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PIPLAN

A TREATMENT PLANNING CODE FOR PION RADIATION THERAPY

by

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Introduction

Computerized treatment planning needs have changed with the relatively recent efforts to utilize charged particles, as well as neutrons, in the treatment of cancer.

Pions, in particular, place special requirements on treatment planning development. Multiple scattering of pions, coupled with beam emittance, for example, necessitates a three-dimensional volume calculation, where conventional treatment planning methods generally calculate in only two dimensions. The pion star dose must include the contributions of the star products: neutrons, protons, deutrons, tritons and heavy charged particles (Z greater than 1). These contributions added to the ionization component of the pions, plus the ionization contributions of the muons and electrons make up the total dose. Biological models need the capability of assigning different relative biological effectiveness coefficients (RBE) to each kind of radiation: low, medium or high LET (lineal energy transfer).

Calculated dose distributions must be based on the best data available regarding patient inhomogeneities: i.e., computerized tomography (CT) data. Such detailed data is essential for an accurate determination of range compensating bolus, as well as dose distributions.

PIPLAN is a treatment planning code developed for pions, utilizing either contour data or CT data for the calculation. It accumulates dose in three dimensions using a ray-tracing model where actual particle trajectories measured in the pion channel represent pencil beams that are traced through the volume.

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Computer Systems

The code is designed to run interactively on a PDP 11/45 (RSX-11D operating system) provided with special hardware devices, such as a contour digitizer, display scope, and life-size plotter. This version is referred to throughout as PIPLAN-RSX. A second version of the code exists on the CDC-7600 and it is this version (PIPLAN-CCF) that carries out the calculation. Both versions are essentially the same, with the exceptions that (1) the calculational module is not contained in PIPLAN-RSX and (2) the CCF version does not have the full I/O capabilities of the RSX version. A third version is PIPLAN-VAX which has the capabilities of PIPLAN-RSX, except for digitizing pen, and is intended to have at some future date all of the calculational capabilities of PIPLAN-CCF.

PIPLAN-RSX or PIPLAN-VAX creates a case file for every patient. Such a file contains (1) CT data, (2) contour data, including surface, target volume and landmark contours, (3) plans and beams data, (4) other pertinent data needed for a calculation, such as range-shifter functions, and (5) calculated dose distributions. This case file can be contained on a magnetic tape and is used for archival storage of patient data, as well as for transporting the data from the PIP-11/45 and VAX to the CDC 7600.

The code requires input information about the patient, the beams used, the type of calculation to be done and the kind of output to be generated. Input is conveyed by a series of commands and numerical data. Output is both alphanumeric and graphic. The PDP 11/45 has a 4010 Tektronix scope that can present temporary displays of either type of output. Hard copies can be made with devices connected to the terminal. PIPLAN-CCF creates displays on microfiche for archival storage.

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Privacy Protection

For patient privacy protection, the user must have a valid password and account to get on either the BIOMED or CCF systems. In addition, PIPLAN-RSX requires passwords before the user can create, modify or read data-files. There are two complete sets of passwords so that patient files can have unique passwords, while the non-patient files can have their own passwords.

Program Modules

PIPLAN is logically divided into six major modules.

The case administration module handles all respects of case-file maintenance. Its master command is *CASE. Commands which are subordinate to *CASE but may be given at any time a case is active are *PURGE, *PRESERVE, *FETCH, and *UPDATE.

The anatomy contour module handles all aspects of entering and editing anatomy and appliance contours. Its master commands are *SHEET, *CONTOUR, *VIEW, and *MOVIE.

The plans module handles plan and beam specifications. Its master commands are *PLAN and *BEAM.

The calculation module computes dose distributions for specified planes. Its master commands are *GO and *GRAPH. This module is currently active only for PIPLAN-CCF.

The mapping module generates a variety of graphic displays. Its master commands are *MAP and *ISOMETRIC.

The utility module consists of several general purpose commands which can be given at any time. Examples are *ROTATE, *DIRECTORY, and *EXIT.

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A complete PIPLAN sequence of operations involves creating a file, linking CT data, entering contours, specifying treatment plans, calculating the dose distribution, and mapping the results. The only operation that requires human intervention is the entering of contours, since PIPLAN uses the surface and target volume to align beams and establish necessary matrices. Thus test runs can be made without identifying a case or using CT data. Of course a calculation needs both contours and plan specification.

At present PIPLAN-RSX is used to define case-files, link CT data, define treatment plans, and export the resulting case file to PIPLAN-CCF via magnetic tape. PIPLAN-CCF can update PIPLAN-RSX specifications, such as for contours or plans, then do the dose calculation and map the results.

Patient Data

The patient anatomy consists of both contours and CT data. PIPLAN needs only the surface and target volume contours to do a calculation. Additional landmark contours, however, are useful to the treatment planner.

Surface contours give the patient's outline and must appear on every sheet with the same contour number. Target volume contours must appear on at least two adjacent slices or sheets and are assigned the density code of the surrounding material.

Although all planes, or sheets, of contours must be parallel, they can be at any orientation to a reference system of coordinate axes that are fixed in any convenient relationship to the patient. Each sheet's position in the parallel stack of planes must be defined.

There is provision for up to 30 slices of contour data for each treatment port corresponding to the slices of CT data needed for that calculation.

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Before contours are entered on a sheet, two special points 20 cm apart are entered. The code uses these points to align the sheet with the others and to define the scale of the data. The data for the contours entered on the sheet can come as direct values from a digitizing table or as numerical information from keyboard. The contours are displayed as they are entered on the sheet. Each contour is assigned a number less than 30 that is used to associate corresponding contours on different planes. Volumes are then effectively created by connecting the vertices of a contour on one plane with the corresponding contour vertices on an adjacent plane. Critical to this procedure are that both contours have the same handedness, the same relative starting point and essentially uniform spacing of vertices around the contours.

Each contour is also assigned a density code from 16 possible values. Codes 1 through 6 are reserved for patient anatomy and depending on an input parameter, the reference number, the anatomy may contain CT data. The remaining density codes are used for other materials, such as water, cerrobend, lucite, parrafin and others.

PIPLAN determines the effective or water-equivalent range at various depths in a patient through the conversion of CT data to pion stopping power ratios. Since PIPLAN does a full three-dimensional calculation, a large bulk of CT data must be available during the calculation. Rapid access requires that this data be in the computer memory, which in turn requires a certain amount of spatial averaging to keep the size within fixed limits. The fetching and averaging of this data for each calculation, after the code speedups described above, require about 20% of the total time. In addition, collecting and transporting the CT data from one computer to the next takes a substantial amount of time.

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The EMI CT scanner diagnostic console offers a wide variety of features for the therapist, and this is the logical device to be used to enter regions of interest (ROI). Usually there are the tumor, the prescription, critical sites, and the patient surface. Unfortunately, in the EMI software, the ROI's are not identifiable as to their purpose. With a special annotation procedure by the therapist and three additional programs, these ROI's and the image data are now fed directly into the patient case file from the CT scan data tape. No restrictions are placed on the therapist as to the order of ROI generation or CT slice, nor on the CT operator when transferring a study to tape. These new programs select the minimum set of data files from the tape in the optimum order to maximize throughput. During the final transfer the ROI pixel description of contours is translated into vector line segments to minimize storage requirements. The resolution of this process is under user control.

Beam Representation

The beam characteristics, position and direction are entered through input parameters. Through use of a tune library consisting of the nine Biomed tunes or beams, the beam data is accessed by PIPLAN and used during the calculation for representation of the pencil beams. This beam tape contains a header with pertinent information about the beam, such as momentum, muon and electron contamination, beam emittance, etc. The header is followed by the actual particle trajectories, characterized by particle type, where 1 = pion, 2 = muon, 3 = electron, and 4 = muon from pion decay.

The three-dimensional calculation of dose utilizes a ray-tracing model, Fig. 1, where actual measured trajectories of beam particles are used to represent pencil beams of pions, muons or electrons.

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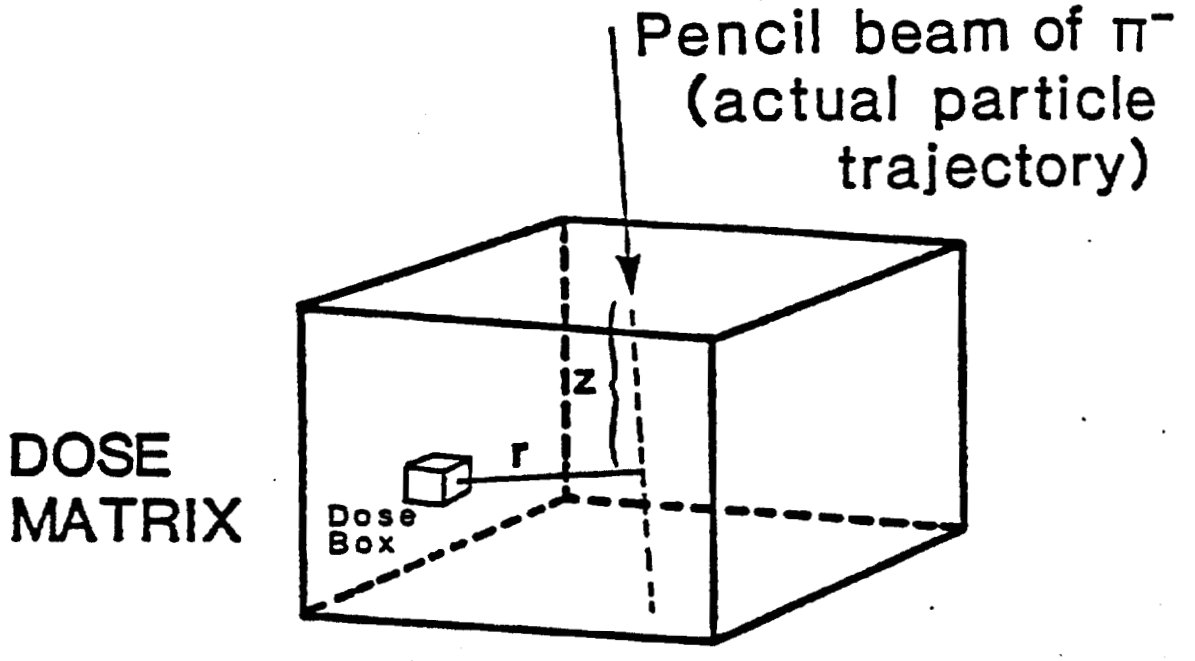

$$D_\pi(z) = N_\pi(z) \left(\frac{dE}{dz}\right)_\pi, \quad D_\mu, D_e \text{ ionizing collisions}$$

$$D_s(z) = \left|\frac{dN_\pi(z)}{dz}\right| \left\{ E_{local} + E_{long\ range} \right\} \text{ star charged products}$$

$$D_T(z,r) = (D_{\pi,\mu,e} + D_s)\, D_{ms}(z,r) + D_{neutron}$$

$$D_{ms}(z,r) = \frac{1}{2\pi\sigma_{ms}^2(z)}\, e^{-r^2/2\sigma_{ms}^2(z)}$$

FIGURE 1

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The contributions to dose of individual pencil beams are accumulated as they pass through various parts of the anatomy (determined by a CT scan) and clinical appliances. The dose distribution for a pencil beam is predetermined analytically in water as the sum of its separate components including the effects of inflight interaction and straggling. This dose is distributed in depth as a function of water-equivalent range along the trajectory, and radially as a function of multiple Coulomb scattering (which is both geometry and energy dependent). Distributing this dose entails accumulating at each point of interest the relative amount of dose at that point from each pencil beam.

Because the treatment beams contain spatially nonuniform ratios of pions, muons, and electrons, and because each particle type has a distinctly different dose distribution, separate calculations are required for each particle type. To model an actual beam then, requires an accurate phase-space representation of pencil beams. PIPLAN uses individually measured trajectories for each beam tune with the spatial coordinates, angles, momentum, and particle type identified.

Each pencil beam contains an analytic description of the dose deposited by a small bundle of monoenergetic particles. There is no statistical uncertainty in the dose deposited by a single pencil beam. However, there is statistical uncertainty in the distribution of pencil beams coming from the particle measuring process. The principal effect is variation in the isodose contours in the plane (x-y) perpendicular to the beam. Dose errors of about ±5% are present due to statistical variation in the flux of particles for the number of events in a PIPLAN calculation of reasonable length.

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To eliminate the statistical variations, a special subset of the beam trajectories is used. For each of the nine beam tunes used for treatments, a two dimensional dose scan is made in the x-y plane for the uncollimated beam in air. Particles are then selected from the measured tune tape so that the air dose distribution is reproduced. The procedure works by filling dose bins and rejecting particles that cause the measured air dose to be exceeded. When this same subset of particles, typically 25,000, is run in PIPLAN, the measured air dose is matched within 1-2%. Thus the air dose measurement becomes the primary beam information in the x-y plane. Multiwire counter efficiency defects and other biases are eliminated from this subset of chamber data.

Range Modulation

The nearly monenergetic pion beams used for clinical treatment result in a peak dose spread only about 3 cm in depth, FWHM. This is too small for most treatments. A mechanical device is placed in the beam that varies the amount of degrader the beam must pass through before entering the patient, which yields a spread-out stopping distribution in depth.

It has been found, for several typical range modulation functions, beam momenta, and clinical geometries, that the radial spread of a pencil beam at various depths in a phantom can be reasonably approximated (to within about 3 percent in relative probability amplitude) with either a Gaussian or an exponential function. Since normalization is required, only one variable is then required to describe the composite radial distribution at each depth for a given modulation function, beam momentum, and geometry. Since modulation functions are designed for each momentum and since the geometry for a given momentum is dominated by a collimator thickness and opening (air gaps), a one-dimensional table of distribution parameters can be precalculated and saved with each modulation function.

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The pencil beam library dose distribution can then be folded with the range modulation function to yield a composite library depth-dose distribution. This library can then be used to describe the distribution for each ray as if it experienced the full range-modulation function. The number of rays required for a given statistical uncertainity is independent of the modulation function.

Increased Resolution

A significant advance was accomplished within the calculational code of PIPLAN that improved the spatial resolution from about 5 to 10 mm on a cubic edge to a 2 mm resolution that is now typically possible. This was accomplished by utilizing the "Large-Core-Memory" (LCM) of the CDC-7600 where all the PIPLAN calculations are made. Expansion of the code into LCM resulted in a somewhat longer calculation time, approximately 25 percent, but which was considered to be a necessary step for the density resolutions that were required.

External Appliances

Typically, all primary and some secondary muons pass through the clinical collimators while pions stop near the distal surface and are captured by high-Z elements. More neutrons are produced from these captures than captures in tissue, but with a different energy spectrum. The collimator and neutron-dose models account for these effects with several adjustable parameters. Additionally, the relatively large air gaps between the collimator and bolus are taken into account with neutron propagation without attenuation.

The collimator is automatically designed by delineating the limits of the target volume on each slice, including adjustable margins and thicknesses. Cerrobend stopping powers are automatically adjusted to

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yield the desired effective-thickness from the finite number of collimator cells in the PIPLAN density-matrix. Life-size collimator templates, with calculated areas of interest, are produced on hardcopy output for collimator fabrication.

Bolus is designed with a parallel beam assumption using CT data and six different modes of alignment of modulated beam with the target volume. All clinical methods used in 2-D bolus design have been implemented, except with much better resolution. Life-size bolus templates are produced on hardcopy output for bolus fabrication.

Coordinate Systems

There is a basic reference system, fixed with respect to the patient, from which all positions and angles are measured. The reference system can be fixed in the most convenient relationship to the patient for each case. For example, it is most convenient to take the Z-axis in the supine patient's midline, with the positive end pointing toward the feet; and the X-axis horizontal, with the positive end toward the patient's left.

Sheets of contours, beams, and isodose maps are all fixed with respect to another coordinate system, the working system, whose origin may be displaced from the origin of the reference system and whose axes may make angles with the axes of the reference system. To relate these two systems, it is convenient to develop the tranformation that will carry the reference system of axes into the working system, regardless of the angle and position of the working system.

The first part of such a transformation is the rotation of the axes to the new angles; this is done in three stages and defines three angles. First is a rotation of the reference system about its Z-axis to give the

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primary system with X_1-, Y_1- and Z_1- axes (Fig. 2).

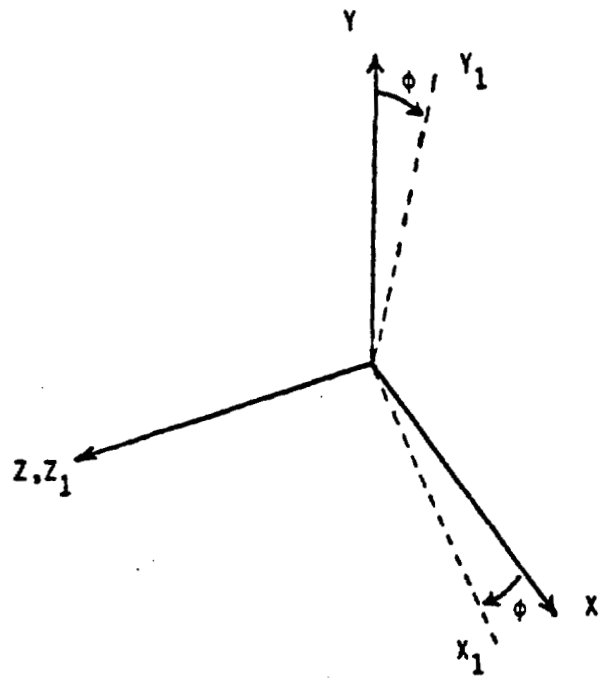

FIGURE 2

The angle of this rotation will be called ϕ. The rotation is positive if X rotates towards Y. Next, a positive direction of rotation of the primary system about its X_1- axis gives the secondary system with X_2-, Y_2- and Z_2- axes. This angle is called θ, and is positive when the rotation carries the Z_1- axis toward the Y_1- axis (Fig. 3).

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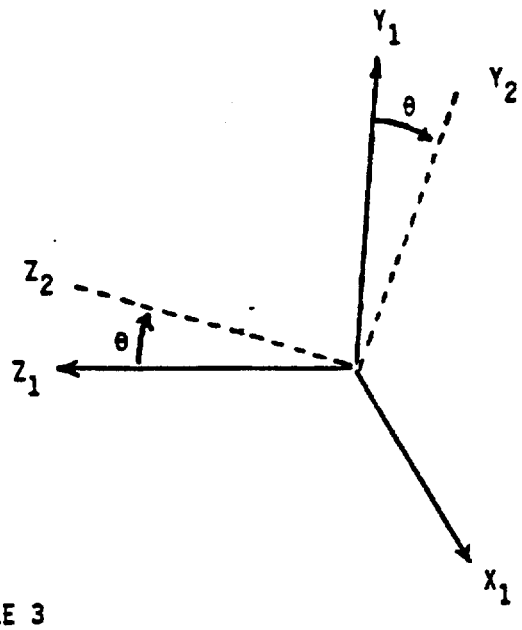

FIGURE 3

Finally there is a rotation of the secondary system about its Z_2- axis to give the tertiary system with X_3-, Y_3- and Z_3- axes. The angle is called β and is positive when the Y_2-axis is carried toward the X_2-axis. These rotations are illustrated in Fig. 4.

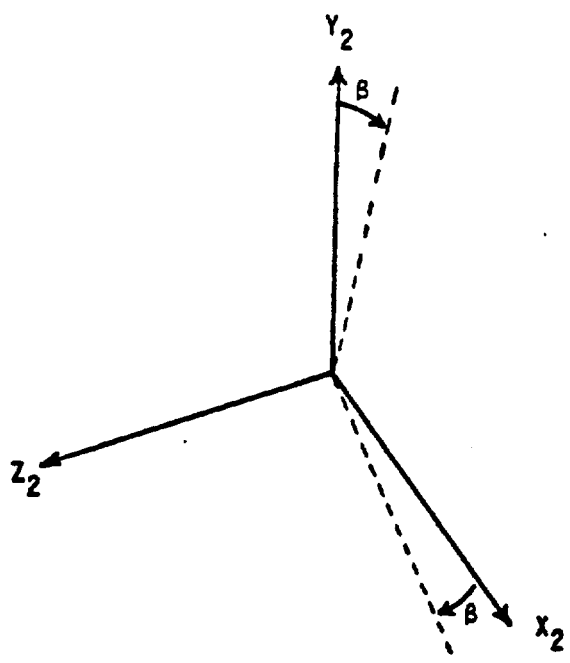

FIGURE 4

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To complete the transformation from the reference to the working system, displacement of the tertiary system without rotation is all that is necessary. The tertiary system origin is moved to the point X=x, Y=y, Z=z in the reference system without changing the angles of the axes; this gives the quarternary system with X_4-, Y_4-, and Z_4- axes. This is sufficient to carry the reference system to any system to any system of the same handedness, but for convenience, one redundant stage is added to the transformation. The quarternary system is translated along its own Z_4- axis to a point Z_4=s, finally giving the working system with X_w-, Y_w-, and Z_w- axes. The displacement of the origin and the translation along the Z_4- axis are shown in Fig. 5.

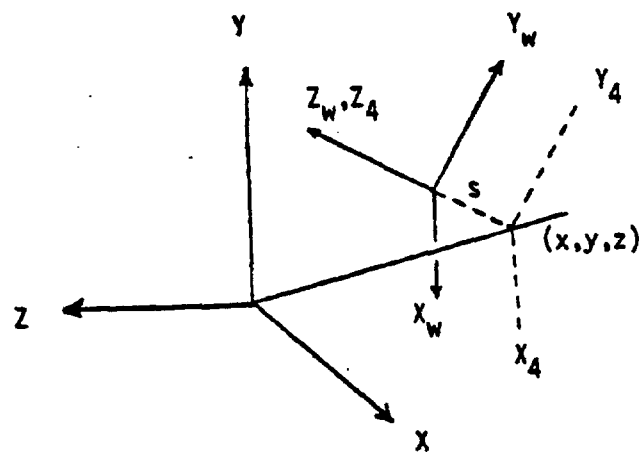

FIGURE 5

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The seven quantities x, y, z, ϕ, θ, β, and s define the working system's position and angle with respect to the reference system. The vector triplet x, y, and z are called the displacements; ϕ, θ, and β are the rotations, and s is called the scan distance. The scan distance is useful whenever a group of parallel planes occur, for example, in the entry of contours.

When entering contours from the digitizing table, it is necessary to relate position on the table to coordinates in the X-Y plane of the working system. This is done by digitizing two special points for each sheet of contours, the first will be at the origin and the second will be at the 20-cm point on the positive X-axis of the working system. This makes the digitized values independent of the position and rotation of the drawing placed on the table. Since the two points need not be 20 cm apart on the table, a magnified or reduced drawing can be used; the points should represent an actual 20 cm on the patient, however.

Summary

PIPLAN is a treatment planning system developed for pions, but with applicability to other radiation modalities. The structure is highly modular so that physics models for the calculation of dose from photon, electron, neutron, or other charged particles can be substituted for the pion models. It utilizes CT data on a pixel-by-pixel basis and accumulates dose in three dimensions.

The interested user is directed to the user manual for detailed descriptions of the extensive list of commands used for creating and calcula a case file. Patient privacy protection, archival storage of data and versatile graphics output are included in the PIPLAN system.

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