TREATMENT PLANNING - PROGRESS AND GOALS

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I. Introduction

The dose deposited by a negative pion along its path is well described by the conventional theory of energy loss of charged particles in matter. At the end of the pion's range, approximately 100 MeV of energy is released in the pion star.* The charged fragments that are produced account for ∿ 35 MeV of this energy, which is subsequently deposited more or less locally. Neutrons account for the remaining energy, which is deposited over greater distances and contributes significantly to whole-body dose. Thus, for a negative pion having a range of ∿ 5 cm in soft tissue, the energy deposited at the end of its path is about equal to the total energy deposited along its path. Also, the radiation emitted in the star has a greater relative biological effectiveness than that produced along the pion's path. Obviously, accurate information regarding the density distribution along the pion's path is required if the location of the large dose deposited at the end of its path is to be accurately determined. In terms of treatment planning, this means that the patient's anatomy, including inhomogeneities must be modeled in some reasonably accurate manner. Complications of finite beam emittance, non-point-source geometry, irregular beam profile distributions, beam contamination, momentum spread, straggling, multiple-scattering, all exacerbate the problem of determining the pion stopping region in a patient; they are all significant and can not be ignored. It is these factors that make treatment planning for negative pion therapy beams substantially more difficult than for the more

* The nuclear disintegration resulting from negative pion absorption by a nucleus is termed a "star".

conventional modalities, requiring a corresponding greater degree of sophistication.

In this report, the computer program PIPLAN, which is the basis of treatment planning development at Los Alamos, is described together with current beam model modifications being made for treatments anticipated in the near future. Possible dose distribution data input schemes are also discussed.

II. PIPLAN

A three-dimensional treatment planning code for pion radiation therapy, PIPLAN[1], was written some years ago at Los Alamos in anticipation of the radiotherapy program now being pursued. At the time of its writing, many assumptions had to be made without benefit of experience regarding the techniques that would be used for treatment; however, as a result of its modular design, in which separate functions are isolated in subroutines, accommodation of future changes in the therapy program was made possible. Although serious modifications are necessary in order to deal with the problems to be faced in the immediate future, PIPLAN remains the basic program for code development in treatment planning.

The requirement of performing routing treatment planning necessitates an interactive input-output operating system. To this end, PIPLAN, which presently runs on the large CDC machines has been split into three parts: an interactive input code, a calculational code, and an interactive output code. These three separate parts of PIPLAN are being modified to run on the BioMed control computer, utilizing special hardware not available on the large computers. The program is structured in such a way that the calculational code could be transported (e.g., by telephone link) to the Central Computing Facility (CCF) for fast calculation in all but the simplest cases.

The calculational algorithm of PIPLAN has a major drawback for initial patient trials - namely, it assumes a two-dimensional scan capability and

prescribes a vertical beam scan and a horizontal patient scan to deliver a uniform dose to a specified treatment volume. For the immediate future, we must have the capability of calculating dose distributions within patients (and phantoms) for a variety of static beams without patient translation. Thus, the calculational code of PIPLAN is now being modified to satisfy these requirements, while all of the input and output display capabilities are being retained.

The input-output display features will determine a treatment planning code's ultimate clinical utility. In PIPLAN, the relevant portions of a patient's anatomy are entered as contours on up to 30 parallel planes, each overlaid with a grid and oriented arbitrarily with respect to a patient-fixed reference system, thus providing a simulation of structures in three dimensions including density inhomogeneities. The contour data for a plane can come directly from a digitizing table or numerically from keyboard or punched cards. It is possible to select a plane, change its position in the parallel stack of planes, and add, modify, or delete contours.

A pencil beam can enter from any direction relative to the patient-fixed reference system, and it can have any weight of dose relative to other beams. The dose resulting from any particular beam can be divided into low- and high-LET fractions. The code also calculates the shape of bolus which may be placed in a beam to reduce the effect of patient surface shape and internal inhomogeneities between the beam's entrance port and the treatment volume.

After the dose distribution has been calculated, the results are displayed under control of input commands. The basic display is a map showing patient contours and isodose contours, but a dot-density display can be substituted. The orientation and position of the map are specified relative to the patient-fixed reference system. There is also a three-dimensional display of either

isodoses or dots that is viewed in plane projection from any direction which may perhaps be useful for producing stereoscopic images.

Typical examples of input and output displays are illustrated in Appendix A.

III. Beam Model

PIPLAN is capable of working with pencil beams of zero width; so, the actual beam must somehow be modeled as a sum of individual pencil beams. This will be done by randomly selecting particles from the multi-wire proportional counter (MWPC) history tape which gives the location (x,y), angle of incidence (θ,ϕ) and momentum (p) of every pion passing through an exit plane at the end of the channel for a particular beam. Each particle thus selected can represent a large number (e.g., 10^6) of pions - i.e., a pencil beam, and is dealt with separately by PIPLAN.

The dose distribution produced by a pencil beam of pions need be calculated only once and, so, can be done as elaborately as desired, including primary ionization, in-flight pion scattering (elastic and inelastic) and absorption, multiple scattering, range straggling, pion star fragments (including neutrons). Also, the ionization dose due to muon and electron beam contaminants must be calculated. Such an elaborate calculation can be carried out with an Oak Ridge-type Monte Carlo code for the central beam momentum p_o. For a particle selected from the MWPC tape with momentum difference $\Delta p = p-p_o$, the dose curve is simply shifted in range. If a ray is calculated to have entered a collimator, it is simply terminated and another ray selected. This approach is feasible because PIPLAN keeps track of the density of the material traversed by the pencil beam from plane to plane. Thus, if the depth is stated in g/cm^2 in the calculation, the dose deposited at a grid point on each plane along the ray's path is calculated accurately to first order. Of course the densities used in PIPLAN can be weighted by the effective stopping power of each material. The deposition of

dose in the radial direction from a given ray could also be calculated in g/cm^2 coordinates. The final dose is arrived at by simply summing the contribution at each grid point on the plane of interest due to all of the rays selected from the MWPC tape.

One obvious advantage of this approach is that because of the random selection of rays from an actual beam, the beam is accurately modeled to some approximation at any time during the calculation - the accuracy improving with the number of rays chosen. Thus, the calculation may be terminated at any time, yielding results that are valid to some approximation.

A disadvantage of this approach is that it will not be possible to generate MWPC history tapes from actual beams after the counters are removed (i.e., in the not-too-distant future). Consequently, we must anticipate the variety of therapy beams that would be used in the future and record the MWPC data at the appropriate channel-parameter settings before removing the counters. If it turns out that theoretical models of the BioMed pion channel are sufficiently accurate, MWPC tapes can then be generated theoretically at any time.

Patient scanning motion and vertical beam scanning can be incorporated when required. Large air gaps between ridge filters or variable energy degraders and the patient's body surface produce significant geometric distortions and can not be tolerated.

IV. Dose Distributions

There are at least three options available for inputting dose distribution data to PIPLAN. First, we can try to produce nearly monoenergetic, narrow beams of several energies and measure depth as well as radial dose distributions in various LET or RBE fractions. Depending on how much collimation is required, such an experiment may not be possible until a very intense pion beam is available. Also, the beam contamination introduced by the collimators may significantly

distort the results. In any case, manpower and time considerations probably make this approach impractical at this time.

A second option is an elaborate Monte Carlo calculation of the Oak Ridge type. Many such calculations have already been carried out[2], some including several LET fractions, range straggling, multiple scattering, and other refinements in various combinations. Certainly, we can get started with some existing calculation, and initiate another at a later time if necessary. The dose distributions can be stored for use in PIPLAN as two-dimensional arrays (depth and radial dependence in g/cm^2), one array per LET fraction. Such calculations have been tested by experiment to some extent; however, a calculation corresponding to our actual beam should be compared to dosimetry data to ensure greater confidence in this vital link of the treatment plan. We emphasize that such a lengthy (and expensive) calculation need be done only once for each therapy beam, not for each treatment plan.

Lastly, the dose distributions can be calculated analytically. This was the original intent in the design of PIPLAN. Indeed, the analytical model developed at Stanford[3] is contained in a subroutine of PIPLAN. We have compared results of Stanford's analytical model with those of Oak Ridge's Monte Carlo calculation (see Appendix B) and have consequently made some changes in some model parameters. We are presently incorporating range straggling and in-flight pion absorption to make a more realistic model. Since star neutrons are expected to deliver a non-negligible fraction of the dose to large treatment volumes[4], we have also included this effect in an approximate manner.

The analytical approach should not be abandoned even if the Monte Carlo approach is adopted since, for simple treatment plans, having an analytical subrouting may make feasible running PIPLAN entirely on the BioMed computer. The large arrays associated with the Monte Carlo approach must be stored in the larger-capacity CDC machines and, so, necessitate exporting the entire calcula-

tional code to the CCF.

V. Directions for the Future

Our immediate task with regard to treatment planning is to make the necessary alterations to PIPLAN to accommodate static rather than oscillating beams and to change isodose data from an input requirement to computed output. At the same time, the beam model described in Section III must be incorporated into PIPLAN. Monte Carlo-generated dose distributions must be tabulated and dove-tailed with the calculational code. With such modifications, PIPLAN should provide a very powerful tool for treatment planning for pion radio therapy at Los Alamos during the forthcoming patient trials. Modifications of PIPLAN to accommodate vertical and horizontal beam scanning can be made at a later time in anticipation of more complex treatments. Re-programming of PIPLAN to make it compatible for use on both the BioMed PDP computer and the CDC machines will continue.

Appendix A. PIPLAN Input-Output Displays

The input-output displays produced by PIPLAN are illustrated for an example of a tumor located in the head and neck of a patient. Figures A1-A4 show the development of the contour representation of the patient's anatomy in the region of interest. Figure A1 contains contour 1 which corresponds to the patient's surface shape in cross section at sheet (or plane) number 1, which happens to be located 39 mm above the origin of the patient-fixed reference system (the positive z-axis extends in a cranial direction, the x- and y-axes extend to the right and ventrally, respectively). The interior density is assigned a value of 100. Sections of the mandible, contours 2 and 3, are then added, followed by the hard palate, contour 4. This stage is shown in Fig. A2, where the interior density of contour 4 is assigned the value 174, corresponding to bone. After the remaining inhomogeneities intersecting sheet 1 are modeled, we proceed to sheet 2 which is located 25 mm above the origin. Figure A3 depicts sheet 2 after contour 9, corresponding to the bodies of the second through fourth cervical vertibra· treated as one piece of bone, has been added. As a final example, Figure A4 shows sheet 5, located at z=-14mm, after the treatment volume, contour 13, has been added to the left of the pharynx. The density input is ignored since it is assumed identical to the surrounding volume.

Figure A5 shows the direction of the beam viewed from above (left figure) and from the right (right figure). The beam emerging from the paper is shown rising in the right figure. In Figure A6, a second, opposing beam has been added. In this example, the single-beam treatment was saved for comparison as Plan 2, and Beam 1 was increased in weight to 140 for Plan 1 - the opposing-beam treatment. The BOL command adds material to each beam ray so that they all have the same total stopping power between the entrance port and the treatment volume.

For each plane of the longitudinal scan there is one display showing each cylinder of stopping pions (assuming a vertically scanned beam, of course) with its entrance dose and the bolus for each entering ray. Such displays are illustrated for each beam, corresponding to the location z=-25mm, in Figures A7 and A8, respectively. The bolus required for each entering beam in this plane is shown at the top of each figure.

The results are illustrated in Figures A9-A14. Isodose contours for sheets located at z=+24mm, +11mm and -23mm are shown in Figures A9-A11. The dose levels corresponding to the contours are given to the left. The contour map of the plane at right angles to the beam directions and passing through the center of the treatment volume is shown in Figure A12.

We have said nothing regarding the handling of administrative data nor of the commands necessary to generate the displays described above. The reader is referred to Reference 1 for these details.

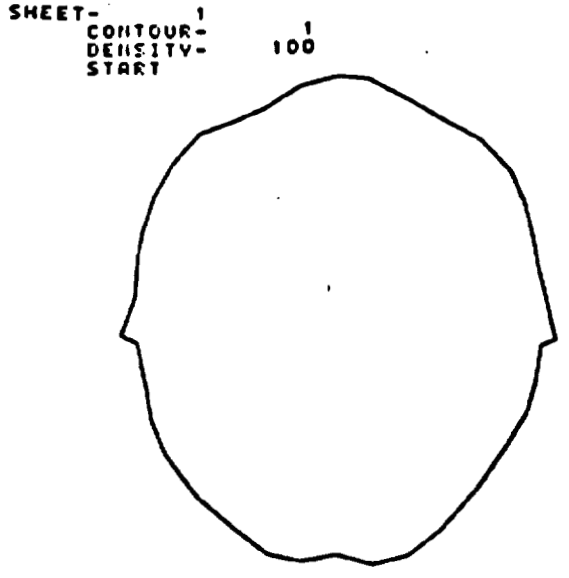
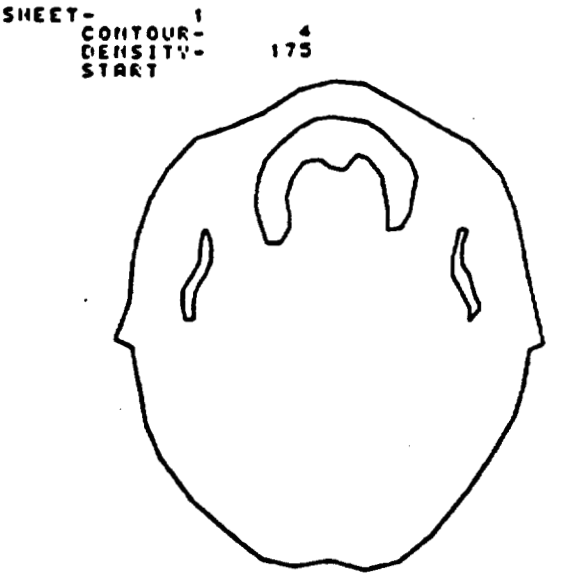


Figure A1



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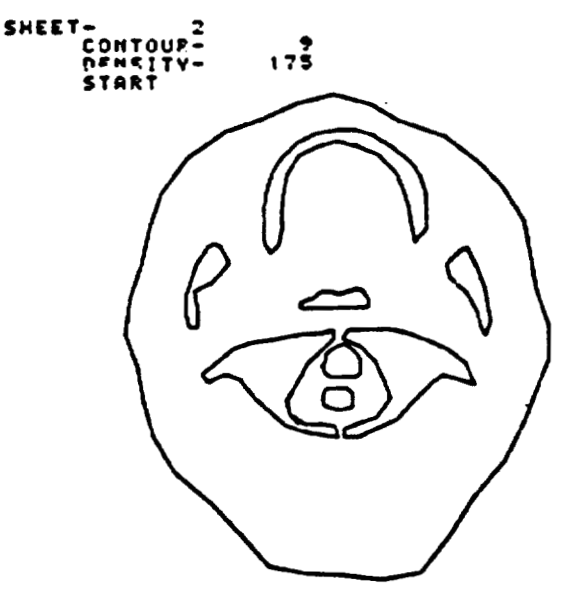

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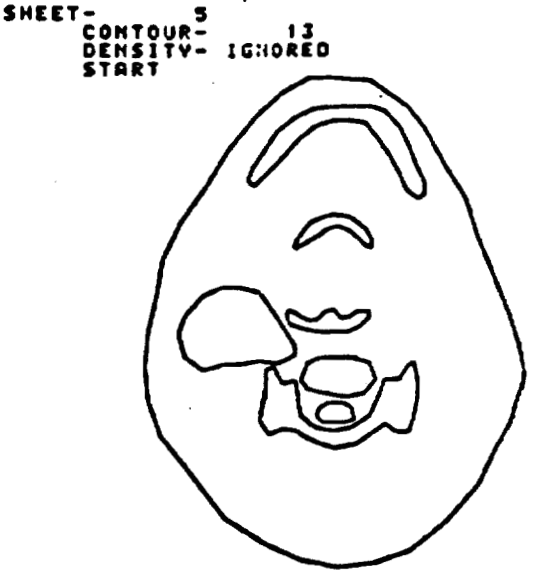

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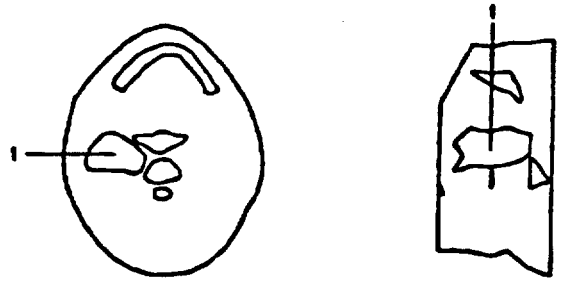

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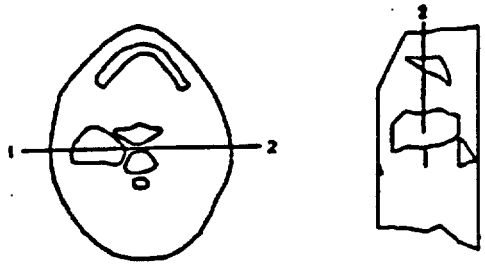

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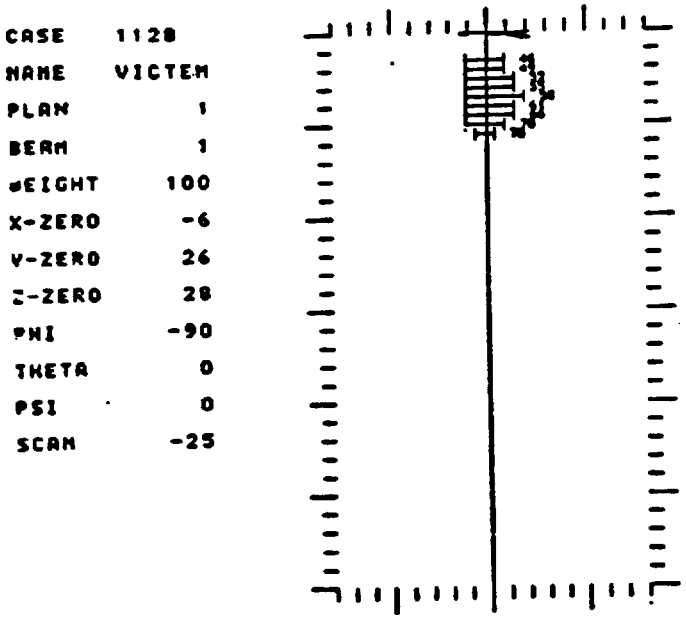

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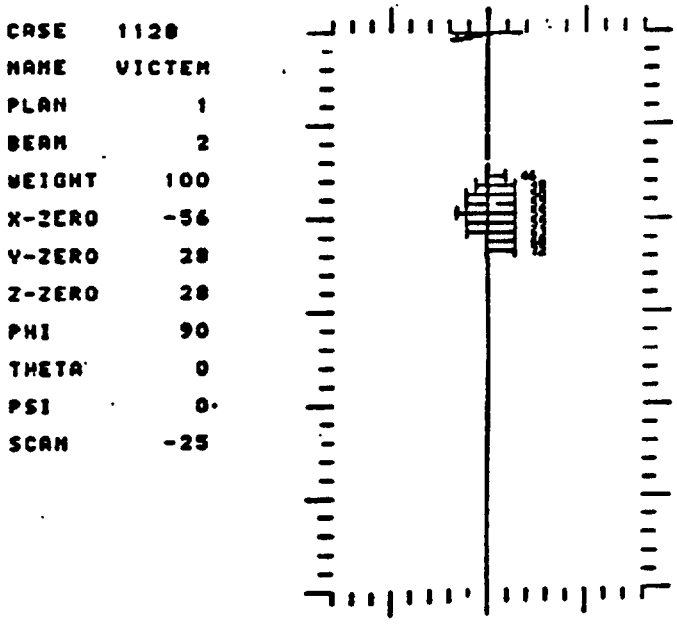

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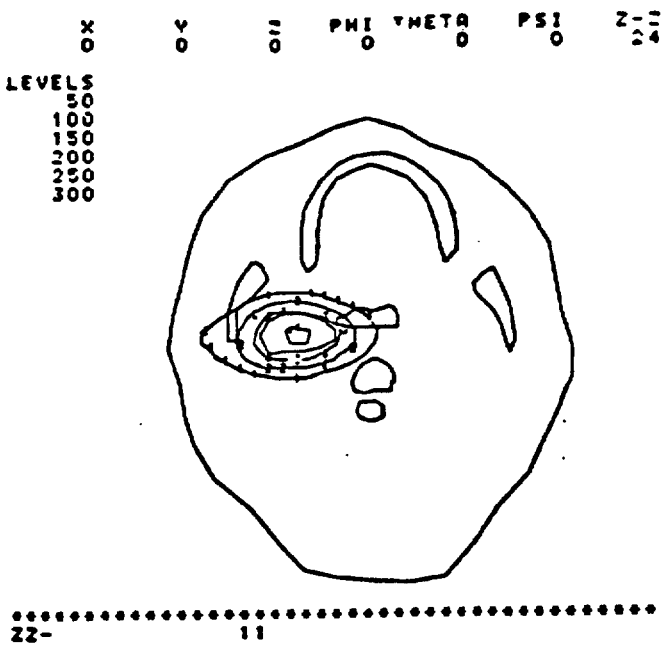

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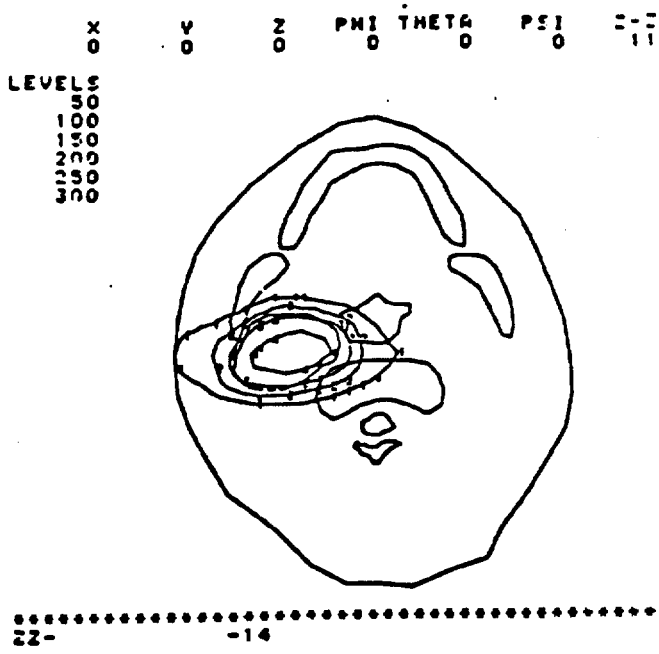

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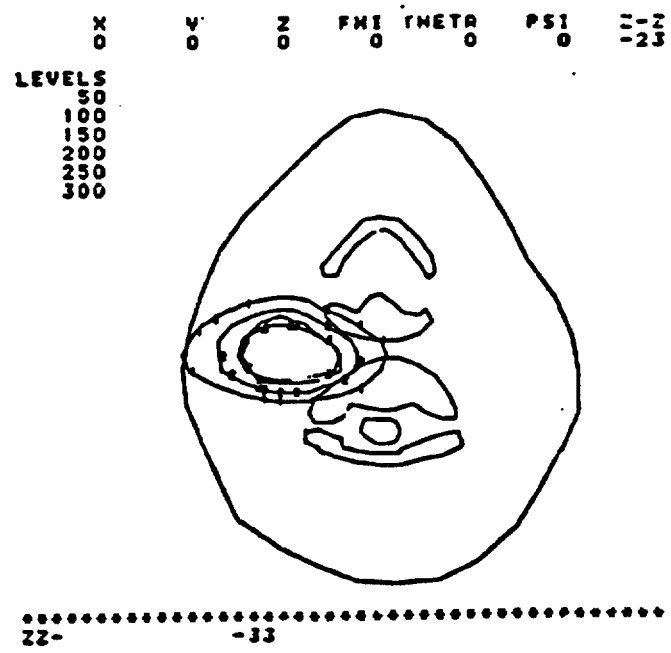

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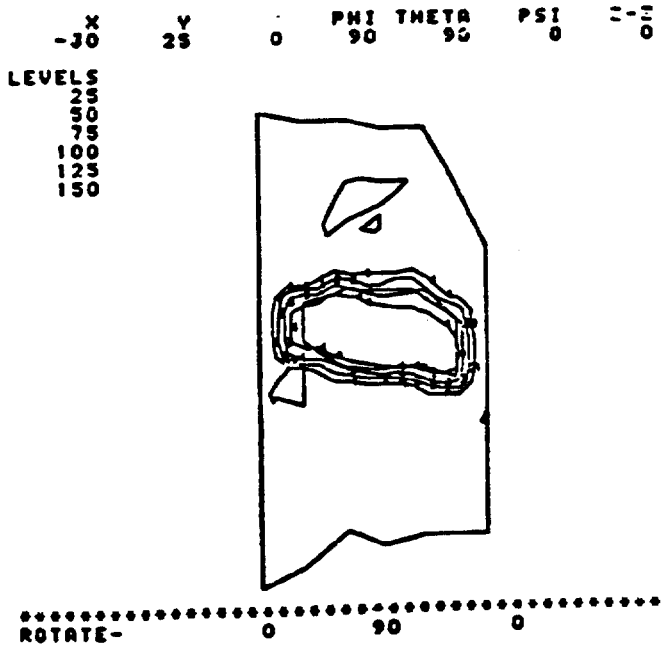

Figure A12

Appendix B. Comparison of Analytic and Monte Carlo Dose Calculations

Using the analytical model developed at Stanford[3], we have tried to fit the results of an Oak Ridge Monte Carlo calculation[2] of the dose distribution in tissue due to a monoenergetic pencil beam of negative pions of 172 MeV/c momentum. The analytical model contains the following features for pions: (a) exponential beam attenuation; (b) range straggling, as it affects the stopping distribution; (c) multiple scattering; and (d) in-flight absorption given by star charged particle energy plus a constant fraction of kinetic energy. This model does not deal with range straggling in the determination of ionization dose nor does it include the dose due to star neutrons, which is small for all but large ($\gtrsim$ 1 ℓ.) treatment volumes.

The Monte Carlo calculation is rather complete in what it includes; however, the results are certainly affected by the sophistication of the physics used within the code to deal with the nuclear and Coulomb interactions. In this respect, the code used (HETC) is something of a "black box" to non-users of the code. One attempt to compare an experimental depth-dose curve with an Oak Ridge calculation - the parameters of which did not exactly match the conditions of the experiment - proved to be reasonably successful[5]. However, much more detailed comparisons should be made in the near future.

In Figure B1 we compare the Stanford analytical model with the Oak Ridge Monte Carlo calculation for both total dose and primary ionization dose for a pure pion beam. We have integrated over radial distributions. The Stanford parameters are used: beam attenuation, z_o=46 cm; range straggling, z_1= 0.027 R_o (where R_o is the incident range); and star charged particle energy, E* = 30MeV. As can be seen, the agreement in the peak region is not at all good. We then changed these parameters to the following set: z_o= 70 cm, z_1 = 0.019 R_o, and E* = 38.1 MeV. As can be seen in Figure B2, the improvement is considerable,

although the tails of the peak are still not well matched. While each of the three changes produced significant effects, the addition of a star neutron dose originating in the peak was insignificant. An attenuation length of 46 cm is rather small, 70 cm being the approximate geometric mean-free-path. Monte Carlo-type calculations indicate a star charged particle energy of 38.1 MeV; however, an early experiment[6] yields a value of about 30 MeV. A more recent experimental value is clearly needed. Although a straggling parameter of $\sigma \simeq .03\ R_o$ is commonly used, the parameter z_1 occurs in a different expression, which, when compared with the Gaussian expression containing σ, yields the value $z_1 = 0.019\ R_o$.

Presently, we are including range straggling in the ionization loss to try to produce a smoother primary ionization peak. Also, we are looking into an accurate treatment of in-flight absorption to replace the current prescription of adding 1/3 of the pion's kinetic energy to E* to obtain the energy of charged particles produced in flight from stars.

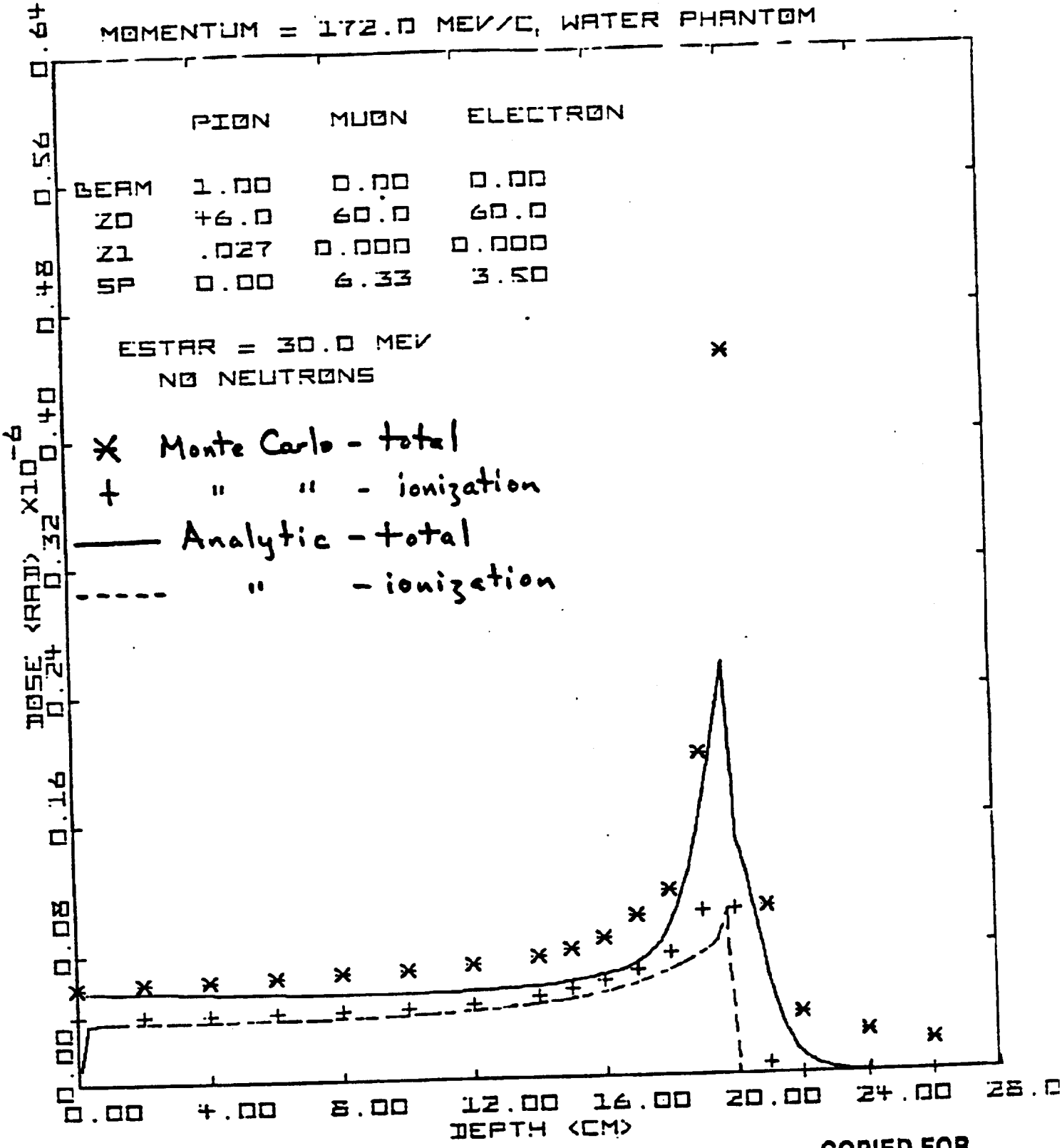

Figure B1

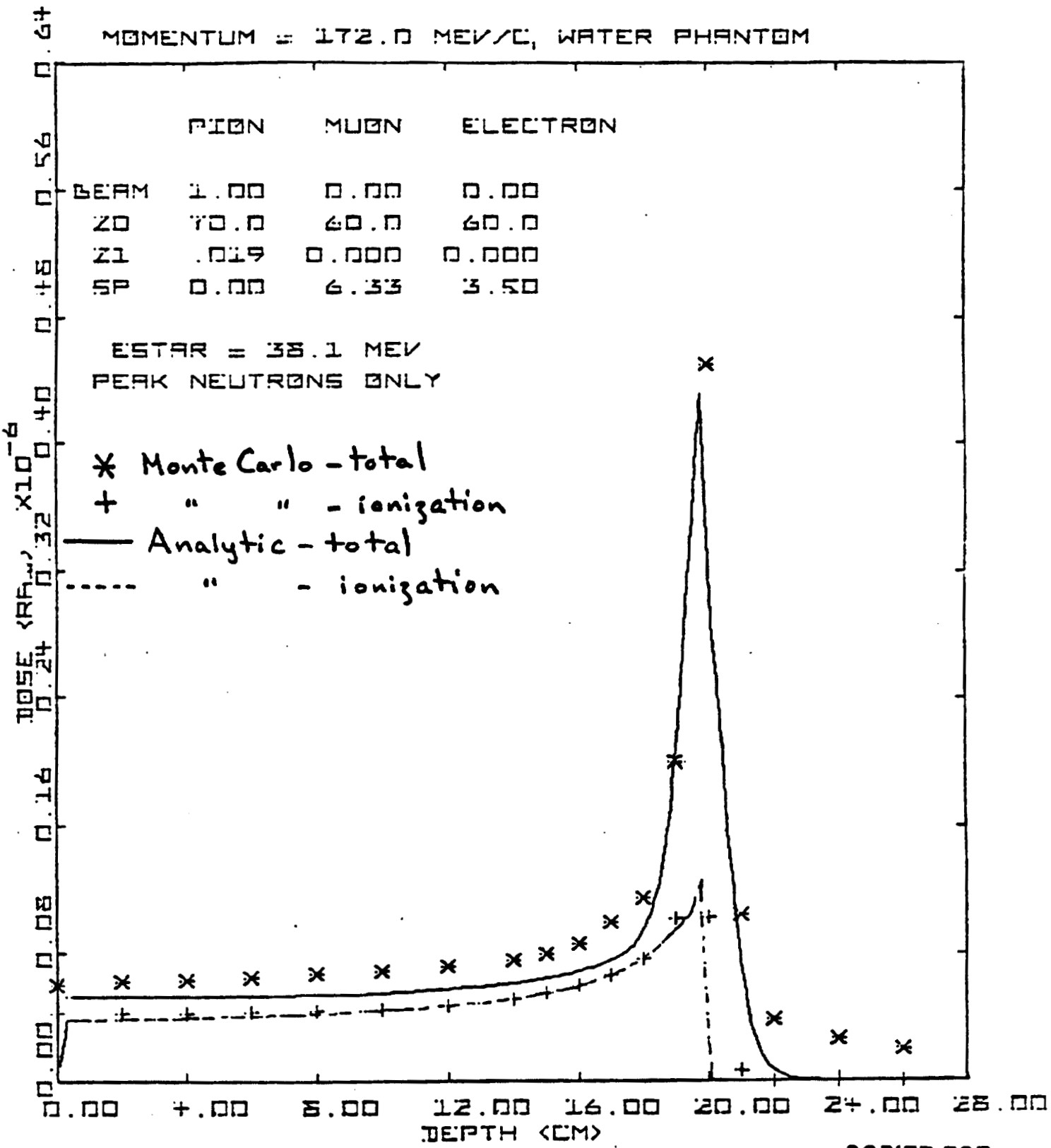

Figure B2

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3. G. C. Li, D. Boyd and H. A. Schwettman, "Pion Dose Calculations Suitable for Treatment Planning", Phys. Med. Biol.19, 436 (1974).

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5. J. F. Dicello, private communication.

6. P. H. Fowler and V. M. Mayes, Proc. Phys. Soc. 92, 377 (1967).