Transmutation Feature Within MCNPX

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ABSTRACT

A feature recently developed for MCNPX [1] is the ability to perform transmutation calculations. Although this capability has been available to users via various post-processing utilities, such as Monteburns [2], it would be the first time this process is entirely automated within MCNPX. Such an enhancement provides many benefits to the user by eliminating the need to learn other post-processing codes, reducing errors in normalizations and auxiliary input, and eliminating file manipulation and tracking issues.

This transmutation option is implemented with a batching scheme that updates material properties at various user-specified time steps. The number of particle histories sampled per batch is also specified by the user. Within each time step, MCNPX tallies a 63-group neutron flux averaged over each material within the geometry. At the end of the time step, the neutron flux data and various 1-group cross sections, along with related isotopic atom densities, are passed through an interface routine to CINDER90 [3]. In its usual fashion, CINDER90 uses the neutron fluxes to perform activation, depletion, and decay. It then updates the isotopic inventory, which then is returned to MCNPX for use during transport of the next time step. As usual, users can perform various time-dependent tallies across the entire simulation process.

During this first phase of the transmutation implementation, we focus on comparisons between MCNPX and Monteburns. As the MCNPX implementation approaches that of Monteburns, it is expected that the results will be quite similar. For a seven-can HEU configuration, we show that the MCNPX and Monteburns k_{eff} results are within a few percent. While these initial results are encouraging, work continues on understanding the differences (e.g., there are notable differences in the cross sections used by MCNPX and CINDER90).

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Three Dimensional Dosimetry Analyses in Radionuclide Therapy using IDL and MCNP-based Software Tools

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ABSTRACT

Objectives: Patient-specific dosimetry methods using the SCMS software tool (that provides input for the MCNP radiation transport simulation code from three dimensional patient image data sets) have been extended using image-based segmentation tools. A user interface has been developed to streamline the processing of data. The objective of this study is to assess the capabilities of these tools in handling phantom and patient data sets taken from a CT-SPECT dual head gamma camera system.

Methods: The SCMS software was installed on Vanderbilt University Medical Center Unix-based machines running the MCNP code. An image-based segmentation tool was written in IDL, which uses CT or MR images to define anatomical structures and SPECT or PET data to establish activity distributions within these structures. Organ identifiers are tied to those established for the Zubal et al. voxel phantom, as is the basis for the SCMS routines. Other IDL routines provide file conversion and other utilities that provide output in the proper format for the SCMS code. Data from phantom studies and existing patient studies at Vanderbilt were processed using these tools.

Results: The SCMS code provides input to the MCNP code, so that three dimensional distributions of radiation dose can be calculated in mixed media (e.g. lung, bone and soft tissue) problems. Some limitations occur in the time needed to obtain results at the individual voxel level for some problems, thus sometimes requiring some grouping of voxel structures. The image segmentation software is flexible and adaptable to many different patient organ geometries and activity distributions, and provides input files for the SCMS code with user identification of organ regions using simultaneous paired image viewing.

Conclusions: The combination of software tools provides a powerful analytical method for three dimensional, image-based analysis of patient radiation dose in radionuclide therapy. Improvements are still needed in the user interface, the codes' ability to correct for image alignment and registration problems, and optimization of MCNP run time for individual problems.

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Shielding calculations in the Core Unloading Device area of the PBMR reactor.

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ABSTRACT

MCNP is extensively used for shielding and criticality calculations in the design phase of the Pebble Bed Modular Reactor (PBMR) project in South Africa. Maintenance work will have to be done timeously on equipment such as the Core Unloading Devices (CUDs), and thus the dose at which personnel will be exposed to, have to be known in the area around such devices.

The CUD area is situated just below the reactor core cavity and is separated from it by a thick concrete floor. Contributions to the dose rates in the CUD area are from four sources, mainly, streaming neutrons from the reactor core and induced gammas in the concrete, the fuel spheres in the defuel tubes which connects the CUDs to the reactor core, fuel spheres in the CUDs and neutron activation of the CUDs.

The MCNP results show that the major contribution to the dose rates in the CUD region is the streaming neutrons coming from the reactor core. A parametric study was then done in determining the thickness of the concrete shielding floor that ensures effective shielding. The modeling of the CUDs and the shielding results obtained with MCNP will be presented.

MCFANG – A <u>M</u>onte <u>C</u>arlo <u>F</u>orward <u>A</u>djoint <u>N</u>eutron <u>G</u>amma code

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ABSTRACT

Evolution of Monte Carlo methods over the last four decades has focused on increased accuracy (through refinements in nuclear data) and efficiency (through development of variance reduction techniques). However, there are many practical problems where the modern abundance of fast computing power removes some of the need for elaborate acceleration techniques.

The computer program MCFANG is a simplified derivative of the powerful, general purpose Monte Carlo code MCBEND. It is intended for situations where human resources are at a premium but computing power is cheap. Nuclear data is represented in multigroup form (neutron, gamma or coupled) which allows the solution of forward or adjoint cases. Some simple and robust variance reduction methods are retained for cases that cannot be solved in analogue mode. The geometry modelling capabilities of MCBEND are retained. Simplicity of use is enhanced by the presence of a graphical user interface for data preparation. MCFANG is aimed at the user who is not an expert in the field of Monte Carlo methods.

BNCT Treatment Planning at the University of Birmingham with NCTPlan

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ABSTRACT

Necessary procedures and supplementary software utilities are documented for the application of the NCTPlan1 code package to the epithermal neutron beam facility at the University of Birmingham for BNCT treatment planning. The local installation and performance characteristics of the PC-based planning system are detailed. A simplified treatment case is then demonstrated, highlighting the overall approach and potential pitfalls, as preparation for initial patient planning work. Beginning with CT scans of a small water-based phantom used to construct the Monte Carlo model, and concluding with an optimised therapy plan, the steps for simulating and optimising a three-field irradiation with the Birmingham epithermal beam are outlined.

A second investigation is performed to determine the validity of two different approximate source/geometry coupling strategies. Efficient treatment planning requires relatively quick transport from the source description location to the patient geometry. An obvious strategy for the Birmingham facility is to use the SSR/SSW card set in MCNP2. Two overlap strategies for this source translocation are available, one requiring an approximate backscattering phantom for SSW generation and the other utilizing a pre-phantom black surface for SSW generation. A slightly modified MCNP compile from the standard NCTPlan installation is required for the SSR phase of the second coupling method. Results indicate that the two source methods both reproduce a full transport calculation, and that the approximate backscatter phantom methodology is preferred.

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Systematic error in pebble's modelling

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ABSTRACT

Due to the impossibility of MCNP to model the geometry of a random distributed system, such as a pebble fuel element, a lot of effort has been made to show the accuracy of lattice-based models. For pebble bed reactors the approximation is used in both distributions of kernels inside the pebbles, and pebbles inside the core. These approximations are usually based in a volume-weighted philosophy, but do not take into account boundary effects due to the intersection of finite bodies with the limiting surface. This fact introduces a systematic bias in the amount of fissile material included in the model of the core, and therefore in all the kcode output variables, from keff to neutron fluxes.

In this work it will be shown the behaviour of this systematic error as a function of the geometry modelled, as well as a method to calculate the proper geometric parameter for the lattice approximation.

Application of Monte Carlo to Intensity Modulated Radiation Therapy

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ABSTRACT

Intensity Modulated Radiation Therapy (IMRT) seeks to deliver highly conformal tumorcidal doses to selected target volumes while conformably avoiding nearby normal tissues and critical structures. In the optimization process, it is assumed that the optimized planned doses can be precisely and accurately delivered to the patient. However, most IMRT planning systems use simplified fast dose calculations during the plan optimization that are historically known to be inaccurate when radiation disequilibrium conditions exist such as near tissue heterogeneities, for small radiation fields, or in dose gradient regions; precisely the conditions often encountered for IMRT. Monte Carlo dose calculation algorithms are not bound by such limitations and can be accurate under all scenarios. Furthermore, by transporting particles through the beam delivery devices (the MLC), Monte Carlo can also accurately determine the fluence incident upon the patient.

The goals of this presentation are to (1) describe intensity-based and leaf-motion based Monte Carlo dose calculation for IMRT and show the impact of this difference on patient plans; (2) describe how Monte Carlo is currently used in our clinic to validate IMRT treatment plans; (3) describe the technical difficulties of using of Monte Carlo for IMRT optimization and (4) discuss potential strategies for overcoming the difficulties and realizing MC IMRT optimization.

Monte Carlo commissioning of photon beams in medical LINACS using wide-field profiles in a water phantom.

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ABSTRACT

Based on the well known fact that in-water dose profiles are very sensitive to the different parameters that define the electron beam incident on the target, we have simulated 40cm x 40cm (SSD=100cm) profiles for several SIEMENS PRIMUS photon beams using the BEAMnrc code. The primary electron beam nominal energy was obtained from a fit of the simulated percentage depth dose with experimental data. Also several 5 cm depth in-water dose profiles were calculated varying the FWHM of the electron beam spacial fluence distribution (supposed to be gaussian). This depth was chosen to have a reduced effect of the water phantom scatter contribution. The results show a significant dependence of these profiles on the beam nominal energy. Additionally, wide field dose profiles depend crucially on a correct simulation of the target, flattening filter and primary collimator. Any changes in the material composition or geometry could be detected using this method, that also allows to crosscheck the determined nominal energy and to calculate the FWHM of the primary beam spacial fluence.

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Use of Monte Carlo simulation to assist in the removal of scatter in quantitative computed radiographic imaging

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ABSTRACT

We are investigating a method of producing quantitative measures of bone mineralization in the monitoring of the healing of tibial shaft fractures using Computed Radiography images. Radiographic images are formed by the detection of primary radiation transmitted through the object and the detection of radiation scattered by the object. Information about the attenuation properties of the object is contained in the primary radiation. In order to perform quantitative analysis on radiographic images, it is essential to remove the scattered radiation contribution from the image. We have investigated a technique of using an analytical model of the scattered radiation distribution to generate a scatter point spread function which was then used to deconvolve the scatter degraded images. This was found to be helpful in the removal of the scatter component. However, this model is applicable to an infinite extent uniform thickness of homogeneous scattering material and therefore required refinement for application to real images of complex composition. Monte Carlo simulation was used to model the clinically used imaging technique, and provided a means of validating the analytical model. Further, it allowed modelling experiments to be conducted so that the input parameters, for the analytical model could be determined more reliably. A mathematical phantom of the lower leg was constructed to simulate the clinical imaging scenario. A physical test phantom consisting of calibrated mass thicknesses of hydroxyapatite place on scattering material was imaged using the Computed Radiography system. Test results using the refined analytical model for scatter deconvolution with both the mathematical and the physical phantoms were encouraging. Using the mathematical phantom with a 100mm air gap, 100mm of soft tissue and bone phantoms of varying mass thicknesses, bone mineral densities were retrieved to within 4% after scatter correction. Tests using the physical phantom with no air gap and 60mm of perspex resulted in a 10% error in bone mineral density after scatter correction. This technique continues to be further refined.

Fast treatment head simulations for photon beams using Directional Radiative Splitting

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ABSTRACT

Introduction: Monte Carlo (MC) simulations of the treatment head of linear accelerators are a valuable tool for the development of source models needed for dose computations in RTP. The vast majority of published treatment head simulations have been performed using the BEAM/BEAMnrc code[1]. Apart from the difficulty to obtain reliable geometry specification from the linear accelerator manufacturers, the main problem when trying to commission a linear accelerator using MC simulations is the very long calculation time. Because the phase space distribution of electrons incident on the photon target are unknown, a large number of simulations with varying incident electron energy and spot size are necessary until good agreement with measured data is found. This paper introduces Directional Radiative Splitting (DRS) for the VMC++ code[2]. DRS is a new variance reduction technique that improves the efficiency of treatment head simulations by more than 2 orders of magnitude compared to BEAMnrc with Selective Bremsstrahlung Splitting (SBS), which was previously the fastest option in BEAMnrc.

Directional Radiative Splitting (DRS): Treatment head simulations (THS) for photon beams are slow because i) without use of any variance reduction techniques (VRT) most of the time is spent tracking electrons and ii) only a small fraction of the bremsstrahlung and scattered photons set in motion (~ 2-3%) escape from the treatment head. DRS addresses i) and ii) by using a complex combination of interaction splitting for processes resulting in the creation of photons, Russian Roulette for interacting photons and the cylindrical symmetry of the upper portion of the treatment head. In addition, it introduces "electron importances" (EI) that are associated with individual regions and components of the treatment head. In regions with higher EI photon interactions result in the creation of more electrons and vice versa. Electrons moving from a region of lower EI to a region with higher EI are split, electrons moving from higher EI to lower EI are subjected to Russian Roulette. The relative EI of regions increases when moving from the top to the bottom of the treatment head.

Results: When DRS is used with the VMC++ code, around 5 (at 18 MV) or 12 (at 6 MV) photons per minute are produced on a 1.53 GHz Athlon CPU in a typical THS that includes the photon target, primary collimator, flattening filter, monitor chamber and photon jaws. This is about a factor of 500 faster than BEAMnrc with SBS. As VMC++ uses a splitting technique for the transport in the patient, thus effectively transporting each photon many times, the time spent for the THS is a small fraction of the CPU time needed for the simulation in the patient (about 10%). One can therefore conclude that a complete THS for each patient dose calculation is possible without a significant increase of CPU time compared to a simulation with an empirical source model.

Future work: Future work will involve the implementation of VMC++ geometry modules for MLC, wedges and compensators. In VMC++ with DRS, most of the CPU time is spent with geometry related checks and therefore the development of extremely fast geometry module implementations is imperative for efficient simulations. The development of an automated beam commissioning process is also envisioned.

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Monte Carlo Simulation of Large Electron Fields at Extended Distances

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ABSTRACT

Development of a Total Skin Electron Treatment (TSET) requires a substantial amount of physical measurements. Therefore, Monte Carlo simulation of TSET can facilitate optimization of this technique. The goal of this study was to simulate a single large electron field produced by a TSET scatterer, at extended distances. Although a combination of beam angles is used in TSET, this simulation was used as the first step for developing a needed TSET optimization process. This study describes the results from simulation of a 6 MeV electron beam scattered by a control scatterer using EGS4 code on a VAX 11/780. Total CPU time was cut to less than half by performing simulations in separate manageable parts. Dnear variable and Presta algorithm were also used to speed up calculations, with no effect on accuracy of results. CPU time for each part was: 10 hours for simulation of a Philips SL-20 treatment head including a flattening scattering foil, air spaces and collimators for 105 initial electrons; and 12 hours for transport of particles from scatterer into a cylindrical water phantom (r=50 cm) at SSD=300cm. To calculate uncertainty limits, calculations were divided into 10 batches (106 initial electrons) and a new starting random generator seed was used for each batch. Generally a good agreement was found between calculated and measured depth dose distributions, dose profiles, and x-ray contamination levels (deviations <1%). However, central axis surface dose and output values were underestimated by 5% and 3% accordingly. Also calculated radial distribution of x-ray contamination were inconsistent with measured values.

Use of the BEAM Monte Carlo Code to calculate surface doses for breast radiotherapy

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ABSTRACT

Introduction: Many women with breast cancer will be treated with radiotherapy. For the majority of these patients, the skin is not part of the clinical target volume, however it is often irradiated to a high dose because of the use of tangential beams, which leads to erythema (reddening of the skin). For other women, where there may be spread of tumour to the skin, it is included in the target volume. For these women, additional material may be added to the patients skin (bolus) to increase the surfaces dose. As the angle of incidence of the radiation beam increases, the surface dose will increase and the depth of dose maximum will decrease. Traditional planning systems are often unable to calculate the dose to the skin due to limitations in their algorithms and inaccuracies in the data for the surface dose.

Methods: Measurements of surface dose both for flat phantoms and curved surfaces were performed on an Elekta SL15 linear accelerator at 6MV using film, extrapolation chamber and Markus chamber at a variety of gantry angles and for a range of field sizes from $5x5cm^2$ to $9x20cm^2$. The accelerator was modelled using the BEAM Monte Carlo code. Electron (ECUT) and photon (PCUT) transport cut-off energies of 0.521MeV and 0.01MeV respectively were used. No range rejection or Bremsstrahlung splitting was used. Phantoms simulated using DOSXYZ.

Results: Surface doses calculated using Monte Carlo agreed well with those measured using a Markus chamber (corrected for over-response using the Rawlinson correction). The Monte Carlo results at a depth of 0.025mm gave values of between 14.8% of Dmax for a $5x5cm^2$ field to 22.3% of Dmax for a $9x20cm^2$ field at normal incidence. These values increased to 53% for a $9x20cm^2$ field at a gantry angle of $75°$. As the gantry angle is increased there is a corresponding decrease in the perpendicular depth of Dmax and the magnitude of the dose at Dmax.

A major component of the skin dose in breast radiotherapy is the exit dose. Decrease in dose at a beam exits the patient has also been investigated and differences of between 11 and 44% for a $10 x10 cm^2$ field were observed in the last 0.05mm as the gantry angle was increased from zero to $75°$.

Conclusion: Results calculated with Monte Carlo agree well with those measured on a linear accelerator. The use of Monte Carlo allows accurate calculation of surface doses for breast radiotherapy.

Inelastic nuclear interactions in Monte Carlo simulations for clinical proton beams

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ABSTRACT

Due to the ballistic properties of protons and the small ranges of secondary electrons, the modelling of electromagnetic processes in proton Monte Carlo simulations is relatively easy. The major uncertainty thus comes from the poorly known inelastic nuclear interaction cross sections that contribute substantially to the total energy transfer and total dose deposition at high-energy clinical proton beams. ICRU report 63 [1] for example, which provides until now the most comprehensive compilation of data, quotes standard uncertainties of up to 10 % on total inelastic cross sections.

In this work, the importance of these contributions from inelastic nuclear interactions was investigated in various topics related to proton dosimetry and dose calculations by Monte Carlo simulations, using the PTRAN [2], GEANT4 [3] and MCNPX [4] codes. These cover perturbation factors in ionisation chambers, fluence perturbation factors to convert dose from one medium to another, water equivalence of graphite for water calorimetry and dose calculations in tissue compositions for treatment planning. The first three topics are summarising and extending earlier work.

Results show that the inelastic nuclear interactions:

1. have small effects in ionisation chamber perturbation factors (though not negligible in corrections of tenths of a percent),

2. can cause fluence perturbations of up to 5 % in the conversion of doses from plastic phantoms and from graphite to water, which show large variations from one inelastic nuclear interaction data set to another,

3. can cause considerable errors in high-energy clinical protons (up to 4% of the total dose) when dose contributions resulting from inelastic interactions are converted from tissue to water or vice versa applying proton stopping power ratios.

We conclude that inelastic nuclear interactions contribute substantially to uncertainties in present day dosimetry and dose calculation practice in proton beams and that more experimental work is needed for quantitatively evaluating the size of their effects.

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Application of Monte Carlo to Four-Dimensional radiotherapy

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ABSTRACT

The Monte Carlo method is generally accepted to be the most dose calculation accurate method, especially in the presence of sharp heterogeneities such as those found in lung tumor geometries. Dose calculation accuracy for lung targets, however, is limited not just the presence of heterogeneities, but also by the fact that the target position is changing with time due to respiratory motion. To account for temporal changes in the target position, the concept of four-dimensional (4D) radiotherapy has been developed. 4DRT is the explicit inclusion of the temporal changes in anatomy during the imaging, planning and delivery of radiotherapy. This work describes the combination of 4DRT with Monte Carlo dose calculations with the goal of achieving accurate dose calculations for moving target volumes in heterogeneous media.

The 4D treatment plan was developed on a 4D CT scan. The 4D CT scan was created by acquiring a series of eight 3D CT image sets at different respiratory phases, and using deformable image registration to map each CT to the end-inhale respiration phase. Contours drawn on the end-inhale CT were then automatically transferred to the CT data sets at the other respiratory phases. Similarly, the treatment plan developed on the end-inhale CT image set was automatically applied to the 3D CT image sets at each respiratory phase using the same the beam arrangement and dose prescription as for the end-inhale plan. The Monte Carlo dose calculation was performed on each of the N (=8) treatment plans and 3D image sets with 1/N fewer particles per calculation than would have been used for a typical 3D plan. Using the deformable mapping, the dose distribution from each respiratory phase was mapped back to the end-inhale CT image set and added to the dose distributions from the other phases. This resulted in a statistical uncertainty in the merged dose distributions equivalent to that of a typical 3D plan. With this method, the 4D calculation time is similar to that for a 3D calculation. Overall, Monte Carlo dose calculation for 4D RT of lung tumors can result in higher dose accuracy because it properly accounts for both the electronic disequilibrium conditions due to the tissue heterogeneities and patient motion. Furthermore, for Monte Carlo, the dose calculation time is independent of the number of 3D CT image sets used in the calculation process, unlike other algorithms for which the calculation time scales linearly with the number of 3D CT image sets used for calculation.

Monte Carlo modelling of a medical linear accelerator and asymmetric field head scatter

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ABSTRACT

The photon beam produced by a linear accelerator is inhomogeneous both in energy and intensity, especially when additional beam-shaping tools such as the physical wedge are employed. Accurate non-Monte Carlo computation of radiation penetration and dose deposition therefore requires comprehensive information about the beam incident on the patient. The required information may be difficult, if not impossible, to obtain by measurement. Although Monte Carlo calculations are still considered to be too slow for routine treatment planning of photon beams, they are used to generate the necessary spectral input for faster alternative algorithms such as the convolution/superposition methods of dose calculation.

We used the Monte Carlo N-Particle radiation transport code MCNP on a personal computer to simulate the MLC-produced open and wedged 6 MV photon fields. For model verification, the depth dose distributions and dose profiles at various depths for different field sizes were simulated and found to be within acceptable limits. The model has been applied to the simulation of asymmetric fields, linear accelerator head scatter studies, and for superposition/convolution model set-up and verification.

Results of linear accelerator characterisation will be presented. Monte Carlo simulated head scatter factors will be compared to measured data, and asymmetric head scatter simulated data will be presented and discussed.

Inter-comparison of electron Monte Carlo dose calculations for EGSnrc, GEANT and Penelope

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ABSTRACT

Introduction: Electron beams with a nominal energy of 4–20 MeV are frequently used in radiotherapy for superficial or deep-seated tumours. Electron therapy is usually performed in regions with heterogeneities such as bone, air cavities, lung and soft tissue, etc. Since electron transport and scatter in matter is strongly influenced by density and material composition, dose calculation in heterogeneous media is extremely challenging. In the present study 3 Monte Carlo electron dose calculation codes: EGSnrc, GEANT and Penelope are inter-compared in water, bone and lung tissue. The study was performed for mono-energetic electron pencil-beams incident on cylindrical slabs, where the following parameters were evaluated:

  ➢ dose deposited as function of depth;
  ➢ energy spectrum at two (2) fixed depths, situated either side of the maximum dose;
  ➢ angular distribution of electrons as a function of the cylinder radius at two (2) fixed depths, situated either side of the maximum dose;
  ➢ electron particle fluence at two (2) fixed depths, situated either side of the maximum dose.

By evaluating these parameters for each Monte Carlo code and inter-comparing them, it is possible to assess how each transport algorithm, scattering algorithms (elastic and inelastic) and cross section data are performing.

Methods: Mono-energetic electron pencil-beams, with nominal energy from 100keV - 20MeV, were modelled perpendicularly incident on a sequence 200 cylindrical scoring slabs, all with identical thickness and radius of 100 cm. The slab thickness varied with the energy of the incident electron beam and was obtained from:

$$SLAB\_THICKNESS \ = \frac{CSD}{100 * \rho} \ ,$$

where CSDA is the continuous slowing down approximation range in g/cm^2 obtained from NIST database and ñ is the density of the slab material in g/cm^3. A phase space file was also generated at depths of 30% and 50% of the CSDA range, where the particle energy, position (x and y co-ordinates) and cosine directors "u,v,w" were kept. The two (2) selected depths correspond to depths before and after the depth at which maximum dose occurs.

In the case of the GEANT Monte Carlo code several electron models and cross section data are available and were assessed. They are (i) standard electromagnetic model (referred to as STD_EM) with 1mm cut-off range, (ii) standard electromagnetic model with 0.001mm cut-off range (referred to as STD_EM_FINE) (iii) Penelope model and (iv) low energy model (referred to LowE).

Results: Preliminary results obtained for the deposited dose as a function of depth for water, bone and lung tissue materials show significant differences between the EGSnrc results and the GEANT (STD_EM, STD_EM_FINE and LowE models) and Penelope values for electron energies below and above 1 MeV (c.f.figure for H_2O dose results obtained for 100keV and 5MeV). However, in the case of 1MeV incident electron energy all Monte Carlo dose prediction are in very good agreement (c.f. following figure for H_2O and BONE dose results).
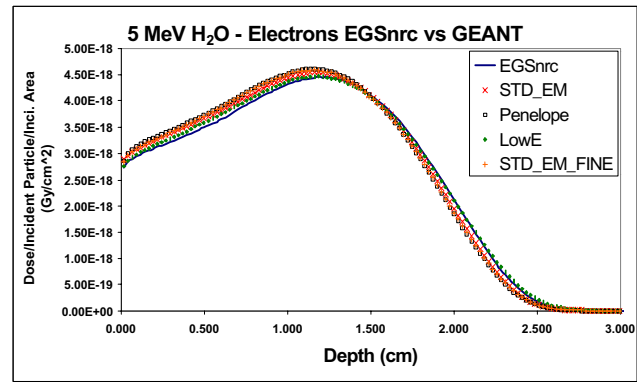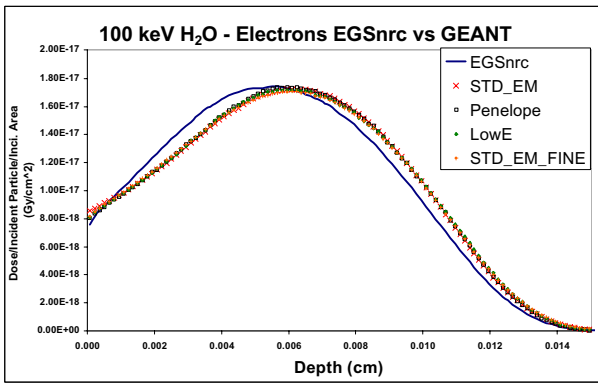
The EGSnrc, GEANT and Penelope Monte Carlo codes use different cross section for electron dose calculation. While EGSnrc use ICRU 37 (1984) restricted collision and radiative stopping powers, GEANT and Penelope use Seltzer and Berger (1985) cross section data. Differences observed in deposited dose for energies below and above 1 MeV, are possibly due to differences in the cross section data and in the scattering (elastic and inelastic) algorithms used. These differences will be assessed by comparing the energy spectrum, angular distribution and particle fluence obtained for various electron energies at two (2) fixed depths, situated either side of the maximum dose.

Conclusions: Preliminary results obtained in water, bone and lung tissue indicate that differences in the cross section data used Monte Carlo code lead to large differences in the deposited dose for electron energies below and above 1MeV.

A parallel implementation of Geant4 application using OOMPI

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Almost of all high energy Monte Carlo simulations require a considerably high CPU time to produce good results. Sometimes we could spent several months in such simulations to achieve low statistical uncertainties. In Medical Physics applications such as treatment planning system for clinical use we need to get a three dimensional (3D) dose distribution from a composition of several fields in few minutes. Standard libraries for high energy Monte Carlo simulations as Geant4, MCNP4, EGS4 can produce good results in few minutes when they run in parallel mode in computer clusters. In this work we present a full object oriented way to parallelize a Geant4 application used for simulate a 3D dose distribution in a simple phantom[1].

Parallel Geant4 applications have been developed with TOP-C library which makes use of MPI to control the execution of parallel tasks. The main problem of TOP-C is its structured design, that can lead to a break of the object oriented feature of all serialized Geant4 applications. OOMPI (Object Oriented MPI) is a C++ class library that implements MPI interface. With this library we can send and receive any object inherited from a special class called OOMPI_Datatype.

We have developed an application to run in one CPU to simulate the 3D dose distribution in a phantom made by a homogeneous box where its material and dimensions can be set by a macro file. The beam particle type and its energy can be selected in the same way as the phantom characteristics. The simulated absorbed dose has been stored in a ROOT 3D histogram class in double precision.

To parallelize that application we needed to add 2 classes, change other 2 classes and the `main()` function. As suggested in Geant4 examples for use with TOP-C we have added a class to handle the state of the random number generator for master and slave nodes. We also added a RunMananger class called ParRunManager responsible to manage the distribution of the jobs and the reception of the results. We have changed the phantom sensitive detector class in order to store data in a temporary histogram object and at the end of a job this object is sent by ParRunManager to the master node. The last one modified class was the analysis class in which we have added a method to merge node simulated data to a main histogram object. In the `main()` function the modifications were about initializing MPI properly.

The application can be started in batch mode as usual. The master node will send only a small number of histories for each node to be processed, in this case we chose 100,000 per node. After sending the number of history for a node the ParRunManager class will choose the seed for the random number engine and send it to that slave node. This process is repeated until all started slave nodes get their jobs. The next step is wait for a result that can be sent from any node in any order. When the master node receives a result it properly stores this result and send a new job to the same slave node. This cycle is repeated until all histories are processed.

References

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Distributing EGS across the NPL United Devices grid

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ABSTRACT

The intranet at NPL links several hundred desktop PCs running a variety of applications, mostly on MS Windows 2000. This is a potentially significant compute resource most of which is idle, most of the time. United Devices Grid MPTM software provides a means to harness this resource for at least some data parallel computational tasks, including radiation transport Monte Carlo simulations. The overall efficiency of such distributed computing systems depends on the ratio of computation to data communication for the tasks to be processed.

The grid consists of a central server, holding a database of compiled applications and their data, and software agents running on desktop workstations. The agents are in regular communication with management software running on the server, which despatches computational tasks as the agents become available. The porting and compilation of applications is carried out by the user on their own PC, from which jobs may be submitted to the grid either interactively, using a web-based interface, or using scripts run from a command prompt. There are several options in porting applications, which in our case were previously running on Linux. The simplest approach uses Cygwin to compile and run source code with minimal changes. In particular, reasonable efficiency can be achieved in some cases without major restructuring of the code. The actual performance obtained in our tests using EGS Monte Carlo simulations will be presented, and preliminary conclusions can be drawn on the scaling behaviour of the system.

GRID-enabling BEAMnrc and "first-class" particle transport

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ABSTRACT

Clinical implementation of Monte Carlo dose calculation is an aspiration of many radiotherapy departments. With increasing demands of complex radiotherapy modalities, the unmatched accuracy of Monte Carlo dose calculation is becoming a necessity. However, long computation time is a major drawback. As a first step in tapping unprecedented computing power to shorten simulation time, we have implemented BEAMnrc and DOSXYZnrc simulations on the Welsh e-Science GRID. We report efforts in GRID-enabling the simulations, and present a set of utility functions designed for streamlining the overall simulation task. With these functions, a complete BEAMnrc/DOSXYZnrc run could be automated by a single command line from the user. We also contrast advantages and disadvantages of GRID computing against those in cluster computing. Finally, we demonstrate BEAMnrc simulation of a linear accelerator using "first-class" EGSnrc transport parameters (e.g. exact boundary crossing, atomic relaxations and Koch & Motz angular sampling.) which, without the elementary GRID solution presented herein, would require 6 months of runtime on a 2.8 GHz Pentium 4.

A simulation for the METAS electron beam primary standard dosimeter

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ABSTRACT

A primary standard for the electron beam dosimetry has been established at METAS since the beginning of 2002, using a chemical dosimeter based on total absorption experiment in a Fricke solution [1]. Recently, a Monte Carlo simulation of the experiment has been undertaken in order to improve the correction factors applied for the losses due to Bremsstrahlung, absorption and scattering in the phantom and the surrounding materials. First results have been obtained using EGSnrc [2], yielding corrections between 2.69% and 8.05% depending on the incident beam energy, which ranges from 5.3 to 22.3 MeV. Furthermore, the simulation allows a better insight into the dose distribution within the solution, for which the local peak dose has been calculated.

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EGSnrc in the cell nucleus

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ABSTRACT

General purpose Monte Carlo codes such as EGSnrc are not usually touted as being useful for the determination of stochastic quantities, firstly because such quantities are generally required at length scales at which the physics assumptions become unreasonable but also because macroscopic source descriptions lead to very inefficient simulations. Standard geometric and importance based variance reduction practices are often invalid due to the way in which energy per event is tallied. There are potential advantages in being able to apply a general purpose codes to microdosimetry problems, in particular being able to use a wider set of materials and to include contributions from upstream and downstream material that may generate complex non-equilibrium fluence. The successful application of EGSnrc to small mm sized air cavities supports its usage in micron size volumes of density 1 gm/cc. The human cell-line, CGL1, is an example of a biological system that shows sensitivity to variations in the energy of low-LET radiation sources (e.g. X-rays and beta sources). The explanation appears to lie in radiation induced damage on the scale of the cell nucleus. Specific energy and lineal energy are stochastic quantities which have been computed with EGSnrc and which unlike dose and LET need to be computed per source particle. In order to achieve reasonable statistics in micron sized volumes for a uniformly distributed source a technique known as detector fluctuation has been used. One approach is to divide the cell layer up into an array of micron sized volumes, however the memory requirement to do this over a scale of cm's quickly escalates to Gbytes. In this paper an alternative method is proposed where events occurring within the cell layer are recorded and at the end of each history, a single energy deposition event is selected at random from the list and translated to deposit the energy at a randomly sampled point within the cell volume. All other events in the particle track are translated accordingly and the total energy deposited within the cell is determined and tallied. Typically hundreds of events need to be post-processed which has an impact on the amount of time it takes to complete the history. The dose-weighted mean lineal energy calculated for a 1x5 micron cylindrical nucleus was 4 keV/micron for a 30 kVp Mo-target X-ray source compared with 0.20 keV/micron for a Sr-90 beta emitter. The biological data from this system indicates a 4-fold difference in RBE for the two radiation sources in the low dose-rate limit which corresponds to an activation threshold of approximately 2 keV/micron deduced from the lineal energy spectra computed for this target size.