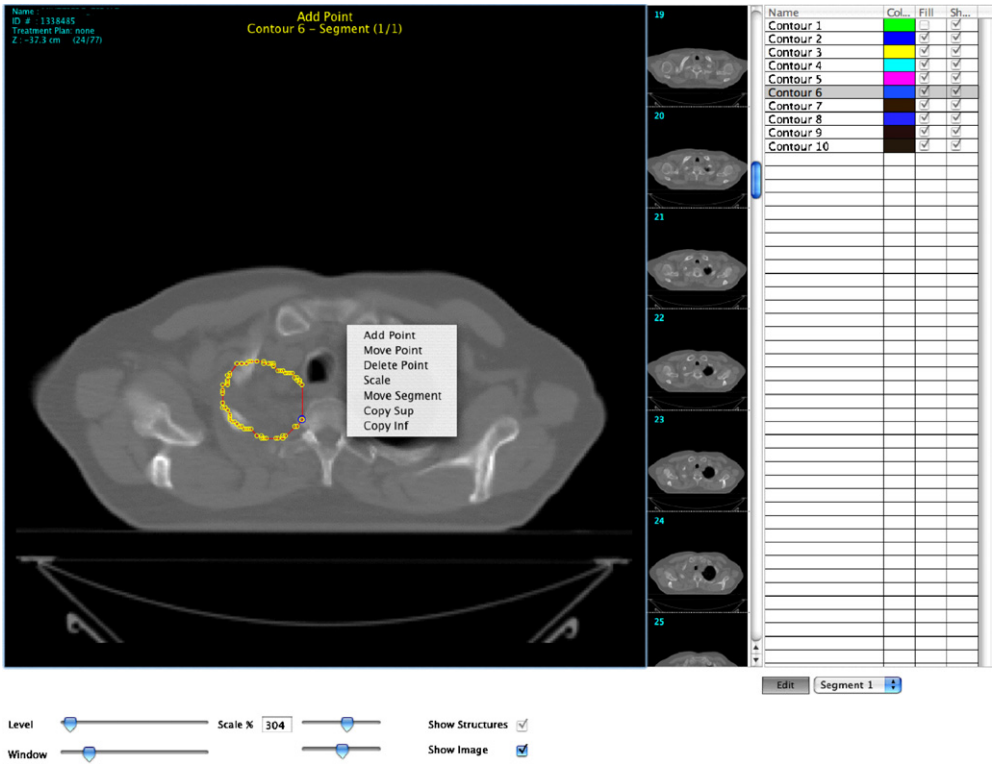


Figure 5. Contour window for editing and creating new contours. The contouring tools include: add point, move point, delete point, scale, move segment, copy sup and copy inf.

does not use the dose distribution uncertainty information. In future releases, propagation of uncertainties needs to be handled properly for dose distribution manipulations. MMCTP also includes a 'paint' dose distribution tool where the user can generate a grid and manually paint dose values one plane at a time. This tool has been used to quantify the DVH calculation accuracy but its future role can define dose constraints for inverse planning techniques.

3.2.2. The contouring window. It was designed for structure contouring where the user may create, edit or delete structures. This window is shown in figure 5 and includes a main canvas for editing contours, thumbnail image preview, a list of structures and some basic display options. Structures are edited individually on the axial planes where a structure may have multiple contour segments per axial plane. Segment editing options include add point, move point, delete point, scale segment, move segment and copy segment to superior or inferior slice. There also exists an auto-contouring tool which contours objects based on CT number constraints. The display options allow the user to change the image window and level, the scale size, the contour transparency settings and Boolean check boxes to show the CT image and or the contours.

4. MMCTP results

4.1. MMCTP validation

Preliminary validation focused on the DVH calculator and patient recalculations. Within MMCTP, DVHs are calculated by interpolating a dose value at the center of each pixel for all

Table 2. Real and MMCTP calculated volumes. The volume error becomes significant with small volumes. In addition to the volume size, the error also depends on the image resolution (pixel width, height and depth). The pixel width × height × depth is the elementary unit of volume. The volumes in this table were calculated on a 256 × 256 image with pixel dimensions of 0.164 × 0.164 cm^2 and an image depth of 0.5 cm.

Volume	MMCTP	
cm^3	cm^3	error (%)
700	699.6	0.1
175	174.9	0.1
87.5	87.4	0.1
25	25.01	0.1
14	12.3	12.1

pixels within a structure where the structure pixels refer to the pixels within a contoured CT image. Dose distributions of simple objects for which the DVH can be manually calculated were created to assess the accuracy of the DVH calculator. The MMCTP DVHs were within an upper limit of 1% to the manually calculated DVHs. The interpolation of the dose distribution grid onto the pixel grid is the main source of discrepancy.

The DVH calculation accuracy is also dependent on the structure volumes. If the volume is not accurate then the DVH is not accurate. The structure volumes are determined from the following process. The structure X, Y cm coordinate points are used to paint a 2D polygon onto an image with the native CT resolution. The number of pixels within the painted polygon determines the structure volume. The structure volume error is a result of the approximation in transferring a curve onto a finite pixel resolution image (partial volume effect). A few basic structures were generated to examine the agreement between manually calculated and MMCTP calculated volumes. If the structure volume is large compared to the volume of one voxel then there is excellent agreement between the MMCTP calculated volumes and the manually calculated volumes. Smaller structure volumes have greater error as there is a higher ratio of edge voxels versus internal voxels. Table 2 summarizes the MMCTP calculated volumes. In conclusion, there is some concern in the DVH accuracy for small volume structures. A solution to this potential problem would be to redefine the structure with additional contour points. Additional contour points reduce the partial volume effect.

4.1.1. Conventional planning systems. Lung patients were recalculated using MMCTP as an extensive test to identify problems throughout MMCTP job control and submission mechanics. These patients were originally planned using CADPlan version 6.2 (Varian Medical Systems Inc., Palo Alto, CA) and thus, the dose distribution was calculated using a pencil beam algorithm with the patient geometry set to homogeneous water. Patient plans were imported within MMCTP for MC dose recalculation. The MMCTP-generated MC input files were compared with manually created MC input files and differences between these files indicate errors within the MC module. It should be noted that the XVMC patient specific density matrix was set to homogeneous water to test the agreement between CADPlan calculated dose distribution for homogeneous water patients and the MC dose distribution. Once the MC dose distribution was calculated, a visual isodose comparison and a DVH comparison were performed. A patient DVH comparison between MMCTP and CADPlan is shown in figure 6 and as expected, the two DVH curves are similar. Since the DVHs are calculated on the same platform, differences seen between the DVHs reflect differences in dose distributions. There

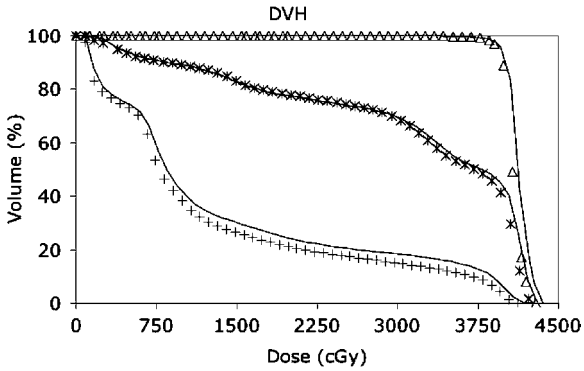


Figure 6. MMCTP patient recalculation with patient geometry set to the density of water; CADPlan DVH (△ CTV, ∗ lung and + heart) and MMCTP DVH (——). MMCTP CTV DVH is slightly right shifted, resulting in a less than 1% dose difference at 90% volume.

is a 1% difference separating the DVH curves for the CTV contour dose at 90% of the volume, although this difference increases to 3% at maximum dose. At first glance, a maximum dose difference suggests a problem with the XVMC normalization factor. However, the normalization factor was ruled out after verifying its accuracy under standard 10×10 cm^2 fields. In addition, the structures in figure 6 all have volumes above 90 cm^3 and thus the DVH volume error is negligible. With proper normalization and an accurate DVH calculator, the maximum dose difference is attributed to a small difference in dose distributions at high dose values and not a result of the analysis process. Within figure 6 there is a noticeable difference throughout the heart DVH. This is a three-field plan with MLC shaped fields where the heart is tangential to the fields. Since the heart is a tangential organ, it is expected that the observed difference is primarily due to beam modeling between MC and pencil beam algorithms. This has been demonstrated by the fact that good agreement was obtained between MLC shaped profiles calculated with MC and experimental profiles in the penumbra of the field whereas penumbra was systematically underestimated with CADPlan (Chetty and Seuntjens 2006).

5. Conclusions

Monte Carlo treatment planning (MCTP) has only now made a slow entry in the clinical environment taking considerably longer than envisioned (Verhaegen and Seuntjens 2005). The main objective of this project was to build a flexible computational radiotherapy research environment which allows for MCTP, outcome analysis and other future research implementations. It is well known that DVHs and outcome analysis must be compared on the same platform to avoid platform dependent effects. A research environment of this type opens the possibility of large-scale retrospective and prospective MC studies.

MMCTP was built as a research platform for the development of patient-specific MC treatment planning for external beam radiation therapy. The MMCTP design consists of a GUI which remotely connects to a computer cluster for MC simulations. MMCTP uses an internal storage format that is flexible in that it allows for future implementation of multi-instance and multi-modality image information. The visualization options, dose matrix operations and DVH tools offer extensive possibilities for plan analysis and comparisons. Plans are imported within MMCTP from commercial treatment planning systems through

well-documented storage protocols such as DICOM_RT and RTOG. MMCTP features a MCTP architecture that uncouples the private patient data from remote calculation engines. This philosophy allows MMCTP to connect to large university-based computer grids so there is no need for expensive computer hardware. Ideally, MMCTP can offer clinics access to MCTP by providing non-specialist people (dosimetrist) a simple interface for MCTP.

MMCTP validation tested cluster communications, MC results, DVH calculations and patient recalculations. Patient recalculations were performed as a validation step to identify potential problems throughout the MC process such as wedge orientations, coordinate systems, couch, gantry and collimator angles. Patient recalculations with the patient geometry set to water should produce similar dose distributions with the conventional heterogeneity uncorrected imported dose distributions. MMCTP DVHs from the MC and conventional dose distribution agreed well for the CTV target.

The MMCTP package will be released for use as a download from our web-page. It is intended that this package be used for radiotherapy research, and not as a clinical application. Improvements, updates and bug fixes are expected and new versions will be posted on our website (http://www.medphys.mcgill.ca/˜mmctp/). MMCTP is designed to run on low-cost hardware and as such, the minimum system requirements are a 1 GHz processor with at least 512 MB of ram.

Acknowledgments

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References

Chetty I J and Seuntjens J P 2006 Monte Carlo-based clinical treatment planning: issues for consideration *Integrating New Technologies into the Clinic: Monte Carlo and Image-Guided Radiation Therapy* (Windsor, Ontario, Canada: AAPM, Medical Physics Publishing)

Constantinou C, Harrington J C and DeWerd L A 1992 An electron density calibration phantom for CT-based treatment planning computers *Med. Phys.* **19** 325–7

Deasy J O, Blanco A I and Clark V H 2003 CERR: A computational environment for radiotherapy research *Med. Phys.* **30** 979–85

Kawrakow I 2000 *VMC++, Electron and Photon Monte Carlo Calculations Optimized for Radiation Treatment Planning: Proc. Monte Carlo 2000 Conf.* (Lisbon: Springer)

Kawrakow I and Fippel M 2000 Investigation of variance reduction techniques for Monte Carlo photon dose calculation using XVMC *Phys. Med. Biol.* **45** 2163–83

Kawrakow I, Fippel M and Friedrich K 1996 3D electron dose calculation using a voxel based Monte Carlo algorithm (VMC) *Med. Phys.* **23** 445–57

Lehmann J *et al* 2005 Monte Carlo treatment planning for molecular target radiotherapy within the MINERVA system *Phys. Med. Biol.* **50** 947–58

Rogers D W O, Faddegon B A, Ding G X, Ma C-M, We J and Mackie T R 1995 BEAM: a Monte Carlo code to simulate radiotherapy treatment units *Med. Phys.* **22** 503–24

Verhaegen F and Seuntjens J 2005 International workshop on current topics in Monte Carlo treatment planning *Phys. Med. Biol.* **50** (5) (editorial)