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Variance Reduction Tools for Making Monte Carlo Radiation Treatment Planning Clinically Useful

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Radiation treatment planning (RTP) for cancer therapy requires the calculation of radiation dose distributions in a computed tomography–scan representation of the body for a given set of beam locations and parameters. This is a difficult problem, which is normally done using approximate pencil-beam convolution methods. These methods lack accuracy near interfaces of dissimilar materials, such as lung/tissue or tissue/bone interfaces. Monte Carlo (MC) methods can be used to very accurately calculate dose distributions for RTP; however, the computer time required to achieve reasonable stochastic uncertainties is currently too great to enable routine clinical usage. Variance reduction methods can be applied to many MC problems to get lower uncertainties for a given calculation time. This proposal was to explore and develop variance reduction techniques from more typical nuclear engineering applications for improving the efficiency (speed) of MC simulations for RTP.

Introduction

The physician's goal in RTP is to maximize dose to the primary target volume (e.g., tumor region) while sparing, or at least reducing as much as possible, dose to the surrounding healthy tissues. Dose to nearby "critical structures" (such as the spinal cord, bladder, optic nerve, etc.) must be kept low or severe injuries to the patient may result.

The current computational tools are based on a simple model: a thin "pencil" beam of radiation striking a large tank of water. The penetration, lateral spread, and ultimate dose to each portion of the tank of water has been parameterized from experimental measurements or time-consuming computer calculations (e.g., analog MC). This one response is then applied many times to the patient geometry, and the effects are totaled to find the patient dose distribution. This method is very fast but is accurate only for patients who look like a large block of water. For real patients, with inhomogeneities such as lungs and sinus cavities of low density and bones and teeth of high density, the pencil beam approach breaks down quickly. Radiation transport depends heavily on the density and the atomic composition of the material. Using an ordinary computed tomography (CT) scan, physicians can develop a detailed model of density and material type for each patient with millimeter resolution. Pencil beam algorithms do not take advantage of this information.

Monte Carlo algorithms[1,2] have been used for many years to calculate dose distributions from radiation treatments.[3] Monte Carlo techniques are considered the most accurate since they simulate the detailed physics of radiation interactions and transport through the regions of the patient—each voxel of the CT scan. The drawback of these methods is the long running times required to calculate the dose in each voxel to a reasonable statistical uncertainty. We consulted with Julian Rosenman, MD, and his staff at the University of North Carolina (UNC) Radiology Department on the needs of clinicians. They run their MC dose calculator, MCRTP, on 100 PC's for 10 to 20 min. The expressed goal for routine clinical use is to have the dose calculator run on a single computer and take 1 to 2 min.

Technical Approach

Variance reduction (VR) methods can be applied to MC radiation transport calculations to reduce the computational time required to achieve the same statistical uncertainty of the final answers as the original, unmodified code (called the 'analog' code). These methods generally reduce the time spent following particles that will not contribute much to the final answer and instead focus on the particles that will. Hence, these techniques require a priori knowledge of particle importance. Each particle is assigned a weight, a value that represents the probability of the particle being followed by the analog code. Some of these methods are fairly simple—such as stopping particles that do not have enough energy to escape the voxel they are currently in, or forcing photons to interact with the patient at least once (and not pass through). More powerful techniques, such as stratified sampling (starting the simulation from a more uniform set of source particles) and the point detector algorithm (finding the contribution of the current particle to every dose response at each interaction), can also be used. These types of methods

have been used to speed up mammographic image simulation codes by orders of magnitude.[4] Of course, the dose distribution problem is more complex than the imaging problem, and it was recognized at the onset of this work that a similar speed up may not be possible.

Other VR approaches are more complex—such as using a faster, non-MC calculation to get an estimate of the dose distribution and then using that estimate in the MC to help guide particle selection, ultimately giving a lower uncertainty in the final result. These methods address the main difficulty associated with using VR techniques, namely, the determination of the problem-dependent VR parameters. A number of recent efforts[5] have focused on the development of automated VR methods based on statistically or deterministically generated importance functions. These efforts have generally been based on the recognition that the adjoint function (i.e., the solution to the adjoint form of the Boltzmann transport equation) has physical significance as a measure of the importance of a particle to some objective function (e.g., dose in some region).[6] It is this physical interpretation that makes the adjoint function well suited for use as an importance function for VR of MC calculations. Hence, many of the recent automated VR efforts that utilize approximate adjoint solutions substantially improve the calculational efficiency and reliability of traditional nuclear applications, while at the same time significantly reduce the time and experience requirements of the user. Based on the success with traditional nuclear application, automated VR was applied to the RTP simulation problem.

Results and Accomplishments

For each voxel, the dose D_i and the stochastic uncertainty σ_i are calculated. A standard figure of merit (FOM) is defined to be the reciprocal of the product of the calculation time T and the square of the uncertainty (variance). For the radiation treatment problem, the dose is calculated in millions of voxels, so the idea of FOM needs to be recast as an average. Similar to Kawrakow,[7] this is done by defining an average relative error s over a group of voxels as

$$s = \frac{1}{N} \sum \frac{\sigma_i}{D_{highest}}$$

where the sum is only over the N voxels with a dose between some minimum dose D_{min} and some maximum dose, D_{max}. $D_{highest}$ is the dose of the highest dose voxel in the entire problem. This allows for the problem to be portioned into low-dose, medium-dose, and high-dose areas. The FOM for groups of voxels is then $1/Ts^2$. Doses and uncertainties from codes with VR were then compared to the analog calculation, an example of which is shown in Fig. 1.

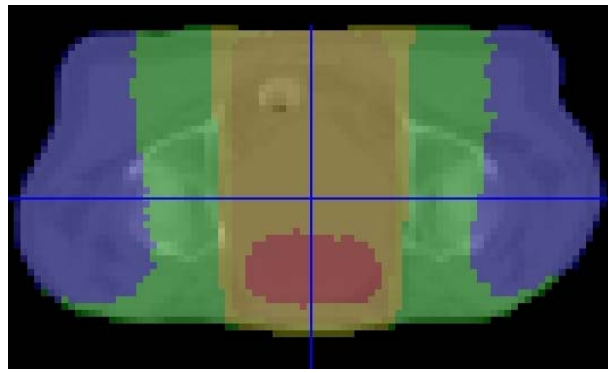

Fig. 1. One slice of a Monte Carlo dose calculation for a single beam prostate therapy. Dose colors are overlayed on the black and white CT values. Red denotes above 90% maximum dose, orange above 50%, yellow above 10%, green above 1%, and blue above 0.1%.

Standard methods for VR fall into categories of modifying the first interaction of the source photons, importance sampling of photons and electrons, particle survival biasing, and changing the photon scatter distributions. For each category, several methods were tried, and for each method listed in Table 1, several sets of parameters were tried. The increase or decrease in FOM listed for each method describes generally how the method performed for all the different cases of parameters. For example, the performance of path-length shortening scheme with respect to one of its parameters is shown in Fig. 2.

Most of these methods changed the distribution of photons throughout the patient. In photon-only problems, some of the above methods gave speed-ups of nearly a factor of 4. But with the small voxel sizes, electrons must be modeled. The electrons deposit dose in many neighboring voxels, so controlling which voxels the photons interact in does not necessarily help reduce the variance on the final energy tally.

In parallel with the above work, automated VR methods based on both deterministic- and stochastic-based importance functions were developed, implemented, and tested with two RTP problems, including one used in a previous VR study.[7] Applicable baseline models and results were generated for both photon-only and coupled photon-electron transport simulations, and metrics for computational efficiency were developed. The methods were developed with the goal of achieving more efficient global dose convergence (i.e., uniform density of simulated particles with the aim of achieving a uniform distribution of statistical uncertainty) without manual intervention (i.e., no manual "tweaking" of VR parameters). The goal of global optimization was based on consultations with the staff at the UNC Radiology Department.

The automated VR methods are based on the concept of importance sampling and represent different strategies for assigning parameters for the standard *weight-window*

Method	Increase/decrease in FOM (%)		
	Low dose	Med. dose	High dose
Modifying the first interaction of the source photons			
Preventing long first interaction distances	6	6	6
Forcing an interaction before leaving the geometry	0	0	15
First interaction distribution in the patient—uniform	–20	40	–20
First interaction distribution in the patient—front	–40	0	35
First interaction distribution in the patient—rear	–50	40	–50
Stratified sampling	0	20	–20
Stratified sampling with variance check	–40	–50	–60
Path-length shortening (Fig. 2)	–25	–25	40
Advanced path-length shortening	–30	30	60
Importance sampling			
Oversampling the edge of the beam	–10	–10	15
Rouletting the core of the source beam	15	15	–35
Source sampling: more spot photons	–40	0	5
Source sampling: more non-spot photons	20	–5	–5
Importance sampling using the source energy	–20	10	20
Electron importance as function of energy	–15	–15	–15
Particle survival biasing			
Interaction splitting	–10	–10	–10
Biasing secondary production	–30	–25	–25
Splitting low energy electrons	0	0	0
Photon scatter distribution sampling			
Compton scatter uniform distribution	–35	–35	–35
Compton scatter right angle biasing	–50	–50	–50

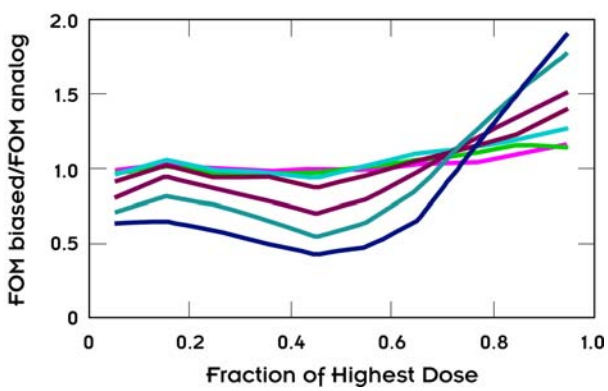

Fig. 2. Results for different levels of biasing (each color) using the path-length shortening scheme. The scheme improves FOM's for higher dose regions at the expense of medium- and lower-dose regions.

and *source-biasing* VR techniques. The weight-window technique is a space- and energy-dependent facility by which splitting and roulette functions are performed, while the source biasing technique enables preferential selection of the source space. The primary methods considered are referred to as (1) individual voxel adjoint–based VR (IVABVR), (2) global adjoint–based VR (GABVR), and (3) global forward–based VR (GFBVR). IVABVR utilizes the consistent adjoint–driven importance sampling (CADIS) methodology,[5] which is based on "traditional" deterministic adjoint functions. This method was applied to evaluate optimization potential of calculated dose in specific voxels and/or localized groups of voxels, while the GABVR and GFBVR methods attempted to reduce overall computational effort by achieving global convergence. For the IVABVR method, the maximum efficiency gain on a voxel-by-voxel basis was less than a factor of 5 and typical gains were less than a factor of 2. For a number of voxels, reductions in efficiency, as compared to the analog (unbiased) case, were observed; this was particularly true for cases that included electron transport.

The GABVR method involved weighting the voxel-wise source for the deterministic adjoint calculation based on the ratio of the maximum to individual voxel response (dose). This method attempted to weight the low-dose regions more heavily (in the adjoint calculation) and thus generate an importance map that would result in global convergence. The GFBVR method, which is similar to work in ref. 8, assigns the importance map directly based on the ratio of maximum to individual voxel response (dose). This method attempts to create a uniform density of simulated particles throughout the problem (patient) in a more direct manner than the GABVR method. Although the GABVR and GFBVR methods are well founded and have been shown to be effective for other problems, neither method demonstrated sufficient efficiency improvement to warrant further development for RTP simulations. This finding is attributed to the computational overhead associated with generating and using the detailed space- and energy-dependent importance map, the inability of the underlying method (the weight window technique) to achieve the desired uniform density of simulated particles, and the inherent characteristics of the RTP problem.

Summary and Conclusions

A VR method that worked for all voxels of the radiation-dose calculation problem without sacrificing any MC accuracy was not found. Methods that improve traditional photon and neutron MC problems did not perform well for this problem, confounded by the electron transport across the small regions.

The results of this work are generally consistent with the results of others who have developed and/or applied a wide variety of different techniques with the goal of improving the efficiency of RTP simulations and hence further demonstrate the obstinate nature of this problem with respect to improvements in computational efficiency.

Despite the lack of significant improvements in computational efficiency, this work is valuable in that traditional MC VR methods were evaluated and adjoint-based VR methods were developed for RTP simulations

for achieving global VR. It is expected that some of these methods will prove effective for other nuclear applications, including deep-penetration problems in which detailed information is sought.

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Identifying a Suitable Methodology to Extract Meaningful Results from Dose Volume Histograms using Statistical Analysis

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External-beam radiation therapy, teletherapy, is used as one of the main treatments for many kinds of cancer. The challenge of teletherapy is to deliver the radiation to effectively eradicate the tumor while minimizing damage to normal tissues and subsequent side effects. The radiation treatment plan includes a set of dose volume histograms (DVHs). Each DVH is a rank percentile curve that displays the fraction volume of a structure (target or some normal organ) that will receive a radiation dose of some value or greater. In this study, we analyzed DVHs and post-treatment bladder complication ratings from 61 patients treated for localized prostate cancer. The study focused on determining if linear discriminant analysis (LDA) could be used to identify features of the bladder DVHs that correlate with post-treatment complications as determined using the Common Toxicity Criteria (CTC) scale. Because of the limited range of CTC ratings and the large variation within CTC groups, LDA was not successful in identifying features of the DVHs that are highly correlated with the CTC toxicity ratings. LDA may perform much better using a larger volume of patient data collected in systematic and controlled manner. Critical to the success of future studies are precise definitions of the CTC groups to be distinguished so that the groups exhibit differences that make discrimination viable.

Introduction

External-beam radiation therapy, teletherapy, has been used since the late 1950s as one of the main treatments for many kinds of cancer and is usually administrated over a period of 5–8 weeks. Because the radiation used to destroy the cancerous cells travels through the body to reach the target, normal tissues which lie along the path to the target receive some of the radiation dose and, as a result, complications due to the radiation may develop in the normal tissues. The challenge of radiation treatment has been to improve the planning and delivery of radiation beams to more effectively target the tumor while keeping damage to normal tissues and subsequent side effects at an acceptable level.

During the past decade, significant advances in the planning and delivery of radiation therapy have been obtained using more energetic radiation generators, advances in computational speed, improved computer graphics, and the wide availability of whole-body computed tomography (CT) scans. One such advance was the development of three-dimensional conformal radiation treatments (3D-CRT). This type of treatment shapes the radiation field to conform to the individual patients' tumor and is delivered with a higher degree of precision than earlier types of teletherapy. Conventional 3D-CRT utilizes a cross-fire, four-field box technique that centers the radiation beams on the target but also includes substantial portions of the intervening normal tissues within the radiation fields.

A newer, more advanced form of radiotherapy delivery, intensity-modulated radiation therapy (IMRT), represents a significant improvement in treatment conformality. IMRT uses many thin beams (beamlets), having small fields to precisely irradiate the target while reducing exposure to other nearby organs. In addition, IMRT allows the intensity of each beamlet to be modulated so that the intensity of the radiation can be varied during the treatment delivery. IMRT produces dose distributions that are far more conformal than can be obtained with standard 3D-CRT. While IMRT reduces radiation exposure to healthy tissues compared to 3D-CRT, these toxicities are not entirely eliminated. The move from standard 3D-CRT to IMRT has resulted in a larger volume of normal tissue being exposed to lower doses.

IMRT allows the radiation oncologist to specify desired doses or dose limits to be delivered to specific regions of normal tissues. Using these goals, specialized software calculates the beam intensity maps that are to be delivered. Once the treatment plan is calculated, a set of dose volume histograms (DVHs) is obtained which depicts the volumes of target and normal tissues that will receive a particular radiation dose. A DVH is a rank percentile

curve that displays the fraction volume of a structure (target or some normal organ) that will receive a radiation dose of some value or greater. Many such curves can be developed by the physician and radiation physicist, and the curve that is ultimately selected as the treatment plan for an individual patient is the decision of the radiation oncologist and medical physicist. A representative set of DVHs used for IMRT planning is presented in Figure 1.

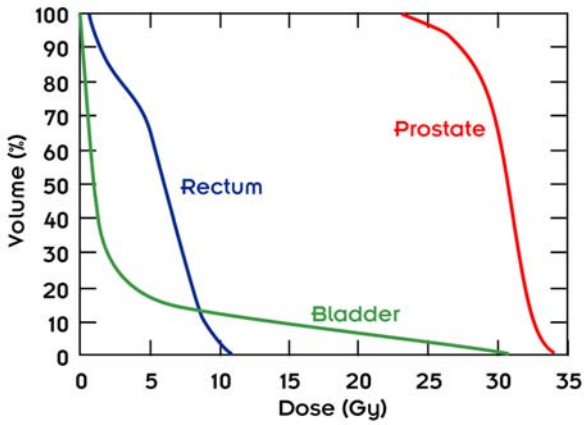

Fig. 1. An example of cumulative dose-volume histograms for IMRT treatment of prostate cancer.

The availability of new methods for treatment planning allows novel distributions of dose across structures of interest to be created. A basic problem of the prescribing physician is to review the created dose distributions to determine whether they are safe to prescribe. The DVH allows the vast amount of information contained in a three-dimensional dose distribution to be reduced to a two-dimensional framework to facilitate review and inter-comparisons among cases. However, building reliable predictors of injury from a set of two-dimensional plots remains a difficult theoretical problem. The purpose of this study was to determine if liner discriminant analysis (LDA) can be successfully applied to identify features of one tissue, the bladder, that correlate with complications after IMRT for prostate cancer. If features of the DVH can be identified that may be used to predict complications, this information would be valuable to aid future IMRT treatment planning.

Technical Approach

Clinical data for this study were provided by the Department of Radiation Oncology at Tufts-New England Medical Center (Tufts-NEMC). The data were obtained retrospectively from patient charts and completely de-identified before sending to the ORNL for analysis. Informed consent was not contained as the approach was approved by the Institutional Review Boards at both Tufts-NEMC and ORNL. Data consisted of treatment planning information and post-treatment bladder complication ratings from 61 patients treated for localized prostate cancer. The irradiation technique consisted of a combination of four co-planar fields using 3D-CRT techniques followed by IMRT. Patient target doses for the four-field treatment varied from 45 to 55 Gy (mean of 45.3 Gy), while target doses for the IMRT varied from 10–28 Gy (mean of 26.4 Gy). The total target dose ranged from 65 to 73 Gy (mean of 71.5 Gy).

Patient treatment information for the four-field treatment was limited to the target dose as DVHs were not consistently available. However, detailed information was provided for the IMRT plans and included the following: (i) the target dose [Gy and % isodine line], (ii) DVH plots, (iii) the prostate total volume [cm^3], and (iv) the bladder total volume [cm^3]. Also provided was the bladder toxicity rating according to the Common Toxicity Criteria (CTC) scale version 2.[1] Table 1 presents a general description of the CTC toxicity scale along with the number of patients assigned to each grade.

A key question in radiation therapy is the following—given that a certain total dose of radiation must be given to kill the cancer cells, are there certain dose distributions that are less likely to lead to post-treatment complications? It has been concluded by the National Institutes of Health and the American Association of Physicists in Medicine that the ability to evaluate and compare the complex dose distributions with respect to expected clinical outcomes has lagged far behind the advances in hardware and software for delivering the treatment.[2] Previous studies have addressed this question by analyzing DVHs to determine if they contain features that correlate to post-treatment complications.[3,4,5] These studies applied techniques such as mechanistic model building, direct comparison of DVHs, permutation tests, and logistic regression. In this study we applied linear discriminant analysis (LDA) to determine if there is a predictive relationship between the DVDs and post-treatment complications. Our approach to discrimination makes use of the entire DVH for each patient, which is in contrast with that published in studies where researchers select only a few points on the curve for discrimination.

Table 1. General patient complication assignment according to the CTC toxicity scale

CTC grade	Complication description	No. of patients
0	No complication	30
1	Minor symptom requiring no treatment	20
2	Minor symptom requiring medication	10
3	Symptom requiring minor surgical intervention	1
4	Symptom requiring major surgical intervention	0

Results and Accomplishments

Thirty-two predictor variables were defined to describe bladder DVHs. The variables representing IMRT boost doses beginning at 0.1 Gy and ending at 31.1 Gy in increments of 1.0 Gy were established. The variable values were defined as the corresponding bladder volumes (either % volume or absolute volume) from the DVHs. Because only one patient was rated toxicity grade 3, three groups were defined: CTC grade 0, 1, and 2/3.

Linear discriminant analysis (LDA) was used to determine if the predictor variables defined from the DVHs could be used to identify combinations of dose and volume that separate DVHs into risk groups for bladder toxicities. Analyses were performed using both percent-of-bladder volume and absolute-bladder volume. Because three CTC groups were defined, two linear discriminant functions (LDFs), denoted as LD1 and LD2, were defined for the three groups of CTC toxicity grades.

The dose-volume values used in the LDA came from the discretization of the DVH curve resulting in a large number of correlated predictor values. It is well known that LDA using high-dimensional, correlated predictors results in an over-fitting of the data. That is, the LDA tends to give overly optimistic results. A variable selection procedure was used to reduce the dimensionality of the problem. We approached the variable selection through all-subsets binary 0,1 regression. (Note that for the two-group case, a standard regression analysis on a binary variable indicating group membership is equivalent to LDA.) Each pair of CTC groups, CTC 0 vs. CTC 1, CTC 0 vs. CTC 2, and CTC 1 vs. CTC 2, was considered. In each of these cases, one group was coded 0 and the other group coded 1 and an all-subsets regression analysis was performed using the possible 32 predictors. The best predictor sets of size 1, 2, and larger were evaluated. This analysis suggested that more than three variables was unwarranted and that a set containing doses 1.1 Gy, 8.1 Gy, and 17.1 Gy along the DVH was among the best (see Fig. 2). Using this three-variable set in an LDA of all three groups resulted in an overall 29 of 61 (47.5%) correct classification rate. A cross-validation procedure was used to estimate how well the LDA might perform for future sample. The cross validation consisted of two steps. First, one patient was omitted and linear classification functions (LCFs) were determined on the remaining 60 patients. Then these LCFs were used to classify the omitted unit into one of the three CTC groups. This process was carried out 61 times, and the number of omitted units correctly classified was used to estimate the classification rate. This procedure resulted in 26 of 61 (42.6%) being correctly classified. The procedure as described above was repeated, replacing percent-of-bladder volume with absolute-bladder volume. Again, a three-variable set containing doses of 1.0, 11.0, and 14.1 Gy was selected for the discriminant analysis. The LDA resulted in an overall 28 of 61 (45.9%) correct classification rate (cross validated rate of 41.0%). Table 2 summarizes the results of these analyses.

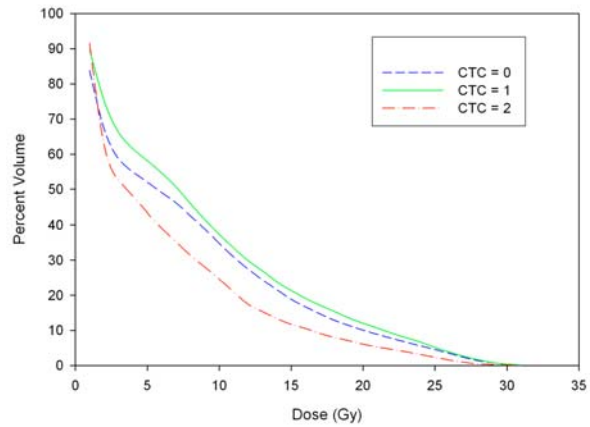

Fig. 2. CTC group means versus dose for percent bladder volume.

As indicated from the results displayed in Table 2, this application of LDA was not successful in identifying features of the DVHs from the IMRT boost doses that are highly correlated with the CTC toxicity ratings. We believe that the lack of success was largely due to two reasons. First, the data used in this study covered a limited range of CTC ratings. The data included only one patient with a CTC = 3 and none with CTC = 4. Second, there was a great deal of variability among DVH curves within each CTC group. Given the limited range of CTC ratings and the large variation within CTC groups, it is doubtful that any procedure would identify combinations of dose and volume that separate DVHs into risk groups for bladder toxicities.

Summary and Conclusions

An important issue facing the biomedical medical research community and recognized by both the National Cancer Institute and regulatory authorities is how to ensure the safety of patient treatment. New devices in radiotherapy offer the potential to create novel dose distributions that may enhance the likelihood of tumor sterilization, but determining which of the new dose distributions are safe is a pressing problem. This study has demonstrated that linear discriminant analysis is an appropriate methodology

Table 2. Summary of linear discriminant analyses

Variables used in the Discriminant Analysis	Dose values selected (Gy)	Classification rate	Cross-validated classification rate
DVH % volume	1.1, 8.1, 17.1	47.5%	42.6%
DVH absolute volume	1.0 , 11.0, 14.1	45.9%	41.0%

for identifying features of radiotherapy DVHs and may be effective in predicting post-treatment complications. The study has also revealed the importance of the quality of the data used in evaluating the methodology.

Large databases of dose volume histograms for structures of interest that include hundreds or thousands of patients are being assembled, often as part of National Cancer Institute (NCI)–sponsored projects in single institutions or cooperative groups. Mathematical and statistical techniques to analyze the vast information data bases are wanting. A pressing need is to derive from the data set reliable predictors that will provide a greater measure of patient safety, allow new treatment delivery techniques to be implemented with more assurance to patients and prescribing physicians, and provide cleaner estimates of complication rates to support the design of large-scale clinical trials. There is now no recognized way to derive such predictors from the acquired dose distributions and to form from them constraints on the dose volume histogram to more effectively guide the treatment planning process. Linear discriminant analysis offers an opportunity to do so, using sophisticated tools developed in the mathematics and statistics communities that remain to be fully explored in clinical radiation oncology.

The analysis done in the report manifests the applicability of Department of Energy (DOE) research into real applications—in this case health care. The potential impact of such a study will also benefit the National Institutes of Health (NIH) programs. As a result, the investigators are applying for follow-on funding to the NIH. A recent report[2] emphasizes the importance of the analysis of the uncertainties in DVH data. A proposal to NIH is being prepared.

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Development of a Three-Dimensional Radioisotope Depletion Method Using Monte Carlo Transport

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Accurate calculation of the depletion of nuclear materials requires careful determination of the neutron flux density and spectrum in the region(s) of interest. Increasing complexity in reactor designs, evolutionary concepts, and nonreactor applications such as safeguards, security, and nonproliferation are beginning to require robust geometrical modeling capabilities to capture neutron transport for complex configurations. Monte Carlo transport methods offer the type of flexibility needed for such applications but will present other difficulties not encountered in deterministic transport methods. The objective of this project is the development of a prototypic code sequence to perform Monte Carlo-based depletion. As part of this effort, approaches will be developed to relate the stochastic uncertainty of the Monte Carlo method to the uncertainty in isotopic predictions, minimize uncertainty via variance reduction, and reduce the computational effort associated with burnup-dependent iterations.

Deterministic solutions have advantages over Monte Carlo simulations for the transport solutions used in coupled depletion analyses because of their ability to generate an accurate spatial distribution of fluxes over a complete problem domain. On the other hand, Monte Carlo methods provide powerful geometric modeling capabilities in three-dimensional domains. Monte Carlo calculations require a large number of neutron-particle simulations to converge on an accurate system response. In order to obtain reasonable local neutron fluxes and power density distributions, significantly more computational effort must be invested. This effort is compounded in a depletion calculation, where transport solutions must be repeated in an iterative sequence alternating with depletion calculations to update isotopic cross sections and inventories. And while deterministic solutions are based on fluxes that are converged to a specified degree over the full problem domain, the nature of Monte Carlo simulations makes it extremely difficult to obtain accurate fluxes in locations that are far removed from the most reactive region of an analysis domain. Since the accuracy of the neutron flux is therefore a function of position in a Monte Carlo simulation, the accuracy of the depletion solution is likewise spatially distributed. If effective depletion based on Monte Carlo transport is to be successfully implemented, these deficiencies must be recognized and addressed.

Coupled Monte Carlo–point depletion methods have been developed elsewhere with varying degrees of success. MOCUP and its more widely used successor MONTEBURNS are based on the MCNP Monte Carlo code coupled with ORIGEN2 for depletion calculations. The German KENOREST system utilizes KENO V.a combined with HAMMER and ORIGEN2. Japan's Toshiba Corporation recently published a description of an in-house system based on MCNP and ORIGEN2. Japan's MVP-BURN and SWAT2 depletion sequence couple the MVP Monte Carlo code to ORIGEN2. Approaches based on MCNP are limited by the slow solution time of that code relative to other Monte Carlo codes such as ORNL's KENO V.a. ORIGEN2 is an older depletion code with known deficiencies and is no longer supported for future development. Additionally, none of these packages consider the effects of error propagation nor implement variance reduction methods to accelerate the solution. Finally, few if any of these systems are maintained under a controlled QA environment.

The current work at ORNL seeks to implement the Monte Carlo transport codes KENO V.a and KENO VI within the TRITON depletion driver module of SCALE, and to study and implement methods to improve the efficacy of iterative depletion based on Monte Carlo transport solutions. Error propagation from the results of Monte Carlo simulations will become a key attribute of such a system. ORNL possesses both adjoint and auto-differentiating versions of ORIGEN-S as developmental tools that have been used previously in propagating data uncertainties into the calculation results. Transitioning this capability to track the effects of flux uncertainties is the next logical step.

This project is still relatively young. Although initial work was started in FY 2003, the majority of the project will be completed in FY 2004. To date, ORNL has modified the TRITON sequence to accept KENO V.a input

and to perform transport solutions driven by TRITON. The SCALE utility code KMART, originally developed to post-process KENO V.a calculations, has been adapted to provide collapsed cross sections and fluxes required by TRITON for setting up ORIGEN-S depletion calculations. TRITON is able to perform full KENO V.a-based depletion calculations for simple fuel pins and is undergoing debugging in application to full assembly depletion analysis.

Potential users of our new depletion codes include the National Nuclear Security Administration, the Office of Nuclear Energy, Science, and Technology, the Office of Science, and the Office of Civilian Radioactive Waste Management within the Department of Energy (DOE). Outside the DOE, other organizations and agencies that would potentially benefit from the results of this work include The Department of Homeland Security, the Department of Defense, and the National Aeronautics and Space Administration. The Nuclear Regulatory Commission has a strong interest in this work and has been following ORNL's progress. The advantages to potential users of a SCALE-based depletion sequence are multifold: SCALE is an easy-to-use system developed around an understandable and simplified input form, ORNL provides formal quality assurance procedures, source-code control, validation and verification of code components that meet many sponsors' needs and ongoing development, testing, and updates. ORNL's SCALE project team provides training and support for users, and ORNL has the capacity to support and protect both proprietary and classified work. Most importantly, ORNL has long been recognized as a world leader in highly accurate and effective Monte Carlo methods (KENO family, MORSE), depletion (ORIGEN family) and automated code sequences (SCALE and its TRITON sequence). ORNL staff have long maintained a productive and cooperative relationship with many of the potential sponsors cited above.