

# ISTITUTO NAZIONALE DI FISICA NUCLEARE

Sezione di Torino

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INFN/TC-92/21  
24 Luglio 1992

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**COMPUTER APPLICATIONS IN ELECTRON BEAM RADIOTHERAPY  
TREATMENT PLANNING**

**Computer applications in electron beam  
radiotherapy treatment planning**

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**Abstract**

A three dimensional Monte Carlo computer code is described. It allows to simulate the electron beam irradiation of a patient using X-ray computed tomography scans as input data. The particle transport is executed by EGS4 code and media data are calculated by its preprocessor PEGS4. The absorbed dose can be evaluated with high spatial resolution in every slice of the patient or in a restricted number of regions of interest called high-resolution zones (HRZ). In the other zones, where high resolution is not necessary for dosimetric purpose, the various organs are divided in several parallelepipeds of homogeneous tissue having different sizes and the dose volume is calculated in each one. With such a division, a considerable reduction of the CPU time is obtained without any reduction of the spatial resolution where the dose distribution is important. Details of the algorithm and its preprocessor SCAN are discussed with their results.

## 1. Introduction

When a high energy electron beam hits a heterogeneous structure, the spatial distribution of the energy transferred to the medium depends on the composition, mass density, size and geometrical contour of the area crossed by the beam. The accurate knowledge of the dose distribution is of great importance in electron beam radiotherapy treatments, because the success of the treatment may greatly be influenced by it [1], but the structural complexity of the human body and its individual variations make such a determination difficult. Due to the random nature of the radiation interaction with matter, Monte Carlo (MC) method can be applied successfully to determinate the dose distributions. It performs the computerized simulation of the passage of the electron through the medium and allows the calculation of the energy transferred to each elementary volume of it. Unfortunately, a MC simulation requires the generation of a large number of stories to obtain a uncertainty in the absorbed dose within the values recommended by ICRU [2] for treatment planning ( $\leq 5$  percent). Consequently a high CPU time is needed to follow all these stories. The problem is greater when the dose distribution has to be determined in a three dimensional (3D) structure obtained using (as input data) X-ray computer tomography (CT) scans of a patient. The CPU time needed to follow a single electron depends, among other parameters, on the total number of crossed volumes and this number is very large when CT input data are used for spatial representation of images. A MC code named "SHAPE" has been used for treatment planning. It simulates electron beam radiotherapy treatments with CPU times smaller than a conventional simulation because a new algorithm which decreases the total number of elementary volumes in the radiated 3D structure is used and describeb in same detail. The reduction acts only on the zones in which it is less important to know the dose distribution with great detail.

## 2. SHAPE code

SHAPE is a Monte Carlo code based on the EGS4 system [3]. It is written in MORTRAN3 [4], a structured language created at SLAC (Stanford Linear Accelerator Center). It simulates electron beam irradiations of complex 3D structures using 3D parallel plane

geometry [5,6] and defining some "high resolution zones" (HRZ), in which the dose is calculated with high spatial resolution (maximum resolution possible is the CT resolution). The program is considered as organized in three main steps: i) acquisition of the 3D data of the patient from the multislice X-ray CT scans and optimization of geometrical boundaries; ii) Monte Carlo simulation of the irradiation field by EGS4 code; iii) dose calculation and graphic representation of the dose distribution.

In step i) a preprocessor named "SCAN" is used. It reads, from disk or magnetic tape, the multislice CT data of the patient and stores them in a CT data matrix. Each CT number is related to the electron density of the patient elementary volume element (called voxel), the geometrical correspondence of the matrix in the simulation is a 3D structure made of parallel slices placed at regular distances and in cylindrical form. The geometrical units of such a structure are voxels with X and Y sizes equal to the CT resolution and the 3rd dimension (Z-axis) equal to the distance between CT slices. To reduce the distance between CT slice a more accurate representation of the real case will be obtained. In the program, in order to determine the corresponding mass density of every voxel, the user selects some intervals of CT numbers and assigns a specific material (identified by a number) to each interval. In this way it is possible to identify the inhomogeneities in the structure. For each material its standard mass density is used. Successively a material matrix having the same size as the CT data matrix and containing the numbers of the materials identified in the structure is constructed. In Fig. 1a an example of materials matrix and its geometrical correspondence is reported. During the simulation of a single particle passage in the medium, the program checks if at each step the particle crosses the boundary of the voxel in which it lies, and when it happens, determines the new voxel and the corresponding mass density. It is evident that, when the total number of voxels crossed by the particles is too large, a high computing time is required for the whole simulation. In order to avoid it, when it is necessary, SCAN diminishes the total number of voxels, according to the geometrical resolution selected by the user. It reduces all the groups of four (or greater) contiguous elements of the materials matrix to one. In this way, the resulting matrix is reduced by a factor four (or greater), but the total number of voxels is also reduced by the same factor. A further reduction of this "reduced matrix" can be executed if the user selects one or

more zones in which to evaluate the dose. For instance, taking into account that normally the irradiation zone with an electron beam is rather small compared to the sizes of the CT image and that the absorbed dose, in zones not crossed by the primary beam, is negligible, the absorbed dose can be only in the zones reached by the primary electrons and in those just next to it. Nevertheless, it is not correct to restrict the simulation only to the selected zones (or HRZ), because the zone external to the HRZ is crossed by several secondary particles (delta-rays, bremsstrahlung photons, etc.). These particles may interact in this zone and return to HRZ or may generate other particles that will cross the HRZ. In order to consider this contribution to the absorbed dose, it is necessary to simulate the zone external to the HRZ too. For this purpose, a "UNION ALGORITHM" was developed (see appendix A), which works in the zones external to the HRZ. It joins all the contiguous voxels inside the same tissue up to obtain several rectangular volumes named "boxes". In this way the organs lying in zones of little interest for the dose evaluation are described by a restricted set of boxes having various sizes. Of course, in the same structure may be present voxels, in HRZ, and boxes in other zones. For simplicity, the general term "boxes" will be used when both these are present in the same phantom. It is important to emphasize that the UNION ALGORITHM does not modify the media contour, in fact at the media interface the same resolution of the reduced matrix is maintained. The result of the UNION ALGORITHM application to the structure of fig. 1a is reported in fig. 1b. In the figure, the resulting matrix or "boxes matrix" and its geometrical correspondence are illustrated. A further application of the program on a Rando phantom CT slice has been studied. The initial CT resolution is  $(1.1 \times 1.1) \text{ cm}^2/\text{voxel}$ . The same slice after the application of the preprocessor SCAN is reduced to  $(2.2 \times 2.2) \text{ cm}^2$  for each voxel. After the application of UNION ALGORITHM, a relatively low number of boxes are present in the zone external to the HRZ. Generally, the resulting boxe number is a function both of the number and sizes of inhomogeneities in a 3D structure. In the more homogeneous zones of the phantom, it can be two or three orders of magnitude less than the initial number of voxels, but also in the heterogeneous zones the reduction is considerable. Of course, the largest possible dimension of an HRZ is the whole phantom. In step (ii), since the minimization of the total number of boxes is reached, the electron beam simulation

starts. Every electron is generated in a random point inside a circular source (representing the LINAC focus) with monochromatic energy and direction cosines. It hits the phantom in a random point inside a rectangular field chosen by the user. At this time the program control is transferred to EGS4 code which follows the primary electron and its secondary particles first in the air gap between the source and phantom surface and later through the phantom. Each particle is discarded when it escapes from the phantom or its energy goes below a cutoff value: ECUT for electrons and PCUT for photons. Media basic data used in this work have been computed by PEGS4 (EGS4 preprocessor). SHAPES stores the energy deposited in each box and when all particles have been followed, it is transformed into absorbed dose. In step (iii), the absorbed dose in each box placed in HRZ is printed out. To obtain an easy to read graphic representation of output doses, we preferred to put the results on single bidimensional planes. In each plane it is possible to represent the whole output matrix of the absorbed doses or isodose curves. The program also allows a visualization of dose with appropriate colors on a color screen printer.

### Monte Carlo simulation

In this paper two examples of complete simulation are described. Only few X-ray CT slices of an antropomorphous Rando phantom were used. The original CT number, after the inhomogeneity contour identification, was replaced by standard densities of the tissue [7,8]: muscle= 1.040 g/cm<sup>3</sup>, air= 1.205 x 10<sup>-3</sup> g/cm<sup>3</sup>, bone= 1.650 g/cm<sup>3</sup>, lung= 0.3 g/cm<sup>3</sup>, and no density variation was considered. The simulation were performed over three head slices and five thorax slices. In both cases, the distance between Ct slices was constant and equal to 2.5 cm. The initial number of CT data, (320x320) for each slice, was reduced by:

- ( a ) grouping the pixels two by two for the head and three by three for the chest-wall, obtaining, respectively, the resolution 2x2 and 3x3 cm<sup>2</sup>/voxel.
  
- ( b ) considering air presence only in the region between source and phantom and vac-

uum in the regions external to the slices.

After this step, the resulting number of voxels within the smallest three dimensional box containing the three slices of the patient was: 15048 voxels for the head case and 50000 voxel for the chest-wall case. In the head case, the relatively low number of resulting voxels allows to consider all the three slices as HRZ. The UNION ALGORITHM was not applied, so the number reported above is the total number of boxes. In the chest-wall case, the high number of resulting voxels needed a further reduction. Defining as HRZ the whole central slice and applying the UNION ALGORITHM on the four slices, we obtained 10000 boxes (HRZ) and 2140 boxes (zones external to HRZ) for a total of 12140 boxes. The incident electrons were restricted to a solid angle defined by the entrance field on the phantom. The kinetic energy of electrons was 17 MeV and the source-skin distance (SSD) 100 cm. Based on the analysis of electron ranges and considering the dimensions of the geometrical regions in our simulations, the selection of the EGS4 transport parameters value was as follows:

AE=ECUT = 521 keV (total energy)

AP=PCUT = 10 keV;

ESTEPE = 4 percent;

field size = (6 x 6) cm<sup>2</sup> for the head simulation; (11 x 11) cm<sup>2</sup> for the chest-wall simulation;

with AE= charged particle creation threshold; ESTEPE= maximum allowable fractional energy loss of charged particle kinetic energy in the charged-particle step. The actual values were chosen where a plateau of ESTEPE stability was observed. The actual values of SMAX (maximum allowable charged-particle step-size) were set to the smallest geometrical dimension of each box (smallest geometrical dimension of interest in the problem). For example, for head simulation SMAX is constant and equal to 2.2 mm; for chest-wall simulation SMAX is constant and equal to 3.3 mm. The computing time required for a total of 800000 electrons (divided in ten batches) generated by the source, was about 7 h for the head simulation and 6.3 h for the chest-wall simulation, on a DEC VAX 8600. The results at the maximum dose have a statistical uncertainty (standard deviation of the mean absorbed dose) of about 3.5 percent.

#### 4. Results

Fig. 2 shows the three simulation head slices of the phantom Rando. This zone, because of the presence of different inhomogeneities, is a good test for any method adopted in the evaluation of the absorbed dose. Just three kinds of media have been simulated in this zone: air ( orophanix), bone (mandible and vertebrae) and muscle. The doses are normalized to the maximum values in muscle, across the three slices. The isodoses distribution shows a backwards shift of isodoses where bone structures are present, with a noticeable dose gradient at the tissue-bone interface. An analog effect, but in opposite direction can be seen at the tissue-air interface. In the simulation of chest-wall electron treatment five slices were set up as input to the program.

#### 5. Conclusions

SHAPE is a powerful program to perform 3D evaluation of the absorbed dose distribution in electron beam radiotherapy, starting from the corresponding X-ray CT scan data which contains anatomic information. The 3D parallel-plane geometry, the application of the UNION ALGORITHM and the definition of HRZ performs the simulation of the irradiation of several contiguous slices with an acceptable computing time. CPU time are comparable to those required for the simulation of electron transport with low cut-off energies in complex geometries. The inclusion of bremsstrahlung generated photons and successive generation of secondary electrons are a large contribution to the large CPU times reported here.

The application of SHAPE in dose evaluation for radiotherapy planning with electron beams is especially relevant when the target volume contains tissue heterogeneities. At present time, SHAPE computing time does not allow the use of the program in daily clinical practice. Nevertheless, for specific kinds of pathologies and standard irradiation techniques, it is possible to obtain results and reference for comparison with the results of other methods. The main limitation is: it does not execute the automatic conversion from CT number to electron density.



Appendix A. UNION ALGORITHM The UNION ALGORITHM (table 1), is applied to the 'reduced matrix'  $IT(I,J,K)$  created by SCAN in order to reduce the number of corresponding voxels. The generic element  $(I,J,K)$  of  $IT$  is the material number of the voxel identified by the components  $I,J,K$ . Each voxel has spatial dimension  $X,Y,Z$ , respectively:  $GAP, GAP, ZTICK$ . Thus  $IT(I,J,K)$  is a 3D array with dimensions  $NX*NY*NZ$ , where  $NX, NY, NZ$  are the dimensions, in the voxel units, of the parallelepiped containing the patient CT slices. the UNION scanning starts at the element  $IT(1,1,1)$  and proceed row by row: that is, initially the component  $I$  varies up to the last matrix element of the first row  $IT(NX,1,1)$ , afterward  $J$  increases by one unit and the scanning starts again on the second row, etc. The method is applied to all the slices until the last element  $IT(NY,NY,NZ)$  of the matrix is reached. The choice of scan as last  $Z$ -dimension is due to the different spatial resolution in this direction ( $Z$ -planes distance is greater than  $X$ - and  $Y$ - planes distance) while the exchange between  $X$  and  $Y$  does not cause appreciable variation on the resulting box number. In the first scanning executed, all the voxels having the same material are joined. In this way, for example on a row, a box  $B1$  with initial dimensions  $L*GAP, GAP, ZTICK$ , ( $1 \leq L \leq NX$  with  $L$  integer) and with the same material can be identified and successfully enlarged until the dimension  $L*GAP, M*GAP, ZTICK$ , ( $\leq M \leq NY$  with  $M$  integer) obtained joining all the contiguous regions  $R1$ . Afterward, the continues on  $Z$ -dimension to control if the boxes superimposed on  $B1$  are present in the contiguous slices and when it happens, joins them up to obtain a rectangular "box" with dimensions  $L*GAP, M*GAP, N*GAP$  ( $1 \leq N \leq NZ$  with  $N$  integer). At this step the box is perfectly identified and the coordinates of two opposite vertices (that define univocally the box) with the box material number are stored in a table. In the  $IT$  matrix, used to create the box, is stored the row number (of the table) in which are memorized the data of the box. In order to avoid confusing this number with the material number that overrides, the row number is increased to 100, and when the union finishes it is restored. This procedure has the double function to label the voxels as no more joinable and to make easy to work of the EGS4 routine HOWFAR. Actually this routine finds the box data in which a generic point in the space  $(XP, YP, ZP)$  lies by simply reading the table to the row pointed by  $IT(XP/GAP+1, YP/GAP+1, ZP/ZTICK+1)$ .

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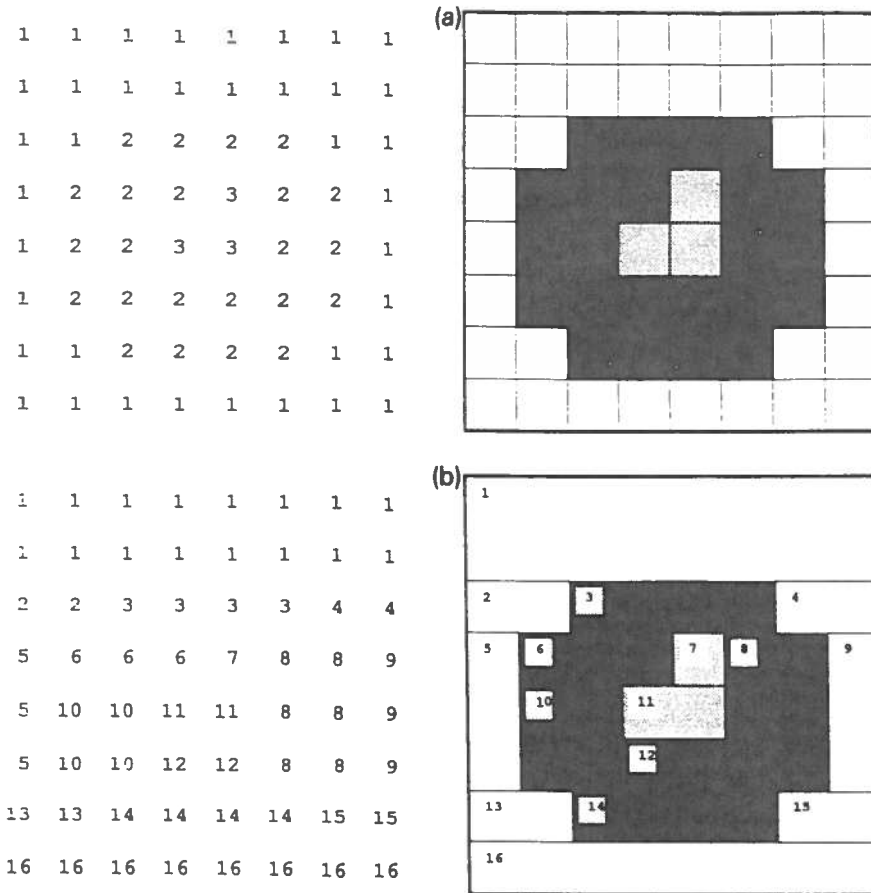


Fig. 1 - (a) An example of material matrix and its geometrical correspondence. (b) The Boxe matrix (obtained by applying the UNION ALGORITHM to the structure of (a) and its geometrical correspondence.

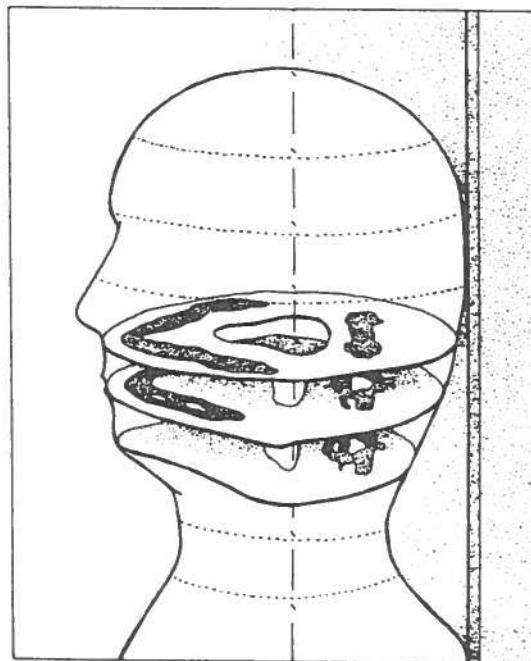


Fig. 2 - Three slices of antropomorphous phantom simulated by SHAPE.

