Prism User's Reference Manual
Version 1.5

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Contents

Chapter 1

About this manual

This manual describes the user interface and user level functions of Version 1.5 of the Prism Radiation Treatment Planning system. It is both a reference manual and functional specification. It is not an introduction to how to use Prism for radiation treatment planning, nor a description of the software design or internal details. For details about the design and implementation of the Prism software, the reader is referred to a separate implementation report [1].

1.1 What you need to know

Readers of this reference manual should already have a basic familiarity with radiation treatment planning, and the way in which the Prism software helps to accomplish this job. To read Chapter 4.1, you should be familiar with the variant of the Unix operating system you are using, the basic concepts of the X window system [2], elementary Common Lisp, and how to install the required Common Lisp software.

1.2 What this manual includes

Included here are a specification of:

- the capabilities of the system,
- its inputs and outputs,
- the computing environment and configuration, and
- the graphical user interface (the control panels).

The information in this report supercedes that contained in all previous reports describing the Prism system capabilities, functions, and user interface.

Chapter 2

Capabilities, inputs and outputs

2.1 Functional capabilities

The Prism system provides the following capabilities:

- Enter, edit, display and store demographics, clinical findings and other information about patients,
- Display and process stored images, including reconstructed sagittal and coronal images (the import of images into the Prism system is done using the Prism DICOM-3 Server system, described in another report [3]),
- Enter, edit, display and store 3-D patient geometry including internal structures and locations of points of interest, based on anatomic data represented in stored image studies, or in films and tracings on paper,
- Enter, edit, display and store 3-D treatment plans consisting of collections of radiation sources including external radiation beams as well as line sources and seeds (brachytherapy),
- Generate and display “digitally reconstructed radiographs” (DRR) or “simulated port films” from stored image studies and treatment beam parameters,
- Prescribe treatments by several different methods, including specifying doses to be delivered by particular radiation sources to specific anatomic points, and specifying the dose to be (nearly) achieved throughout extended volumes,
- Calculate doses at points and/or in 3-D volumes, display doses as isodose contours superimposed on anatomy and markers (“landmarks”), and store computed dose distributions for subsequent display, analysis and comparison, by using external utilities such as the products of the NCI RTPT project.
- Produce hardcopy output presenting the data and/or results of all the preceding operations, in graphic form when appropriate (including images — the system can produce hardcopy of gray scale or color images together with all the color graphics, if a color PostScript printer is available),

- Save treatment setup data for subsequent download to computer controlled accelerators, using DICOM-RT.

All capabilities can be invoked and operated interactively at a workstation.

Capabilities will be provided in different configurations to support different applications. For production clinical work there is a configuration that provides a stable collection of operations and is easy to use. Different configurations will support research and development.

2.2 Components and products of the planning task

From the clinical user's point of view there are several different components that the user must enter, acquire or create in the course of the planning task. Each component may be stored in the planning system between planning sessions and will remain there to be recalled as needed until some special operation is performed to remove it.

Case The identifying information, clinical findings, anatomic data and points of interest associated with a patient in a particular treatment position for a series of treatments. If any of the anatomic data are derived from images, the case can be also associated with a particular image study.

There may be more than one case associated with a patient (e.g. if anatomic data derived from different image studies are used, or if the same patient returns with different clinical findings after completing one course of treatment). Or there may be several successive but distinct cases derived from a single image study (e.g. as more contours are entered).

A case may include as a component a list of one or more plans.

Image study A set of image data (a series of related 2-dimensional images collected in a single imaging session, with the patient in the treatment position).

There is never more than one image study associated with a case. However, a given patient may have multiple cases on file, as well as multiple image studies.

Image studies are optional, in the sense that it is possible to create a case and treatment plans from which doses can be computed even if there is no image study available, for example by entering contours from a digitizer. A single image study may be associated with more than one case, as different subsets of anatomy may be drawn on the same set of images.

Plan A collection of radiation sources associated with a particular case, along with a dose calculation region. A plan usually includes one or more isodose levels. Typically there will be several (or many) plans created for each case.

From the clinical user's point of view there are several products that can be produced, once a plan has been created:

Chart Text that briefly summarizes a plan, which can be printed and enclosed in the patient's chart. The chart identifies the patient case and plan, with sufficient information to differentiate it from all other plans and cases for the same patient. The chart may contain additional information about the case. It identifies and describes all the radiation sources, including beams, line sources and seeds. It shows the total dose delivered to each point from all sources (including external beams, line sources and seeds), and also the dose delivered to each point from each external beam. The chart may contain additional optional information, such as the coordinates in the patient coordinate system of the points of interest and line sources and seeds.

The charts produced by the Prism planning system are described in section 2.6.

Plot A line drawing of a view of a plan. A plot can show everything described in section 2.5, on a color PostScript printer, and everything except images on a pen plotter. In addition, the plot can be produced at any specified magnification (e.g., actual size, exactly one-half actual size, etc.) relative to the patient, not the size on the display.

The plotted output contains additional information, not present in the view. In the upper left corner, department ID (see sections 2.6 and 4.2), patient name, plan name, plan time stamp and plot magnification are printed. In the upper right corner, the Prism logo and version number appear. At the bottom is the text describing the position and orientation of the pictured plane, the maximum dose, the grid size, and the isodose levels. In the case of a beam's eye view the beam name appears below the orientation, and no isodose contours are included.

Dose contours on the plot are color coded as on the view display, with a few exceptions (yellow and white on the display are black on the plot). The list of isodose levels is similarly color coded to provide a key. The dose level numbers are drawn on the isodose lines on the display or plot. Points of interest that have been specified as "invisible" do not appear on the plot. When points do appear, their labels are as close as possible to the actual point location. Image data, such as CT gray scale data, will appear on plots produced for PostScript capable printers (this includes printers that are supported by a PostScript filter such as the `ghostscript` program).

Dose distribution The 3-D dose distribution array calculated for a particular plan may be written out to the Prism file system for further analysis and display.

Other items Additional software tools such as those provided by the Radiotherapy Treatment Planning Tools Project may produce additional outputs. They are described in their separate manuals.

Charts and plots can be produced from a plan quite rapidly, so the system does not provide any way to store these. A temporary file is created, and it is queued to a printer or plotter. It is not automatically deleted. However, subsequent printing and plotting operations may overwrite the file. Dose distributions may take an appreciable time to calculate, but nevertheless, in general we do not expect to store dose distributions because they take up a large amount of disk storage, and there are design problems in consistently saving and restoring a stored dose distribution with a plan. A plot can be produced without having computed a dose distribution, in which case, no isodose curves will appear on the plot.

2.3 The shared treatment planning database

A list of patients and the corresponding stored image studies, cases and plans constitutes a treatment planning database. A database can be shared among a group of users, so that when any user in the group stores something in the database, it becomes available to other users in the group.

There may be several such databases for different groups of users (e.g. the actual list of patients for whom clinical planning is done, which is shared by the dosimetrists, clinical physicists and physicians; a list of cases for testing and demonstrations which is shared by researchers and software developers etc.). In general not all databases will be available to all users, but some users may have more than one database available to them.

The Prism system determines where to find each database from variables that are set when the user's Prism session starts up. This is customizable by each user and is further described in section 4.2.

For each patient, there may be several (or many) stored image studies, cases, and plans. Users may produce charts and plots from any of these at any time. It is important that the system maintain the correct correspondences between these items (e.g. which plans are associated with which cases, etc.) and that users can easily tell which stored plans (etc.) correspond to a particular chart or plot. These problems are solved in the following way:

Each chart, plot and stored dose distribution is associated with a single plan. Therefore, each chart and plot are clearly labelled with the patient identification (name and unique identifier created by the system), and a unique plan identification. The unique patient case identification is a time stamp assigned by the system and updated each time the patient case data are changed in any significant way (see page 90). Similarly, the plan identification is also a time stamp assigned by the system and updated each time the plan is changed in any significant way (see page 102). Users may include other information in the plan to help identify it (e.g. descriptive text), but the time stamp can always be used to distinguish one plan from another (very similar) one. In particular, users can retrieve the stored plan that was used to produce a particular chart or plot, if in fact the plan and its case were stored in either the checkpoint database or shared database.

Each plan is in turn associated with a single case, and (possibly) a single image study. The system stores these correspondences internally in the file system and in working memory. Selecting a plan is only possible through prior selection of the corresponding case. To derive anatomic data for a case (i.e., organ, tumor and target contours), a user may select any of a patient's image studies, and to create a plan, a user may select any of a patient's cases.

2.4 Dose computation

This section describes what can be computed by the dose computation program. The algorithms and physics are described in another report [4].

2.4.1 Types of radiation sources

The system can compute doses from external beams composed of photons, neutrons, or electrons, as well as from radioactive line sources or seeds.

For external beams, both fixed fields and arc treatments are supported. An arc treatment is simulated by computing a series of closely spaced fixed fields, in effect performing a stepwise numerical integration over gantry angle. Arc therapy capability includes all external beam types, photon, neutron and electron.

The following types of collimation systems are supported for both photon and neutron beams:

- Symmetric rectangular fields created by standard collimators.
- Asymmetric rectangular fields created by variable-jaw collimators, as long as no collimator jaw crosses over the central axis ("over-centering").
- Irregular fields created by multileaf collimators (MLC), including over-centered leaves that cross over the central axis.

Any number of shielding blocks may be combined with either the symmetric or asymmetric rectangular types of photon fields, but not with MLC fields.

The electron beam dose computation model supports rectangular electron fields created with applicator cones that are provided by the accelerator manufacturer, and *with* blocking formed by metal cutouts.

Any of these fields may be oriented using any available therapy machine motions, including collimator rotation and couch rotation. In other words, fields may be arbitrarily oblique. Any field (including oblique fields) may be an arc (or moving) field. Any type of field may be combined with any other type in a plan. For photons and neutrons, the isocenter may be outside the patient, i.e., treatment setups at "extended SSD" are supported, but the central axis of the beam *must intersect* the patient volume somewhere. Setups where a beam central axis projects past the patient without intersecting it are *not* supported.

Note that if there is no skin outline or the skin (or "external contours") is not assigned a density, the Prism dose computation will fail, and the user's session may be aborted unexpectedly.

There is no theoretical upper limit to the number of fields (including arcs) that may be included in a plan. In particular, it is possible in principle to model conformal therapy plans that include scores of fields. Available system resources (virtual and physical memory, cpu speed) may, however, introduce practical limits at run time.

The following types of brachytherapy sources are supported in the Prism system:

- point sources (seeds)
- (uniform) line sources

A variety of isotopes and activity levels may be modelled, by entering the appropriate specifications in the Prism source catalog. Chapter 15 describes the facility for entering a source into the Prism source catalog.

Source locations in the patient may be entered into the system from orthogonal films, using the digitizer or the workstation keyboard.

Any number of line sources or seeds may be included in a plan, and all these radiation source types (external beam, line source and seed) may be combined arbitrarily in a plan.

2.4.2 What the system produces

On demand, the system will compute the doses to some set of points from all the radiation sources in any plan created by the user for the current case (consisting of anatomy and other data). It is possible to create multiple plans for a given case. This is described in more detail in following sections. Two options are provided regarding the collection of points at which doses are calculated:

1. the (small) set of (arbitrarily located) points of interest in the plan, and,
2. the 3-D array of points in a rectangular volume.

The first option is fast and is provided to support rapid interactive optimization of plans. The system calculates the dose to each of the points of interest explicitly, rather than interpolating them from doses calculated on a regular grid. This improves accuracy and makes it possible for doses to be calculated at points that lie outside any pre-defined calculation grid.

The second option calculates 3-D dose distributions. The calculation grid may be located anywhere in the patient volume and its length in the X, Y and Z directions can be varied independently (e.g. it is a “rectangular prism” of any width, length, and height). The user can specify the resolution (distance between grid points) by selecting one of three standard grid spacings. The same spacing is used in each direction. The grid is always oriented parallel to the patient coordinate system; it is never oblique or “tilted”.

The computation creates a separate dose array (or list, for points of interest) for each radiation source (e.g field). In the case where the only change in a plan has been to the strength or weight of one or more sources, the Prism system computes the new dose distribution by simply scaling the previously computed arrays and summing them together to form a new combined dose array. This permits a plan to be “renormalized” or “differently weighted” very rapidly.

On demand, the system can save a computed dose distribution in a file for subsequent processing or analysis. This is a temporary storage, not archival for later retrieval. The data in this temporary file can be used by external software tools such as those from the RTPT project.

2.5 Graphic displays

In this section we describe the graphics that may be displayed on the workstation. In order to describe and implement these, we have chosen some coordinate system conventions. Chapter 3 specifies the Prism system conventions for the patient coordinate system and the other coordinate systems, for the anatomy, beams and views, and transformations between them. The conventions used in Prism for gantry angle, couch angle and collimator angle are also specified there.

The relation between the Prism machine settings and the actual machine settings for various machines is described in detail in Appendix A.

The system displays these kinds of objects:

1. Anatomic structures
2. Tumor volumes
3. Target volumes

4. Points of interest, including labelling text
5. Beams (including blocks and wedges)
6. Line sources and seeds
7. Dose calculation regions
8. Dose distributions
9. CT or other image studies

It is possible for the user to have these objects displayed in several kinds of views on the display screen as well as plotted on a hardcopy device. The system provides these kinds of views:

1. Transverse views
2. Sagittal views
3. Coronal views
4. Beam's-eye views (only for plans in which one or more external beams is present)
5. Oblique views (only for brachytherapy sources)
6. Room views, showing solid model visualization of organs and other objects (work in progress, not fully functional, and not described yet in the following sections)

Each kind of view (except the room view) is described in greater detail in the following sections. The way in which these views are created is described in section 13, the plan panel. The view control panel is described in section 16. In addition, the manual editing functions provide temporary views of the data for use in the editing operation.

2.5.1 Transverse, coronal and sagittal views

The transverse, coronal and sagittal views are treated similarly. Each view, except the room view, is characterized by a *viewing plane,* which is specified by the plane's Z, Y, or X coordinate in the patient coordinate system for transverse, coronal and sagittal views, respectively.

The patient is modeled in the *treatment* position. The patient coordinate system is really associated with the couch, and does not invert if the patient is prone rather than supine.

The transverse view is oriented in the conventional way for transverse CT studies, with the $+Y$ axis pointed up and the $+X$ axis pointed to the viewer's right. Thus this view shows the cross section as seen looking toward the gantry from the end of the couch.

The coronal view is oriented with the $-Z$ axis pointed up and the $+X$ axis pointed to the viewer's right, so a coronal view of a supine patient's head is oriented as in a conventional portrait, viewed from front to back. If the patient is prone, the view is from back to front, i.e., the view is looking down on the couch from above.

The sagittal view is oriented with the $+Z$ axis pointed to the right and the $+Y$ axis pointed up, so a sagittal view is oriented as if the viewer were seeing a supine patient from the patient's right, with the head towards the viewer's left. If the patient is prone, the view still shows the head towards the viewer's left, as seen from the patient's left.

Views are initially scaled and positioned so that the contents appear appropriately centered and sized, but this is only approximate. The goal is to have the contents sufficiently fill, but do not exceed, the available display area and roughly the same amount of surrounding blank space appears on the right as on the left, and on the top as on the bottom. This is done automatically by the view creation process, but the algorithm is simple and may not always create the best presentation. Once displayed, views may be manually rescaled and also "panned" (i.e., the origin may be moved).

Objects are depicted as follows:

Contours Contours that lie in or near the viewing plane are drawn as connected line segments. In this context, "near" means within some small distance, i.e., a fraction of a millimeter, to accomodate round-off errors in determining or specifying plane positions.

Contours that are not parallel to the viewing plane but that intersect it are indicated by markers at each point of intersection.

All the contours of an anatomic object are the same color in all the views, but contours corresponding to different objects may be of different colors, including "invisible".

Points Points of interest that lie within 0.01 mm of the plane of the view are indicated by a marker centered on the point, optionally accompanied by the point number.

Beams Each beam is depicted by showing the intersection of the beam portal, as defined by the collimating system, with the view plane, as described in [5]: if the beam central axis is in the view plane, diverging fanlines are drawn; an oblique rectangular beam appears as an elongated lozenge, etc. Electron beams are also depicted in the same way, using the portal defined by the cutout plate and the collimating cone.

Blocks Blocks are depicted using a method similar to that of beam portals. Individual blocks may be shown in different colors than their beams and different from each other.

Isocenter The beam central axis and isocenter are displayed in the same color as the beam portal, as follows: the intersection of the beam central axis and the view plane is shown as a +, unless the beam central axis is coplanar with the view plane (within 0.01 mm). In the latter case, the isocenter is shown as a diamond shape, and the central axis may be shown as a line with centimeter tick marks on it. If neither the + nor the diamond is seen, the beam central axis does not intersect the view plane.

Wedges A wedge, if present, is drawn in the same color as the beam portal, and is pictured to make it easy to identify the direction of the wedge gradient. The *shape* and *orientation* of the pictured wedge is determined by the direction of the wedge gradient. This gradient is defined by a vector in the collimator coordinate system that points toward the toe of the wedge and always lies on one of the four collimator coordinate system axes $+x$, $-x$, $+y$, $-y$ (which one depends on the wedge rotation angle). The wedge shape is determined by projecting this vector into the view plane (using the usual 3D transformation techniques). The wedge is shown as an isosceles triangle with one angle at the point (toe end) of the projected vector and its unequal side at the heel end of the projected vector. The length of this heel side is chosen so the triangle appears long and sharply pointed when the wedge gradient vector is parallel to the view plane. As the angle between the wedge gradient vector and the view plane increases, the triangle will appear shorter. The *location* of the pictured wedge is determined by projecting the beam's central axis ray (starting at the beam source) into the viewing plane. If the projected location of the beam source lies outside the viewing window, the wedge is pictured on the ray just inside the window border. If the projected location of the beam source lies inside the window, the wedge is pictured at that location (the beam source).

Dose Calculation Region The rectangular prism enclosing the calculation grid may intersect the view plane, determining a rectangle. The corners of this rectangle are indicated by "angle brackets". The length of the vertical and horizontal legs of these angle brackets are equal to the grid spacing in those directions (according to the current scale of the view).

Dose Distribution Dose distributions may be shown as isodose contours. Contours corresponding to different dose levels may be different colors. These may optionally be displayed if a dose array corresponding to the current plan, and intersecting the plane of the view, is available. It is not necessary that the grid points of the the dose array lie exactly on the view plane; if two dose array planes lie on either side of the view plane, the doses in the view plane are determined by linear interpolation. Each dose contour displayed is labelled by the corresponding dose value, and by the color, with a color/dose key on the plan panel. The dose shown is the total dose for the specified monitor units from each beam. If you adjust the monitor units so that a specified point receives a dose of 100.0, then the isodose levels effectively represent percent of dose to that point. Other methods for visualization of dose distributions may be provided as experimentation demonstrates their feasibility and usefulness.

CT Studies These objects must be handled differently in the three views. In each case, the display of image data is at the user's option. In a transverse view, a CT image whose thickness includes the viewing plane may be displayed. A coronal view on the other hand may render a reformatted image created by selecting and replicating appropriate horizontal raster lines from each transverse (axial) image in the study, while a sagittal view perform the same type of reconstruction on appropriate vertical lines of pixels from transverse images.

Line sources Line sources are depicted in all views except beam's eye views, whether in the plane or not, projected to the view plane, with dashed texture indicating the part of the line that is behind the viewing plane. They are optionally labeled by numbers. (When displaying line sources, if we use the dashed line style to indicate "behind the view plane" we need to be sure the ends are solid, not an invisible part of the dashed line.)

Seeds Seeds are also depicted in all views except beam's eye views, whether in the plane or not, projected to the view plane, as plus signs if in front of the view, as minus signs if behind the view, and as small circles if within 1 mm of the view plane. Seeds may optionally be labeled with their numbers to the upper right of the symbol.

2.5.2 Beam's eye views

These views are drawn to show the anatomy and other information as seen from a viewpoint at the virtual source point of a particular beam in a plan. The view plane is the plane through the beam's isocenter and orthogonal to the beam central axis. The beam's eye view is always oriented so that the view top is towards the machine gantry (i.e., the axis of gantry rotation is a vertical line in the view, and the direction towards the machine is "up").

The central axis of the beam for which this is the beam's eye view is initially in the exact center of the beam's eye view. Initially, the view is drawn at such a scale that all patient anatomy appears in the view. If the couch rotation is zero, the patient's Z axis is pointed straight down on the display (e.g. the patient is oriented head-up). When the couch rotates, the view point remains fixed, and the anatomy changes its projected appearance. When the collimator rotates, if the collimator is a rectangular collimator, the outline of the collimator and blocks move, not the patient anatomy.

This is sufficient to determine the transformation from the beam and patient coordinate systems to the view and screen coordinate systems.

Objects in beam's eye views are depicted as follows:

Contours Contours are drawn as wireframe "hoops" in proper perspective. Colors of each organ are the same as in the other views.

Points All points of interest are projected in proper perspective, to the isocenter plane, with numbers.

Beams All beams appear in the view; each field and any blocks are drawn as portal outlines that represent the intersection of the beam with the view plane. For electron beams the cutout outline is shown and it rotates as the collimator angle is changed. If the collimator is a multileaf collimator, the portal outline is shown, and it does *not* rotate as the collimator angle is changed. The multileaf collimator actual leaf positions may optionally be shown. They will rotate as the collimator angle is changed.

Colors for beams, blocks, and wedges, are the same as in cross-sectional views.

Isocenter A crosshair appears at the point where the beam central axis (of the beam for which the beam's eye view is drawn) intersects the view plane (this is the projection of the isocenter, or the actual isocenter for the plane at position 0.0). The isocenter and central axis of each of the other beams are depicted as in the cross sectional views.

Wedges The wedge (if present) is drawn as a narrow isosceles triangle with its sharp angle pointed toward the wedge toe. If the wedge orientation angle is 0 or 180, the wedge picture is centered on the collimator $-x$ axis near the view border (and points parallel to the collimator $+y$ or $-y$ axis, respectively). If the wedge orientation angle is 90 or 270, the wedge picture is centered on the collimator $+y$ axis near the view border.

Dose distributions Dose calculation regions and dose distributions do not appear.

CT Studies A digitally reconstructed radiograph from CT or other image data may appear.

Line sources and seeds Line sources and seeds do *not* appear in a beam's eye view.

2.5.3 Presentation

A view occupies a single window on the display, so it may be moved, “popped to the top” or manipulated by any of the standard operations provided by the window manager. Several views (in the corresponding windows) may be visible at the same time. All views are “active” views, that is, if an object in the plan is updated, all views showing that object are updated to reflect the change. Further, views provide some interactive input, e.g., the locator bars that control the view positions for other views, and the dose calculation grid, whose corners may be “dragged” with the mouse and on-screen pointer.

Any view that is visible can accept input. For details on what kinds of input are possible in views, see section 16, which describes the view panel. The input focus is controlled by the X window manager, according to the particular window manager in use on the computer, and each user’s choice of X window manager configuration. This is not controlled by the Prism system.

2.6 Contents of chart printout

Prism produces a PostScript file suitable for printing on any PostScript capable printer (or one for which a PostScript preprocessor such as `ghostscript` is available). If a PostScript previewer such as `ghostview` or `gv` is available, the chart file may be previewed on the workstation screen.

On every page of the chart, the left margin is large enough for hole punching and binding. The top margin is large enough for stapling. Each section described below begins on a new page.

2.6.1 Title page and combined doses section

The top of the first page has a title section. On the left side are two lines of text identification, usually the department name and institution name. In the upper right, the Prism logo appears, with the Prism system version number. On the right side, the following text appears below the Prism logo:

```
            APPROVED BY:

ATTENDING: ____________ DATE _____

RESIDENT:  ____________ DATE _____

PHYSICIST: ____________ DATE _____

THERAPIST: ____________ DATE _____

BILLED: __________________________
```

Next on the first page, and *at the top of every following page*, is printed the patient name, case ID (timestamp), patient ID, hospital ID, plan name (possibly abbreviated), plan time stamp, and the page number in sequence, as in “page 2 of 5”. This will make it easy to reassemble the chart in case it gets jumbled in the printer hopper.

Next on the first page is the contents of the comments attribute of the case, then the text `DS:` followed by the dosimetrist's name. This is followed by the plan comments.

Next there is a list of organ names and densities for all organs that were used as inhomogeneity information in the dose calculation (external beam only).

If selected by the Prism user in the chart dialog box and if point doses for all beams were computed, a list of points with the combined doses appears, with total dose only, followed by the x,y,z coords for each point. The information is left justified and the space on the right is available for users to add small drawings and handwritten notes. The x and y coordinates are given to one decimal place. The z coordinate of each point listed is given to three decimal places. This makes it easier to find the z-plane of a particular point in the easel or point editor, since these planes may initially be defined to three decimal places.

2.6.2 External beam setup and dosimetry

This section is designed to help therapists set up treatments. It includes both machine settings and dosimetry information, unlike the previous version of Prism in which these were in separate sections.

This part is arranged as a table with the beams in up to four vertical columns. If there are more than four beams, this section is repeated as necessary, with each succeeding group of four (or fewer) beams put on a new page.

At the top of each column the beam name is printed as three lines of 10 characters each, as entered in the beam panel.

Below the beam name, the setup information appears. The setup information should be correct for the particular machine specified, in the machine-specific coordinate system, not the Prism universal coordinate system. Therefore, to set up the planned treatment correctly, it should only be necessary to enter the numbers from the chart into the machine console.

This requires Prism to perform the scaling for each machine motion on every type of machine available. The scaling conventions for University of Washington machines are in Appendix A.

Linear dimensions (SSD, Collimator X etc.) are in cm, to nearest mm (one digit after decimal point). Angles are in degrees (rounded to nearest integer).

These items are appropriate for photon, electron and neutron beams; for electron beams, a few items are different from photons and neutrons, as noted below.

Beam name e.g., `left lateral`,

Machine e.g., `SL20A-6MV-MLC`,

Particle e.g., `PHOTONS`,

Energy for photons, a nominal energy (from the machine specification file), e.g., `6MV`, for electrons the actual energy selected, e.g., `6 MeV`, for neutrons a string from the machine file,

Monitor units/fraction The monitor units per fraction, rounded to the nearest whole number. No decimal point nor decimal digits should appear.

Number of fractions

SSD Source-to-skin distance (computed by Prism), or `MISS` if the central axis does not intersect the patient volume.

Wedge The text description string naming the selected wedge, or `None` if no wedge.

Wedge Rotation an angle (degrees) specifying the wedge orientation, according to the convention of the machine manufacturer, or `None` if no wedge is selected. See Appendix A for guidance on assigning wedge rotations. Even with a wedge, an angle appears here only if the particular machine provides this capability, otherwise this is blank.

Collimators Not only are the scaling conventions different on the machines, but the number and types of items, and even *naming* conventions are also different. So really the row labels, not just the numbers, will depend on the machine. And if there is more than one kind of machine in a plan, well . . . . For example, Varian has "Upper Set" and "Lower Set", while Elekta has X1, X2, Y1, Y2. See Appendix A.

The following two entries suggest a layout convention. The actual row labels should differ. For electron beams, the X and Y numbers are the same, the *nominal* size of the applicator cone.

Collimator X If independent jaws, two numbers. If leaf collimator, also two numbers, giving widest opening on each side. This information is useful at the simulator and when making port films. See Appendix A for guidance in choosing which pair of collimators is the X pair.

Collimator Y Same format as for Collimator X.

Gantry Gantry angle in degrees (for arcs this is the nominal "start" angle.)

Arc size `Fixed` when no arc (the usual case), or a number of degrees.

Collimator Rotation the collimator angle setting according to the machine manufacturer's convention (see Appendix A).

Couch Rotation The scaling conventions for this differ even among the Varian machines! See Appendix A.

Blocks `Blocks` or `None` or `Leaf`. Always `Leaf` for leaf collimated fields.

Table linear motions are always relative to the table home position, but can be used as offsets from an initial patient setup with the alignment lasers. They are also useful for the dosimetrists. So, these are in *Prism* coordinates, not machine specific coordinates.

Table height

Table lateral

Table longitudinal

Start Angle For arcs, this is the initial gantry angle, repeated here along with the following, for convenience.

Stop Angle Computed and printed assuming *clockwise* rotation. This means it could be a lower value than the start angle on some machines.

Arc size Repeated from above.

MU per degree The value for a *single* fraction is computed and printed.

Depth of isocenter Calculated from SSD and SAD. `EXTEND` if isocenter is not within patient, and blank if the central axis misses the patient.

Collimator X For rectangular jaw collimators, the width of the opening in the X direction. For leaf collimated fields, the width in the X direction of the the smallest rectangle that encloses the portal (that is also parallel to the collimator X and Y axes).

Collimator Y Same format as Collimator X.

Equivalent Square Computed, only for photons and neutrons. In cm, to nearest mm (e.g `12.4`. For rectangular fields, this is the value of w_c from the dose computation methods technical report [4], section 2.3.1. For leaf collimated fields, this is the value of w_p from [4], section 2.4.1. If the beam's central axis misses the patient, this field is blank.

Output Factor (ROF) Computed, only for photons and neutrons. This is $O(w_c)$ for rectangular collimated fields and $O_p(w_p)$ for leaf collimated fields. Given to three decimal points, e.g. `0.917`. If the beam's central axis misses the patient, this field is blank.

TPR at Iso TPR at depth of isocenter, accounts for missing block scatter. Computed, only for photons and neutrons, as described in [4], it is the term D_b in equation 2.1. For rectangular collimated fields, it is described in section 2.3 of [4] and for leaf collimated fields, it is described in section 2.4 of [4]. Given to 3 decimal points, eg. `0.728`. If the isocenter is outside the patient, this quantity cannot be computed, and instead, `EXTEND` is printed. If the beam's central axis misses the patient, this field is blank.

Tray factor `None` if no blocks, which means it has value 1.0. Given to three decimal points, e.g. `0.974`.

Attenuation factor The number put in by the dosimetrist as part of the beam specification for this beam (see also Chapter 5).

2.6.3 Dose per treatment by field and total dose by field

The dose per treatment by field includes a column listing the points of interest by name and number, and a column for each treatment beam, with the beam name, and on the line corresponding to each point, the dose to that point from that beam. The page accomodates up to four beams. If there are more points than fit on the page, the list is continued with the same beams on additional pages as required. If there are more than four beams, additional pages are printed, until all beams are printed.

The column headings appear on every page.

The total dose by field pages are in the same format, except that on the first page an additional column appears, after the point names but before any beams, showing the total dose to each point from all beams. Although this information also appears on the first page of the chart, it is repeated here for convenience.

2.6.4 Line sources

For linear sources, there are two additional sections of the chart printout, “LINEAR SOURCES” and “TOTAL DOSE BY SOURCE”. This includes source endpoint coordinates, both raw (original input, e.g., from orthogonal films) and the reduced three dimensional space coordinates.

2.6.5 Seeds

For seeds there is only one additional section, “SEED INFORMATION” listing the characteristics of the seeds, and no section listing dose per seed. This section also includes raw and reduced coordinates for each seed.

2.6.6 Miscellaneous

At the end of the printout there is a bitmap (halftone) portait of the dosimetrist.[1]

2.7 Other chart printouts

There are three other chart printouts, a special page for leaf settings for treatment machines with multileaf collimators (MLC), a special page of information associated with the transfer of treatment setup information to the UW Clinical Neutron Therapy System (Neutron chart), and a special page of information associated with the transfer of treatment setup informaiton to the Elekta linear accelerators using the DICOM-RT facility.

2.7.1 Leaf collimator settings

For each leaf collimated field, a page can be printed that shows all the leaf settings in a convenient format for the machine. This chart is a separate printout that contains all leaf settings, along with other identifying information to associate the chart with a unique patient, case, plan, and beam.

2.7.2 Neutron charts

The contents of the Neutron chart are described in Chapter 10, which describes the neutron beam data transfer panel.

---

[1] Well, still not in this version, but soon. . .

Chapter 3

Coordinate conventions in Prism

The coordinate system definitions used by Prism largely agree with those discussed in [5]. Unless otherwise specified, the scale is in centimeters and angular transformation rotations in the positive direction are counterclockwise as seen from the positive axis, looking toward the origin of the coordinate system. The units for all angular coordinates are degrees.

Prism makes use of the following coordinate systems: *treatment room space*, *gantry space*, *collimator space*, *couch space*, *patient space*, *view plane space*, and *screen space*. Objects with a spatial or visual extent are defined in one of these coordinate systems, and their coordinates may be transformed between systems for the purposes of graphic display.

3.1 Patient space

The axes of the patient space are parallel to those of the couch space. The origin of this space is defined by a clinician or dosimetrist only when entering data from a digitizer. When data are entered from CT images, the origin is already defined by the data in the image files. When a patient is scanned we have a convention for determining the patient origin in the image, described here.

Image data for Prism are stored in sets of files, with a file for the information about the images in a set and separate files for the binary image data, one file per image. Images from CT or MR studies are organized into “image sets”. An image set is assigned an “id” number similarly to the case “id” number, i.e., it is relative to a given patient, and associated with a given patient. Each image within the set is assigned an image ID, which should be the “slice number” from the CT scanner file.

It is also important that the `origin` attribute of each image be set according to a fixed convention so that the relation between the patient coordinate system and the image pixels is known to users of Prism. Our convention for this is that the patient space origin of a 2-D CT image is determined by information from the DICOM data transmission from the CT scanner. Usually the origin is at the center of the image, corresponding to the intersection of the laser positioning lights on the scanner. The patient space location of the (0,0) pixel is therefore computed from the image size specified in the image file from the scanner. This convention is followed so that external markings on the patient or a patient positioning device can accurately reproduce the positioning of the patient in the treatment machine room. Prism sets the “table position” at the patient origin, so the treatment machine couch motions represent absolute displacements from this initial position.

The geometric data describing the patient's anatomy and the treatment regions are defined in a patient coordinate system, with user-specified origin, Z axis increasing toward the patient's feet, X axis increasing toward the patient's left side and Y axis increasing toward the front of the patient (see figure 3.1).

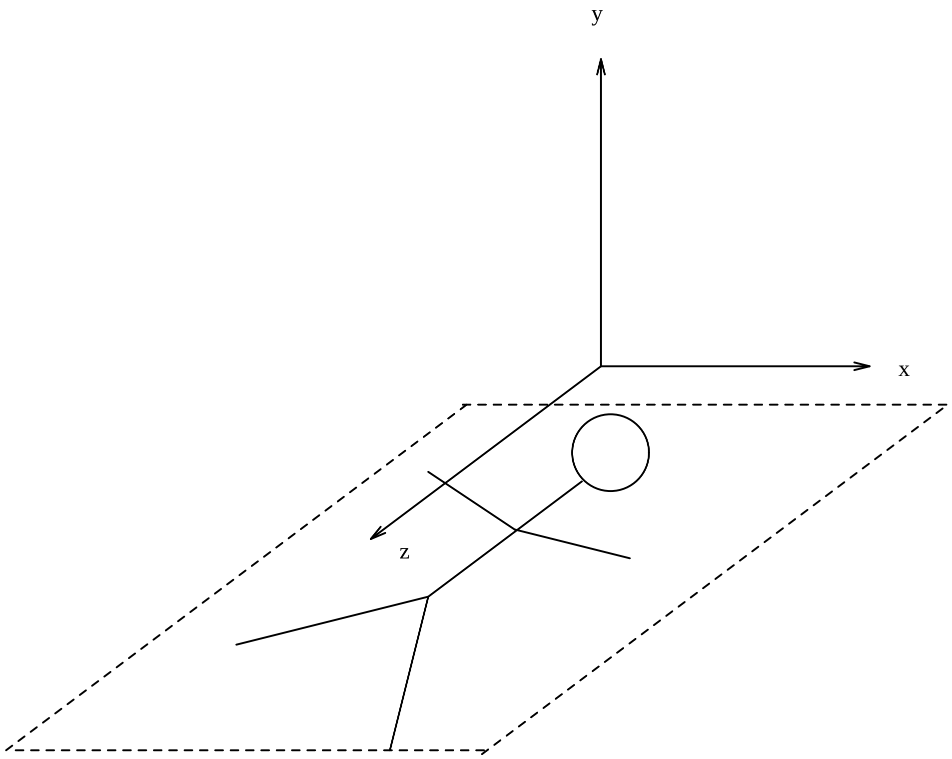

Figure 3.1: The patient coordinate system

The patient coordinate system is related to the external beam treatment couch coordinate system by computing or specifying the location of the beam isocenter in the patient coordinate system when the patient is on the couch and the couch is at its "home" position. In the Prism system, the couch is at home position when all three couch linear motion settings are at 0.0 (couch height, couch lateral position, couch longitudinal position). The convention used in the Prism system is that under this condition, the beam isocenter is at the patient coordinate system origin. See page 107 for further explanation.

3.2 Couch space

The origin of this space is the treatment machine isocenter. The y-axis points directly up, and the x-axis and z-axis are rotated from their counterparts in the treatment room space by a turntable angle t. See figure 3.2.

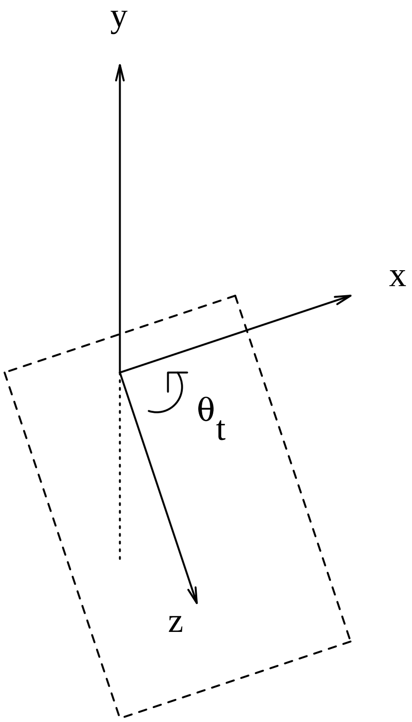

Figure 3.2: The couch coordinate space

3.3 Treatment room space

The origin of this space is at the treatment machine isocenter. The x-axis points to the right when the viewer faces the treatment machine gantry protractor, the y-axis points directly up, and the z-axis is the axis of gantry rotation and points directly away from the machine. See figure 3.3.

3.4 Gantry space

The origin of this space is at the treatment machine isocenter. The x-axis points to the right when facing the treatment machine, the y-axis is the axis of gantry rotation and points directly toward the machine, and the z-axis points directly toward the beam source. The gantry space is obtained from the treatment room space by rotating -90 degrees about the x-axis and then rotating by the gantry angle g around the new y-axis. See figure 3.4.

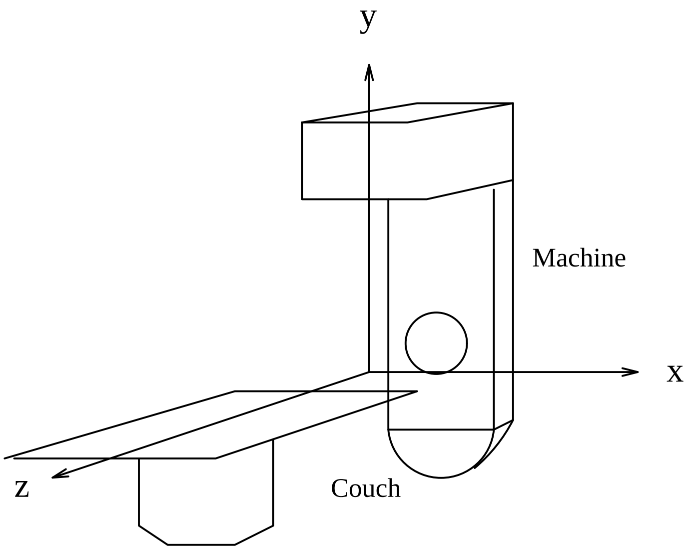

Figure 3.3: The treatment room coordinate space (in this picture the couch is at “home” position, with couch angle 0.0

3.5 Collimator space

The origin of this space is the treatment machine isocenter. The x-axis and y-axis are rotated from their counterparts in the gantry space by the collimator angle c, and the z-axis points toward the beam source (the apparent source of the radiation beam). See figure 3.5.

3.6 View space

Prism includes the concept of a view space, a single planar cross-sectional view of the patient. Three kinds of cross-sectional views are provided by the Prism system: transverse, sagittal and coronal views. These are planes that are normal to the patient space z-axis, x-axis and y-axis, respectively. Associated with a view plane is a two-dimensional coordinate system, and a scalar value determining which plane in patient space corresponds to the view plane. The origin in the view plane is the intersection with the plane of a line normal to the plane and through the patient origin.

3.7 Screen space

In order to generate graphic displays of Prism objects shown in the various kinds of views, an additional coordinate system, screen space, is needed. This space is a two-dimensional space which represents the window on the display console. The origin of this space is in the upper left corner of the screen. The x-axis points to the right and the y-axis points down. Furthermore, the scale is in

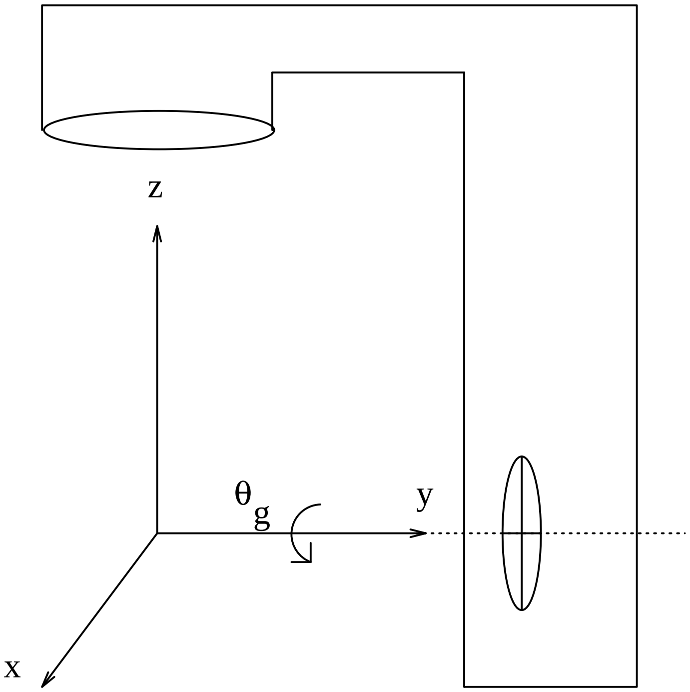

Figure 3.4: The gantry coordinate space

pixels, rather than centimeters. Screen space can be derived from view space by inverting the y-axis and re-scaling (described below). See figure 3.6.

The natural coordinate system for describing beams is collimator space. Most other graphical objects, like anatomy, tumors, and points (referred to below as contour or point based), are defined in patient space. The coordinates of these structures must be transformed to view space (and then to screen space) for the appropriate view being displayed.

For cross-sectional views the patient space origin is initially centered in the view; in a beam's eye view, the origin is initially set so that the isocenter of the corresponding beam is at the center of the view window.

When an image is drawn into a view, the location of the patient space origin in the view must be reset by Prism to match the image data.

3.8 Plot space

The plot space is a cross section or projection of coordinates from patient space and is scaled from life size according to the selected plot magnification.

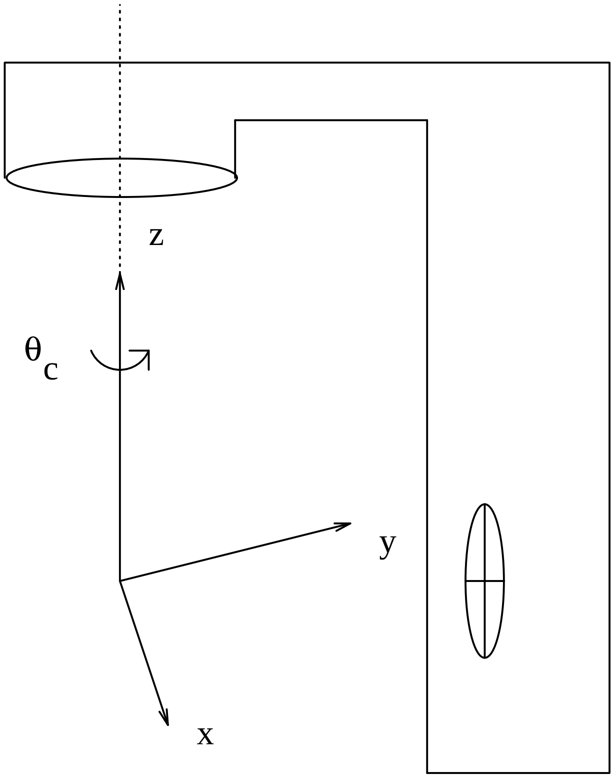

Figure 3.5: The collimator coordinate space

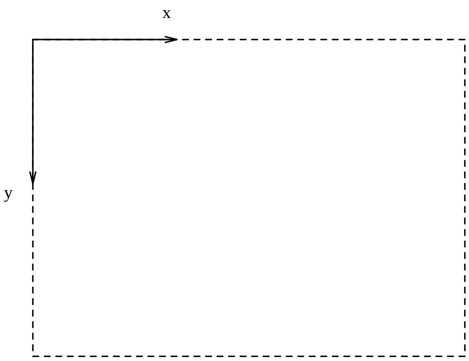

Figure 3.6: The screen coordinate space

Chapter 4

User environment and customization

4.1 Equipment requirements and setup

This section describes the equipment requirements, some specific details on setting up specialized equipment, and instructions for building an executable Prism image using Allegro Common Lisp.

The computer on which Prism runs must provide a Common LISP [6] software system which includes programming support compliant with the X Window System [2] at the level of the X protocol. Prism uses the CLX package [7], the Common LISP binding of the X window system protocol, analogous to Xlib for C programs, for graphics and other user interface features. A set of OpenGL or equivalent libraries (`libGL` and `libGLU`) is also required. Silicon Graphics OpenGL is known to work as is Mesa-3.4 on HP-UX 10.20 and Red Hat Linux 7.x, 8 and 9. The display on which the Prism user interface appears must provide an X server capable of creating and managing a large number of windows and pixmaps. Several X server implementations for MS-Windows systems appear to work, each with some limitations.

The current version of Prism only works with Allegro Common Lisp, from Franz, Inc., Berkeley, CA. Version 6.2 or later is required.

The display environment must also provide a reasonable window manager such as `twm`, *Motif*, KDE or Gnome. It is also possible to display Prism windows on a Macintosh or MS/Windows computer, with the use of a suitable X server and the native window manager of either of those systems. However, no Prism code depends on the choice of window manager, and Prism does not use any graphical user interface libraries other than the Common LISP binding of X (CLX) and OpenGL through GLX. These decisions are all aimed at achieving portability across different workstation environments.

It is possible to run the Prism program on one computer and display on another, or display on an X terminal. The computer used for display must be running an X server capable of accepting connections via TCP/IP and the computer running Prism needs X client support, i.e., it does not need to be running an X server, but only the TCP/IP and other software to allow the Prism client to make a connection to the remote display. In this respect, Prism works exactly like any other ordinary X application program and it uses the UNIX `DISPLAY` environment variable to determine the location of the display. Note that the Prism X connection can *not* be tunneled through an `ssh` connection, because of a CLX bug that does not allow the display number to be non-zero. We hope to fix this in a future release.

The hardware (including graphics) capabilities required by the Prism radiotherapy planning system are simple. The graphic display must be at least 8 bits deep (24 bits is preferred), and provide up to 256 gray levels as well as a variety of colors. The Prism code does not depend on CPU architecture (RISC or not, 32 bit or 64 bit), and most modern workstations are adequate in terms of CPU performance. Prism runs adequately on a 233 MHz Pentium with Red Hat Linux 7. A minimum of 64 megabytes (MB) of memory is required, but in general, the more memory, the higher the performance, particularly when using large CT image studies (Prism can handle unlimited numbers of CT images in a study, and 100 to 200 is typical). A display of 1024 by 768 pixels is useable but not desirable. A display of 1280 by 1024 pixels is adequate. The Prism software uses all three buttons on the standard mouse supported by the X window system. If you have a two button mouse, configure your X server to emulate the middle button by holding down the two buttons simultaneously.

The Prism software uses the default screen and root window depth, visual and pixmap formats, as well as the default colormap. If other programs are running that have already allocated many color entries in the default colormap, Prism will not run. In this case, it is necessary to terminate the other program(s) to free up the colormap space, then restart Prism. With a 24 bit display, this is rarely a problem.

Prism prints charts on any printer that supports PostScript level 2, including indirect support using a conversion program like `ghostscript`, through standard printer queues, so no special setup is required except to set up the printers and print queues according to the system in use, and put the print queue names in the appropriate global configuration variable as described in Section 4.2. Similarly, the plotted output is sent through a printer queue to the plotter. Plotters using PostScript, such as the Tektronix Phaser 790, can print color plot data on gray scale images. Plotters that do HP-GL can be used for plots without images. The only requirements are that the printer queue should be set up to *not* print a “banner” page or otherwise modify the stream of data going to the plotter.

Digitizer input is through a serial port, configured to whatever digitizer is available, as long as the serial port can be read from by a non privileged program. The name of the serial port device must be provided in a configuration file, as described in Section 4.2. The digitizer in use at the University of Washington is the SAC model GP-9. Others can be used, if they provide an output format that is similar to the GP-9. The digitizer software expects a large digitizing area with menu boxes defined at the bottom (closest to the user), with fixed dimensions.

There is no other special hardware for Prism.

The Prism software consists of a collection of Common Lisp source files. The files include the SLIK user interface kit [8], a set of four files called the Polygons system, two files implementing a rule-interpreter [9], and the Prism files themselves. To create an executable Prism assuming you have all the source files, take the following steps:

1. If they are not already available, install a Common Lisp environment with CLX and CLOS preloaded, compliant with the documents cited above. At UW, we use Allegro Common Lisp, a product from Franz, Inc., Berkeley, California. The procedure for installing this software is vendor specific.

2. unpack the Prism tar file into a convenient local directory. This should create several subdirectories corresponding to the subsystems of Prism and the `systemdefs` directory, containing the subsystem definitions.

3. Make sure you have an X11R6 compliant X server, and the two main OpenGL or equivalent libraries, `libGL.so` and `libGLU.so`. (In some systems the extension may be `.sl`) You may have to modify the file `gl-support.cl` to define the correct locations for the Xlib and GL libraries.

4. A number of site-specific global constants may be customized to the local computing environment, as discussed in Section 4.2.

5. If the location of the `prism.config` file is different from the default (see section 4.2.2), you must edit the `prism-globals.cl` file, modifying the form:

   ```
   (defvar *config-directory*
     "/radonc/prism/" "The directory of the prism.config file")
   ```

   This form specifies the directory that Prism will look in to find the `prism.config` file. Redefine the form to specify the directory where your `prism.config` file will be located. Unlike the other variables, the value of `*config-directory*` cannot be overridden in the `prism.config` file itself.

6. If the local Common Lisp environment expects source files to have a suffix other than `.cl`, rename all the files in the source directory to have the appropriate suffix. Make sure your Common Lisp system is defined in or consistent with the defaults in the `defsystem.cl` file. This software package is documented in a companion (PostScript) file, `defsystem.ps` available from the same source as the Prism source files.

7. Invoke Lisp in the directory in which you unpacked the Prism tar file. The command to invoke Lisp is specific to the local computing environment. At UW, we use Allegro Common Lisp, and the command to invoke lisp is `alisp8`, which runs the version with 8 bit character set and ANSI style conversion to upper case of input to `read`.

8. Type `(load "config")` to the Lisp prompt, which loads the defsystem module and defines the location of the system definition files.

9. Type `(mk:load-system :prism)` to the Lisp prompt to load the system. It may take a few minutes to load all the source files.

10. Type `(mk:compile-system :prism)` to the Lisp prompt to compile the system. It may take several minutes for the system to compile.

11. Save the compiled system to a dumped Lisp image, in a manner such that the system will evaluate the `pr:prism-top-level` form when the executable Lisp image is invoked from the operating system prompt. The command to do this is:

```
(pr:dump-prism-image)
```

12. Exit Lisp. The Allegro Common Lisp command to exit is `(exit)` or `:exit`.
13. Place the lisp image you created into the `/radonc/prism/` directory, where you should also have the `prism.config` file.

Prism may be run by defining a shell command alias, *prism*, as follows:

```
alias prism "alisp8 -I /radonc/prism/prism.dxl"
```

Running Prism requires a proper license from Franz, Inc. and also requires that the Allegro CL installation remain on the computer, as the program depends on files from the Allegro CL installed environment.

The Prism data directories must also be set up. There should be a main data directory, and several subdirectories, one for case data, one for image data, and one for measured beam data. In addition, each user who wishes to have the work-in-progress feature should have a local directory where he/she can store temporary plans, work in progress. The case directory starts out with a blank file called `patient.index` and another called `case.index`. These files need to be created initially by hand.

(add comments on directory protections, ownership, groups and user private groups)

4.2 User and site customization

A system-wide customization file allows some Prism parameters to be tailored to the site configuration without changing any code. Each Prism user may also have a customization file setting additional Prism parameters that can take values according to each user's individual preference. These are described in the following sections.

4.2.1 The `.prismrc` user customization file

The `.prismrc` file, in the user's home directory, contains text that sets Prism global variables to values other than their defaults, so that each user may tailor these settings to their own environment or preferences. The global variables are all in the `prism` package in the Common Lisp package system, so the file must begin with `(in-package :prism)` which makes that package the current one while the file is read in.

Case database: the pathname for the directory containing the Prism case archives. Variable name: `*patient-database*`

Image database: the pathname for the directory containing the Prism image database. Variable name: `*image-database*`

Checkpoint database: the pathname for the directory containing the local checkpoint database. Variable name: `*local-database*`

Therapy machine database: the pathname for the directory containing the machine data to be used in this Prism session. Variable name: `*therapy-machine-database*`

Machine index directory: the pathname for the directory containing the machine index files that specify the actual machine data file names corresponding to the generic machine names in the Prism plans. Variable name: `*machine-index-directory*`

Structure set directory: the pathname for the directory containing the Prism organs, tumors and targets written by the Prism DICOM server from structure sets received e.g. from a CT simulator. Variable name: `*structure-database*`

Plotter file: the pathname of a file in which to store a plot before it is printed. Variable name: `*plotter-file*`

Chart file: the pathname of a file in which to store a chart before it is printed. Variable name: `*chart-file*`

Dose grid coarse granularity: a single-float, indicating the dimensions of a voxel in a coarse dose grid, in cm. Variable name: `*coarse-grid-size*`

Dose grid medium granularity: a single-float, indicating the dimensions of a voxel in a medium dose grid, in cm. Variable name: `*medium-grid-size*`

Dose grid fine granularity: a single-float, indicating the dimensions of a voxel in a fine dose grid, in cm. Variable name: `*fine-grid-size*`

Minimum dose grid size: the minimum allowable size, in centimeters, of the length, width, or depth of the dose grid. Variable name: `*minimum-grid-size*`

Ruler default color: symbol in the SLIK package, to specify the color in which the ruler should appear initially in a contour editor, point editor or view. Variable name: `*ruler-color*`

Easel drawing region size: this is an unquoted symbol, either `medium` or `large`, specifying how big the drawing region in the Easel should be, corresponding respectively to 512 and 768. If you put any other number or symbol in, the results are unpredictable. Variable name: `*easel-size*`

Neutron setup file: this is a string specifying the full pathname of the file to contain neutron therapy system setup data. Variable name: `*neutron-setup-file*`

Neutron chart file: this is a string specifying the full pathname of the file to which the neutron chart information is written. Variable name: `*neutron-chart-file*`

MLC chart file: this is a string specifying the full pathname of the file to which multileaf collimator setup information is written. Variable name: `*mlc-chart-file*`

The format of this file is a series of Common Lisp expressions. Each expression is a `setf` form, to change the value of the variable to the desired one.

An example `.prismrc` file is as follows:

```
(in-package :prism)
(setf *patient-database* "/prismdata/cases/")   ; case database
(setf *image-database* "/prismdata/images/")    ; image database
(setf *local-database* "~/prismlocal/")         ; checkpoint database
(setf *therapy-machine-database*
      "/prismdata/beamdata/")                   ; machine data
(setf *machine-index-directory*
      "/prismdata/beamdata/")                   ; machine filenames
(setf *structure-database*                      ; temporary storage
      "/prismdata/structures/")                 ; for structure sets
(setf *plotter-file* "~/plot.plt")              ; plotter file
(setf *chart-file* "chart.dat")                 ; chart file
(setf *ruler-color* 'sl:green)                  ; default ruler color
(setf *coarse-grid-size* 2.0)                   ; coarse dose grid size
(setf *medium-grid-size* 1.0)                   ; medium dose grid size
(setf *fine-grid-size* 0.5)                     ; fine dose grid size
(setf *minimum-grid-size* 4.0)                  ; minimum dose grid size
(setf *easel-size* medium)                      ; easel drawing region
(setf *neutron-setup-file* "~/neutron.dat")     ; neutron setup file
(setf *neutron-chart-file* "~/neutron.cht")     ; neutron chart file
(setf *mlc-chart-file* "~/mlc.cht")             ; mlc chart file
```

4.2.2 The `prism.config` system configuration file

In addition to the user modifiable global variables, there is a second set of global parameters that are system-wide, and should be set by a Prism system administrator. They are the same for all users, but are specific to the computer system on which Prism is run, and are contained in a file called `prism.config`. This file is assumed to be in a directory named `/radonc/prism` and if it is not, one of the Prism source code modules will need to be changed. (See section 4.1.) Any of the user-specific configuration parameters can also be set in this file, to provide system-wide user defaults in the absence of user-specific parameter values.

Spooler command: the command string to spool a chart or plotter file, as known by the system's print spooler. Variable name: `*spooler-command*`

Plotter destinations: an association list of pairs, where each pair consists of a print queue name and a symbol specifying the type of the plotter device for that print queue. Variable name: `*plotters*`

Chart printer destinations: a list of strings, each of which is the name of a print queue spooling to a printer capable of printing PostScript, either directly or through a filter such as Ghostscript. One of these should be the string, `File only`, which provides the option of writing a file but not printing it on a printer. The file will be written in the user's current directory and the file name will be as specified by the `*chart-file*` parameter. Variable name: `*postscript-printers*`

Hardcopy header: a list of two strings, constituting the text header to appear on all charts and plots. Variable name: `*hardcopy-header*`

Digitizer device names: an association list of *(hostname, devicename)* pairs, indicating the device file name for the digitizer interface corresponding to each computer on which Prism is run. Each *hostname* and *devicename* is a string. Variable name: `*digitizer-devices*`

Following is an example of a `prism.config` file:

```
(in-package :prism)
(setf *spooler-command* "lp -c -d")    ; chart & plot spool cmd
(setf *plotters* '(("ps184" ps-plot)
   ("PS File only" ps-plot)
   ("hp7550a" hp7550a-plot)
   ("dj455c" hp455c-plot)))
(setf *postscript-printers* '("ps146b" "ps136" "File Only"))
(setf *hardcopy-header*                ; header on charts & plots
  '("Radiation Oncology Department"
    "University of Washington"))
(setf *digitizer-devices*           ; digitizer device names
  '(("violin1" "/dev/ttyS0")        ; example for Red Hat Linux 7
    ("violin2" "/dev/ttyS0")
    ("viola"   "/dev/ttyS0")))
```

4.3 User level functions

For clinical users, a self-contained[1] executable image is provided, that can be run by typing a single command, `prism`, at the operating system command interpreter prompt (e.g., UNIX shell). The user's login environment and/or the system configuration will be set up so that this command succeeds in activating the Prism program. This is one of the very few instances where clinical users must interact directly with the operating system; however, they need only issue exactly the command which is described to them.

It is possible to run the Prism program on one computer and display on another, or on an X terminal. If the user wishes to have the display appear somewhere else than the computer (host) on which the program is being run, the user must first be sure that the `DISPLAY` environment variable is set to the display at the user's desk. If the user is running Prism in an `xdm` session, e.g., on an X terminal, this is automatic. If the user has connected to the Prism host by using `telnet` or a similar remote login facility, he/she must type a command to set the `DISPLAY`. In this respect, Prism works exactly like any other ordinary X application program.

The system responds by displaying the patient panel (Chapter 11) with no current patient case selected. The user may then select a case from the shared database or from his/her checkpoint database. The user's checkpoint database is a local, or private, database of patients, cases and plans, like the shared database but owned by that user and independent of other users and independent of the shared file system. A user's stored work in progress is not part of any shared database; it is only available to the user who created it or by explicit reference in the use of the "retrieve" function. This is further described in section 11.3.

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[1] Not entirely - it may require that the supporting Common Lisp system be installed and licensed, e.g., Allegro CL^{TM} from Franz, Inc.

A user’s current case and plans are stored in the shared database only by performing explicit “archive” operations (see section 11.3 for a description of the archive functions).

When the user ends a planning session, work in progress is *not* automatically saved for that user. If a session ends abnormally due to program or system failure, work in progress may be lost; automatic checkpointing is not provided. However, the user may periodically invoke a manual checkpointing function to minimize lost data and save work in progress. The manual checkpointing function writes the current case and/or plans into the user’s checkpoint database.

Certain aspects of the Prism environment can be tailored for each user. These include such things as the location of the Prism archival patient database and image database, and the location of the user’s personal checkpoint database. All such user configurable information is contained in a text file, located in the user’s home directory, and named `.prismrc`, in the style of typical user configurable programs in the UNIX operating system environment. The contents of the `.prismrc` file are specified in Section 4.2.1.

It is possible for two persons to work on and archive changes to the same case in general (as long as each set of changes is added to the database separately). Changes may be made sequentially, i.e., a user makes a change and archives it. The second user selects the archived case and makes further changes. They also may be made in parallel, i.e., two different users may each create a new case or plan, and archive his/her work, but the changes show up as separate cases or plans, and cannot be merged.

It is possible in any planning session to create and operate on multiple plans for the current case, limited only by system resources (such as dynamic memory).

A view shows a graphic visualization of the case and a plan. There may be several views displayed at any time, for the same case and plan. More than one plan may be displayed at any time, for the same case. Therefore, there must be some clear way to indicate the scope or context of each operation. The way in which plan and case data in general are displayed solves this problem.

For each kind of Prism system object that is manipulated by the user there are one or more control panels on the screen. They are the means by which an object’s attributes may be specified or altered. If altering an attribute involves graphic data entry, a temporary window may be created for this purpose. However, when an attribute of an object is changed, *all views* that depict the object will be updated. In addition, when a *view’s* scale factor, position or other attributes are changed, *all objects* depicted in that view are redrawn and redisplayed. Similiarly, when attributes of a beam are changed, any *beam’s eye view* for that beam will be updated.

Some data will be entered graphically, such as by drawing on the screen with a mouse, in a window, typically when a CT image is displayed in that window. It is also possible to enter graphical data by using a sonic digitizer. Use of the workstation keyboard to enter locations by typing coordinates is in general *not* supported. Exceptions are noted in the descriptions of the individual control panels.

4.4 The Prism graphical user interface

The Prism Radiation Treatment Planning system user interface is distributed among several task-specific windows we call *panels*, which act as a front end for those components of the system which actually carry out various functions related to radiotherapy planning. A patient panel manages administrative information about the current patient case. When you start the Prism system the patient panel appears on the screen. There is always one and only one patient panel present in a given Prism session. Individual panels for plans, beams and other component objects control their respective domains, and view windows display graphical renditions of patient anatomy and beam portals. In addition, a graphic editing panel called the "Volume Editor" provides for the delineation and modification of patient anatomy, tumors and targets. A point editor panel provides a facility for specifying and modifying points of interest in the 3-dimensional patient space, at which the dose is specifically computed. The plan panel includes controls for the specification, computation and display of dosimetric information for a plan. There can be zero or more of any of these component-specific panels during the Prism session.

All visible panels can accept input and their controls can be manipulated by the user. The input focus for the mouse and keyboard is controlled by the X window manager, according to the particular window manager in use on the computer, and each user's choice of X window manager configuration. This is not controlled by the Prism system.

The general appearance and style of the control panels can be changed by setting a few parameters that determine foreground and background colors and border style. The two most commonly used are: 1) set the foreground to black, the background to grey, and the border style to "raised", which gives a kind of "3-D" look and feel, and 2) set the foreground to white, the background to black, and the border style to "flat", which gives a stark outline look and feel. An example of the flat style is shown in figure 4.1. All the rest of the figures in this report, however, are shown in the grey "3-D" style.

4.4.1 Control panels

In addition to the case and plans, other types of objects in the Prism system include: organs, tumors, targets, points of interest, beams, line sources, seeds, dose distributions, and others. For some types of objects that can be part of a case or plan, there is an associated type of control panel, where each instance of the panel controls a single instance of the Prism object. These include: plans, beams, and views. For some collections of objects, there is a single panel to create and edit all the instances of the collection(s). These include: anatomy (organs, tumors and targets), and points of interest. Instead of a control panel for each organ, tumor or target, there is a single panel, the volume editor, with which the user enters or modifies all the anatomy. Similarly, there is a single panel to create and modify all the points of interest.

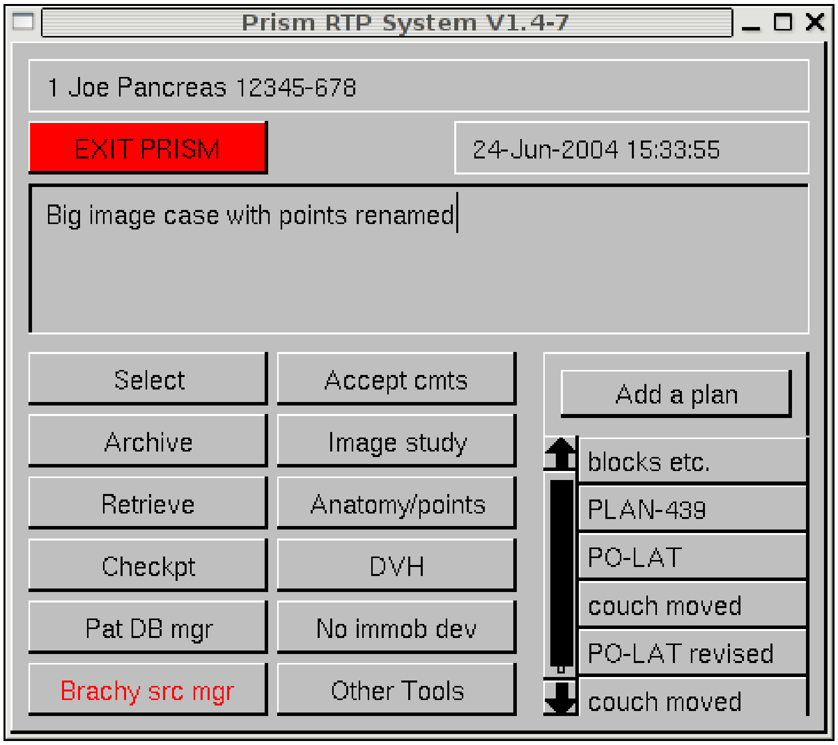
Each panel except the patient panel contains a `Delete Panel` button, and panels that each control a single instance of an object usually provide one or more `Copy` buttons.

The `Delete Panel` button simply removes the control panel from the display, without altering the object (essentially this "deselects" the object). This is a way to declutter the display.

The `Copy` button creates a copy of the object attached to the control panel, and makes a control panel for it. This provides a method for creating a similar but altered instance without the effort of manual duplication. Facilities for copying items are described in the sections on the panels for those types of objects.

Prism panels generally conform to the following pattern:

- Titlebar: A region at the top of the panel, containing the panel name. The titlebar is provided



1 Joe Pancreas 12345-678

24-Jun-2004 15:33:55

Big image case with points renamed

Figure 4.1: The patient panel, shown in white on black (flat) style.

by the local window manager, if the user has configured the window manager to provide this on top level windows. Most panel titlebars simply have a label identifying the type of panel.

- Buttons: Usually a column of buttons, on the left side of the panel, that perform simple functions, like those described above. On some panels the buttons may be in multiple columns.

- Task specific content: The dials, sliders, graphic displays, etc. that you use to adjust numerical parameters, enter text information, or manipulate the display, comprising the majority of the panel's contents.

4.4.2 User interface guidelines

We follow several guidelines in order to make the many parts of the Prism user interface consistent in appearance and behavior. These guidelines should be followed as the system expands, so that consistency and simplicity will be maintained.

In the following, *unmap* means that the window disappears from the screen (i.e., it is unmapped in the X window system sense). To *left-click* a control (such as a button) with the mouse means to position the screen pointer over the control, and to depress and release the left mouse button. *Center-clicking* and *right-clicking*[2] are similarly defined. *Dragging* an object on the screen with the mouse means to hold the pointer over the object, depress one of the mouse buttons and move the mouse while the button is depressed. If no button is specified for a mouse click or drag, the left button is implied.

In the “flat” black and white style, a button is “off” when it shows the label as white, on a black background. It is “on” when the colors are reversed, i.e., black text on a white background.

In the “3-D” grey style, a button is “off” when it has a slightly raised look, as if it were illuminated from the upper left. It is “on” when it appears slightly depressed (from the same lighting angle).

The guidelines are as follows:

- *Window manager*

  The Prism software does not interact directly with the window manager, but a window manager is required. The window manager does not need to be running on the same system as Prism. A Macintosh or MS/Windows computer running an X server that interacts with the local window manager should also work. Most any reasonable one will do. Prism is known to work with `twm`, the *Motif* window manager, KDE and Gnome window managers on Linux, the Hewlett-Packard Visual User Environment (HP-VUE), the Common Desktop Environment (CDE) on the HP-UX operating systems for the HP Unix workstations, CDE on the DEC Alpha with Digital UNIX, DECwindows for Digital UNIX, Silicon Graphics IRIX/`4Dwm`, and Sun OpenLook. It will also work with a Macintosh or MS/Windows system as the display, with a sufficiently robust X server package such as Exodus, Xwin32 or similar.

  Prism windows may be moved or iconified by the user in order to manage his/her workspace. Prism will allow the windows to be resized but will do nothing about it. Therefore if a window is made larger, the extra space will be blank, and if a window is made smaller the contents will be clipped, i.e., part of the panel will not be visible.

  However, the user must *not* attempt to “Close” or delete Prism windows by using the window manager. This will almost certainly cause a Prism session to terminate abnormally.

- *Mouse buttons*

  More detailed hardware requirements for a computer and operating system to run Prism are specified in Section 4.1. We note here just that this configuration requires either a 3-button mouse or the equivalent functionality, in addition to an X window display. If a single button or two button mouse is used with for example a Macintosh or PC, the user must refer to the directions for the X server software for the Macintosh or PC to find out how to emulate the missing mouse buttons.

  When we refer to the *left* mouse button, this means the button that is designated as button number 1 in the X window system setup. It is possible to reconfigure your workstation so that button number one is the *right* mouse button. If you do so, references in this document and

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[2] Some systems may be equipped with a two button mouse, in which case the X window system configuration should be set up to emulate the middle mouse button by simultaneously depressing both buttons.

all other Prism reports that mention the left or right buttons will be reversed. Everything will work otherwise exactly the same, except with the left and right buttons interchanged.

Some books and reports on the X window system and other mouse oriented software use the terms “left-click”, “center-click” and “right-click”. These simply mean “press the left (center, right) mouse button while the pointer on the screen is over a button or other user interface device.”

The left mouse button is used to do selection in the system (click on menus, click on buttons, select objects from lists, etc.). The middle button usually implements a “delete” function. The right mouse button implements various context dependent operations. In views and the contour and point editors it implements a background “panning” facility; in the contour and point editors it is also used to change the color of temporary foreground objects, like landmarks and the ruler (see for example the discussion of the contour editor in Section 17.5).

- *Dials and sliders*

  The controls that appear in the Prism user interface may be directly manipulated, i.e., in order to move a dial, use the mouse to move the pointer to the dial (with the buttons up), and either point to the desired new dial arrow position and press and release the mouse left button, or, put the pointer on the dial arrow, press and hold the left button and drag the arrow to the desired new position. If the computer is in heavy use, the response may lag behind the mouse motion. You release the mouse button in order to leave the dial arrow at the new position. Sliders work the same way – you may either position the pointer at the desired new slider position and click the left mouse button, or “grab and drag” the slider to its new position.

- *Text input*

  In Prism panels there are places where a box for a short line of text input may be present. This “textline” will have a thin vertical line in it that serves as a text input cursor. In order to type data into a textline, you make the textline window have input focus, using whatever method your window manager provides, then you position the pointer over the textline box, and type on the keyboard. Each character will appear as you type it. Except for `<DELETE>` and `<BACKSPACE>`, both of which erase the last character typed and back up the cursor one space, control (non-printing) characters are ignored.

  Pressing the middle mouse button while the pointer is in a textline will erase the contents of the textline. This is useful if the user wishes to simply enter a replacement line of text, and is faster than “backspacing” over the existing text.

  Any text input box which requires a numerical input will check (when the `<RETURN>` key is pressed) that the input consists of a properly formed number, and that it is within an allowable range. If the user types unusable input and presses the `<RETURN>` key, Prism will display a message informing the user of the acceptable range, the unusable contents will be erased, and normal operation of Prism will continue when the user presses the “Acknowledge” button on the message box.

  Some cautions are necessary when typing text information in Prism treatment plans.

1. The printers use the PostScript^{TM} printer control language. PostScript uses the right and left parenthesis characters in a special way, which makes it very problematic to include them in text in a chart. Until we figure out a way around this problem, users should *not* use parentheses anywhere in Prism treatment plan text. Sometimes it will work but often it results in print requests simply disappearing without being printed. If you find that a chart does not print, but simply disappears from the system, please check if you have used parentheses (most often because of a typo).

   As far as we are able to determine, the bracket (`[]`) and brace (`{}`) characters do not cause problems, and are OK to use.

2. When typing numbers into text boxes you must be careful not to use the backslash (`\`) character. It causes the program to treat the next character input as special and can cause the program to fail.

- *Dialog box composition*

  A dialog box's *title bar* displays the name of the operation or menu item which caused it to be displayed. Several types of dialog boxes appear in the operation of the Prism system. They are described below. When a dialog box is displayed, the rest of the panels will not respond to user interaction, and any mouse clicks, pointer motion, or keystrokes while the pointer is in another Prism panel, will be ignored. The user must complete the interaction with the dialog box before proceeding with any other interaction with Prism.

- *Menus*

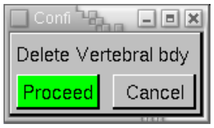
  Menus may be of two kinds, *radio menus*, in which only one item may be selected at a time, and selecting an item deselects the item previously selected (e.g., the popup menu for color selection), and *multiple selection menus*, in which several items may be selected simultaneously.

A *message box* simply displays some information, such as that an operation could not be performed. Figure 4.2 shows an example from the contour drawing facilities. A button at the bottom of the window is labeled `Acknowledge`; until this button is left-clicked, all other user interaction in the Prism system is ignored. When the button is left-clicked, the message box is unmapped and normal interaction proceeds.

Contour not accepted.
Some segments would cross each other.

Figure 4.2: Sample message box

A *confirmation box* displays a warning message and prompts whether to continue. An example is shown in figure 4.3. Its two buttons are labeled `Proceed` and `Cancel`, and they behave similarly to `Accept` and `Cancel`, respectively, in a query box. Until one or the other button is left-clicked, all other user interaction in the Prism system is ignored. When one of the buttons is pressed, the confirmation box is unmapped and normal interaction proceeds.



Delete Vertebral bdy

Figure 4.3: Sample confirmation box

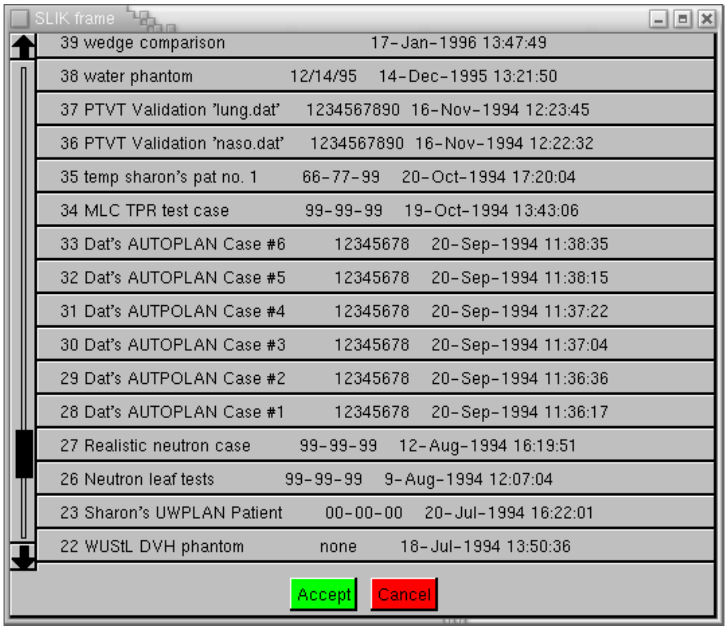
A *query box* gathers information from the user. See figure 4.4 for an example. In this type of box, two buttons appear, horizontally aligned and toward the bottom of the window. The left button is labeled `Accept` and the right `Cancel`. Acceptance causes the system to commit the information to its store and proceed with the action which brought the box into existence, while cancellation causes the entered information to be discarded and restores the state of the system before the operation was commenced. Pressing either button causes the window to unmap. Interaction with other elements of the Prism system may not proceed until the query is completed.

4.4.3 Selector panels - lists of objects

On the patient panel, as well as on the plan panel and other panels in the Prism system, there are subpanels called “selector panels”, which provide for creation and editing of objects that are kept together as a set. These include, for example, on the patient panel, `plans`; on the volume editor (the anatomy editing panel), `organs`, `tumors`, and `targets`; on the plan panel, `beams`, `dose levels`, and `views`, and on the beam panel, `blocks`. For these types of objects, organs for instance, several instances such as the skin (patient outline), brain, spinal cord, and eyes may exist simultaneously. The purpose of the subpanels is to provide access to all the components at random, as reasonably as possible, so one may select an object and thereby bring up on the screen a control panel for manipulating that object. You can add new objects of a given category easily also.

At the top of each subpanel is an `Add` button whose label is specific to the type of object managed by that subpanel (eg: `Add Plan`). Below each button is a scrolling list of the existing instances of that type of object. The `Add` button, in conjunction with the left and middle mouse buttons, provide a means for adding new items to a list, for bringing up a control panel for any item in a list (more than one panel may be on the screen at any given time), and for deletion of items from the list.

Pressing the `Add` button makes a new instance of the type of object listed in that subpanel, and selects that instance (usually this means: to create a control panel for it). For some types of objects, e.g., *targets* and *views*, a dialog box will appear that provides specialized operations or different



```
39 wedge comparison                              17-Jan-1996 13:47:49
38 water phantom                    12/14/95    14-Dec-1995 13:21:50
37 PTVT Validation 'lung.dat'     1234567890  16-Nov-1994 12:23:45
36 PTVT Validation 'naso.dat'     1234567890  16-Nov-1994 12:22:32
35 temp sharon's pat no. 1          66-77-99    20-Oct-1994 17:20:04
34 MLC TPR test case                99-99-99    19-Oct-1994 13:43:06
33 Dat's AUTOPLAN Case #6         12345678    20-Sep-1994 11:38:35
32 Dat's AUTOPLAN Case #5         12345678    20-Sep-1994 11:38:15
31 Dat's AUTPOLAN Case #4         12345678    20-Sep-1994 11:37:22
30 Dat's AUTOPLAN Case #3         12345678    20-Sep-1994 11:37:04
29 Dat's AUTPOLAN Case #2         12345678    20-Sep-1994 11:36:36
28 Dat's AUTOPLAN Case #1         12345678    20-Sep-1994 11:36:17
27 Realistic neutron case           99-99-99    12-Aug-1994 16:19:51
26 Neutron leaf tests             99-99-99    9-Aug-1994 12:07:04
23 Sharon's UWPLAN Patient          00-00-00    20-Jul-1994 16:22:01
22 WUStL DVH phantom                  none       18-Jul-1994 13:50:36
```

Figure 4.4: Sample query box

mechanisms for creating and adding the object.

When an item from the list is selected with the *left* mouse button, a control panel for that particular item is created, and the item is highlighted. The user then may modify any attributes of that object. Except for the organs, tumors and targets on the easel panel, where only one object may be selected at any one time, more than one control panel may be created (i.e. more than one object may be manipulated at any time). However, a single object is associated with at most a single control panel, and a single control panel is always associated with the same object throughout the existence of the control panel. The user may remove that object's control panel without deleting the object itself, either by clicking with the left mouse button on the highlighted item in the list or on the `Delete Panel` button of the control panel.

When an item in the list is selected with the *middle* mouse button, that object is deleted. Before the deletion proceeds, a confirmation dialog box appears, allowing the user to either confirm the deletion or cancel it. If a panel is displayed for that object, and the object is deleted, the panel is removed. Also, if the object is deleted, its button is removed from the corresponding list. In the volume editor, if an object is already selected, it cannot be deleted. In all other panels, an already selected object can be deleted.

When a new object is created, default values for some attributes are assigned, which of course may be changed by the user. But in general, when a new instance of some Prism object is created, it has valid values for all attributes.

Each button corresponding to an object has a label, the *name* attribute of the object it represents. If the user (or some action in Prism) changes the name of an object, the button for that object changes its label to the new name. For objects that have a color attribute, e.g., organs, tumors, targets, beams, the color of the button label (or the background color when the button is on) is the color of the object. If the user changes the color of the object, the button color will also change to the new color. Note that views do not have a color attribute, and their buttons are not colored.

4.4.4 Images, window and level

In control panels and views that can display images, there may be an `Image` button, that displays an image if available, in the background. If this button is present, the image can be toggled on or off. There are also `Window` and `Level` sliderboxes that provide the usual “window” and “level” controls of medical image display. The numbers for window correspond to Hounsfield units, for CT, and the level numbers are Hounsfield units displaced upward by 1024, i.e., a value of 1024 is roughly the level for water, 0 is air, and numbers above about 1500 or so correspond to bone.

4.4.5 Objects and declutter

Many control panels that display contoured objects, beam portals, etc., such as the various portal editing panels and the view panels, include a button labeled “Objects”. This button provides a declutter function, so that some of the objects in the treatment plan can be made invisible in a particular control panel or view. For details, see section 16.2.6.

Chapter 5

Beam panel

The beam panel allows the user to manipulate the attributes of a radiation beam, such as the gantry angle or the collimator width, through direct manipulation dials, sliders, buttons and text fields. Beam portals are visible in the graphical views of patient anatomy and any changes made to a beam's attributes through the controls in this panel are immediately apparent in those views which render an area through which the beam passes (and which belong to the same plan).

On the left side of the panel are buttons for various functions. At the top of the left side of the beam panel is the standard *Delete panel* button which, when pressed, closes the control panel.

5.1 The `Copy` operations

There are four buttons for copying beams: `Copy Here`, `Copy 90`, `Copy 180`, and `Copy 270`. These options allow for the copying of beams into reflected beam geometries, changing other attributes as described below.

The new beam is given an arbitrary name, of the form `BEAM-nnn`, where `nnn` is an arbitrary number. The user may modify or replace this name by typing in the name textline, as described below. The system does *not* assign fixed numbers to beams.

The `Copy` buttons each create a new beam, with almost the same parameters as the one on whose panel the button was pressed. The actions vary slightly depending on the desired shift in gantry angle.

5.1.1 The `Copy here` operation

The `Copy here` button makes a copy of the beam with the same parameters. This can be useful in order to explore for example wedged and unwedged beams that need to be combined in arbitrary ways to create the effect of a wedge of arbitrary angle. The new beam is given a new name, and any wedge selected is deselected, i.e., the new beam never has a wedge, but all other parameters are replicas of the original.

5.1.2 The `Copy 90` and `Copy 270` operations

The `Copy 90` button is useful for creating wedged pair plans or four field box plans. All of the new beam's settings are the same as the original beam, except its gantry angle is advanced by 90 degrees. The `Copy 270` button works similarly, creating a new beam at 90 degrees to the original in the opposite direction as for `Copy 90`.

When a beam is copied with a gantry angle increment of 90 degrees or 270 degrees, the original beam is not changed, and the copied beam is almost like the original. *There are no blocks or wedges in the copied beam.* The collimator rotation angle in the copied beam is the same as the original, and the collimator jaw settings (or multileaf portal, or electron cutout shape) remain the same also. This will achieve the (usually) desired effect of preserving the length of the field (along the axis of gantry rotation, usually along the patient's long axis) and achieving a similar field width.

5.1.3 The `Copy 180` operation

The `Copy 180` button creates parallel opposed fields. Most of the settings for the new beam are the same as pictured on the beam panel of the first beam (so the isocenter of the new beam is at the same place). The *gantry angle* is 180 degrees opposed.

When a beam is copied with a gantry angle increment of 180 degrees, the original beam is not changed and the copied beam should be a reflection of the original. This means that the projections of both fields coincide exactly in the plane through the mutual isocenter that is perpendicular to the mutual central axes. Blocks are copied as well (they are reflected). The new beam will *not* have a wedge selected even if the original did. The new beam's collimator angle will be set depending on the machine type, initial collimator angle, and wedge (see Table 5.1).

There are usually several different ways to achieve the intended reflection by choosing different combinations of collimator rotation angle, jaw settings, and wedge orientation. To simplify treatment setups, the Prism `Copy 180` operation is designed to avoid unnecessary differences between the original and copied fields. In particular, collimator rotation for the neutron beam is time consuming and should be avoided if possible by adjusting collimator jaws/leaf settings or rotating wedges instead. On the other hand, the Elekta machines have wedges that can *not* be rotated independently, and the collimator may have to be rotated to achieve the desired wedge orientation.

The following table (Table 5.1) details all the cases for the Prism `Copy Beam` operation for a 180 degree gantry shift, i.e., an opposed beam. The behavior described for the CNTS collimator is the same as in previous versions of Prism. For the others, there is some slight change. If there is no entry in the "Blocks" column, the x coordinates are reflected. In the "New coll angle" column, c is the original collimator angle and c' is the new collimator angle.

The several coordinate systems are defined in Chapter 3. Note that rotation angles are always positive numbers in the range 0 – 359.9 degrees.

The table merely describes some special cases of the general solution: one could design the program to *always* accomplish `Copy 180` by reflecting the field (and everything in it, including jaws, leaves, blocks, and the wedge gradient) around the gantry coordinate system y-axis. In the general case, Prism accomplishes this by using collimator rotation to reflect the collimator y-axis about the gantry y-axis. This ensures that the jaws (or leaves) in the two fields will be parallel. Then it is only necessary to reflect the collimator x-coordinates of every feature.

CNTS (neutron) collimator

Old coll angle	Wedge	Coll set mods	Blocks	New coll angle
90, 270	any,none	$y_{inf} \leftrightarrow y_{sup}$	reflect y	$c' = c$
all others		$x_{inf} \leftrightarrow x_{sup}$		$c' = 360 - c$ $0 = 0,\ 180 = 180$

SL20 modeled as Variable Jaw Collimator

Old coll angle	Wedge	Coll set mods	Blocks	New coll angle
90, 270	internal	$x_{inf} \leftrightarrow x_{sup}$		$90 \leftrightarrow 270$
	none	$y_{inf} \leftrightarrow y_{sup}$	reflect y	$c' = c$
all others		$x_{inf} \leftrightarrow x_{sup}$		$c' = 360 - c$ $0 = 0,\ 180 = 180$

SL20 modeled as Multileaf Collimator

Old coll angle	Wedge	Coll set mods	Blocks	New coll angle
90, 270	internal	reflect portal x	N/A	$90 \leftrightarrow 270$
	external,none	reflect portal x	N/A	$c' = c$
0, 180	internal,none	reflect portal x	N/A	$c' = c$
	external	reflect portal x	N/A	$0 \leftrightarrow 180$
all others	any,none	reflect portal x	N/A	$c' = 360 - c$

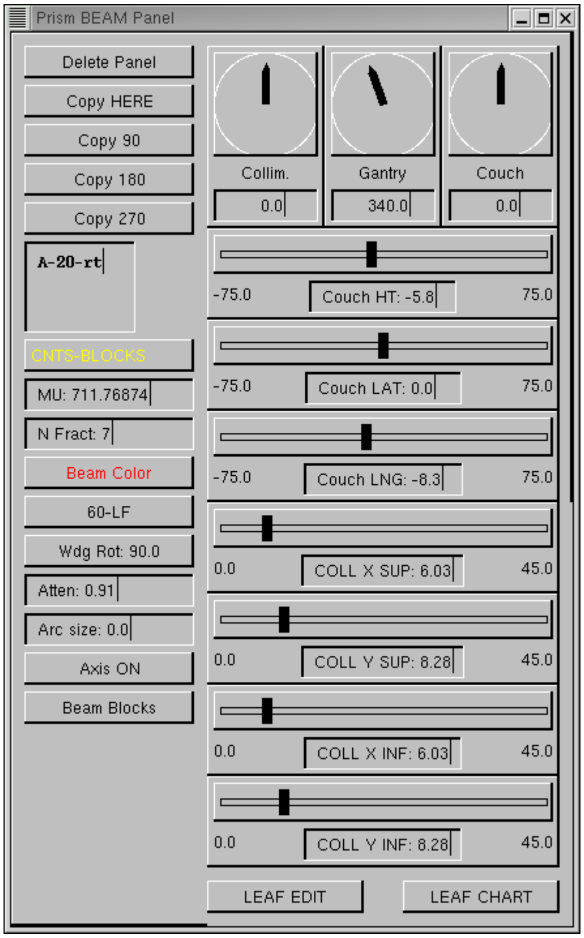
Symmetric Jaw Collimator (e.g. CLINAC 4)

Old coll angle	Wedge	Coll set mods	Blocks	New coll angle
90, 270	wedge			$90 \leftrightarrow 270$
	none		reflect y	$c' = c$
all others				$c' = 360 - c$ $0 = 0,\ 180 = 180$

Table 5.1: Copy 180: Original and copied settings

This table suggests how best to choose the Prism collimator coordinate system for each machine. In machines where the field shape is most closely defined by leaves or asymmetric jaws, the direction of leaf (or asymmetric jaw) motion should be parallel to the collimator system x axis; that is, the leaves (or asymmetric jaws) should define collimator system x coordinates. This should ensure that leaf settings fitted to the reflected portal shapes will coincide exactly.

There are cases where the operation described in the table might not be possible. Some machines have limited collimator rotation and might not always be able to reach the new collimator angle demanded. Prism does not enforce any limits on collimator angle setting, so the user must be aware of the limits on the particular machine selected.



Collim. 0.0

Gantry 340.0

Couch 0.0

A-20-rt

MU: 711.76874

N Fract: 7

Atten: 0.91

Arc size: 0.0

Couch HT: -5.8

Couch LAT: 0.0

Couch LNG: -8.3

COLL X SUP: 6.03

COLL Y SUP: 8.28

COLL X INF: 6.03

COLL Y INF: 8.28

Figure 5.1: The beam panel

5.2 Beam control buttons and textlines

5.2.1 Beam name

The *Beam Name* text field displays the name of the beam. The user may edit this name and put in any text desired, including a number, for example, `1 Left Lateral`, or `1A Lt. Lat. Boost`. The beam name can be up to three separate lines of text, with a maximum of 10 characters per line. Since this field is a multi-line box, the middle button does not erase the data as for a single line text field. In any of the three lines, characters entered beyond the limit of 10 are discarded.

5.2.2 Machine

The *Machine* button displays the name of the selected machine, e.g., `SL20A-6MV-MLC`. Pressing it pops up a menu of machine names from the local database of available treatment machines. The first machine name on the menu of names from the machine index file in the therapy machine database serves as a default machine, which is displayed on the *Machine* button when a new beam is created. (The exception is a new beam created by the `Copy` buttons, which uses the same machine as the original beam.)

When the machine type is changed, any blocks are retained with the beam, unless the new machine type is one for which blocks are not supported, in which case the blocks are deleted. For all types of machines, if a wedge was present it is deleted. This is necessary because there is no general correspondence between the wedges for one machine and the wedges for another.

Blocks cannot be used with a machine of type MLC, or with electron beams. The MLC shaping capability should be able to produce any desired aperture for photons or neutrons. For electron beams, the cutout serves in lieu of blocks. The system will not prevent you from entering a block in these cases, but it will be ignored in the dose calculation. This is (in the case of neutrons and photons) a limitation of the current dose computation model. Note that if a block is entered for an MLC or electron machine, a tray factor will be printed on the chart, but it is not used in the dose calculation.

5.2.3 Monitor Units

The *Monitor Units* text field, labeled `MU:`, displays the total number of monitor units for the beam. Any number of significant digits after the decimal point can be entered here, but the value range is from 0.0 to 10,000.0.

5.2.4 Number of Fractions

The *Number of Fractions* text field, labeled `N Fract:`, displays the number of fractions for the beam.

5.2.5 Color

The `Color` button, when pressed, pops up a menu of colors to choose from. When a new color is selected all views showing that beam are updated to show the beam in the new color. The button label is shown in the current beam color.

5.2.6 Attenuation Factor

The *Attenuation Factor* text field displays an additional attenuation factor (beyond the tray factor which is in the beam data file) that the dosimetrist may enter. When a new beam is created this is initially set to 1.0 and is labeled `Atten:`.

5.2.7 Arc Size

The *Arc Size* text field displays the size of the arc if this field is specified to be for arc therapy. A value of 0.0 in this field specifies no arc (this is the default). The arc rotation is assumed to increase clockwise from the gantry angle as the start angle. There is no visual display of arc ending angle; only the starting position of the arc is shown in views.

5.2.8 Axis On

The *Axis On* button toggles between `Axis ON` and `Axis OFF` and controls whether the central axis of the beam and accompanying tic marks is displayed for any views in which the beam's central axis lies in the plane of the view.

5.3 Wedges

5.3.1 Wedge selection

The *Wedge* button has the name of the selected wedge (or `No wedge`) on the button. Pressing it pops up a menu of available wedges for the currently selected machine. Different machines may have different assortments of wedges available, and the list that appears is specific to the current machine type for the beam. If wedges are not available for use with the selected machine, the menu lists only one choice, `No wedge`.

5.3.2 Wedge Rotation

The *Wedge Rotation* button displays an angle, corresponding to the wedge rotation angle relative to the collimator coordinate system. This also varies with machine type, and the menu that is popped up in order to select the orientation angle reflects that. The button shows `Wdg Rot:` and the angle, unless no wedge is selected. If no wedge is selected this field is blank. When no wedges are available for use with the selected machine, the menu is not available.

5.4 Blocks

The beam panel contains a "Beam Blocks" button, which brings up the block editing panel (see chapter 6).

5.5 Machine rotations

The upper right section of the beam panel is taken up with three dials, one each for the gantry angle, the collimator angle and the couch angle.

The Prism system uses a set of coordinate systems and conventions which is independent of any particular treatment machine manufacturer's coordinate system. Consequently, all components of the Prism user interface conform to the coordinate systems used by Prism, and all aspects of planning are done with reference to these systems. Translations of treatment machine set up parameters from Prism's coordinate system to a local manufacturer's system are made on the hardcopy of the part of the plan containing the treatment machine set up information. This correspondence is detailed in Appendix A for all treatment machines in use at the University of Washington. When using the Prism system, you can preview what the translation produces by making a chart with the "File only" destination, and then using a PostScript preview program such as `ghostview` or `gv`.

The Prism conventions for gantry, couch and collimator angles are as follows:

Gantry angle: when the gantry angle of a beam in the Prism system is 0.0, the gantry is set so that the beam is directed down at the couch from above. The gantry angle value increases as the gantry rotates *clockwise* as seen from the far end of the couch looking toward the isocenter and the gantry itself (when the couch is perpendicular to the plane of rotation of the gantry, i.e., couch angle 0.0).

Couch angle: when the couch angle in the Prism system is 0.0, the couch is perpendicular to the plane of rotation of the gantry, i.e., at "home" position. The couch angle increases as the couch rotates *counterclockwise* as seen from *above*.

Collimator angle: when the collimator angle in the Prism system is 0.0, the collimator is at "home" position. The corresponding machine specific collimator angle setting for machines in use at the University of Washington Radiation Oncology Department is specified in Appendix A. The collimator angle in the Prism system increases as the collimator rotates *counterclockwise*, as seen from the target inside the machine, through the collimator system, toward the isocenter.

5.6 Couch linear motions

Below the dials there are three sliders for couch lateral, longitudinal and height motions. The values displayed are in cm and represent displacement (distances) from the couch "home" position. See pages 30 and 107 for further explanation. The limits on vertical motion (couch height) are +/- 75.0 cm. The default limits on the other two motions are the same, but these are configurable parameters that can be changed as described in section 4.2.

5.7 Collimator subpanels

The machine type determines the type of collimator system and settings available. The beam panel has a collimator subpanel that is changed as needed to provide the proper sliders or controls for the type of collimator on the selected machine. The collimator subpanel may have zero to four sliders for collimator settings. The number of sliders depends on the type of machine. Their number and labels change as appropriate when a different machine is selected.

If the collimator type is a multileaf collimator, no collimator sliders appear. Instead a MLC collimator subpanel appears in this area. The MLC subpanel includes a *Source to Film Distance* text field like the one in the block editing panel. There are no `Name` or `Color` fields, since these are determined by the field itself, and there is no `Delete Portal` button because there is always a portal (the portal is initially a 10.0 cm square when a new field is created).

For electron beams, an electron collimator subpanel provides the relevant controls, described in section 5.7.2.

The available collimator controls correspond to the collimator type as follows:

Symmetric jaw: Sliders for X and Y jaw.

Combination jaw: Sliders for X superior, X inferior, and Y jaws.

Variable jaw: (also called *Asymmetric*) Sliders for X superior, Y superior, X inferior, and Y inferior jaws.

Multileaf: Text field for source to film distance. Buttons for beam portal drawing and leaf display (Chapter 9), and leaf chart printout. The leaf chart button, when pressed, produces a printed multileaf collimator chart (see section 2.7.1).

Neutron: Sliders for X superior, Y superior, X inferior, and Y inferior jaws. Buttons for leaf display (Chapter 9) and leaf chart printout (as described above).

Electron: Buttons for applicator selection (cone size) and cutout drawing (beam portal). See section 5.7.2 for details.

5.7.1 Changing machine type

When the machine type is changed, and the new machine has a different type of collimator than the original, the new collimator settings are chosen to match reasonably closely with the old ones, as specified in Table 5.2. For this purpose, the neutron beam collimator behaves the same as an *asymmetric* collimator, and an electron beam behaves similarly to an *MLC*. The MLC and VJC variants of each of the Elekta machines are considered *different* machine types. When a photon beam is changed to an electron beam, the cutout contour is computed from the collimator settings, but the electron cone size is set to the default value of 10 cm.

5.7.2 The electron cutout editing panel

The electron cutout editing panel includes some controls in the space normally occupied by the collimator controls on the beam panel.

- a `CONE:` button, which, when pressed, displays a menu of the available electron applicator cone sizes, from which the user can select. The applicator cone size appears as a part of the button label. When an electron machine is selected as the machine type for a beam, the applicator cone size is set to a default value, 10 cm.
- a `CUTOUT CONTOUR` button that brings up a contour editor, with the usual Accept, Clear, Mode buttons and magnification slider, but without any other controls. The title bar of the contour editor panel has on it the name of the beam to which this cutout belongs. This contour editor displays anatomy and points of interest as in a beam's eye view, and provides for

Old coll.	New collimator type				
type	Symmetric	Combination	Asymmetric	MLC	Electron
Symmetric	same	$x_{sup} = x_{inf} = x/2$ $y = y$	$x_{sup} = x_{inf} = x/2$ $y_{sup} = y_{inf} = y/2$	compute portal	like MLC
Combination	$x = x_{sup} + x_{inf}$ $y = y$	same	same for x $y_{sup} = y_{inf} = y/2$	compute portal	like MLC
Asymmetric	$x = x_{sup} + x_{inf}$ $y = y_{sup} + y_{inf}$	same for x $y = y_{sup} + y_{inf}$	same	compute portal	like MLC
MLC	$x = y = 10$	$x_{sup} = x_{inf} = 5$ $y = 10$	$x_{sup} = x_{inf} = 5$ $y_{sup} = y_{inf} = 5$	same	like MLC
Electron	$x = y =$ cone size (cs)	$x_{sup} = x_{inf} = cs/2$ $y = cs$	$x_{sup} = x_{inf} = cs/2$ $y_{sup} = y_{inf} = cs/2$	compute portal	same

Table 5.2: Relation of new collimator settings to old when a beam's collimator type is changed

drawing a cutout contour. The applicator nominal square field size at isocenter is displayed as part of the background. The initial contour is a square corresponding to the current applicator size. When the `Accept` button on the contour editor is pressed, the cutout contour in the electron beam is updated, unless the contour being edited has less than three points or is self-intersecting, as for other contours. The electron cutout contour editing panel remains on the screen until the `Beam portal` button is pressed again, which removes the contour editing panel, without changing the electron cutout contour (i.e., deleting the panel does *not* "accept" the contour in the contour editor).

In the contour editor, it is understood that the contour defines the opening inside the cutout (not the outside of the cutout material — the user should not draw in the surrounding square border of the cutout material). The user should not draw a contour larger than the applicator size, but the Prism system does not check for this. If the contour is larger than the applicator aperture, the electron dose calculation will fail.

When the digitizer is used, the hardcopy is usually a cutout film. As with blocks, the user should place the hardcopy on the digitizer tablet in a fixed orientation with respect to the patient (actually, fixed in the gantry coordinate system), regardless of of collimator rotation. As with blocks, the user should determine the gantry angle and the collimator angle before drawing the cutout.

The electron cutout editing panel does not require any `Name` or `Color` fields, since these are determined by the field itself, and there is no `Delete Cutout` button because there is always a cutout.

Chapter 6

Block editing panel

The block editing panel (figure 6.1) contains a contour editor for drawing the block outline and buttons and textlines for setting the block name, color and transmission. The title bar of the block editing panel has on it the name of the beam to which the block belongs. A single block editing panel provides access to all the blocks for a given beam. Blocks may be added, selected or deleted without closing and reopening the panel.

6.1 Block outline drawing

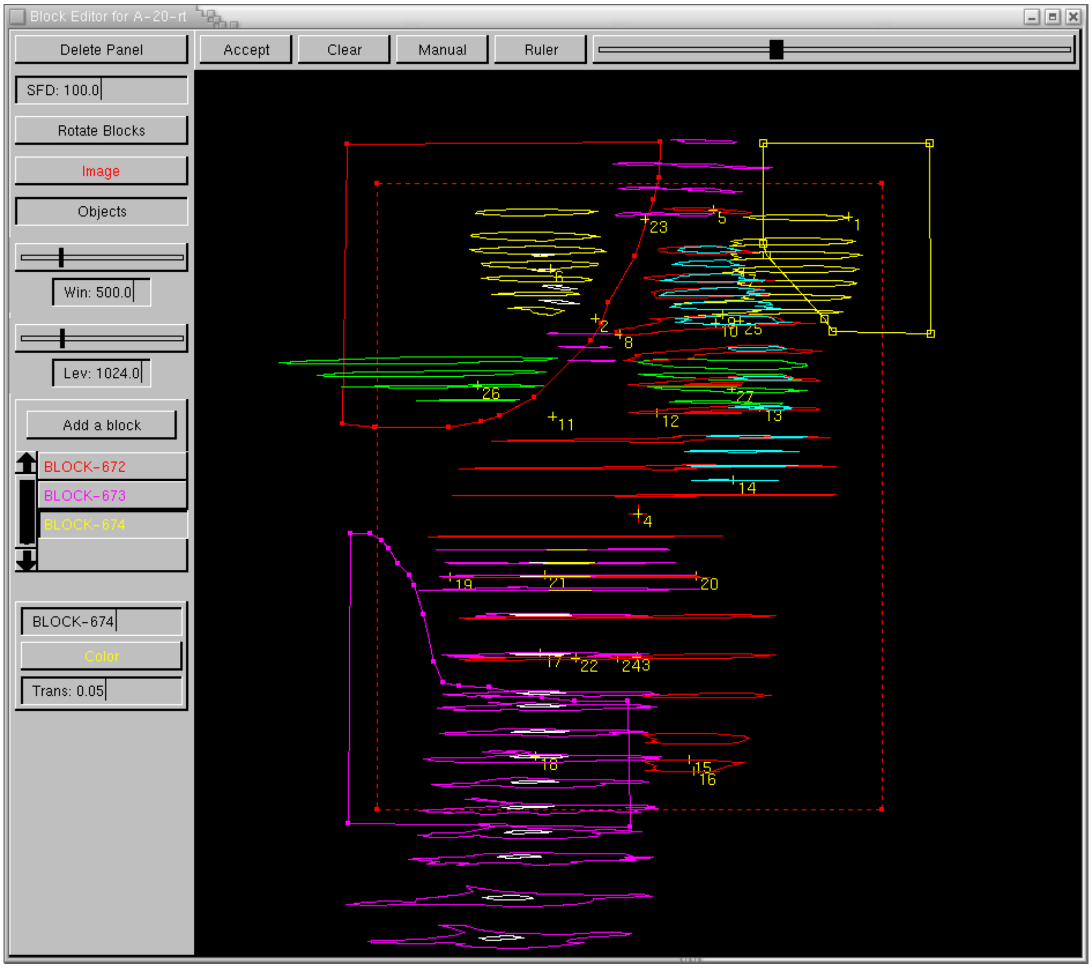
The control region of the block contour editor is like that described in section 17.5, except that the `Automatic` mode is inactive for block entry. The ruler and landmark functions are available. The ruler scale applies to the plane of the isocenter since that is the plane of the drawing region.

The drawing region of the block panel contour editor shows a “beam’s eye view” in the display region, showing all the projected contours for anatomy, tumors and targets, as well as points of interest projected to the view plane. This view also shows the outlines of any other blocks already entered for that beam, and the field aperture defined by the collimator angle and the collimator jaws. The view depicts everything the same way as a beam’s eye view at the plane of the isocenter, so the projected anatomy is always displayed the same way independent of the collimator angle, and the rectangular field aperture, along with any blocks already defined, is displayed rotated by the amount of the collimator angle.

When block contours are entered in manual mode (using the mouse and display), Prism determines the scale factor automatically and neither the Source to Film Distance nor the digitizer magnification factor has any effect. This mode may be useful when all the necessary anatomy is delineated already and therefore appears in the block editing display as in a beam’s eye view.

6.2 Film orientation on the digitizer

There is a digitizer entry mode for block contours. This enables block contours to be digitized from simulator films. The film always goes onto the digitizer tablet in the same orientation *with respect to the gantry*, regardless of the collimator angle or the film casette orientation. (In other words, the hardcopy is understood to be fixed in the *gantry coordinate system.*) For example, in the usual case



SFD: 100.0

Win: 500.0

Lev: 1024.0

BLOCK-674

Trans: 0.05

Figure 6.1: The block editing panel

where the couch rotation is zero and the patient's head is toward the gantry, the film always goes on the tablet with the patient's head up, as in a portrait. Depending on the casette orientation, the film's longer dimension might go left-right or up-down; no matter, as long as the patient's *head* is toward the top.

The anatomy is portrayed in the contour editor display in the same orientation as it appears in the hardcopy on the digitizer tablet, regardless of the collimator angle or casette orientation. The origin on the digitizer hardcopy must be the *beam central axis*.

The user should take care to select the gantry angle and the collimator angle before drawing (or digitizing) blocks. Then, when the user draws (or digitizes) the block contour, that new block will appear in the contour editor display (and in the plan) in the proper orientation. However, if the user subsequently changes the collimator angle, the blocks will rotate with the collimator, and will move out of the orientation that the user entered. If the rotation is 90, 180 or 270 degrees, the *Rotate blocks* function can be used to reposition the blocks. If it becomes necessary to change the collimator angle by some other amount, the user will have to re-enter all the block contours. Of course if the user changes the gantry angle, the blocks will need to be redrawn also.

The display will *not* update with changes in the beam gantry angle, couch angle, or couch translational motions. If any of these parameters are changed, the block editing panel should be deleted and reselected in order to get the proper beam's eye view display.

6.3 Other controls

In addition to the contour editor, the block editing panel includes *Delete Panel*, a textline for entering *Source to Film Distance*, a button for rotating the blocks, a selector panel for adding, selecting and deleting blocks, a `Name` textline, a `Color` button, and a textline for entering a block transmission factor.

6.3.1 Source to Film Distance

The *Source to Film Distance* text field (labeled `SFD:`) affects the default scale factor from cm on the digitizer hardcopy to cm in the gantry coordinate system. When the digitizer is selected, the digitizer magnification factor is set to the ratio of the source-to-film distance and the source-to-axis distance. For block entry with the digitizer, users may enter the actual Source to Film Distance in cm, or put a film magnification factor in the subsequent dialog box. The value of Source to Film Distance defaults to the beam's source-to-axis-distance each time a block editing panel is selected; its value is not part of the stored plan data (Prism stores block contour dimensions referenced to isocenter distance, regardless of source to film distance used during data entry). If you put the actual Source to Film Distance in cm, the Mag. factor dialog box will already have the appropriate magnification factor and all you need to do is press "Accept". This does *not* work in reverse, i.e., the number you put in the Mag. factor dialog box does not affect the value in the SFD textline.

6.3.2 Rotation of blocks

There is a button labeled `Rotate Blocks` just below the SFD textline. When this button is pressed, a menu containing three rotation angles ($90°$, $180°$, and $270°$) is popped up. When one of these angles is selected by the user, all the blocks for the beam are rotated around the collimator by the angle specified, in the counter-clockwise direction. This operation roughly models the rotation of the blocking tray on the treatment machine head, and is provided so that users of the system do not need to re-digitize previously entered blocks if they later decide to change the beam's collimator angle to accommodate a wedge.

6.3.3 Image button

This button operates the same as for a *beam's eye view* in the view panel, as described in chapter 16.

6.3.4 Objects button

This button operates the same as in the view panel, described in chapter 16.

6.3.5 Window and level sliders

These sliders operate the same as in the view panel, described in chapter 16.

6.3.6 Block selector panel

Below the sliders there is a selector panel for adding, deleting and selecting blocks. Only one block can be selected at a time. It is possible to delete all the blocks (one by one) if the user decides, after entering one or more, that the beam should not have any blocks.

6.3.7 Name

Each block can be given a name, which is entered in the textline directly below the selector panel. A default name may appear here when a block is added using the block selector panel. The name entered in the textline also appears in the block selector panel after the text is registered (by pressing “Enter”).

6.3.8 Color

Below the name textline there is a color button for setting the color of each block.

6.3.9 Block Transmission

The *Block Transmission* text field (labeled `Trans:`), below the color button, represents an estimated effective block transmission factor, usually near 0.0; it defaults to 0.05. The allowed range of values is from 0.0 to 1.0.

Chapter 7

Brachytherapy sources panel

The brachytherapy panel provides the facilities for selection of brachytherapy source types and entry of the source locations. It contains control buttons for selecting source type (line sources or seeds) and entry methods (XYZ or orthogonal films) for source coordinate entry, two subpanels for selection of sources and specification of source attributes, and a subpanel for display of dose rates and total doses from the entire group of sources to individual points.

The various input modes provide for editing or re-entering coordinates of a single source or a whole group of sources, as described below. The source attributes subpanels at the bottom of the brachytherapy panel provide editing of attributes of a single source at a time. There are two subpanels, one for seeds and one for line sources. It is possible to make a plan containing both seeds and line sources (and external beams). Access to either subpanel is available at any time the brachytherapy panel is displayed.

All these subpanels are described in the remainder of this section. The brachytherapy panel is shown in figure 7.1.

It is possible to add some line sources, and then add some seeds (or seeds first and then line sources, or even different kinds of seeds). It is possible to create a plan combining line sources and seeds (and even external beams, though the meaning of total dose becomes problematic in that case), and it is possible to mix different types of line sources and different types of seeds in the same plan.

7.1 Source data entry controls

In the upper left, in addition to the usual `Del Panel` button, for removing the brachytherapy panel, there is a two element radio menu for selecting either seeds or line sources. This pertains to the operation of the other data entry controls in the upper part of the brachytherapy panel. Next to it there is a four element radio menu, to select the coordinate entry method. Next, on the right, there is a subpanel for coordinate entry. The details of this panel depend on the combination of source type and entry mode.

Below the coordinate entry subpanel is a subpanel for specifying attributes of sources being added to the plan. These attributes are: the source model, source strength, and application time. This panel can also be used to change any of these attributes for a range of sources, and the subpanel

Curr: 1
End: 1
X: 0.0
Y: 0.0
Z: 0.0

Ir192-TG43 Daskalov C=1.11 A=0.97
Source strength: 1.0 U
Application time: 1.0 Hours
Source number range: First: Last:

Point name	Dose rate	Total dose
21 POINT-317	81.1	2558.5
22 coord origin	14.6	417.7

	Source type	Strength		Perm	App. time	X	Y	Z	Delta Z
1	Ir-192 seed orig C=7.90 A=1.00	0.665	mgRa	P	38.0	-2.61	-1.81	-6.29	
2	Ir-192 seed orig C=7.90 A=1.00	0.333	mgRa	P	38.0	-2.63	-1.78	-5.28	
3	Ir-192 seed orig C=7.90 A=1.00	0.333	mgRa	P	38.0	-2.71	-1.80	-4.27	
4	Ir-192 seed orig C=7.90 A=1.00	0.665	mgRa	P	38.0	-2.21	-0.63	-5.46	
5	Ir-192 seed orig C=7.90 A=1.00	0.333	mgRa	P	38.0	-2.28	-0.63	-4.47	
6	Ir-192 seed orig C=7.90 A=1.00	0.333	mgRa	P	38.0	-2.37	-0.69	-3.41	

Figure 7.1: The brachytherapy panel

can also be used to delete a range of sources.

The button for selecting the specific source model (isotope, etc.) brings up a popup menu of available source models from the source catalog (see section 15). This popup menu contains either the line source types in the source catalog, or the seed source types in the source catalog, depending on the setting of the source type button. The source types are defined using the source table management panel, described in Chapter 15.

7.1.1 Adding sources

New sources are added by selecting either seeds or line sources, and then using either the XYZ or Ortho films entry mode, with either the keyboard or the digitizer (see section 7.2). As the coordinates are entered, the new sources are assigned other attributes according to the settings on the attributes subpanel in the center of the brachytherapy panel.

The default application time is 1.0 hours, and the default activity is 1.0 source strength units. However, the user can set these to some other initial value, and enter a set of sources using the new values as defaults. The default values will revert to 1.0 the next time the brachytherapy panel is opened. The source strength unit depends on the type of source, as described in section 15. It is possible to have in the source type catalog different source types with the same isotope and different source strength units, eg., Ir-192 specified in mgRa and Ir-192 specified in mCi, or other units.

There is no built in limit to the number of sources in a plan. The allowable range of application times is from 0.0 to 10000.0 hours. The allowable range of activity or source strength is from 0.0 to 100.0 source strength units.

7.1.2 Deleting sources

A range of sources may be deleted by entering the ID number of the first source in the range, in the textline labeled `First:`, and the ID number of the last source in the range in the textline labeled `Last:` and then pressing the `Delete` button.

7.1.3 Modifying sources

It is possible to assign some of these attributes to whole groups of seeds simultaneously, as well as individually. For each of the three attributes that can be changed, there is a `Change` button to the left of the attribute specification. Pressing the `Change` button modifies all the sources in the range specified in the `First` and `Last` textlines.

7.2 Source coordinate entry

There are several ways to enter or edit the source locations in the patient's body. They are selected by a radio menu on the upper left of the brachytherapy panel. The menu buttons for selecting the coordinate entry mode are labeled according to the entry mode, either `XYZ`, `Ortho`, `Table shift`, or `Images`. Only two of these, the XYZ and Ortho films methods, are implemented. Transverse sections, template panels, and stereo shift film entry are not supported in this release.

In both source coordinate entry methods, the user types in the `Curr:` textline the starting ID number of a source to be entered (or re-entered, which is also allowed). The `End:` textline should contain the ID number for the last source to be entered or re-entered. The sources will be sequentially added or updated, by ID number. Each time the user presses the `Enter` button, the data currently in the coordinate textlines is stored and the `Current:` ID number is incremented, until the `End:` ID number is reached. After that, no further increments are made.

7.2.1 Keyboard entry and XYZ method

The user may type into the textlines provided in the coordinate entry subpanel, the actual (not magnified) x,y,z coordinates in space of the seeds or the two ends of each of the line sources. This entry mode is provided for creating “standard geometry” template plans, such as eye plaques, idealized planar geometries for seed preplans, and other such plans.

The process is:

1. enter the starting ID as Curr and the ending ID as End,
2. type in the X, Y, and Z coordinates of the first source and press `Enter`,
3. type in the X, Y, and Z coordinates of the next source and press `Enter`,
4. repeat the above step until the last set of coordinates is entered.

Any single source can be re-entered by putting its ID number in as the Curr value. Any range of sources can also be re-entered similarly. The user does *not* have to keep entering coordinates until the End ID is reached. You can change the Curr ID any time, to skip around. This is also true of keyboard entry of orthogonal film data when typing the numbers in, instead of using a digitizer.

7.2.2 Orthogonal films

The brachytherapy panel includes a capability for input from orthogonal films on the digitizer. As explained in the list of buttons and text fields below, any combination of: either AP or PA, and either left or right lateral, can be used.

In this input mode, shown in figure 7.1, the following buttons and textlines appear in the coordinate entry subpanel:

- A button for specifying either AP or PA film. Either can be used but the user must select which, using this button. The button toggles between these two choices. The default is AP.
- A textline for specifying magnification factor for the AP (or PA) film on the digitizer. This number is kept with the plan data as well as the raw input coordinates from the film.
- A button for specifying either right or left lateral film. Either can be used but the user must select which, using this button. The button toggles between these two choices. The default is left lateral.
- A textline for specifying magnification factor for the Lateral film on the digitizer. This number is kept with the plan data as well as the raw input coordinates from the film.

When adding sources or modifying source coordinates, if the digitizer has not been used previously in the current Prism session, the user is asked to digitize the lower left and upper right corners, to determine the digitizer scale, for conversion from digitizer counts to actual cm on the digitizer. This is not the magnification factor, which pertains to the films themselves. The user must be sure to enter the magnification factor in the appropriate textline for each film, before proceeding.

Then the user is prompted for input first from the AP film, for all the sources, and then from the Lateral film for all the sources.

For each film, the user is prompted to digitize the origin, once for each set of sources to be entered, then the source locations in sequence (for seeds) or the first and second end for each source (for line sources). The user must keep track of which ends are which. The ID of the source to be entered and the label (A or B) of the end to be entered, are displayed in a prompt box on the screen.

The origin should be a user selected anatomic point easily identifiable on each film. The origin is not the digitizer origin but the patient coordinate origin, so that the data from the two films may be correlated correctly.

There is no automatic seed or line source sorting or coordinate matching in the Prism system.

Each film must be placed on the digitizer so that the negative z-axis, the direction from the patient's feet to the head, is pointing toward the top of the digitizer. The film should be placed on the digitizer for the AP film, as it would be if you were looking toward the patient and the film, from the X-ray source. For the lateral film, similarly, it should be as seen from the X-ray source, but rotated so that the patient's head is at the top of the digitizer. It is possible to put and leave both films on the digitizer at the same time, since an origin is entered separately for each.

The data are graphically displayed on the screen as you enter them, in any views that are displayed. By displaying a coronal view and a sagittal view, you can visualize the sources as seen on the AP and lateral films, respectively, although the orientations may not be the same.

7.3 Source attribute editing

The brachytherapy panel has two subpanels at the bottom, showing line sources in one, and seeds in the other. These subpanels provides editing of the non-geometric attributes of the sources, i.e., display color, type, activity, insertion time, etc. (whether sources are visible is implied by color).

7.3.1 Arrow buttons

In the subpanel, there is a table containing a row of buttons and textlines for up to six sources. Up and down arrows will shift the list to display additional sources. Left-clicking on an arrow will move the list by one row, and center-clicking will move it ten rows at a time.

7.3.2 Source color (the number button)

In each row, starting on the left, the first field is a button labeled by the source number, assigned by the Prism system, when it is added to the list. The color of the label on this button is the display color of the source. When you press the source number button, a popup color menu appears, to change the color of the source.

7.3.3 Source type for each source

The next field is a button whose label identifies the source type, model, etc. Pressing this button brings up a popup menu of source types to choose from, so that the type of each source may be individually specified or changed.

7.3.4 Activity and units for each source

The next field is a textline for displaying (and editing) the source strength. Following the numerical value of the source strength is a label from the source catalog identifying the units of source strength. The user may change the source strength of any source at any time.

7.3.5 Application time for each source

The next field is a textline for editing the application time. The units are hours. The user may change the values for any source at any time. This value can be specified to any desired precision, up to 8 decimal places, eg., a value of 0.00000001 hours is acceptable, but no more than 8 significant digits are used, so 100.000001 hours will be rounded to 100.0 hours.

7.3.6 Display of geometric information for each source

The remaining columns are readouts, showing different information depending on whether line sources or seeds are displayed.

When line sources are displayed in the subpanel, the readouts show the active length, the nominal physical length, and the computed physical length of each source, where active length and nominal physical length are values taken from the source catalog. They are displayed to provide additional assurance, besides the type label, that the right sources were selected and that the coordinate entry produced reasonable results.

When seeds are displayed in the subpanel, the additional columns show for each seed the X, Y, and Z values of the seed coordinates derived from the data entry, and the difference between Z values determined from the two films (for orthogonal film entry) similarly to provide a check on the coordinate entry procedure.

7.4 The point dose subpanel

In the upper right of the brachytherapy panel, there is a subpanel for displaying the total doses to any specified points of interest from all the sources, line sources and seeds combined. The first column contains up and down arrow buttons that can be used to scroll through the points if there are too many to display in the available space on the panel. The point names are shown in the second column. The dose rate for the combined effect of all sources, in rads per hour, is shown in the next column, and the total dose for the specified application times (can be different for different sources) is shown in the last column. At the top is a “Compute Dose” button. When pressed, this will cause computation of all the doses to all points from all sources.

If the user enters a new dose rate or total dose for a point, either new activities or new application times are computed for all sources, and the doses of all the other points are updated accordingly. There are two buttons to the right, above the dose rate and total dose columns. When one is pressed, the other turns off, and vice versa. This selection controls what happens when a new number is entered for total dose to any point. If the time button is on, the application time for all sources is rescaled to produce the specified dose. If the activity button (labeled “Act.”) is on, entering a new dose for a point will cause the activites to be rescaled. In either case, the proportions of times and activites will be kept. So, if some sources have double the activity of others, that ratio will be maintained even though the values may be increased or decreased.

Chapter 8

Dose-volume histogram (DVH) panel

The DVH panel provides a facility for inspecting the quality of a treatment plan. Figure 8.1 shows a sample DVH panel, for a critical structure, i.e. an “organ”.

8.1 DVH panel buttons

8.1.1 Bin Size

The `Bin Size[cGy]` textline specifies the width per bin for the display of the dose-volume histogram. The default value is 2cGy.

8.1.2 Max Dose

The `Max Dose[cGy]` readout represents the maximum value of the displayed dose-volume histogram.

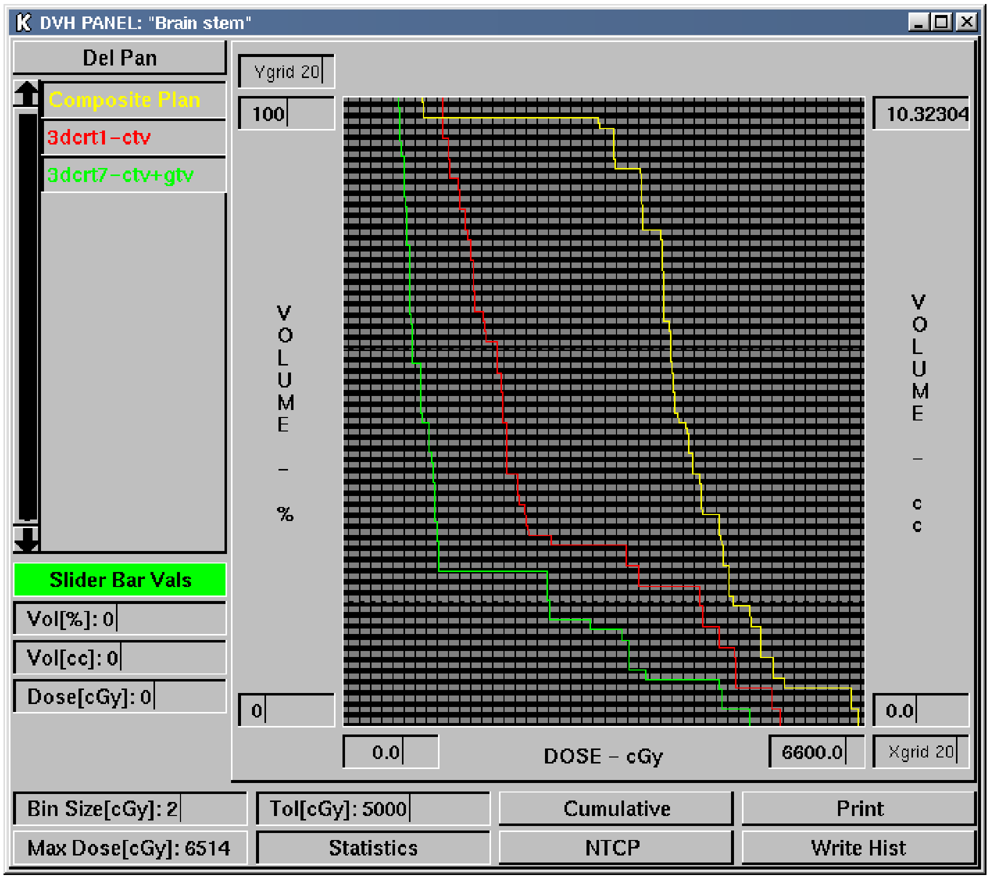
8.1.3 Prescription/Tolerance dose

Depending on the object selected the field is labeled `Prescr[cGy]` or `Tol[cGy]`. It displays either the prescribed dose (in cGy) for the Planning Target Volume (PTV)/Clinical Target Volume (GTV) or the tolerance dose for other organs. If the prescribed dose has not been previously entered in the volume editor panel the text field is set to a default value of 0.0. Entering a value updates the corresponding field in the volume editor panel.

(-> Update of display not yet implemented!). (Is it necessary to describe where the dose is prescribed to?)

8.1.4 Statistics

The `Statistics` button brings up a table which reports information regarding the quality of each plan. The plan quality specification criteria correspond to the recommendations by the Intensity Modulated Radiation Therapy Collaborative Working Group [10]. Note that prior to selecting the `Statistics` button a value has to be entered in the `Prescr[cGy]` field. The calculations for



Vol[%]: 0
Vol[cc]: 0
Dose[cGy]: 0
Bin Size[cGy]: 2
Tol[cGy]: 5000
Max Dose[cGy]: 6514

Figure 8.1: The dose-volume histogram (DVH) panel

the statistics panel are based on a bin size of unity and not on the value entered in the `Bin Size` textline. If a large bin size has been chosen for the display, this may result in a slight discrepancy between the statistics values calculated and the plot display. Only the plans which are selected in the DVH panel are analysed. The criteria are as follows:

D_{100} Dose that covers 100% of the PTV/CTV or organ, i.e. the minimal dose.

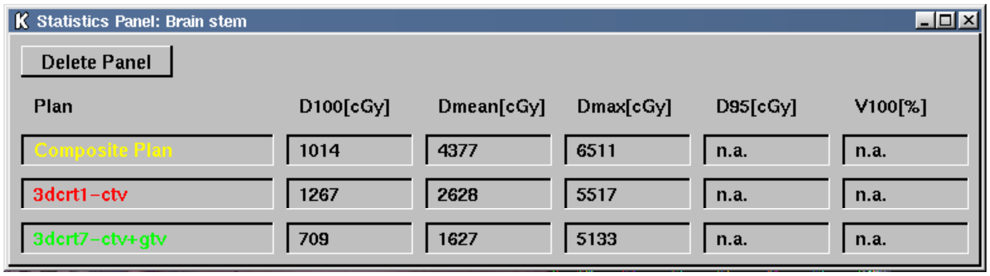
D_{Mean} The mean dose.

D_{Max} The maximum dose.

D_{95} Dose that covers 95% of the PTV/CTV.

V_{100} Percentage of the PTV/CTV that receives the prescribed dose.

An example of a statistics panel is shown in Figure 8.2. Note that the D_{95} and V_{100} values can only be attributed to the PTV/CTV. For organs, the D_{95} and V_{100} readouts are set to “n.a.” , denoting “not applicable”. Any change in Prism which will result in the modification of the dose distribution, and consequently the DVH, will close the statistics panel (-> not yet implemented). Note that if the D_{100} value is zero it is very likely that the dose grid does not cover the entire object.



Plan	D100[cGy]	Dmean[cGy]	Dmax[cGy]	D95[cGy]	V100[%]
Composite Plan	1014	4377	6511	n.a.	n.a.
3dcrt1-ctv	1267	2628	5517	n.a.	n.a.
3dcrt7-ctv+gtv	709	1627	5133	n.a.	n.a.

Figure 8.2: The statistics panel

8.1.5 Cumulative/Differential DVH

This button toggles between `Cumulative` and `Differential`. The graphical dose-volume histogram display changes appropriately.

8.1.6 Biological Models for the Tumor Complication Probability (TCP) and the Normal Tissue Complication Probability (NTCP)

Depending on the object selected the button is either labeled `TCP` or `NTCP` and on selection the appropriate model is activated and the corresponding panel is displayed.

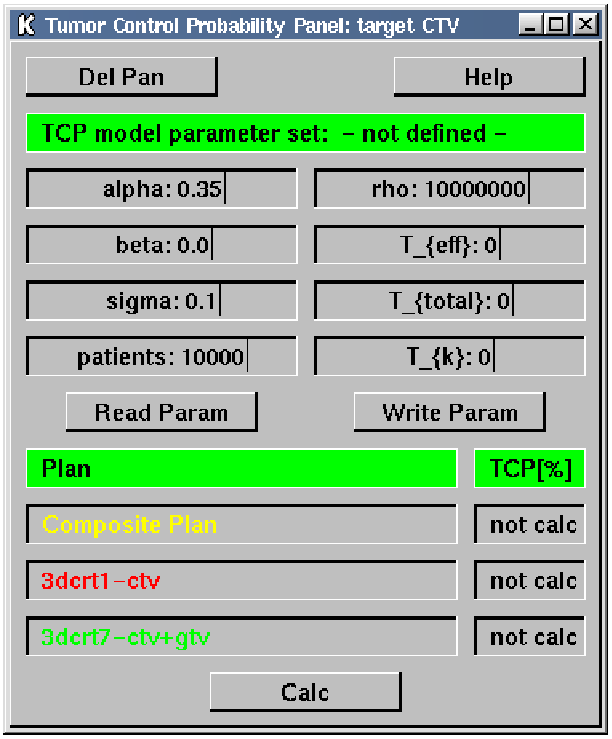
TCP panel

The TCP panel is subdivided into two regions as shown in Figure 8.3. Parameters which are required for the TCP model can be entered in the top half, denoted “TCP model parameter set:”. The default parameter set is denoted “- not defined -”. The parameters are explained in the following.

α_0 Parameter referring to the linear term in the linear-quadratic (LQ) model [11]. The valid range of alpha is: $0.001 \leq \alpha_0 \leq 1\text{Gy}^{-1}$.

β Parameter referring to the quadratic term in the LQ-model. Note that for low dose fractions ($\leq$ 2Gy) the β term can be ignored, i.e. β can be set to zero. The valid range of β is: $0 \leq \beta \leq 0.2\text{Gy}^{-1}$.

ρ The uniform density of clonogenic cells in the tumor. The recommended value is $10^7 cm^{-3}$ [12].



Tumor Control Probability Panel: target CTV

TCP model parameter set: – not defined –

alpha: 0.35
rho: 10000000
beta: 0.0
T_{eff}: 0
sigma: 0.1
T_{total}: 0
patients: 10000
T_{k}: 0

Plan	TCP[%]
Composite Plan	not calc
3dcrt1–ctv	not calc
3dcrt7–ctv+gtv	not calc

Figure 8.3: The TCP panel

σ To incorporate patient heterogeneity, i.e. the intrinsic radio-sensitivity of different patients, a Gaussian distribution of the mean α_0 value is assumed for a population of patients. The standard deviation σ describes the width of the Gaussian distribution with mean α_0.

`Patients` The number of patients with varying α_0. For each patient a random α_i is generated (Gaussian distribution). The larger the number of patients is set the longer it takes to calculate the TCP but the smaller is the variance of the TCP value when the calculations are repeated with the same settings. The recommended minimum value is 10^3 – 10^4 [12]. The final choice is therefore a trade-off between speed and accuracy, i.e. reproducibility, of the TCP result.

T_{Eff} The effective doubling time of tumor clonogens (in days).

T_{Total} The overall treatment time (in days).

T_K The time between first treatment and the start of tumor proliferation (in days). It is also referred to as the “kick-off” time.

Note that if the effects of tumor re-population during the course of radiation therapy are not desired to be included into the TCP calculations, any of the time dependent values, i.e. T_{Eff}, T_{Total} or T_K may be set to zero.

Each plan selected in the DVH panel is listed in the bottom half of the TCP panel (see Figure 8.3), denoted “Plan”, in combination with a readout for the TCP value. Selecting the `Calc` button starts the TCP calculation(s). The default value for the TCP readout is “not calc”, denoting that the TCP value has not yet been calculated. During the calculation of the TCP “calc...” is displayed in the corresponding readout indicating the progress of the calculations before the final value is displayed.

The buttons `Write` and `Read` enable the operator to store and retrieve, respectively, sets of parameters. User defined parameter sets can be stored by selecting the `Write` button. A descriptive name can be assigned, such as e.g. `breast 55Gy` or `head and neck 70Gy`. The TCP parameter sets are stored in the `tcp-data` file in the `/prismdata` directory. When the `Read` button is selected, a radio-scrolling-list appears with the available parameter sets which have been stored previously (see Figure 8.4). On selection of the `Accept` button the respective parameters appear in the textline readouts in the TCP panel and the name of the selected parameter set is updated.

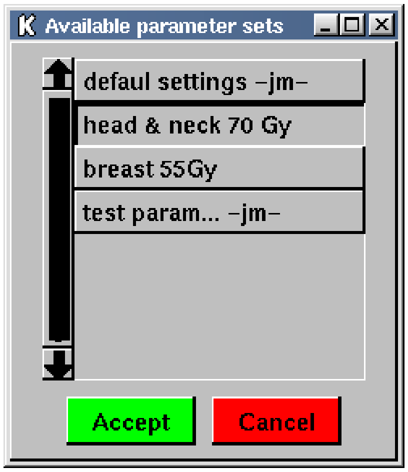


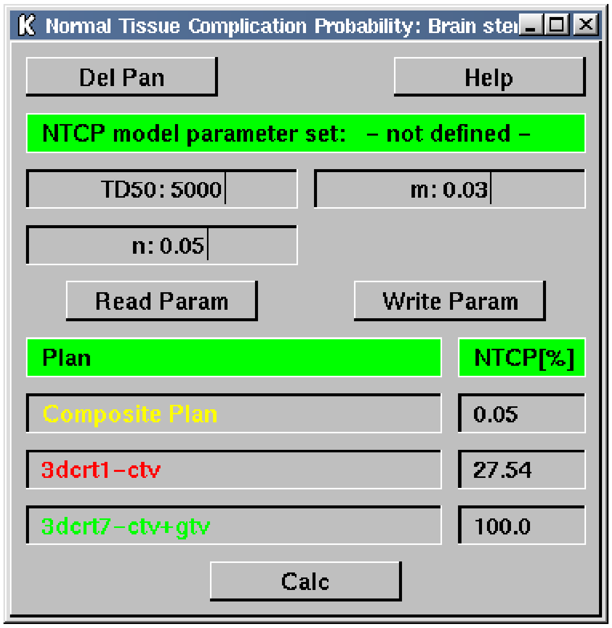
Figure 8.4: Read parameter set

The `Help` button (see Figure 8.3) displays a brief description of the parameters for the TCP model.

Any change in Prism which will result in the modification of the dose distribution, and consequently the DVH, will close the TCP/NTCP panel (-> not yet implemented).

NTCP panel

The design structure of the NTCP panel (Figure 8.5) is analogous to the TCP panel. The NTCP parameters are stored in the `ntcp-data` file in the `/prismdata` directory. The `Read`, `Write`, `Help` and `Calc` buttons have the same functions as for the TCP panel with respect to the NTCP calculations. The parameters required for the NTCP model are as follows [13, 14]:



NTCP model parameter set: – not defined –

TD50: 5000

m: 0.03

n: 0.05

Plan	NTCP[%]
Composite Plan	0.05
3dcrt1-ctv	27.54
3dcrt7-ctv+gtv	100.0

Figure 8.5: The NTCP panel

$TD50$ The dose to a reference volume (in Gy) that would result in 50% complication probability after 5 years.

n Parameter describing the volume dependence. The valid range of n is: $0.001 \leq n \leq 1.5$

m Parameter describing the slope of NTCP vs. dose. The valid range of m is: $0.001 \leq m \leq 1$.

8.1.7 Print

8.1.8 Write Hist

Chapter 9

MLC panel

The MLC editing panel is used to define portal shapes for fields created by multileaf collimators (MLC). It also provides a display of leaf positions and controls for setting individual leaves. Additional functions aid in matching leaves to a portal outline, and vice versa.

The title bar of the portal editing panel has on it the name of the beam to which this MLC belongs. It provides a "beam's-eye-view" of projected anatomy and points of interest, and also shows the beam portal aperture that the user defined. The user can draw the portal on the screen, or use the digitizer (i.e., with a simulator film), observing the same conventions about hardcopy (film) placement, source-to-film distance, etc., as for blocks.

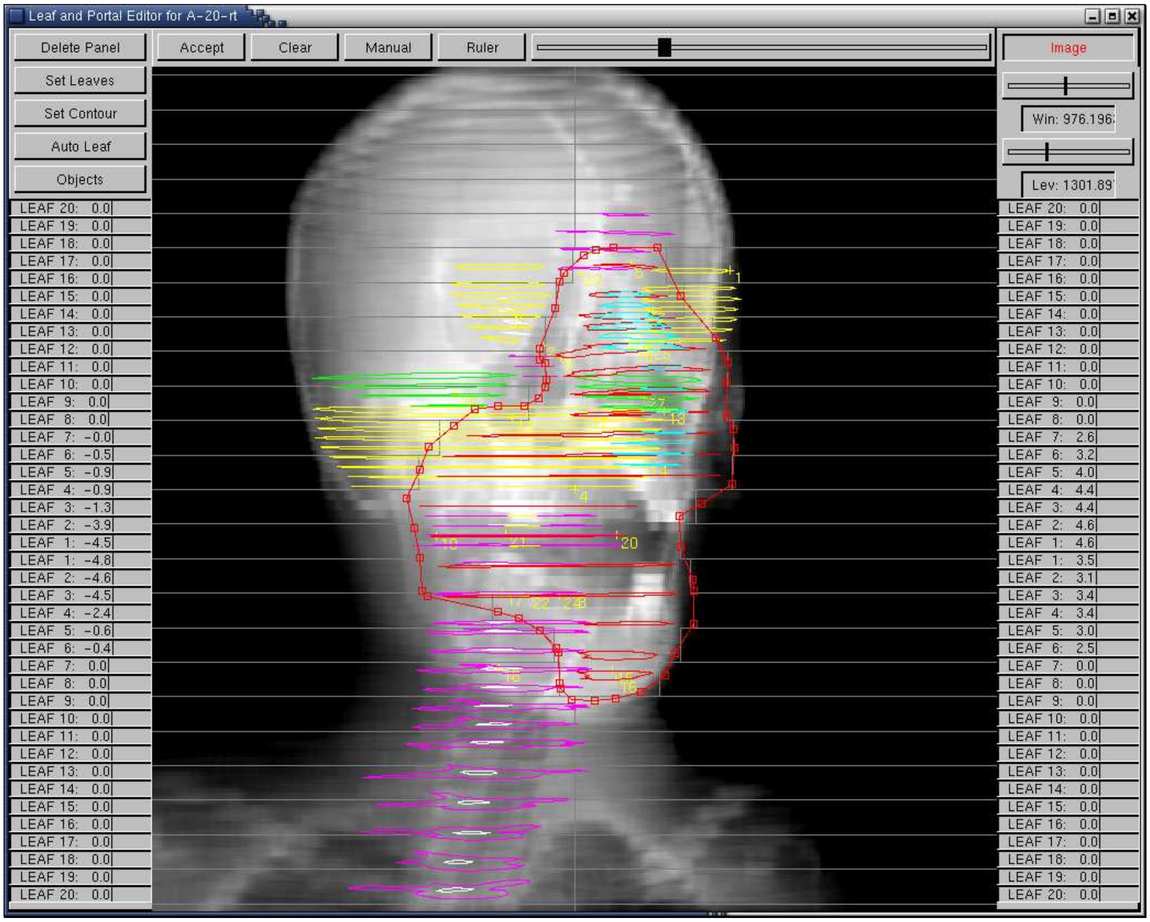
As for the block editing panel and the electron cutout editing panel, the display does *not* update when you change the beam gantry angle, the couch angle or any translational motion of the couch.

However, there is one very important difference from the block editing and electron cutout editing panels. *The portal shape remains in the same orientation when the collimator is rotated*. In other words, the portal shape is fixed with respect to *the target anatomy*, not the collimator. (The portal shape is fixed in the gantry coordinate system, not the collimator coordinate system.)

The user should enter a portal shape that conforms closely to the projected target anatomy (possibly enlarged by some suitable margin for penumbra). The user should *not* attempt to draw the actual stepped portal shape created by the collimator leaves. A facility is included in this panel to generate such a portal automatically, once the leaf settings are entered in the leaf textlines.

9.1 MLC contour drawing

The MLC panel contains a central display region, showing a beam's eye view display of the treatment volume. Across the top of this subpanel is the same row of controls found in other graphical editors in Prism, including an "Accept" button, a "Clear" button, an edit mode button, a "Ruler" button, and a scale slider. The MLC portal contour may be modified or drawn manually, just as contours are drawn in the volume editor (section 17.5).



Win: 976.196
Lev: 1301.89

LEAF 20: 0.0	LEAF 20: 0.0
LEAF 19: 0.0	LEAF 19: 0.0
LEAF 18: 0.0	LEAF 18: 0.0
LEAF 17: 0.0	LEAF 17: 0.0
LEAF 16: 0.0	LEAF 16: 0.0
LEAF 15: 0.0	LEAF 15: 0.0
LEAF 14: 0.0	LEAF 14: 0.0
LEAF 13: 0.0	LEAF 13: 0.0
LEAF 12: 0.0	LEAF 12: 0.0
LEAF 11: 0.0	LEAF 11: 0.0
LEAF 10: 0.0	LEAF 10: 0.0
LEAF 9: 0.0	LEAF 9: 0.0
LEAF 8: 0.0	LEAF 8: 0.0
LEAF 7: -0.0	LEAF 7: 2.6
LEAF 6: -0.5	LEAF 6: 3.2
LEAF 5: -0.9	LEAF 5: 4.0
LEAF 4: -0.9	LEAF 4: 4.4
LEAF 3: -1.3	LEAF 3: 4.4
LEAF 2: -3.9	LEAF 2: 4.6
LEAF 1: -4.5	LEAF 1: 4.6
LEAF 1: -4.8	LEAF 1: 3.5
LEAF 2: -4.6	LEAF 2: 3.1
LEAF 3: -4.5	LEAF 3: 3.4
LEAF 4: -2.4	LEAF 4: 3.4
LEAF 5: -0.6	LEAF 5: 3.0
LEAF 6: -0.4	LEAF 6: 2.5
LEAF 7: 0.0	LEAF 7: 0.0
LEAF 8: 0.0	LEAF 8: 0.0
LEAF 9: 0.0	LEAF 9: 0.0
LEAF 10: 0.0	LEAF 10: 0.0
LEAF 11: 0.0	LEAF 11: 0.0
LEAF 12: 0.0	LEAF 12: 0.0
LEAF 13: 0.0	LEAF 13: 0.0
LEAF 14: 0.0	LEAF 14: 0.0
LEAF 15: 0.0	LEAF 15: 0.0
LEAF 16: 0.0	LEAF 16: 0.0
LEAF 17: 0.0	LEAF 17: 0.0
LEAF 18: 0.0	LEAF 18: 0.0
LEAF 19: 0.0	LEAF 19: 0.0
LEAF 20: 0.0	LEAF 20: 0.0

Figure 9.1: The MLC panel

9.1.1 Accept

If the user accepts the portal contour by pressing the `Accept` button, the *contour*, not the leaf settings, is updated in the beam. The leaf settings are never stored; they are recalculated each time the panel is selected.

9.1.2 Clear

The Clear button works exactly as in the volume editor, erasing the portal contour, and allowing the user to redraw a portal contour either by sketching or point by point.

9.1.3 Edit mode

The usual modes are available here, *Manual* for sketching with the mouse, *Digitizer* for drawing the portal from a simulator film or a paper drawing, *Landmark* for putting landmarks on the display. *Auto* mode is inactive in the MLC panel.

9.1.4 Ruler

The ruler is also available and works as it does in the other editors.

9.1.5 Scale slider

The user may rescale the display, by moving the scale slider, as in other editor panels and the view panel. Similarly, the display may be panned (moved laterally) by dragging the mouse in the drawing region with the right mouse button depressed, as in other editor panels and the view panel.

9.2 Leaf settings

The leaf editing capability in this panel allows users to see how multileaf collimator leaves will fit to a portal shape. It also provides an alternative way for users to define the portal shape. Instead of entering a polygonal portal contour they can enter the leaf settings. The panel includes three buttons for facilitating the matching of leaf settings and portal shape, a *Set contour* button, a *Set leaves* button, and a *Auto leaf* button.

When the Leaf editing panel appears for a machine with a standard multileaf collimator, Prism calculates the leaf settings that best fit the (polygonal) portal shape at the current collimator rotation angle. Leaves at these settings are graphically displayed, superimposed upon a beam's eye view of projected anatomy and points. See figure 9.1. The leaf settings also appear numerically in the columns of text fields on either side of the panel. The user may edit in new leaf positions by typing into these text fields. The display updates after each new leaf position is entered.

Leaves are labeled in the text fields as they are on the actual treatment machine — for example, figure 9.1 depicts the multileaf collimator for the SL20 therapy machine. Note that the values of the leaves in the text fields are in the Prism gantry coordinate system, and not the coordinate system of any particular vendor. This means that the numbers in the text fields on the left side of the Leaf panel will typically be negative, indicating that the corresponding leaves are pulled back from the centerline, leaving an open field. This convention may disagree with the convention used by a particular vendor — for example, the leaf postions are positive on both sides of the collimator on Elekta SL20 treatment machines.

When the collimator angle is zero, the leaf text fields that appear at the top of the screen are the ones that are closest to the treatment machine gantry, and each leaf text field on the screen is close to the location of the leaf itself in the beam's eye view. As the collimator is rotated, the location of leaves in the view will rotate accordingly, and will no longer line up with the text fields on the sides of the Leaf editor. The text fields near the top of the screen will no longer correspond to the leaves closest to the treatment machine gantry either. In particular, if the collimator angle is $180°$, then editing a leaf position text field in the upper left part of the Leaf panel will cause a leaf in the lower right part of the beam's eye view of the panel to change location.

9.2.1 Set contour

When the *Set contour* button is pressed, the portal contour that exactly represents the current leaf positions is computed, and this contour replaces the current contour. This allows the user to set the leaves at the positions desired, and then to automatically create a contour that matches them.

9.2.2 Set leaves

When the *Set leaves* button is pressed, each of the leaves is set to a value that positions the center of the leaf on the current portal contour. These leaf settings will replace any previous ones in the panel. This allows the user to get a manual "best fit" of the leaves to the desired portal shape.

This only will have an effect if there are no unaccepted modifications of the current contour, i.e., if the Accept button is on, it must be pressed first.

9.2.3 Auto leaf

When the *Auto leaf* button is off, and the user rotates the collimator using the dial or a typed angle entry on the beam panel, the leaf display rotates in the MLC panel, but the individual leaf settings stay fixed at their current values. However, when this button is turned on, as the collimator rotates, the leaf settings are automatically adjusted to match the portal outline. This allows the user to rotate the collimator to determine the collimator angle at which the best match can be obtained between the desired portal and the actual shapes of the individual leaves.

9.3 Leaf editing with the UW CNTS

The Clinical Neutron Therapy System at the University of Washington has a multileaf collimator but is presently modelled in Prism as a machine with a "CNTS collimator", which is essentially a variable jaw collimator, with blocks, for the purposes of dose computation. To support this, the Leaf editing panel provides special capabilities for machines with CNTS collimators. When the Leaf editing panel is selected for a beam with machine that has a CNTS collimator, Prism calculates leaf positions to best match the portal formed by the four collimator jaws and all blocks. In this case, when the user presses the *Accept* button in the MLC panel, Prism replaces any blocks with a single C-shaped block that exactly matches the portal defined by the MLC panel.

Note that when the collimator angle of such a machine is changed, the rectangular jaws of the collimator, blocks, and stepped collimator portal all rotate in unison around the beam's central axis. The contour does not change shape as it rotates, since the collimator portal is literally rotating as the collimator angle changes in this case.

9.4 Image display

Pressing the *Image display* button will generate a DRR (digital reconstructed radiograph) in the display, if an image set is available, just as in a regular Prism beam's eye view.

9.5 Objects – the declutter function

As in views (see section 16.2.6), the *Objects* button brings up a scrolling list of all the objects displayed in the MLC panel. The user can deselect any of them in order to declutter the display.

Chapter 10

Neutron panel

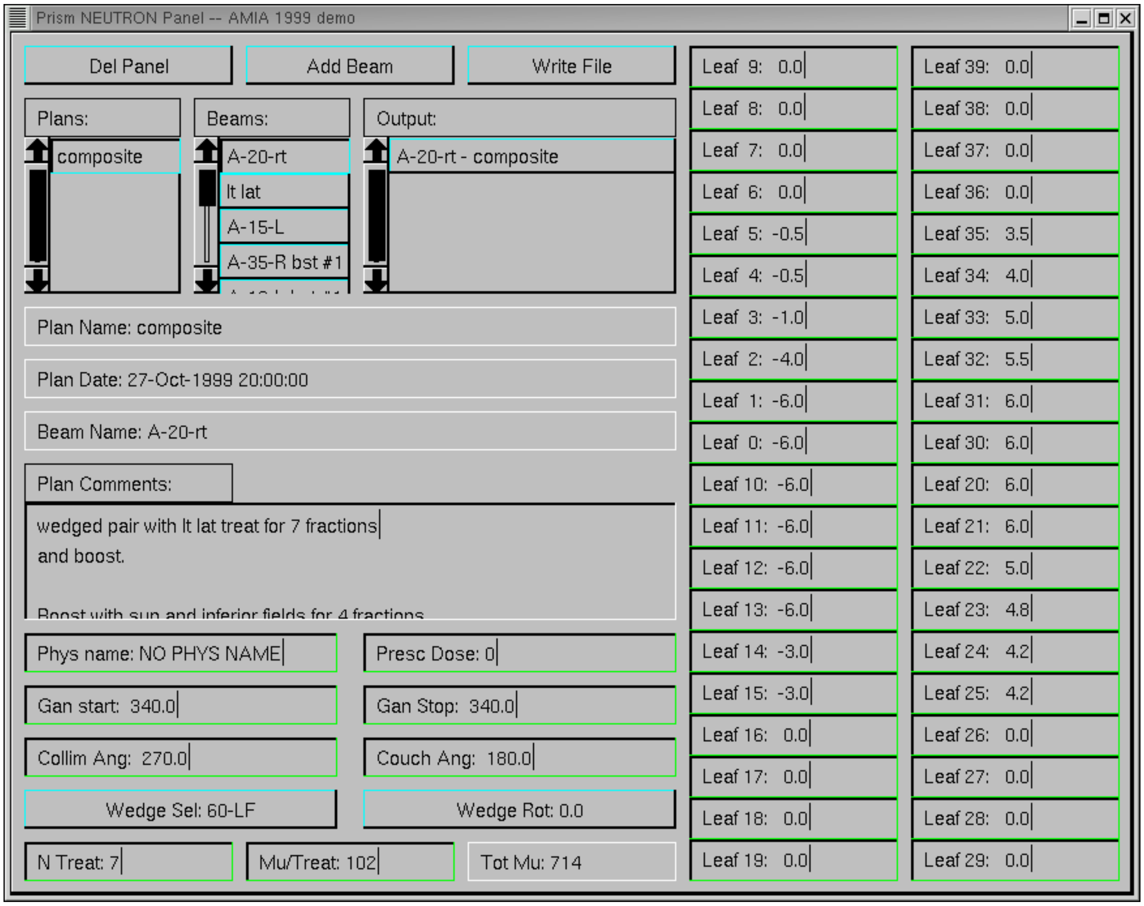
The Prism neutron panel enables the user to write a data file from the current case that contains information used to set up the treatment machinery in the Clinical Neutron Therapy System (CNTS) at the University of Washington. It is not intended to be portable to other sites. This facility also copies the output file from the computer running Prism to another computer at UW, and appends it to a master patient data set for the CNTS system. This facility also generates a hardcopy chart for each field that is output and transferred. Subsequent stages of the transfer process (such as actually loading the output file into the CNTS controls) are accomplished by facilities outside of Prism.

It is intended that all preparation of beam setup information will be done in Prism, so that subsequent editing of the converted file by the cyclotron therapy technologists or other staff members will not be necessary.

The Neutron panel provides flexibility in choosing which beams to transfer. The user many transfer some, but not all, beams from a particular Prism plan, or may transfer a group of fields selected from more than one Prism plan. It is usual to transfer additional fields for the same patient on different days, after physicians and dosimetrists revise the plan or add boost fields.

When the user selects the “Neutron” facility from the list of available tools on the tools panel, the neutron panel appears (see figure 10.1). The borders and contents of the buttons, readouts, and text fields on the Neutron panel are color coded so that users will be better able to distinguish the function of each control on the panel. Buttons are displayed in cyan, readouts in white, and text fields in green. Furthermore, when the user begins editing any text field, its border and contents will change from green to red, signifying that the data in the text field is volatile, and is not currently stored in the system. After the user presses the RETURN key, the border and contents of the text field change back to green. This minimizes the possibility of confusion over whether the contents of a particular text field has previously been accepted into the system (by the pressing of the `RETURN` key).

After the neutron panel appears, the user should first select a plan from the scrolling list of plans on the left side of the panel, labeled “Plans”. Once a plan has been selected, all the neutron beams of the plan will be listed in the scrolling list of beams directly adjacent to the list of plans, labeled “Beams”. The plan’s and date will appear in readouts directly beneath the three scrolling lists. The first three lines of the plan’s comments will also appear in the comments box, labeled “Plan Comments”, below the plan name and plan date readouts.



Prism NEUTRON Panel -- AMIA 1999 demo

Plans: composite

Beams: A-20-rt, lt lat, A-15-L, A-35-R bst #1

Output: A-20-rt - composite

Plan Name: composite

Plan Date: 27-Oct-1999 20:00:00

Beam Name: A-20-rt

Plan Comments:

wedged pair with lt lat treat for 7 fractions
and boost.

Boost with sup and inferior fields for 4 fractions

Phys name: NO PHYS NAME

Presc Dose: 0

Gan start: 340.0

Gan Stop: 340.0

Collim Ang: 270.0

Couch Ang: 180.0

Wedge Sel: 60-LF

Wedge Rot: 0.0

N Treat: 7

Mu/Treat: 102

Tot Mu: 714

Leaf 9: 0.0	Leaf 39: 0.0
Leaf 8: 0.0	Leaf 38: 0.0
Leaf 7: 0.0	Leaf 37: 0.0
Leaf 6: 0.0	Leaf 36: 0.0
Leaf 5: -0.5	Leaf 35: 3.5
Leaf 4: -0.5	Leaf 34: 4.0
Leaf 3: -1.0	Leaf 33: 5.0
Leaf 2: -4.0	Leaf 32: 5.5
Leaf 1: -6.0	Leaf 31: 6.0
Leaf 0: -6.0	Leaf 30: 6.0
Leaf 10: -6.0	Leaf 20: 6.0
Leaf 11: -6.0	Leaf 21: 6.0
Leaf 12: -6.0	Leaf 22: 5.0
Leaf 13: -6.0	Leaf 23: 4.8
Leaf 14: -3.0	Leaf 24: 4.2
Leaf 15: -3.0	Leaf 25: 4.2
Leaf 16: 0.0	Leaf 26: 0.0
Leaf 17: 0.0	Leaf 27: 0.0
Leaf 18: 0.0	Leaf 28: 0.0
Leaf 19: 0.0	Leaf 29: 0.0

Figure 10.1: The neutron panel

Once a plan has been selected, the user may select one of its beams. The full name of the beam will appear in a readout directly below the plan name and date readouts, and the current values of a number of beam attributes will appear in the columns of readouts and text fields in the lower left portion of the panel. The beam's collimator leaf settings appear in a set of text fields on the right side of the panel.

Prism calculates the leaf settings that best fit the multileaf collimator portal at the current collimator rotation angle. These leaf settings are the same as appear in the Prism Leaf Editing panel.

The leaf settings and other setup information are displayed to help the therapist determine whether the beam should be written to the neutron setup file. Settings are not expressed in the machine-independent coordinate system used in the Prism Beam panel. Instead, settings on the Neutron panel are expressed in the machine-specific coordinate system used at the neutron therapy console and on the neutron treatment room wall displays.

With the exception of the plan comments box, beam name, plan name, plan date, and total monitor units readouts, any of the other text fields containing beam specific information on the Neutron panel may be edited. The beam's wedge selection and wedge rotation may be edited by pressing either of the two buttons on the bottom row on the left hand side of the panel – in either case, a menu of options will appear[1].

This facility does allow the user to add a few items of information used in CNTS that are not modelled in Prism. These are the Physician Name and Prescribed Dose, presented in text fields just below the scrolling lists of beams and plans. This information will be written to the file along with the plan and beam specific information. When the Neutron panel is selected, the Prescribed Dose defaults to 0 and the Physician Name defaults to "NO PHYS NAME". The contents of these two text fields do not change when a new plan or beam is selected, and their contents have no significance to the rest of Prism[2].

To the right of the scrolling list of beams is an output list of beam and plan names, labeled "Output", that will be written to the neutron setup file. When the Neutron panel first appears, this list is empty.

Three buttons appear at the top of the panel. The "Add Beam" button causes the currently displayed beam to be added to the output list (along with the name of the currently selected plan, for identification purposes). As long as the Neutron panel is visible, the user may continue to select different plans and beams, and accept particular beams (or not). The list may contain beams from different plans. Beams can be deleted from the list in the usual way (with the middle mouse button).

The "Write File" button causes a confirmation box to appear. If the user confirms, the neutron setup file is opened, all the beams in the output list are written out, and the file is closed. The file is then automaticaly transferred to another computer and is appended to the master patient data set there. The transfer takes a few seconds. When the transfer is complete, a chart options dialog box is displayed, for neutron field charts (see below).

If the user cancels from the initial confirmation box, no file is written or transferred. If the "Write File" button is pressed several times, then several output files will be appended to the master data set. The "Delete Panel" button unmaps the Neutron panel, without writing any setup file. If the "Delete Panel" button is pressed before the "Write File" button, the Neutron panel is unmapped, and no output file will be written.

For each beam transferred, a neutron chart is printed, detailing the changes that were made to the beam. The destination printer at which these charts are to be printed, and number of copies of each chart, may be specified in the chart options dialog box that is displayed immediately after the neutron file transfer completes. The header on each chart is similar in appearance to the first page of the main Prism chart, which is printed from the plan panel. The current plan and beam, and the transfer date are also printed on the neutron chart. Field attributes that were modified with the Neutron panel before being written out are highlighted on the chart.

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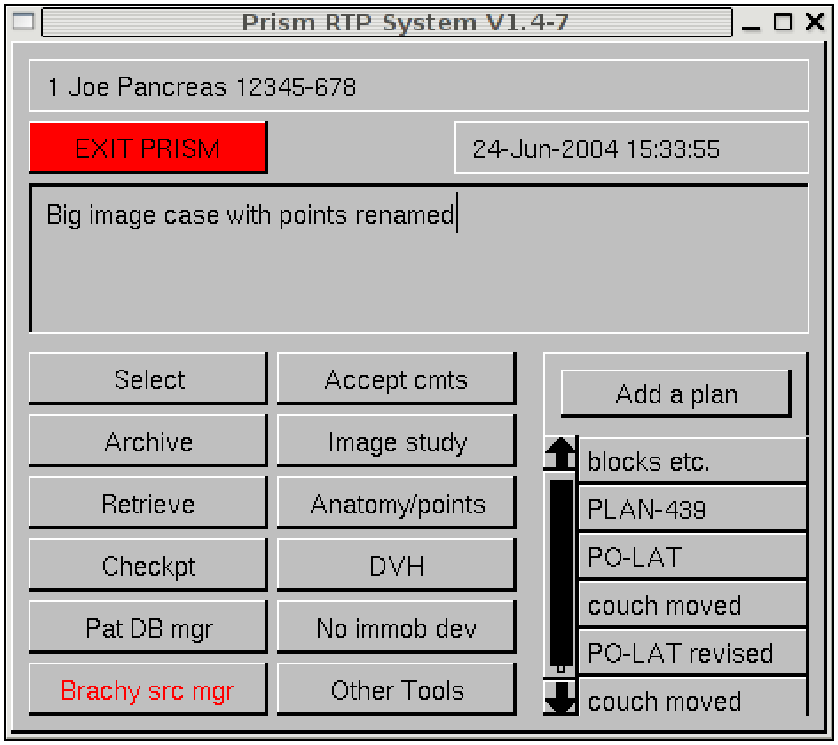
[1] We plan to remove the capability to edit settings from the Neutron panel. The recommended procedure is to edit settings in the Prism Beam panel.

[2] These items are not used by the new neutron therapy control system and we plan to remove them from the Neutron panel.

Chapter 11

Patient panel



1 Joe Pancreas 12345-678

24-Jun-2004 15:33:55

Big image case with points renamed

Figure 11.1: The patient panel

The patient panel is always present. It contains an `Exit` button, access to the patient database and the user's local work in progress, and other controls that provide for creating and editing the current case. Several special software tools are also accessible through buttons and subpanels of the patient panel.

The patient panel provides buttons for bringing up specialized panels to handle groups of objects, e.g., the anatomy editor and the points of interest editor. Also it includes a scrolling list of plans associated with the current case. There is an "Add" button for adding a new plan, and selecting a plan by left clicking a button in the list brings up a plan panel (described in Chapter 13).

11.1 Ending the Prism session: the Exit button

Just below the patient name readout, on the left, is a button used for ending the Prism session, the `Exit` button. When the `Exit` button is pressed, a confirmation box appears, with `Proceed` and `Cancel` buttons. If the user presses the `Cancel` button, his/her session continues. If the user presses the `Proceed` button, the Prism session terminates. The user's work in progress is *not* automatically saved. There is a shared archive system for keeping *permanent* copies of *completed* work, and a checkpoint facility for each user to keep *temporary* copies of his/her *work in progress*. The patient data archive system and the checkpoint facility are described in more detail below.

11.2 Patient and case identification

The panel includes at the top a readout displaying the patient's name and hospital ID (neither are editable here). This information is entered (and modified if necessary) with the database management panel described in Chapter 12. The `Pat DB mgr` button on the patient panel brings up the database management panel. The database management panel is also used for entering new patients in the archive master patient list, and deleting temporary or other data no longer needed (see chapter 12).

11.2.1 Case timestamp

A timestamp readout appears on the right under the name and hospital ID. This timestamp is updated when patient anatomy or other data are altered.

The following changes to a patient case will cause the patient timestamp to be updated. Note that this is *not* the same list as in section 13.8, the changes which will cause dose computation results to be invalidated. Note also that adding, deleting or changing a *plan* will *not* change the patient case timestamp.

- Changing the case's comments.
- Adding an organ, tumor, or target to the case.
- Deleting an organ, tumor, or target from the case.
- For any existing organ, tumor, or target:
  - Adding, deleting, or replacing (changing) any contours.
  - Changing the name.

- Changing any of the following organ attributes:
  - Density.
  - Tolerance dose.
- Changing any of the following tumor attributes:
  - T-stage.
  - N-stage.
  - Cell type.
  - Site.
  - Region.
  - Side.
  - Fixed.
  - Pulmonary risk.
- Changing any of the following target attributes:
  - Site.
  - Required dose (labeled PD)
  - Region.
  - Type (labeled Initial or Boost or blank)
  - Nodes.
- Adding points to the case.
- Deleting points from the case.
- Changing the name or location of any existing point.

11.2.2 Case Comments

Just below the readouts and exit button is a text box for the user to enter comments on the case, or a case description. This box allows entry and editing of any number of lines of text. Only three lines are visible at any time, but the lines can be scrolled up and down with the cursor arrow keys. Lines can be inserted and deleted. This is implemented with a SLIK textbox. For a complete description of how a textbox works, see [8]. This text information can be entered or modified at any time during the Prism session (except of course when the system is waiting for the user to respond to a dialog box, or when a dose computation is in progress).

The `Accept cmts` button will turn “on” when any changes are made to the comments after the last archive or checkpoint operation. When the user types in the text box, the modifications are not made part of the case until the user “accepts” the changes by pressing the `Accept cmts` button. This turns the button “off” until further changes in the text are made.

11.3 The patient database and checkpoint facility

This section describes the buttons on the patient panel that provide functions pertaining to the patient and checkpoint databases.

11.3.1 Select

The `Select` button is used to obtain a case from the archive or start a new case on a patient by designating the patient from the archive patient list. This function involves a sequence[1] of dialog boxes.

The first is a warning about losing current data, described below.

The next is a small textline for (optionally) providing a match string to use so that only patients whose entries in the patient list match some part of the match string. It may be left blank, in which case, the entire patient list is displayed in the next step. The match string is compared with all the information displayed in the patient selection list, including the patient ID number assigned by the Prism system, the patient's name, the hospital ID, and the date the patient was entered in the system. The string does not have to be at the beginning of a field. For example, using "1997" will include in the list all patients with entry date in the year 1997, but will also include a patient whose Prism ID is (or includes) 1997. Using "john" will include in the list patients whose first name is John, or last name has john in it, e.g., Johnson, etc. The match process does not do any other filtering other than equating upper case and lower case, i.e., dashes and spaces in dates or hospital IDs are included in the comparision, so `4 Jul 2004` is *different* from `4-Jul-2004`, though both will match on just `2004`.

The next dialog box is a query box with a scrolling list of patients available in the database. New patients are *not* entered this way, but are put in separately with the patient and image data management panel described in chapter 12. When one of the patients is selected and the `Accept` button is pressed, the query box is replaced with a second query box with a scrolling list of cases for the selected patient, including an entry for starting a new case. When one of the cases is selected and the `Accept` button in the query box is pressed, that selected case is read from the archive and made the current case, replacing any previous current case.

It is possible that the selected case data were previously removed from the shared database (e.g., after being copied to tape for long term off line storage) and the data are therefore not present in the database. In this case, a message box appears informing the user that the selected case is unavailable, and nothing in the user's session is changed.

When a case is selected, read in and made the current case, the case that was previously the current case will be replaced, and any changes made to that previous case after the last time it was archived or checkpointed will be lost. To aid in preventing loss of work, if the current case has unarchived changes at the time the `Select` button is pressed, a confirmation box with a warning about the possibility of losing work is popped up. If the user presses the `Cancel` button in the confirmation box, nothing in the user's session is changed and the selection process is done.

When a new selection (either by the Select or Retrieve buttons) is completed and the new case is read in, the new information is displayed in the patient panel. All other panels and subpanels are

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[1] In this version, unfortunately we just decided to extend this, instead of rethinking it to be less sequential. Maybe revise this in a later version.

removed from the screen.

In this context, a case includes all plans associated with the case.

11.3.2 Archive

The `Archive` button causes the current case to be saved to the patient database. If the case has changed since retrieved or last archived (or checkpointed) it is eligible for archiving, and the border of the time stamp readout will be red. If no changes that update the time stamp have been made since the last archive (or checkpoint) operation the case will not be saved and a message box informing the user will appear. If the archive operation is successful, a message box informing the user will appear. Any plans associated with the case are also archived. The dose distributions and views for a plan are *never* archived or checkpointed. When a case is archived, the time stamp border color changes back to white.

If a patient has *not* been selected from the archive or checkpoint database, along with either starting a new case or retrieving an old one to work on, any data entered cannot be stored in either the archive or checkpoint database. The user *must first* select a patient, *and* either an old case or the `new case` option before entering patient or plan data. If the user presses the Archive or Checkpoint buttons before selecting a patient, a message box will appear informing the user they must select a patient first.

Changes to plans do not update the case time stamp and do not make the case subject to archival. When plans are added or modified, they are archived individually from the plan panel. The plan is added to the existing plans associated with the current case in the archive. This is further described in section 13 on page 101. However, when a *case* is archived all the plans are archived with it. Only *subsequent* changes and additions to plans require separate action. The archive and checkpoint operations always *add* a copy of the current case or plan to the archives. They never modify or replace or delete data.

11.3.3 Checkpoint and Retrieve

The `Retrieve` button and the `Checkpt` button work exactly the same way as the `Select` button and the `Archive` button, respectively, except that they use a local database for the current user rather than the shared database of patient archive data. In order to use this checkpoint facility, the user must have a checkpoint directory containing an initially empty file, called `case.index`. The pathname of this checkpoint directory is specified in the user's Prism customization file, `.prismrc` in the user's home directory. If the user has no customization file, the pathname is taken from the Prism system configuration file, or a default value. See appendix 4.2.1 for default values and details about customizing Prism. The checkpoint facility is used for storing work in progress, and protecting against inadvertent or unexpected termination of Prism.

The pathname of the user's current checkpoint directory is displayed in a dialog box containing a textline. The user may change this information to specify any other directory he/she wishes, where there is a valid set of Prism checkpoint data files. By doing so, the user may retrieve a case from another user's checkpoint directory, provided the user has read access to the other user's files and directory. This is intended to allow one user to work on a case and another to continue it, *without adding incomplete work to the archive*.

When the user presses the `Retrieve` button a dialog box appears, containing the user's current checkpoint directory name. If the user wishes to retrieve data from another checkpoint directory, that of another user, for example, the user should change the directory in this dialog box to the one desired. The directory and the files in that directory must be accessible. If the file or directory permissions are not set for read access the operation will fail, and a message box will appear informing the user.

To create or edit a treatment plan, *even if it is to be only in your checkpoint database*, you must create and select an entry for the *patient* in the *archive* database. You do *not* create independent entries for patients in the checkpoint database. It is *not* an independent database, but only temporary storage with respect to some archival database.

Note that if a case or plan is *checkpointed* it cannot be subsequently archived unless some further change is made to it after the checkpointing operation.

11.4 Patient data entry facilities

11.4.1 Image study

The `Image study` button, when pressed, causes the image study associated with the current case to be read from the image database into working memory. A case may have at most one image study associated with it, but the same image study can be associated with any number of cases. If no image study is yet associated with the case, this button acts as a "Select study" button and a query box containing a scrolling list of available image studies is popped up when the button is pressed. When one of the image studies is selected and the `Accept` button in the query box is pressed, the selected image study is permanently associated with the current case. Images derived from the selected study may be displayed in the graphical views and easels described later in this document. When the case is added to the archives, a reference to the selected image study is kept with the case, so the image study may be read into working memory in the future without again going through the selection process.[2] If the image study data have already been read into working memory, pressing the `Image study` button has no effect.

11.4.2 Anatomy

The `Anatomy` button, when pressed, brings up an anatomy editor panel, called the "Volume Editor", for entering and editing anatomic objects, including organs, tumors, targets and points. It is more fully described in Chapter 17.

11.4.3 Immobilization device

The `Immobilization device` button shows the name of the specified immobilization device on the button, or the text `no immob. device`. When pressed it pops up a menu of the possible

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[2] This reference is just the image set number, a simple integer. This means that if you delete the image study and later send another image study to the Prism system from an image source (a CT scanner), the wrong set will be associated with this case. Until a more sophisticated indexing scheme is developed, it is advised to keep the image study in the Prism file system as long as it may be needed.

selections for this item. Possible immobilization devices that can appear on the menu are: No device, Mask, Alpha Cradle and Plaster Shell. This information is used in the Planning Target Volume Tool (PTVT) described in section 17.1.3.

11.5 Additional functions on the patient panel

11.5.1 Other software tools

Access to specialized software tools external to the main Prism system is provided by the `Other Tools` button.

11.5.2 Brachytherapy source catalog manager

The Brachytherapy source catalog manager provides a panel for defining new brachytherapy source types, and for line sources generating a table of modified Sievert integral values to be used in the line source dose calculation. It is described in Chapter 15.

11.6 Plans

On the right side of the patient panel, there is a subpanel implemented as a scrolling list, providing for creation and editing of treatment plans for the specified anatomy etc. The operation of this and other similar "selector panels" is described in section 4.4.3.

Chapter 12

Patient database manager panel

The patient database contains a master patient list, which is maintained with the patient database panel. This panel also includes functions for deleting cases, plans and image sets, from the archives and the user's checkpoint directory, when they are no longer needed. It includes the capability to delete image studies when they are no longer needed. The "delete study" operation shows a list of stored image studies in the stored database for the selected patient and allows the user to select one study, which is then deleted from the shared database. These operations are needed to recover disk space.

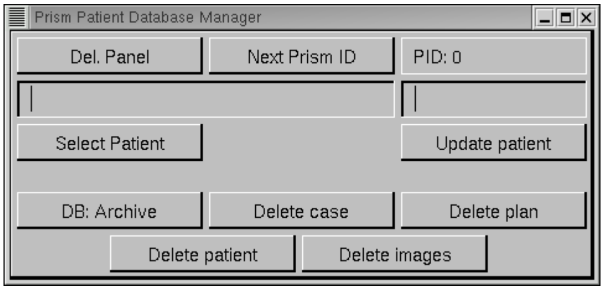


Figure 12.1: The patient database panel

12.1 Patient list management

The patient list contains an entry for each patient, consisting of the patient's name, hospital assigned ID, a sequence number assigned by the Prism system when first entered (Prism ID), and a date on which the entry was created. To facilitate accuracy, it is possible to update the patient name and hospital ID to correct typing or spelling errors. A patient must first be added to the patient list before any cases or treatment plans can be created for that patient.

12.1.1 Next Prism ID

Pressing this button sets the PID readout to the next available Prism ID or sequence number, not yet assigned to a patient. Also the patient name textline and hospital ID textline are reset to blank. This is the first step in entering a new patient.

12.1.2 PID (Prism ID)

This is a readout showing the Prism ID for the patient whose name and hospital ID are displayed.

12.1.3 Patient name

The patient name for a new entry can be typed in this textline, or for an existing patient, the name can be erased and retyped to correct a previous data entry error. The change is registered when the user presses the `Update patient` button.

12.1.4 Patient hospital ID

The hospital ID for a new entry can be typed in this textline, or for an existing patient, the hospital ID can be erased and retyped to correct a previous data entry error. The change is registered when the user presses the `Update patient` button.

12.1.5 Select patient

Pressing this button brings up the patient list, from which the user can select a patient. The selected patient's name, Prism ID and hospital ID are then displayed in their respective places. As in the patient panel, the matching function does an exact comparision, except for equating upper case, so that dashes, spaces, colons, and the lack thereof, are all considered different.

12.1.6 Update patient

Pressing this button replaces the patient name and hospital ID for the entry in the patient list corresponding to the displayed Prism ID, using the contents of the textlines on the panel.

12.2 Database management

This panel also provides some functions for deleting cases, individual plans, entire collections of cases for a patient, and image sets, from any of the archival or checkpoint databases, and patients from checkpoint databases.

12.2.1 DB: Database selection

The `DB:` button brings up a menu of databases to select which one the operations will affect. The name of the selected database is shown as the label on the button.

12.2.2 Delete case

Pressing the `Delete case` button brings up the patient selection panel, then the case selection panel, to specify the case to delete. After selecting a case, a confirmation box will appear, to make sure the user wants to proceed with the deletion.

12.2.3 Delete plan

Pressing the `Delete plan` button brings up the patient selection panel, then the case selection panel, to specify the case to delete. After selecting a case, the user may select any of the plans for that case. A confirmation box will appear, to make sure the user wants to proceed with the deletion.

12.2.4 Delete patient

This operation is applied *only* to the user's checkpoint directory. A patient *cannot* be deleted from the archive.

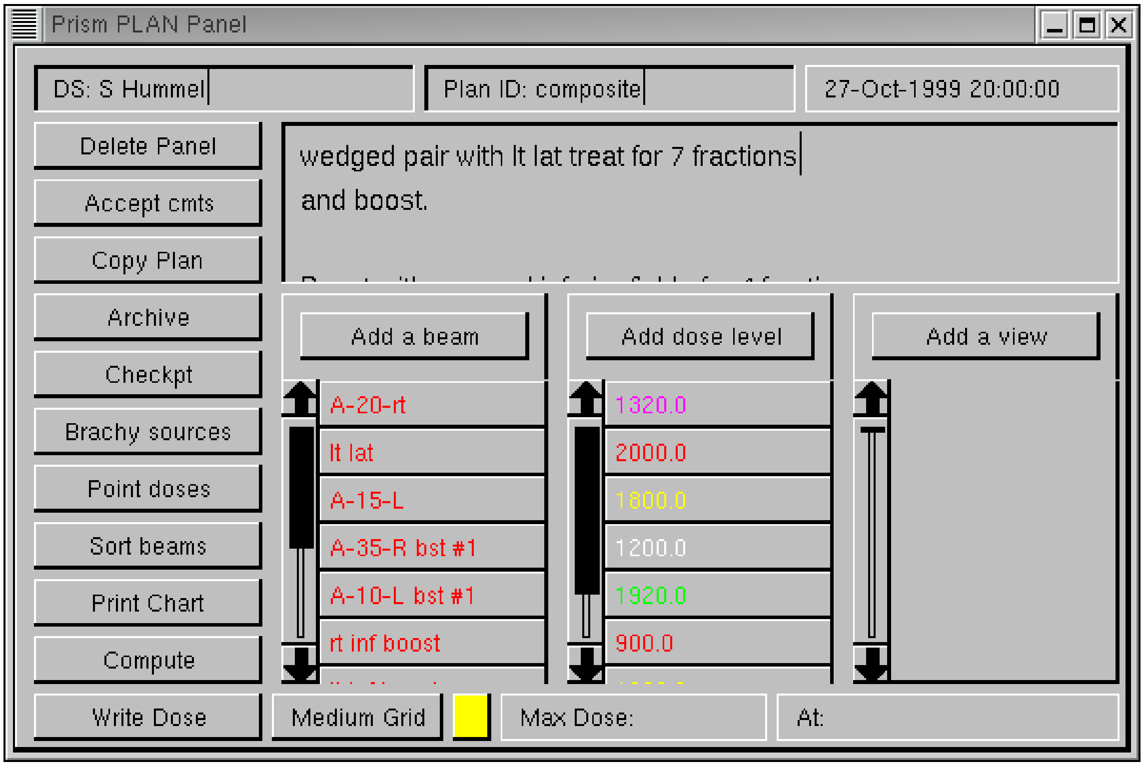
The `Delete patient` button brings up the patient selection panel, listing *only* the patients for whom there are cases in the user's checkpoint directory. When a patient is selected, a confirmation box will appear, to make sure the user wants to proceed with the deletion. This operation deletes *all* the cases in the user's checkpoint directory, under a specific patient. The patient entry in the patient list is retained, since this is independent of the checkpoint directory and can be seen in the Select and Archive operations.

12.2.5 Delete images

The `Delete images` button brings up a list of all image sets in the Prism image database, for all patients. When the user selects one for deletion, a confirmation box will appear, to make sure the user wants to proceed with the deletion. This operation deletes all the images in the selected set, as well as the image set file, and the entry in the image index.

Chapter 13

Plan panel



DS: S Hummel

Plan ID: composite

27-Oct-1999 20:00:00

wedged pair with lt lat treat for 7 fractions
and boost.

A-20-rt
lt lat
A-15-L
A-35-R bst #1
A-10-L bst #1
rt inf boost

1320.0
2000.0
1800.0
1200.0
1920.0
900.0

Figure 13.1: The plan panel

The plan panel provides access to all the components of a plan, consisting of radiation sources, views, and dose calculation results. As there may be multiple plans for a patient, there may be multiple plan panels on the screen. The plan panel includes text fields at the top for the dosimetrist's name and the plan name (called plan ID). There is also a text readout for the plan timestamp. Below these text fields, there is a text box for entry of multiple lines of comments. On the left side of the panel there is a column of buttons for various functions, described in the following paragraphs. Below the comments box, there are (from left to right) three selector panels, a selector panel for beams included in the plan, a selector panel for isodose levels, and a selector panel for views to display the plan. Below them are: a button for the dose grid granularity, a small solid colored button to select the color of the dose grid in the views, and text readouts for the maximum dose in the dose grid and the coordinates in the patient coordinate system for the point of maximum dose.

Figure 13.1 shows the plan panel.

Dose volume histograms may be computed and displayed with the DVH panel (Chapter 8) accessible from the Patient Panel (Chapter 11).

13.1 Text information

Across the top of the plan panel, there is a text line for the plan author (dosimetrist, labeled `DS:`), and a short text line for a brief plan identification text, labeled `Plan ID:`.

Below the top row, there is a text box in which the user can enter and edit any number of lines of text to be printed with the plan information on the paper chart. Only three lines are displayed but more can be entered, and the user can scroll the text by using the up and down arrow cursor keys on the keyboard. This works the same way as the text box on the patient panel.

There is an `Accept cmts` button on the plan panel, in the button area, which is used to copy the text box contents into the plan data. It works the same way as the corresponding button in the patient panel.

13.2 Plan timestamp

At the upper right of the plan panel there is a readout for the plan timestamp.

When any significant part of a plan is altered, the timestamp of the plan is automatically set to the current time of day. The following is a complete enumeration of the changes to a plan and its components which cause its timestamp to be reset:

- Changing a plan's name, comments, or author.
- Changing the granularity of the plan's dose grid.
- Changing the size or location of the plan's dose grid.
- Adding a beam, seed, or line source to a plan.
- Deleting a beam, seed, or line source from a plan.
- Changing any of the following beam attributes:
  - Name

  - Therapy machine
  - Gantry angle
  - Arc size
  - Collimator angle
  - Monitor units
  - Number of treatments
  - Couch lateral
  - Couch longitudinal
  - Couch height
  - Couch angle
  - Wedge ID (i.e., which wedge if any)
  - Wedge orientation
  - Attenuation factor

- Changing any collimator settings (including changing the portal of a multileaf collimator or the cutout portal of an electron beam).

- Inserting a block into any of a plan’s beams.

- Deleting a block from any of a plan’s beams.

- Changing the following block attributes:

  - Name
  - Block outline, or contour
  - Transmission factor

- Changing any of the following line source attributes:

  - Source type
  - Activity
  - Treatment time
  - Endpoint coordinates

- Changing any of the following seed attributes:

  - Source type
  - Activity
  - Treatment time
  - Location

13.3 Plan panel function buttons

13.3.1 Copy Plan

The `Copy Plan` button creates a copy of the plan attached to the plan panel, and adds it to the plans for the current patient. The new plan is given an arbitrary (unique) name, which may be edited by the user. The beams and other objects in the new plan are given the *same* names as in the old plan, however, since the intent is that the *contents* of the plan should be copied exactly.

13.3.2 Archive

The `Archive` button adds the plan to the shared (archival) database under the case of which it is a part. This function is used when a plan has been added or modified, but no further changes have been made to the anatomy or other case data besides the plans. If the non-plan data for the current case has not yet been saved to the shared database, or it has been saved but subsequently has been modified, a message box informs the user that the plan data can not be saved until the case is archived (see the patient panel archive operations described on page 92).

Dose distributions are never archived or checkpointed. Also, views are not archived or checkpointed. The display colors associated with each object (organs, beams etc.) *are* stored in the archive and checkpoint databases along with the objects.

13.3.3 Checkpt

The `Checkpt` button functions exactly like the `Archive` button except that it writes the data into the user's local checkpoint database instead of the shared archive.

13.3.4 Brachy Sources

Pressing the `Brachy Sources` button brings up a panel for input of line sources, e.g., for a Fletcher applicator, or for entry of seeds from orthogonal films, and for special types of applicators. This panel also provides access to specialized panels for applicatiors like the Syed or the prostate seed template. The Brachytherapy sources panel is described in Chapter 7.

13.3.5 Point Doses

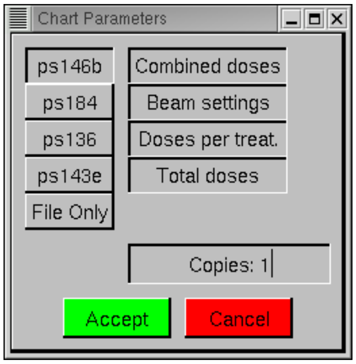
The `Point Doses` button brings up a display of the patient's points of interest and associated dose information, the dose "spreadsheet". It is described in Chapter 14.

13.3.6 Sort Beams

The `Sort Beams` button brings up a panel with a pair of scrolling lists, labeled "Old list" and "New list". Initially in the left (Old) list are all the beams of the plan. The right (New) list is empty. The user may click on any beam in either list. Clicking on a beam transfers it to the other list, left to right or vice versa. This panel is used to reorder the beams, so that related beams are listed next to each other, on the display and on the chart. When the `Accept` button is pressed, the beams are put back into the plan in the order of the new list, followed by any remaining in the old list.

13.3.7 Print Chart

The `Print Chart` button prints information about the plan and the case containing it in a form suitable for inclusion in the patient's chart. A dialog box will query about the printer queue and other information. Figure 13.2 shows this dialog box. There is a textline for number of copies (an integer in the range 1–9, with default value 1) and a menu for selection of the printer queue. Pressing a menu option selects that printer queue. One of the printer queue selections may be `File only`. If this is selected, a chart text file is written but not printed on a printer. This file is a PostScript file and may be displayed on the screen with a PostScript previewer such as `ghostview` or `gv`.



Copies: 1

Figure 13.2: The chart dialog box

The chart dialog box also provides the option of printing only parts of the chart. A menu of the parts or sections appears in the dialog box, with all parts initially selected. The user may deselect any parts, and only the selected parts will be printed.

The chart printout is produced by creating and printing a PostScript file, so the output can be sent to any printer or print queue capable of printing PostScript. This file may also be displayed and reviewed at the user's workstation, by using a PostScript previewer program such as `ghostview` or `gv`. The file is written in the user's home directory.

It is possible to produce the chart *quickly* – in particular, it is only be necessary to calculate the doses to the points that actually appear on the chart, not the 3-D dose distribution.

For contents of the printout, see Section 2.6.

Note that to obtain paper graphic output (on a large format color printer, for example) you perform that operation with respect to a particular view of the plan, and so the controls for performing that operation are on the view panel (Chapter 16), not on the plan panel.

13.3.8 Compute dose

The user requests that dose be computed for the three dimensional dose grid by pressing the plan panel's `Compute` button. Once the dose computation is started, it computes the dose grid values for each of the plan's radiation sources in sequence. When the dose computation finishes all the plan's sources, the resulting dose information from each source is scaled by that source's strength (e.g., monitor units for beams) and the scaled results are summed together internally. These sums represent the total dose to the grid for this plan.

If any of the beams in the plan has its central axis positioned so that the central axis does not intersect the patient skin, no dose for that beam is computed, and no isodose contours can be displayed for the plan. When the dose computation reaches such a beam, a message is typed out in the terminal window in which the Prism session was started. If the calculation was for point doses, a message box appears; if the calculation was for the dose matrix (the Compute button), the calculation stops when that beam is reached and then a message box appears.

While the computation is in progress, the `Compute dose` button is "on", i.e., displayed with foreground and background reversed. During dose computation, no part of the entire Prism user interface will respond to actions by the user. When the dose computation is completed for all sources in the plan, the `Compute` button turns "off" i.e., it reverts to its normal display, and normal interaction resumes.

13.4 Dose specification

Prism can compute dose to a three-dimensional grid of regularly spaced sample points in patient space. The size, location, and resolution of the dose grid must be specified in order for the dose throughout its volume to be computed. When a plan is created these are given default values; the user has the option to change them. The sides of the grid are always parallel to the axes of patient space; the grid is never tilted or skewed.

The grid corners are displayed in all cross sectional views as "corner markers". Each includes a small "grab box". These are also described in Chapter 16, the View panel.

The size and location of the grid is initially set in the three dimensions such that it just encloses the patient anatomy. The size and location can then be adjusted by dragging any of the grid corner markers by its grab box in any cross sectional view, using the left mouse button and pointer.

13.4.1 Dose grid resolution

The user specifies the grid resolution by pressing a button on the plan panel (bottom, next to "Write dose"), whose label indicates the currently selected resolution. This displays a pop-up menu of three standard grid spacings, from which the user may choose one. The three choices are: `Coarse`, `Medium` and `Fine`, corresponding to spacings of 2.0 cm, 1.0 cm and 0.5 cm respectively[1]. If the grid spacing of a plan retrieved from the file system matches one of these standard choices, the corresponding label is displayed. If the stored grid spacing does not match one of the standard choices, the actual value in cm is displayed as the button label. If the user chooses a different one from the menu, of course the appropriate label is then used.

This means that the grid may not necessarily have the same number of samples in the three directions. The number of samples is computed from the corner locations and the resolution. The

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[1] The actual values may be adjusted in the `prism.config` or `.prismrc` files, and are based on experience to determine the most useful spacings

Prism software may automatically slightly adjust the spacing between points in the dose grid when the `Compute dose` button is pressed, because the number of samples must be a whole number in each direction. So the nominal value associated with the “Coarse”, “Medium” or “Fine” setting will be approximate, but the locations of the corners are depicted exactly, and the lengths of the corner markers indicating the size of the grid spacing will be correct as well. So, if the user selects a grid with nominal 1.0 cm spacing, the actual spacing may be slightly more or less than 1.0 cm, but the true spacing and corner locations will be shown on the display and plot.

13.4.2 Dose grid color

The color of the dose grid corner markers and grab boxes is set by using a solid colored button to the right of the grid spacing button. This button is colored the same as the grid markers. Pressing it brings up a popup color menu from which the user may select a named color. When the `Accept` button on the popup color menu is pressed, the grid markers change to the new color and so does the color button.

13.5 Adding a beam

Below the text fields and next to the buttons, on the right side, the plan panel contains three subpanels, each of which contains an `Add` button and a scrolling list. The leftmost pane lists the beams contained in the plan, the middle one lists the isodose levels, and the one on the right lists the views. Selecting an item in a list creates a control panel for that item, just as in the patient panel. Deleting (selecting with middle mouse button) works as in the patient panel.

When adding a new beam to a plan, the new beam is assigned initially the following (default) values:

gantry angle	0.0
arc size	0.0
collimator angle	0.0
monitor units (MU)	100.0
no. of fractions (N)	1
couch lateral	0.0
couch longitudinal	0.0

couch height	0.0
couch angle	0.0
wedge	none
wedge rotation (rot.)	none
attenuation factor	1.0
display color	red

The initial selection of treatment machine depends on the order of entries in the treatment machines database, and is the first entry in the machine index file in the therapy machine database in use for this Prism session.

The order that fields are listed in their scrolling list of beams on the plan panel (and also on the Point-Dose panel, and on the chart) will be consistently the order in which they are entered, with new beams being added at the end of the list. If you save and recover a plan, this order will not change in any of those places.

In order to relate the machine (couch, gantry and collimator) coordinate systems to the patient coordinate system (the organ contours and other contours), the Prism system uses a fixed convention. The location of the machine isocenter, in the *patient* coordinate system, when the couch is at its “home” position (i.e., all linear motion settings are at 0.0 as above) for new plans is defined *automatically* by the Prism system to be the patient coordinate system origin. This means that when a beam is added to a plan in which this setting is in effect, the isocenter of the new beam is at the patient origin. Then changing the couch settings (couch lateral, longitudinal or vertical position) will move the isocenter to any other desired location within the patient.

This convention requires that the user give some care to the way that image studies are done and data are entered from the digitizer.

When contours for organs and other anatomy are drawn on CT images, the patient coordinate origin is automatically defined to be at the center of the first slice scanned, i.e., at the intersection of the CT laser alignment lights. In this case, the couch settings on the beam will represent absolute displacements from the known setup with the CT alignment marks. If the CT scan has been done so that the first image in the image set is through the tumor, to place the origin in the area of the tumor, this is very convenient. When scanning the patient, place markings on the patient at the position of the CT alignment lights and the first slice position. Then when actually treating the patient, to position the isocenter, you simply first position the patient so the lasers match the markings on the patient, then move the patient from that position by the amounts of each of the couch positions on the printed chart, i.e., you use the couch settings as displacements from the initial setup.

When entering data from the digitizer, the *user* defines the location of the patient coordinate system origin. Generally it is a good idea to choose a location that can be related to external landmarks on the patient. If the position of the isocenter (for an isocentric plan) is known, this is usually a good choice for the origin. However, if using CT data in the patient case, the CT image data will have already defined the patient space origin, and you must know where that is.

13.6 Adding a view

The “New view parameters” query box, shown in figure 13.3, appears when you press the `Add view` button on the plan panel. It determines the type and size of a new view, and the beam of the view for beam’s eye views. There is no `Cancel` button in this query box; unwanted views can be deleted from the plan panel (see the discussion of the Plan panel in section 13). After the `Accept` button of this query box is pressed, a new view with the specified characteristics is created and mapped to the screen.

When a view is created it is given default values as follows:

Origin	depends on type of view
Scale	10.0 pixels/cm
Position	0.0
Locator bars	ON (both local and remote)
Window	500
Level	1024

For transverse, coronal and sagittal views, the view origin is set so that the *patient space origin* is centered in the view.

For beam’s eye views, the origin is set so that the isocenter of the beam associated with the view is in the center of the view.

The view origin (not the patient origin) may be moved by “panning” with the right mouse button,

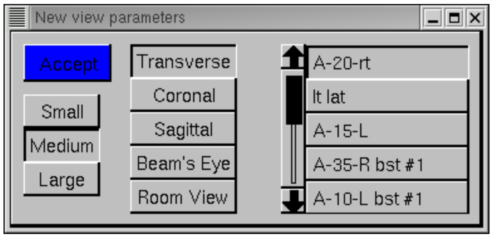


Figure 13.3: New view parameters query box

and the scale changed with the scale slider. These work when images are displayed, as well as when only line graphics are displayed.

When a beam is deleted from a plan, if there are any beam's eye views for that beam, they are deleted also.

13.7 Dose display controls

13.7.1 Dose maximum

Two readouts display respectively the highest dose found in the plan's dose grid, and the X, Y, and Z coordinates in patient space of this point of highest dose. When there are no valid dose results computed, these readouts are blank.

13.7.2 Isolevel surfaces

Since the dose grid has three-dimensional extent, a dose threshold value corresponds to a surface embedded within the grid. A set of dose surfaces is associated with a plan. Each surface is characterized by a threshold value and a color. The threshold value determines the location and shape of the surface in space. In each of the plan's orthogonal views that intersects the surface, a set of curves determined by the intersection of the surface and view appears in the view, in the surface's color. In some view positions no curves can appear, e.g., if the view is located beyond the region containing a certain dose level.

On the plan panel, there is a selector panel containing buttons corresponding to values for dose surfaces to display. Any number of dose levels can be specified, each with its own color, selected from one of the standard Prism colors. The button label color corresponds to the color of the corresponding isodose curves in the views. The dose threshold values can be changed at any time by selecting any of the buttons, as for any other selector panel. This brings up a dose level panel (see figure 13.4), a small panel with a "Delete panel" button, a color button, and an adjustable sliderbox with which to change the dose level value.

The adjustable sliderbox has a slider and a textline to control the dose level value. The right and left textlines are adjustable upper and lower limits for the value. They can be changed to give the slider more precision as needed. Pressing the Surface Color button brings up a popup color menu from which the user can change the color assigned to that isodose level. When the user manipulates the slider, either by using the screen pointer to drag or reposition the slider knob, or by typing a new value into the text field below the slider, the surface's threshold, and its appearance in the plan's views, changes interactively.

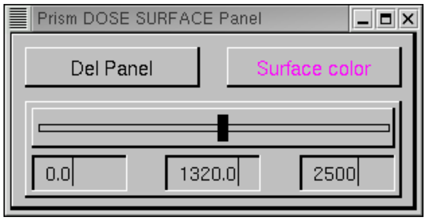


Figure 13.4: The isodose level panel

13.8 Dose display constraints

Unlike other relationships in Prism, the dose display can not automatically be maintained in a consistent state, because the dose computation can take an appreciable time. Therefore, the user has to request a dose computation by using the `Compute dose` button described above. The results of the dose computation are displayed after the dose computation is completed. Any time the user makes a change in the plan or anatomy which would invalidate the dose computation results, the dose display is erased and cannot be redisplayed until a new dose computation is completed.

If the user defines a new source or deletes an existing source from the system or changes some attribute of a source that would have an effect on dose computation (like the gantry angle of a beam), then all dose displays become unavailable, since the summed dose result is no longer up to date. The user must press the `Compute` button on the plan panel again to request dose computation for the source or sources that have changed. After dose computation has finished, the combined dose is recomputed and dose displays become available again. Any specified dose surfaces that are displayable in any views will then be drawn automatically.

Similarly, if the patient's anatomy, table position, or the plan's dose grid specificiation changes or is turned on or off, all dose displays become unavailable, and the user must press the `Compute` button again. In this case, all beams etc. will be recomputed and of course it will take longer than recomputing a single beam.

Certain operations do not require recomputation of the doses but only require recomputing the weighted sum of the doses from each source. In these cases it is not necessary to press the `Compute` button, and the display will update quickly (if not immediately). In particular, changing the monitor units of a beam, the activity of a brachytherapy source, or the treatment time of a brachytherapy source, results in immediate update of the display without further user action.

The following specific changes to the patient case or plan data will cause the dose computation results for a source and therefore the dose display *and* list of doses to points of interest to be invalidated:

- A change to the patient's set of organs. This includes any of the following:
  - A change to any existing organ contour.
  - The deletion of a contour from an organ.
  - The addition of a contour to an organ.
  - The deletion of an entire organ.
  - The addition of a new organ.
  - A change to the density attribute of an existing organ.

  These changes invalidate the results for all sources.
- A change to an attribute of the source that would affect the computation of dose from that source.

  For beams, this consists of the following:
  - A change to the beam's gantry angle.
  - A change to the beam's collimator angle.
  - A change to the beam's couch angle.
  - A change to the beam's couch lateral motion.
  - A change to the beam's couch longitudinal motion.
  - A change to the beam's couch height motion.
  - A change to any of the beam's collimator jaw positions or portal outline (for MLC, electrons, etc.).
  - Changing the beam's collimator type.
  - Changing the beam's wedge ID.
  - Changing the beam's wedge rotation.
  - Changing the beam's treatment machine.
  - Inserting a block into the beam.
  - Deleting a block from the beam.
  - Changing either of the following block attributes:
    - Outline or contour
    - Transmission factor.
  - Changing the attenuation factor.

For line sources, this consists of the following:

- Source type
- Endpoint coordinates

For seeds, this consists of the following:

- Source type
- Location

Adding a radiation source invalidates the summed dose results of the plan containing that source. Deleting a radiation source causes the summed dose results of the plan to be recomputed automatically, and all dose surfaces to be recomputed and redisplayed.

The following changes to the plan will cause the dose arrays of all radiation sources to be invalidated:

- A change to the position or extent of the dose grid boundary.
- A change to the dose grid granularity.

The following changes to the patient case will cause the list of doses to points of interest of all radiation sources to be invalidated:

- The addition of a new point of interest.
- The deletion of an existing point of interest.
- A change to the location of an existing point of interest.

Chapter 14

Point dose panel

The user can prescribe and/or display doses to points of interest by using the point dose panel. The point dose panel can be used *without* computing the dose to a three-dimensional volume of space. Although the description following refers to beams, line sources (but not seeds) are also supported.

The panel resembles a table, with beam names along the column headings, and point names along the row headings. There are arrow buttons above and below the list of point names, as well as to the left and right of the list of beam names. The `Del Pnl` button is in the upper-left corner of the panel, and when pressed, causes the panel to close. See figure 14.1.

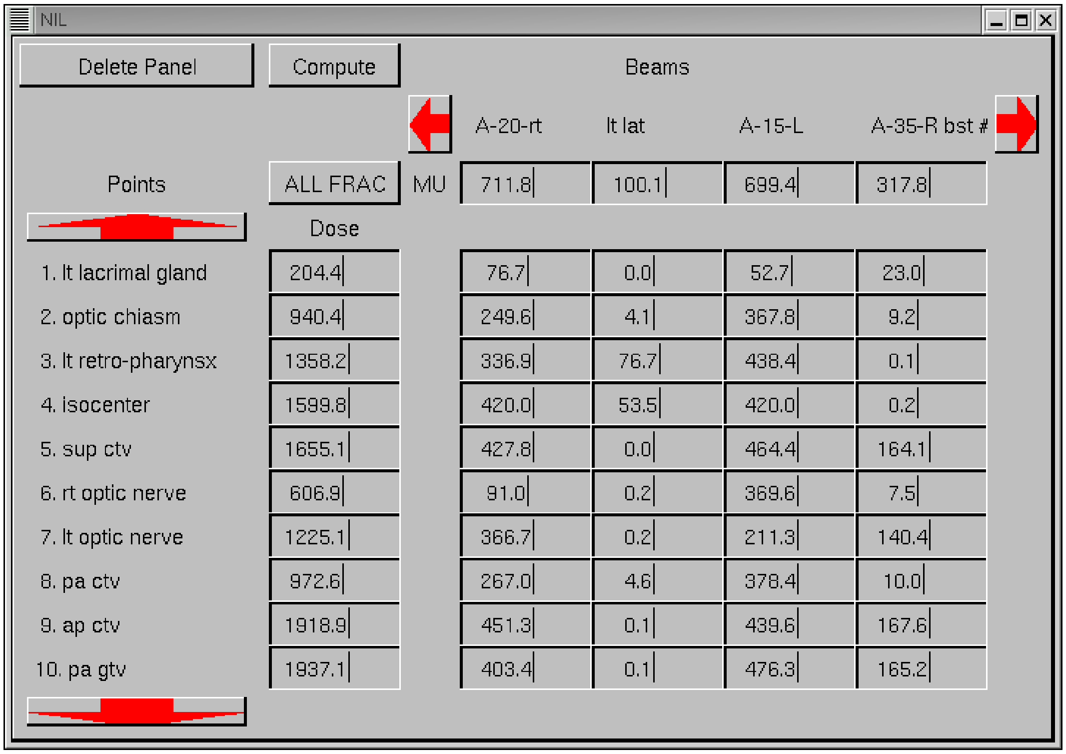
The cells of the table are user-editable text fields, with the exception of the cell at the top of the first column of numbers (below the Compute button). This cell contains a button for toggling the display mode (see section 14.2 below). The first column of the table is labeled `Dose`. Each number in that column represents the dose received by a particular point for all beams. The first row of the table is labeled `MU`. Each number in that row represents the monitor units for a particular beam. The number in each internal cell of the table represents an absolute dose received by a particular point under a particular beam.

14.1 Compute point doses

The `Compute` button, when pressed, will run a dose calculation for all the points of interest. This calculation is separate from and independent of the three dimensional dose grid calculation. The doses to the points are *not* computed by interpolation of the dose grid.

14.2 All fractions/one fraction

On the Point dose panel there is a button that toggles the panel's display mode. When the button is labeled `All Frac`, the dose information and monitor units displayed in the rest of the table are computed for all fractions of the entire treatment. When labeled `One Frac`, the doses and monitor units are computed for a single fraction. The user may toggle between the two modes by pressing this button; the numbers on the table will update accordingly. When the button is set to `One Frac` the dose per fraction is computed based on the number of fractions of the first beam in the collection



Points	Dose	A-20-rt	lt lat	A-15-L	A-35-R bst #
MU		711.8	100.1	699.4	317.8
1. lt lacrimal gland	204.4	76.7	0.0	52.7	23.0
2. optic chiasm	940.4	249.6	4.1	367.8	9.2
3. lt retro-pharynsx	1358.2	336.9	76.7	438.4	0.1
4. isocenter	1599.8	420.0	53.5	420.0	0.2
5. sup ctv	1655.1	427.8	0.0	464.4	164.1
6. rt optic nerve	606.9	91.0	0.2	369.6	7.5
7. lt optic nerve	1225.1	366.7	0.2	211.3	140.4
8. pa ctv	972.6	267.0	4.6	378.4	10.0
9. ap ctv	1918.9	451.3	0.1	439.6	167.6
10. pa gtv	1937.1	403.4	0.1	476.3	165.2

Figure 14.1: The point dose panel

of beams, and all other beams are assumed to have the same number of fractions. When the beams do not all have the same number of fractions the display will not go into this mode.

Line sources and seeds, even if present, are not displayed in this panel, and the total dose to each point, displayed in this panel, *does not* include the dose from the line sources and seeds in the plan.

14.3 Arrow buttons

The arrow buttons control which of the patient's points of interest and the plan's beams are visible in the table at any given time. When the plan contains more beams and line sources than there is space for in the table, the user can press the arrow buttons to the left and right of the list of beam names on the table to scroll the table forward and backward through the plan's full set of defined beams and line sources. By pressing the left mouse button over the left or right arrow buttons, the user can scroll the table a beam at a time. If there are more than four beams, then by pressing the middle mouse button the table can be scrolled four beams at a time, causing the table's entire interior to change.

When the patient case contains more points of interest than there is space for in the table, the user can press the arrow buttons above and below the list of point names on the table to scroll the table forward and backward through the patient's full set of defined points of interest. By pressing the left mouse button over the up or down arrow buttons, the user can scroll the table a point at a time. If there are more than ten points, then by pressing the middle mouse button the table can scrolled ten points at a time, causing the table's entire interior to change.

14.4 Values in the table cells

The value at each table cell is determined from a point's computed dose per monitor unit under a particular beam and the monitor units for that beam. The user can modify the contents of any table cell, as follows:

1. The monitor units of a single beam (or the insertion time of a single source) can be changed by editing one of the cells in the first row of the table, and pressing the `<RETURN>` key. This causes the absolute dose to all points under that beam to update, reflecting the new monitor units setting. If the monitor units setting for a beam is 0.0, then the dose to all points under that beam will naturally be 0.0 as well.

2. The absolute dose to a particular point from a particular beam or line source can be changed by editing one of the table's internal cells, and pressing the `<RETURN>` key. This causes the monitor units for that beam to be adjusted so that the absolute dose to the point just edited equals the newly edited value. The change in monitor units in turn causes the absolute dose values for all the other points under that beam to update, reflecting the new monitor units setting. Note that if the dose per monitor unit for a particular point under a particular beam is 0.0, then the absolute dose displayed in the corresponding cell of the table will read 0.0 as well. In this case, the value in the cell will remain 0.0 if the user attempts to change it, and no other cells in the table will update after the attempt either. This prevents divide by zero errors. If a beam contributes no dose to a point, no amount of MU will make a non-zero dose at that point.

3. The total dose to a particular point can be changed by editing one of the cells in the first column of the table, and pressing the `<RETURN>` key. This causes the monitor units for all beams to be adjusted by the same scaling factor, so that the total absolute dose to the point just edited equals the newly edited value. After the monitor units of each beam is adjusted, the total dose to all points under that beam is updated. Thus, the contents of all the editable cells of the table change as a result.

None of these operations has any effect on the line sources or seeds present in a plan. There is a separate point dose display on the brachytherapy panel, described in chapter 7.

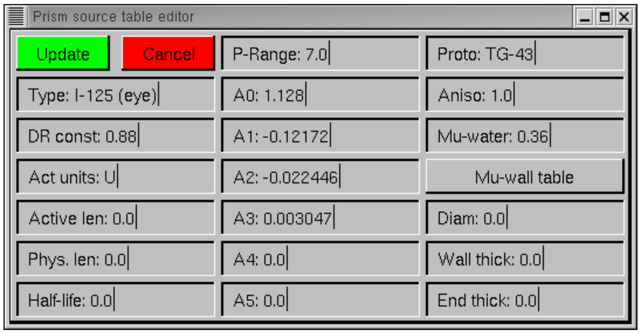
It is not necessary to compute dose to a three-dimensional volume of space before using the point dose panel. If a dose volume has been created, however, any views containing isodose contours will update after the user causes a beam's monitor units to change from the table in the point dose panel.

Note that if the point dose panel is currently displayed on the screen, the table will automatically update if the user changes the monitor units of a beam from a different part of Prism (e.g. in a beam panel). This will immediately cause the table to update to reflect the new dose values for the points and beams in the table. Changing anything else, which would require a new dose computation cycle, will simply cause all entries in the table to become blank.

Chapter 15

Source catalog panel

The source catalog panel provides a facility for entering data about the various types of sealed radioactive sources that Prism supports. These include both linear sources such as Cesium capsules for intracavitary radiotherapy, and seeds such as iridium, gold and iodine. The source catalog panel is shown in figure 15.1.



P-Range: 7.0
Proto: TG-43
Type: I-125 (eye)
A0: 1.128
Aniso: 1.0
DR const: 0.88
A1: -0.12172
Mu-water: 0.36
Act units: U
A2: -0.022446
Active len: 0.0
A3: 0.003047
Diam: 0.0
Phys. len: 0.0
A4: 0.0
Wall thick: 0.0
Half-life: 0.0
A5: 0.0
End thick: 0.0

Figure 15.1: The source catalog editing panel

The source catalog panel is a dialog panel, and while it is active, no other interaction with Prism panels is accepted. If the user presses the `Update` button, the source catalog entry selected is modified for the current Prism session. If the active length parameter is non-zero, a new Sievert integral table is generated. A dialog box then appears, asking if the user wishes to update the source catalog file. If the user presses “Proceed” in this query box, the source catalog file is rewritten with the new parameters.

The panel includes textlines for entering a source type label and numeric data items, and a button that brings up yet another panel for entering wall attenuation coefficients.

All the numeric parameters are as described in the Prism Dose Computation Methods report [4], chapter 4.

15.1 Source type

The source type is a string, that labels this source type. This label appears in the source type selection menus, and will be printed on the chart.

15.2 Gamma factor

The gamma factor is a number, chosen to correspond to the source strength units utilized in creating a plan with this source type.

15.3 Active length

The active length is the linear extent (in cm) of actual radioactive material in the source, if it is a linear source, such as a Cesium capsule. This number should be 0.0 for a seed type.

15.4 Physical length

The physical length is 0.0 for a seed type. For a linear source, it is the actual physical length of the capsule, in cm.

15.5 Polynomial range

The polynomial range (in cm) determines the maximum radial distance from the source (or the source center for line sources) at which the Meisberger polynomial correction for tissue scatter and attenuation is used. For distances beyond this number, an exponential correction is used.

15.6 Polynomial coefficients

The polynomial coefficients are four numbers, A0, A1, A2, A3, that correspond to the coefficients of the Meisberger third order polynomial tissue correction factor.

15.7 Water attenuation

The water attenuation (labeled `Mu-water`) is used in the exponential tissue correction factor.

15.8 Wall attenuation

The wall attenuation (labeled `Mu-wall`) is used in computing the Sievert integral and the end dose rate values, as specified in [4]. On the possibility that the spectrum of the radioactive isotope is polyenergetic, there is a short table that allows the user to specify wall attenuation as a function of thickness. This table appears when the button is pressed. The values on the left are the wall thicknesses and cannot be changed. The values on the right are the corresponding attenuation factors and can be changed by the user.

15.9 Source diameter

The source diameter (in cm) is the diameter of the actual radioactive material inside the source, for a linear source, and is used in computing the “effective diameter” as described in [4].

15.10 Wall thickness

The wall thickness (in cm) is also used in computing the “effective diameter” and is the actual (radial) wall thickness of the capsule for a linear source.

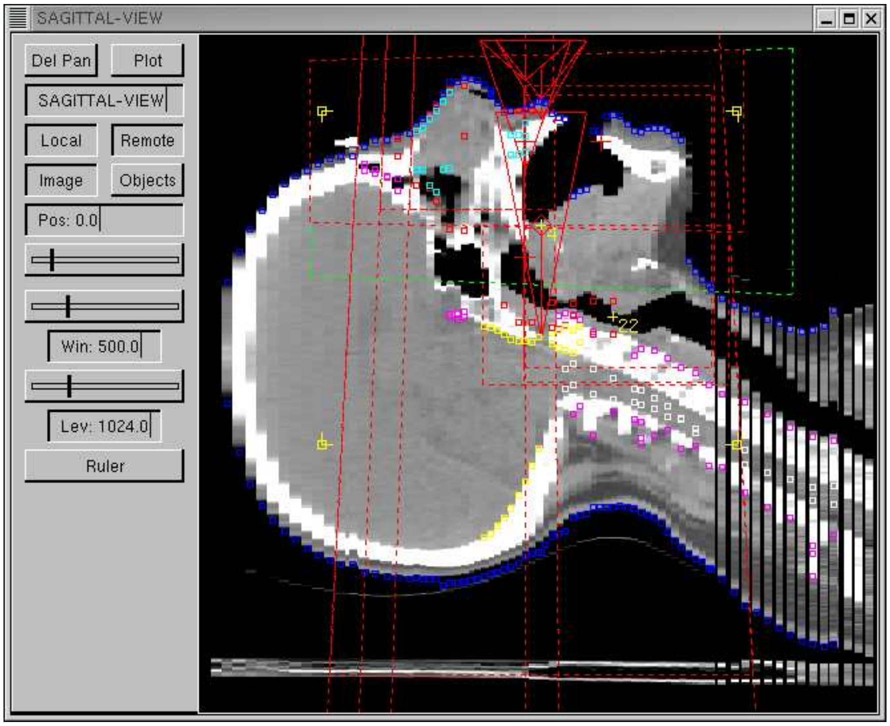
15.11 Endcap thickness

The endcap thickness is the actual thickness (in cm) of the end cap of the linear source capsule. Typical linear sources are in fact asymmetric in regard to this parameter, but the dose calculation treats the source as symmetric, so it is up to the physicist’s judgement how best to approximate this number.

Chapter 16

View panel

While all of the previously described panels control or specify objects pertaining to patients or therapy plans, a view panel controls a graphical rendition of patient anatomy, tumors, targets, beams, points, and dose distributions. A view panel is composed of a picture and controls.



SAGITTAL-VIEW

Pos: 0.0

Win: 500.0

Lev: 1024.0

Figure 16.1: The view panel

16.1 The picture area

The picture, or rendering portion, displays anatomy, tumors, targets, points, beams and dose information in wireframe format, and optionally an underlying image. Sectional views display a two-dimensional, orthogonal slice of patient anatomy, while beam's eye views give a perspective rendering with the viewpoint at the beam source.

Section 2.5 gives all the details of how all the various Prism objects (anatomy, beams, points of interest, etc.) are depicted in the views.

16.1.1 Locators

Cross-sectional views are additionally capable of displaying *locators*, horizontal or vertical lines, to indicate and manipulate the location of orthogonal views of the same plan. Given two orthogonal views, *A* and *B*, the locator for view *A* is overlaid on view *B* at the intersection of their respective view planes. A sectional view of course does not display locators for views of an identical type. A transverse view may for instance show a horizontal locator for a coronal view and a vertical one for a sagittal view but no locators for other transverse views.

Users may move the locator back and forth by pressing and holding the left mouse button while the pointer is on a grab box placed at the end of the locator near the scale legend. Then moving the pointer while the button is held down will move the locator to a new position. Only the locator is updated while it is in motion; the associated view and locators for it in other views are redisplayed only when the mouse button is released.

Moving the locator to a new position updates the view position of the view corresponding to that locator. No rounding is done, so it may be that moving a locator bar for a transverse view (eg. in a coronal view) will put the transverse view at a position that does not correspond with any CT image or contours. They are simply not displayed, unless they are within the small zone immediately around that value of position. This is further explained below.

16.1.2 Dose grid corner markers

In addition to the locator bars, Prism displays "corner markers" indicating the extent of the three-dimensional dose calculation grid, an array of regularly spaced sample points in patient space at which the dose can be computed. This information is the basis for dose displays such as isodose contours in a cross-sectional view. The sides of the grid are always parallel to the axes of patient space; the grid is never tilted or skewed. The grid corners are displayed in all cross sectional views as "corner markers". Each includes a small "grab box". These grab boxes can be dragged with the left mouse button down, in the view, to change the extent of the dose calculation region. As they are dragged, all the corner markers in all the views will update. This involves sufficient computing that the display may lag behind the pointer motion and take a few seconds to catch up after the user stops moving the pointer and releases the left mouse button.

Oblique planes are also provided. At this time, they only display line sources and seeds. The view plane can be rotated quickly using two small dials that control the rotation about each of two axes. In the future, these oblique views will display internal anatomy as intersections like the coronal and sagittal views, and they also will be able to display an oblique reformatted CT in the background. When the plane is rotated, the background image will be erased, but can be restored with the `Show Image` button.

16.1.3 Panning the view

The graphical contents of the view can be panned by holding the pointer over any part of the view's picture area and dragging with the *right* mouse button. This facility is available even when an image is displayed in the view.

16.2 View panel controls

The view panel contains a number of controls in a column along the left side: a `Delete Panel` button, a `Plot` button, a `View Name` textline, a `Local` locator button, a `Remote` locator button, an `Image` button, an `Objects` button, a `View Position` text field, a `Scale` slider, and sliders and text fields for adjusting image grayscale (`Window` and `Level`).

The `Delete Panel` button (labeled `Del`) removes the view panel from the display but does not delete the view from the plan.

16.2.1 Plots

The `Plot` button is adjacent to the `Delete` button and, when pressed, causes a dialog box to appear that contains options for hardcopy of the view's contents to be plotted. The dialog box (figure 16.2) includes:

- a menu for selecting the plotter on which to produce the plot (i.e., the name of the plotter queue),
- a menu to select paper size (plot area),
- a textline for specification of plot magnification,
- a textline for number of copies,
- a button to specify if the plot background should be black or white,
- a Cancel button, to cancel the plot request,
- an Accept button, to proceed with the plot.

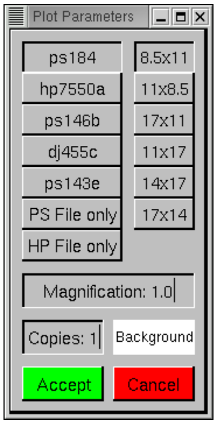
A white rectangle appears on the view indicating what part of the view will be on the plot. It may not be visible if the view magnification factor is high, putting the rectangle outside the view window. The rectangle will change with plot size selection. The "panning" capability of the view panel (right mouse button) provides a way to center a region of interest in the plot area, as the rectangle will remain fixed while the contents move relative to it.

The paper size menu displays a range of possible paper sizes and orientations, although not all plotters or printers support all paper sizes. If a paper size is chosen that a printer or plotter does not support, the plot will be clipped to the actual paper size in the printer.

The plot magnification is relative to actual life size.

The “background” button will be colored with either a black or a white background. The background color of the button corresponds to the background fill color for the plot, when an image is displayed on the plot. The default color is white. If no image is present on the plot, the background will be white, regardless of the button setting. Although a white background is not as visually appealing as a black background, it gives a considerable saving on ink or toner.

The Prism system supports the Hewlett-Packard model HP7550A pen plotter, the Hewlett-Packard Design-Jet 450 series ink jet printers and any PostScript capable color printer, such as the Tektronix/Xerox Phaser 790. If the printer supports PostScript paper size selection and has multiple paper trays, the plot will automatically direct the selection of the paper tray.



Magnification: 1.0

Copies: 1

Figure 16.2: The Plot dialog box

16.2.2 Locator controls

The *Local Locator* and *Remote Locator* buttons are beneath the *Delete Panel* and `Plot` buttons respectively. When the *Local Locator* button (labeled `Local`) is on, locators for other intersecting views may appear in this view; when it is off, no locators appear in this view. When the *Remote Locator* button (labeled `Remote`) is on, the locator for this view may appear in other intersecting views; when it is off, no locator for this view will appear in any other views. In order for a locator for an intersecting view A to appear in a given view B, the `Remote` button of view A and the `Local` button of view B must both be on; turning off either causes the locator for view A to disappear from view B. As for most other buttons, a button is “on” when it appears depressed (shaded rendition style) or the background and foreground are reversed (flat black/white rendition style).

The default settings of these locator buttons for a new view is that they are both on.

16.2.3 View Name

The *View Name* text field (unlabeled) provides a way to change the name of a view whenever necessary to clarify what is being shown on the screen. It shows the view name assigned at view creation, and can be changed anytime.

16.2.4 View Position

The *View Position* text field (labeled `Pos`) controls the position of the plane of the view along the axis of the patient coordinate system to which the view is orthogonal. This value is the view's z-coordinate for transverse views, y-coordinate for coronal views, x-coordinate for sagittal views, and the distance of the plane of the view from the isocenter toward the beam source, for beam's eye views.

If the value of the view position in a transverse view does not match the position of any contours, e.g., for organs, tumors and targets, then only the beam portals will be visible. If the view plane does not intersect the beams then of course the beams will not be visible either. To match here means that the position of the view and the z coordinate of the contour must be within an amount ϵ of each other. This parameter is called `*display-epsilon*` and may be set in the system wide parameter file (see section 4.2). The default is 0.001 cm, and it is recommended that it not be changed.

16.2.5 Image

The `Image` button controls the display of image data in the view. It is effective only if an image study has been loaded, otherwise the button has no effect. For transverse views, turning the `Image` button on causes an image at the z-coordinate determined by the view plane's position to appear in the view, if such an image exists (otherwise, nothing happens). The threshold for considering two things to be in the same plane is a configurable parameter (see section 4.2). For coronal and sagittal views, turning on the button causes a reformatted image to be computed at the view plane's position, if possible, and to be displayed in the view.

For beam's eye views, a DRR (digital reconstructed radiograph) is computed if an image set is present. This may take some time, as much as a minute. Progress messages are written to the terminal window, and portions of the DRR image are displayed progressively as they are computed.

16.2.6 Objects

The `Objects` button brings up a scrolling list of all the objects displayed in the view. The user can deselect any object, i.e., turn off its button in the list, causing it to not appear in the view. This is used to declutter a busy display, for example, a plan with many beams, blocks, or anatomical contours that are obscuring each other.

16.2.7 Display scale

The `Scale` slider controls the magnification of the objects in the view. The contents of the view are magnified as the slider is dragged to the right. On faster workstations, the update may be fast enough to drag the slider.

16.2.8 Image window and level

The `Window` and `Level` sliders and text fields determine the width and midpoint respectively, of the view's linear grayscale pixel intensity map. This map in turn determines the brightness and degree of contrast between features of the image which appears in the view. Image pixels whose values are below the bottom of the window appear black; those whose values are above the top of the window appear white, and those in between appear a shade of gray determined by the location of their value in the map. Changing either of these text fields or sliders causes the image to be redisplayed under the new mapping.

Chapter 17

Volume editor

The volume editor is a composite control panel that supports the creation and editing of organs, tumors, and targets. The volume editor panel also provides entry and edit of points of interest.

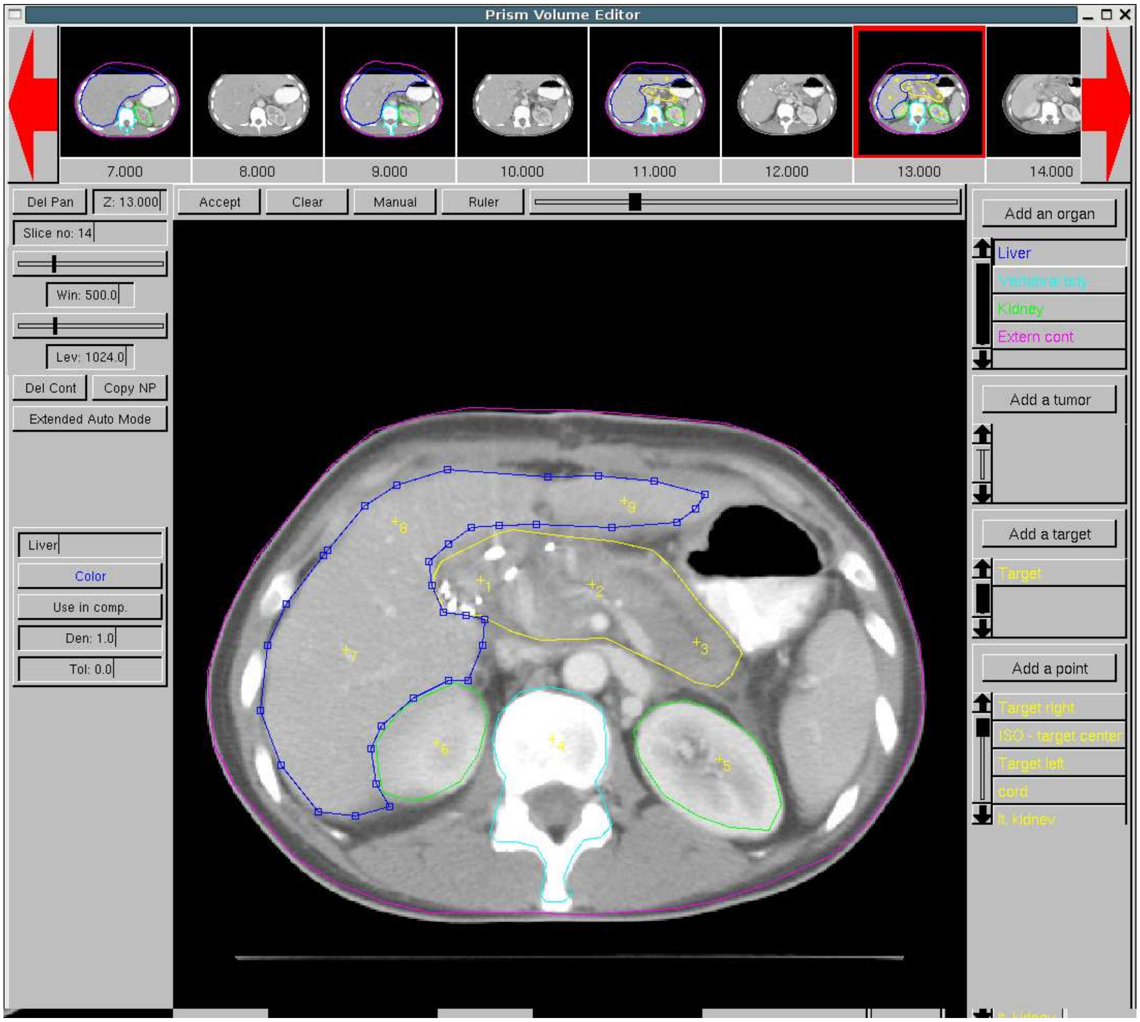
A single volume editor panel is created from the patient panel by pressing the Anatomy button. It is used to create and edit all anatomical structures. On the right side of the volume editor there are three selector panels, one each for `organs`, `tumors`, and `targets`. These selector panels work similarly to the others in Prism, except that when an object is added or selected, it becomes the focus of the volume editor panel, rather than having a separate panel created for it. Also, only one object among the three selector panels can be selected at any time. When the user selects an object, the object previously selected is deselected, i.e., the three lists act like a combined “radio menu”.

When the user brings up the volume editor, if there are any organs, tumors or targets, the first object (organ, tumor or target) encountered among the three lists becomes the initial selection. If there are none of these objects in the case yet, the volume editor automatically creates an organ with default values and no contours, and selects it.

When one of the *Add* buttons (in a selector panel) is pressed or when an existing object in one of the selector panels is selected, the newly created or selected object becomes the focus of the volume editor operations. If there was volatile data in the contour editor part of the volume editor, it will be discarded. Volatile data (a contour entered but not “accepted”, or a modified contour that has not been accepted, i.e., updated into the object) are indicated by the “Accept” button in the contour editor part of the volume editor. This button turns on when a contour is drawn or modified, or when the “Clear” button is pressed. The contour is accepted when the user turns the button *off* by pressing it when it is on. The button is automatically reset (turned off) when the user changes planes, or selects a different object.

In the volume editor, an object cannot be deleted if it is the currently selected object. The user must select some other object first. This means that once the volume editor is used, the patient case will contain at least one organ, tumor or target. You cannot delete them all.

The volume editor will display images or previously contoured anatomical structures, but the volume editor panel is capable of editing only the anatomical structure currently selected. Beam portals and isodose contours do not appear in the volume editor or in any of its subpanels, because they are associated with plans, and there can be multiple plans. Images may appear in the volume editor but they are not required.



Z: 13.000

Slice no: 14

Win: 500.0

Lev: 1024.0

Liver

Den: 1.0

Tol: 0.0

Figure 17.1: The volume editor

In addition to the selector panels and some controls of its own, the volume editor contains three additional control panels within it — a *filmstrip*, a *contour editor*, and an *attribute editor*. The filmstrip appears across the top of the volume editor, the contour editor in the volume editor's center, the attribute editor along the volume editor's lower left side, and the volume editor's own controls on its left side in the middle of the panel.

The volume editor can be one of two sizes, determined by the `*easel-size*` parameter, which may be set in the user's `.prismrc` file (appendix 4.2.1). The `medium` size makes the contour editor area 512 by 512 pixels, enough to display a standard CT image at normal resolution.

This may be a little small for drawing contours on small head cross sections or other small images. The `large` size makes the contour editor area 768 by 768 pixels, which is a 1.5 times magnification of standard CT image data. There is no restriction on the value of this parameter, except that it should be a reasonable size relative to the screen resolution in use.

When a new anatomy object is created, default values for some attributes are assigned, which of course may be changed by the user. The defaults are as follows:

- Organs: density is initially set to “None” and the organ is designated as “not used in the dose computation” (referred to as “Ignore in comp.”), display color is green, and there are no contours.
- Tumors: display color is cyan, and there are no contours.
- Targets: display color is blue, “how derived” is set to “Manual” unless one of the automated options described below is used, and there are no contours unless one of the automated options is used.

When an organ or a tumor is added, it becomes the volume editor focus, and manual editing can proceed. For targets, there may be more options, and they are described in the following section.

17.1 Creation of targets

When the user presses the `Add target` button above the target list subpanel in the volume editor, if there is at least one tumor with two or more contours defined (there could be several tumors), a dialog box will appear, to choose one of the three mechanisms for creating the new target. The dialog box has a three item radio menu, containing the items `Manual`, `Linear` and `PTVT`, along with `Accept` and `Cancel` buttons. If there are no tumors already defined, or only one contour for each tumor, a target with defaults as specified above is created and becomes the current object in the volume editor, without any dialog box.

17.1.1 Creating targets manually

Selecting `Manual editing with easel` or pressing the `Cancel` button simply creates a default target and makes it the current object in the volume editor.

17.1.2 Creating targets by trilinear volume expansion

The panel labeled “Prism Linear Volume Expansion Editor” consists of a scrolling list of tumors defined for this case, a text entry field for the expansion margin (in centimeters) to be used, and an `Accept` button. The same amount of expansion is used in all directions. The user identifies a tumor to be used for volume expansion by selecting it from the scrolling list, and edits the text entry field to provide the desired margin. Only tumors that have at least two contours will appear in the list. When the panel appears, the text field already has present a default value of 0.5 cm. You can change this value to whatever you would like to use. Pressing the “Accept” button causes the expansion mechanism to apply the specified margin to the tumor to create a target. The target is then added to

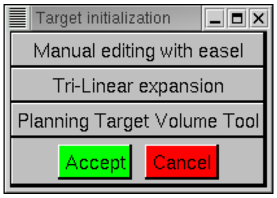


Figure 17.2: The volume expansion panel

the list of existing targets for this case. During the time that this panel is displayed, the rest of the system will not respond to other user input.

17.1.3 Creating targets with PTVT

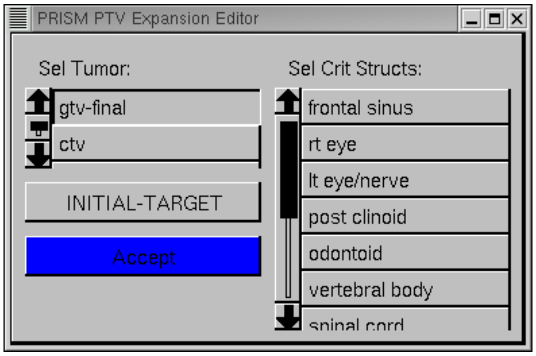


Figure 17.3: The PTVT panel

The Planning Target Volume Tool panel consists of a scrolling list of tumors defined for this case, a scrolling list of organs defined for the case, a button to specify either an “Initial” or a “Boost” target volume, and an `Accept` button. The user selects a gross tumor volume (GTV) or clinical tumor volume (CTV) from the list of tumors, and selects a set of *critical structures* from the list of organs. Only tumors that have at least two contours will appear in the list. Critical structures are organs that are sensitive to radiation and that should be excluded from the resulting target volume.

The user should *not* select the patient surface (skin) as a critical structure, since doing so will produce a target volume with no contours. The Prism system does not prevent this; it is up to the user to remember which is the patient surface.

Pressing the `Accept` button causes PTVT to compute a set of margins for the selected tumor, based upon the current patient immobilization device and the attributes of the selected tumor (see section 17.6 for information on editing a tumor's attributes). The margins are applied to the tumor to create a target, which is then added to the list of existing targets for this case. Critical structures are excluded from the target volume by PTVT. During the time that this panel is displayed, the rest of the system will not respond to other user input.

If attributes of the selected tumor are missing, the PTVT algorithm still generates a target volume, using default values for the missing information. The target produced may initially have no contours.

Planning target volume generation is further discussed in [15].

17.2 Using the volume editor

One anatomical object at a time can be edited by the volume editor, but if there are several anatomic objects in the patient case, the user may freely switch between objects without deselecting and reselecting the volume editor.

Upon creation of the volume editor, the sequence of images and existing anatomical contours associated with this case, if any, appears in miniature in the volume editor's filmstrip. If there are planes in which contours have been drawn but there are no images (e.g., if the contours were entered using the sonic digitizer), those planes also may appear in the filmstrip, with a black background. The part of the sequence visible in the filmstrip can be paged forward or backward a frame at a time by left-clicking[1] the arrow button at the upper left side of the panel for increasingly negative z values (toward the gantry) and the arrow button at the upper right side of the panel for increasingly positive z values (toward the viewer). Center-clicking on the filmstrip arrow buttons will page the filmstrip by five frames at a time.

17.2.1 Selecting a plane in which to edit

A plane is selected for editing by left-clicking on one of the miniature images in the filmstrip, or by entering a slice Z value into the volume editor's Z text field (If no image study should be available you may enter contours in their correct planesby entering the appropriate Z values in this text field). In the former case, a full-scale version of the selected image appears in the contour editor; in both cases, contours from anatomical objects previously created may appear in the contour editor, but these contours are not editable until the object they belong to is selected.

You can always enter a contour at a new Z plane by typing a new value into the volume editor's Z text field, whether an image study is present or not.

There is also a `Slice no.` register, that displays and allows selection of the display plane by image slice number if an image study is present.

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[1] this and related terms are defined on page 44

17.2.2 Editing a contour in the selected plane

If the selected object already has a contour at the selected plane, an editable copy of the contour appears in the contour editor. A series of small square *grab boxes* at the vertices of the editable contour always distinguishes it from other non-editable contours appearing in the same plane. Grab boxes are involved in editing operations; these operations are discussed in detail below. An existing contour can be hand edited with the pointer and mouse. If no contour yet exists for the selected object at the selected plane, a contour may be added by hand with the pointer and mouse, or generated with an autocontouring algorithm (if an image exists and is displayed), or entered with a digitizing tablet.

The autocontouring algorithm works well for high contrast objects such as skin, lungs and bone. It does not do well in delineating internal soft tissues when they are contiguous, e.g., liver, prostate.

17.2.3 Updating the selected anatomic object

Both contours edited from existing contours and new contours generated from scratch are *accepted* when finished by pressing the contour editor's `Accept` button, when it is on, i.e., by turning it off. If the button is already off, this means that there is no volatile or new data in the contour editor. When a contour is initially drawn, and when it is modified, the accept button turns on. This includes pressing the `Clear` button but not the `Delete contour` button. It also includes adding vertices, moving vertices, deleting vertices and using the autocontour facility.

Before being accepted, the contour has no existence beyond the confines of the contour editor, and can be arbitrarily manipulated without having any effect on the rest of the system. Once accepted, the contour is added to the selected anatomical object and associated with the current transverse plane selected in the volume editor. If a contour for that plane already was present in the object, it is replaced by the new one. When a contour is accepted, any views present that might show it will be updated and any dose calculation results that depend on it will be invalidated. Dose calculation results depend on the anatomy contours (only for objects assigned a density) but not on tumor or target contours. If isodose curves were displayed they will be erased. If a volume editor containing a contour that has yet to be accepted is itself deleted, the editable copy of the contour is discarded and the rest of the system is unaffected by any changes that had been made to that copy.

The Prism system (and the Volume Editor in particular) can *not* accept anatomic objects that have bifurcations along the z axis, i.e., that would require two or more disjoint contours in a single z plane. This includes things like bronchi. If such objects are to be put into Prism, they should be split into two or more adjoining parts, each of which is not bifurcated.

An existing contour can be deleted by selecting its plane and pressing the `Delete Contour` button on the volume editor. When a contour is deleted by the volume editor, the effect on the selected object is immediate.

17.2.4 Editing nonspatial attributes

Textual attributes of the volume editor's selected anatomical object can be edited with the volume editor's attribute editor, which contains text fields or other controls for all such attributes. The contents of the attribute editor are specific to the kind of anatomical object currently being edited by the volume editor. The effect of modifying an attribute of an object via the attribute editor is immediate, meaning that an attribute changes as soon as the interaction with the attribute editor control corresponding to that attribute is complete. For text fields, this means, when you press the `<RETURN>` key on the keyboard. For popup menus, or other such dialog boxes, this means, when you press the `Accept` button or the `Cancel` button.

Typically, a user selects the volume editor, adds or edits the contours for the various anatomic objects on a plane by plane basis (manually, with autocontouring, or using the digitizing tablet), and then deletes the volume editor panel, signifying the completion of editing operations for the anatomy. The changes to the contours of an object during editing by the volume editor (that is, after a new or modified contour is accepted, or after an existing contour is deleted) are immediately reflected in any relevant views.

17.3 Volume Editor controls

The volume editor contains a number of controls of its own, which are not part of any of the three subpanels contained within it. These controls manage operations upon the volume editor itself or handle functions which cannot be properly contained within any of the volume editor subpanels.

The *Delete Panel* button (labeled `Del Pan`) deselects the anatomical object being edited and closes the volume editor. If a contour was being edited by the contour editor and was not yet accepted at the time the volume editor is closed, the editable version of that contour is discarded and the original is unchanged.

17.3.1 Delete Contour

The *Delete Contour* button (labeled `Del Cont`) immediately deletes the contour currently being edited from the selected anatomical object.

17.3.2 Copy NP

The *Copy Contour from Nearest Plane* button (labeled `Copy NP`) copies the object contour from the nearest plane edited to the current plane of the contour editor. This mechanism is useful when contours of a given object do not vary much from plane to plane, and when it would be easier to copy and modify a contour from a nearby plane, rather than to create a new contour altogether for each plane. If there are two planes that are both equidistant (and closest) to the current plane, then the contour from the plane with the lesser z value is copied. If there is no contour available to copy, the button has no effect, except that an acknowledge box appears, indicating “No nearest contour”.

17.3.3 Z

The `Z` text field displays the Z value of the transverse plane currently highlighted with a red border in the filmstrip, if such a plane exists in the filmstrip and is visible, and indicates the plane to which the contour editor is set. If a new value is entered into this text field, the list of existing planes for this study is searched and the plane with the matching Z value is selected, if such a plane exists. The filmstrip adjusts itself so that the frame corresponding to the selected plane is visible in this case, and this frame becomes highlighted. The contour editor plane is also set to the selected plane, and the selected image and contours in this plane are displayed there, if any exist. If the value entered into the `Z` text field does not match (to within a parametrized value) any of the existing planes for the current case, no filmstrip frames are highlighted and the contour editor is reset to an empty plane. The slice number field is blank. When a contour is drawn into this plane and accepted, the new plane is added to the list of planes for this study, and then appears in the filmstrip.

If you have drawn a contour in the current plane but not "accepted" it by pressing the `Accept` button in the contour editor, and you then select a new plane either by typing in a new Z value and pressing the `<RETURN>` key, or by selecting a frame in the filmstrip, the contour you drew will be discarded.

17.3.4 Slice no.

The `Slice no.` text field displays the slice number of the image currently displayed in the background of the contour editor (and highlighted in the filmstrip), if there is an image in the current plane. If there is no image in the current plane, this text field is blank. The user may type in the slice number for an image whose plane he/she wishes to select, just as with the Z text field. If there is an image with that slice number, the corresponding Z plane is selected as above. If there is no such slice number, a message box will appear informing the user, and the text field will be blank. Similarly if there is no image study, the message will appear when the user enters any slice number. If the slice number is negative, an acknowledge box appears with the message, "Please enter a number between 0 and 500".

17.3.5 Window and Level

The *Window* and *Level* text fields (labeled `Win:` and `Lev:` respectively) control the gray scale window and level of the image in the contour editor's drawing region and the images in the filmstrip's frames. Entering new values into either of these text fields causes the window and level of these images to change to the specified new values.

17.4 Filmstrip

The principal component of the filmstrip is a scrollable, horizontal sequence of transverse images derived from the image study associated with the current plan. These images are displayed at a resolution of 128x128 pixels in the filmstrip's *viewport*, and can be scrolled in either direction a frame at a time by left-clicking the mouse over either of the red arrow buttons on each side of the viewport. Center-clicking the mouse over the filmstrip arrow buttons will scroll the filmstrip five frames at a time (if there are more than five frames beyond the visible part of the filmstrip, otherwise the middle button will have no effect). The Z value of each transverse image is displayed directly below the image (rounded to the nearest 0.1 mm). Each image also contains contours for any anatomy, tumors, or targets which have previously been drawn in that plane with other volume editor panels. Clicking the left mouse button while the pointer is on a particular frame in the filmstrip selects that plane, causes it to highlight in the viewport and causes it to be displayed at full size in the contour editor.

17.5 Contour editor

Below the filmstrip is the contour editor, a facility for creating and editing organ, tumor, and target contours. It consists of a drawing region for interactively adding, editing, or deleting contours and a control region for invoking or modifying the state or mode of the contour editor. The contour editor is also used as a component in the block editing panel (section 6), the multileaf collimator editing panel (section 9), and the electron beam cutout contour editing panel (section 5.7.2). In those cases some functions are not available; differences from its use here are described in each of those sections.

The contour editor's control region consists of a set of buttons and other controls which collectively control a variety of contour editor functions.

17.5.1 Accept

The `Accept` button causes the contour being edited to be closed, if it was open, and to be added to the current organ, tumor or target. If the user is editing an existing contour, the new contour replaces the old one. The `Accept` button must be pressed to update the object with the new contour. The action required is that the button is turned off, not on. If the button is not on, there is no new data to accept, so the operation would be redundant. Nevertheless it can be done by the user turning the button on and then off, i.e., with two successive clicks.

To be *accepted* a contour must satisfy several conditions. First, no accepted contour may cross over itself. Such a contour will not be accepted if the `Accept` button is pressed; a message box is displayed instead, giving the reason why. Second, no contour may have any adjacent pairs of coincident vertices. Such vertices are checked for and automatically stripped out during the accept operation. Finally, no closed contour may have less than three vertices.

An open (or closed) contour with less than three vertices cannot be accepted; instead, a message box is displayed stating the reason why. It is possible to delete vertices with the middle mouse button, reducing the number of vertices below three in a *closed* contour during contour editing, but the resulting contour will not be accepted when the `Accept` button is pressed.

17.5.2 Clear

The `Clear` button causes the contour currently being edited to be erased, and allows the user to start over, with no contour vertices. The `Clear` button is a strictly volatile operation and *cannot* be used to delete a contour from the anatomical object selected by the volume editor, since after a contour is erased with the `Clear` operation, it contains less than three vertices and will not be accepted. A contour is *deleted* from an object with the `Delete Contour` button on the volume editor.

17.5.3 Ruler

The `Ruler` button creates and places an interactive, movable, resizable, reangleable ruler marked in centimeter intervals according to the current magnification. Grab disks appear at each end, one open and one closed. Clicking and dragging on either with the left mouse button causes that end of the ruler to be repositioned — the other end stays fixed, causing the ruler to be lengthened or shortened. The ruler "unrolls" from the open grab disk, in that the tic marks are generated and consumed at that end as the ruler is resized. Dragging any part of the spine of the ruler with the left mouse button causes the entire ruler to be relocated along with the pointer. A ruler is associated with the drawing region of the contour editor in which it is created. It persists in the drawing region across different spatial planes but does not persist from session to session. Also, one may delete a ruler with a middle mouse click, and change the ruler's color via a right mouse click with a popup color menu. For these two operations the pointer must be on the long axis of the ruler. Otherwise there is no effect. Clicking the ends or the tic marks (off the axis) will not bring up the color menu or delete the ruler. Rulers do not move with the anatomy and landmarks when the magnification of the contour editor drawing region changes. Similarly, the ruler does not move when the "panning" option is used. However, when the magnification changes, the spacing between the ruler's tic marks does change accordingly. When the ruler is on the screen, the ruler button label displays the ruler's current length in cm, to the nearest 0.01 cm (0.1 mm).

17.5.4 Drawing Mode Button

The *Drawing Mode Button* switches among four modes. The modes are: `Manual`, `Automatic`, `Landmark` and `Digitizer`. Each is a way that you can use the pointer and the mouse (or the sonic digitizer) to draw or edit contours and landmarks. The mode currently in effect is displayed as the button label. The default mode is Manual. Pressing the button brings up a popup menu listing the four modes. These drawing modes are described in section 17.5.6.

In `Digitizer` mode the system accepts input from a sonic digitizer. As long as this mode is in effect, Prism ignores (discards) keyboard and mouse activity and only accepts input from the digitizer. Digitizer input mode remains in effect until the user digitizes in the *Done (Exit)* box on the digitizer tablet. Then Prism returns to manual, automatic or landmark mode, whichever was previously in effect.

17.5.5 Scale slider

A `Scale` slider allows for changing the scale factor at which the graphics in the contour editor are displayed. This provides a "zoom" operation.

Panning, a related operation, is controlled by dragging the pointer across the drawing region with the right mouse button held down, while the pointer is not on a contour vertex, ruler or landmark.

17.5.6 Drawing region

When a Z plane has been specified by clicking on one of the filmstrip's frames (see above), or by entering a slice number, a large format version of the transverse plane at the specified Z level appears in the contour editor's drawing region. Entering or editing a value in the Z text field of the volume editor will also render a large format version of the specified plane if such a plane contains any data.

An image and/or other previously contoured structures may appear in the drawing region, but such structures are only editable by the contour editor if the structure is selected on the right side of the volume editor panel. If there is no contour for the currently selected object, by drawing directly into drawing region with the mouse, a new contour for the object being edited may be added at the specified Z level. If there is a contour for the currently selected object, that existing contour may be modified or removed. If a contour is editable in the selected plane, it will appear with grab boxes at its vertices.

Contours are displayed as vertices connected by line segments. At each vertex, a grab box is displayed. If the contour is open, the last vertex added has a grab box that is filled in, and all other grab boxes are hollowed out. A contour which has been closed appears as a continuous chain, all grab boxes hollowed out, and may not be opened again.

The drawing area may also contain small circles called *Landmarks*. Landmarks are intended solely as temporary memory aids — they are not saved with the patient data and do not persist from session to session. A landmark is not attached to the spatial plane on which it is drawn but reappears on subsequent planes in the drawing area, until it is deleted. Landmarks do not appear in views or on plots. Placing a landmark is analogous to making a temporary mark on the CRT screen, assuming the registration and magnification of the displayed data remains consistent from plane to plane. However, if registration or magnification changes (pan or zoom), the landmark's location changes appropriately.

The effect of the mouse buttons and pointer motion depends on the current mode. There are two kinds of actions, those that take place when the pointer is over an object that can be manipulated, e.g. a contour vertex or a landmark, and those that take place when the pointer is not over any such object.

The following list describes what happens when a mouse button is pressed while the pointer is over an object. This is the same in *all modes* except `Digitizer` mode (because in `Digitizer` mode the mouse has no effect except as used explicitly for entry of the digitizer magnification factor).

Contour vertex: If the pointer is placed over the grab box of an existing contour vertex and the *left* mouse button held down, the contour vertex represented by the grab box can be dragged to a new location.

Clicking on the *middle* mouse button while the pointer is over a contour vertex grab box deletes the vertex and any segments adjacent to it. If the box was not at an endpoint, the two grab boxes which were at the other ends of the deleted segments are then connected together by a replacement segment. The number of segments in a *closed* contour can be reduced below three, in which case, when there are two vertices, the contour is "degenerate", a double straight line, when there is one, a totally "degenerate" contour, and deleting the one remaining vertex has the same effect as the `Clear` button.

When the contour was closed, and the number of vertices is two, you cannot add vertices except by clicking on the line segment connecting them. When the number of vertices drops to one, you can not add vertices, and must delete it or use the Clear button to start over.

The *right* mouse button has no effect when the pointer is over a vertex grab box.

Contour segment: If the pointer is placed over an existing contour segment and the *left* mouse button is clicked, that contour segment is broken into two at the pointer's location, a new vertex is added to the contour at that point, and correspondingly a new grab box appears between the two contour segments.

The *middle* and *right* mouse buttons have no effect when the pointer is over a contour segment.

Landmark: Once placed, a landmark may be moved by dragging it with the *left* mouse button, in a manner similar to dragging contour vertices.

A landmark is deleted by positioning the pointer over the landmark and pressing the *middle* mouse button.

The color of the landmark may be changed by positioning the pointer over the landmark and pressing the *right* mouse button. A color popup menu appears from which the user may then select the color.

The following describes what actions take place when the mouse buttons are pressed while the pointer is *not* over an object as described above.

Pressing the *right* mouse button and then moving the pointer will "pan" the view, i.e., the origin in the view is shifted by the amount and direction that the pointer moves. This operation is independent of mode, except that it is, of course, disabled in `Digitizer` mode.

Pressing the *middle* mouse button while the pointer is not over any moveable or editable object has no effect in the contour editor.

Pressing the *left* mouse button has an effect that depends on the drawing mode, as follows:

Manual mode: If the contour is open and the pointer is not over an object, then depressing the left mouse button causes a new segment to be added from the leading segment of the contour to the pointer. A new leading grab box is added to the new end of the contour, and the old leading grab box is hollowed out. If the mouse is then moved while the left button is held down, a freehand curve may be traced out from the leading grab box by the pointer. When the left mouse button is finally released, the curve is automatically converted into a chain of segments, separated by grab boxes, closely approximating the curve. This conversion process begins at the leading grab box and ends at the pointer.

Automatic mode: Automatic mode may be used to contour around structures whose interior and exterior significantly contrast each other in the underlying image. In this mode, the user places the mouse pointer over some part of the image and clicks with the left mouse button. This causes a line to be autocontoured through the image starting at a point to the right of the pointer where the intensity level just increases (a presumed boundary); the line is then automatically segmented in the same way that a line drawn by freehand sketch in manual mode is. This causes the previous contour to be erased and a new one to be set down. If the resulting contour is unacceptable, the pointer may be moved and the left mouse button re-clicked. This operation uses the image data after it is put through the gray scale map and displayed. Adjusting the window and level values may help make the automatic contouring process more effective, since the operation uses the mapped image as displayed, not the original image data. The pointer should be placed just to the left of a visible boundary in which the brightness of the image is increasing to the right.

When Automatic mode is selected, it is possible to use the Extended Autocontour facility. Pressing this button provides some additional controls just below it. There are text fields to specify the range of Z values to include for automatic contouring, a mode selection button, a

Clear button (that will erase all the contours in the specified range), and an object type button (the only useful object type at present is External, referring to the skin contours). The mode selection button determines what is done when the autocontour function finds an already existing contour at a particular Z plane. It can replace it with the new one, it can stop at that plane (even though there are still more planes to do), it can use the existing contour instead of the new one, or it can ignore the existing one, and just add the new one.

It is also possible to autocontour the inside of a low density region by placing the pointer inside the region near the right edge.

If no image is displayed, the autocontouring function is not enabled, even though it appears on the popup menu associated with the mode button.

Landmark mode: Clicking with the left mouse button while the pointer is not over a selectable object in the drawing area creates and places a small movable circle in the drawing region. Landmarks are not identified with any particular anatomical contour or image.

Digitizer mode: Mouse and pointer action are ignored, except for input of digitizer magnification factor at the beginning of a cycle of digitizer entry.

17.5.7 Digitizer

Contours may also be entered with a *digitizing tablet.* This mechanism is commonly used to enter contours when no image study is available, but it can also be used to enter contours from films, e.g., multiformat films produced by the CT film printer.

The user selects the digitizer by pressing the *Mode* button in the contour editor control region, and selecting `Digitizer` from the popup menu. When a Prism session starts, the Prism software determines if a digitizer is available on the workstation currently in use, by referring to the table described in section 4.2. If the digitizer is not connected, or turned off, but the table specifies that it is available, selecting digitizer input mode will cause the Prism session to get stuck. In this case the Prism user can interrupt the program by typing `^C` (Control-C), and then `:exit` at the terminal window where the Prism program was started. In this case all data that were not archived or checkpointed will be lost. If the table does not specify a digitizer as available for the computer in use, selecting digitizer input will just result in a message box informing the user.

Once the user has selected the digitizer, Prism can only respond to the digitizer; it ignores (discards) any typing or mouse activity, except when prompting for entry of the digitizer magnification factor. In digitizer mode the user controls the session by striking the digitizer stylus in marked regions on the digitizer tablet. This takes the place of clicking the mouse.

The first time the digitizer is selected in a Prism session, the user is prompted to digitize two calibration points that are permanently marked on the tablet itself. This calibration only needs to be done once for the duration of the Prism session, regardless of whether the user is entering contours, or beam portals, or blocks or electron beam cutouts. The prompt is in a window on the screen, like a message box, except that there is no `Acknowledge` button, and the box is unmapped when the points requested are digitized. Because of an unsolved problem with how the X window system works, the first message may be blank, but the user should proceed anyway as if it said, “Please digitize the lower left calibration point”.

Each time digitizer mode is selected, a dialog box appears containing a text field for the digitizer magnification factor (labeled `Mag:`). This dialog box displays the magnification factor that will be in effect during digitizer input mode. This factor is initialized to 1.0 when the volume editor is created. The user should enter an appropriate value before digitizing from a hardcopy image which is not life size. This factor is actually the magnification of the hardcopy image, so that an image which is smaller than life size has a magnification factor less than one. Prism uses the reciprocal of this magnification factor to scale from cm on the digitizer tablet to cm in the object space. In subsequent selections of digitizer mode from the same volume editor, the previously entered magnification factor appears in the dialog box. When the volume editor is deleted, the magnification factor reverts to 1.0, for subsequent volume editor invokations.

After entering and/or accepting the magnification factor, a dialog box appears asking the user to digitize the origin point. This dialog box may also be blank. You should proceed anyway. The origin point is chosen by the user and is fixed on the hardcopy image (not the tablet). The user should choose an origin point that can be easily and repeatably identified in the hardcopy. This origin is used to define the object space coordinate system for the current plane in the contour editor.

After entering the origin, the user may digitize contour points or invoke editing functions by pressing the digitizer stylus on the tablet. As each point is digitized, it appears in the contour editor, connected to the previously entered point by a segment. Editing operations may be invoked by using the stylus in three of the four marked regions of the digitizing tablet, labeled `Delete last, Delete all (Start Over), Close contour, Done (Exit)`.

The most recently added contour segment may be deleted with `Delete last`, all points may be discarded with `Delete all (Start over)`, and the contour may be “accepted” with `Done (Exit)`. The `Close contour` box on the digitizer is ignored if you digitize a point within it. Digitizing `Done (Exit)` is like pressing the contour editor’s `Accept` button, and in addition it deselects the digitizer, returning control to the keyboard and mouse. The contour editor mode returns to its previous state.

17.6 Attribute editor

To the left of the contour editor is the attribute editor, which consists of a set of text fields and buttons for entering or modifying textual or numerical information associated with the anatomical object specified for this volume editor. Every instance of the attribute editor has at least a `Name` text field and a `Color` button.

17.6.1 Name

The `Name` text field displays the name of the object currently being edited; entering a new name causes the name to be updated in the appropriate scrolling list in the patient panel.

17.6.2 Color

The `Color` button displays its label in the color associated with the object. When pressed, it brings up a popup color menu, from which the user may select any of the standard colors. Selecting a new color changes the color of all contours of the object currently being edited.

17.6.3 Other attributes

The other particular kinds of information are different for each type of anatomic object, and consequently, the contents of the attribute editor differ from one type of anatomical object to the next. These are the attributes for each type of anatomic object:

Organ: For an organ the attribute editor has:

- a button that toggles between two values, specifying that the organ is either used in the dose computation or ignored by the dose computation (for obliquity and inhomogeneity corrections). The button is labeled either `Use in comp` or `Ignore in comp`. Pressing the button changes it from one state to the other.
- a textline for density assigned to the organ. It has label `Density:` and either `none` or a number. If the button above is set to `Ignore in comp` this textline shows `none` and the value cannot be altered by user input. If the button is set to `Use in comp`, the textline shows a number, initially 1.0; it can then be changed by the user. Input is checked for validity, i.e., it must be a well formed number, greater than or equal to 0.0.
- a textline for tolerance dose. It has label `Tol:` and a number. Input is checked for validity, similarly to the `Density` textline.

Tumor: For a tumor the attribute editor has the following buttons, each of which pops up a menu of the valid choices for each attribute. They are only used in the PTVT automated target generation tool and are explained further in [15].

- Site
- T-stage
- N-stage
- Cell type
- Region
- Side
- Fixed or not fixed
- Pulm Risk

Target: For a target the attribute editor has:

- Site
- Prescribed dose (PD)
- Region
- Target type (Initial or boost)

- Nodes

The site, region and target type are buttons like the tumor attributes. The prescribed dose is a numeric textline, and nodes is a textline.

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Appendix A

Machine motion scaling and printed settings

This section explains how to interpret therapy machine settings (such as gantry angle, etc.) on charts printed by the Prism treatment planning system. We also list here particulars of machine motion conventions, scaling, and motion limits for all machines in use at the Radiation Oncology Department of the University of Washington Medical Center.

In a Prism planning session at the workstation, every machine motion is represented the same way. For example, gantry angle zero is always the "home" position that puts the gantry at the top of its rotation, with the beam pointing straight down. The Prism coordinate system conventions are explained in detail in Chapter 3 of this report.

On the Prism chart, motions are represented in each machine's own coordinate system. The gantry "home" position is called zero degrees for the neutron machine and the Philips SL20, but 180 degrees for Varian machines. Therefore, the numbers that appear on the Prism panels on the workstation screen are sometimes different from the numbers printed on the chart. This section explains the differences for all the machines now in use in the Department of Radiation Oncology at the University of Washington.

A.1 Gantry angle

Table A.1 lists the correspondence between the Prism gantry angle scaling conventions and those of all the machines in use at the Radiation Oncology Department of the University of Washington Medical Center.

For the gantry, *Home* is the machine coordinate system value for the angle that puts the gantry at the top of its rotation, with the beam pointing straight down. In the Prism system this gantry angle is 0 degrees.

For the gantry, *Dir* is the direction of increasing gantry angle in the machine's coordinate system. It is clockwise (cw) or counterclockwise (ccw) seen from the isocenter looking toward the gantry protractor. In the Prism system, the gantry angle increases clockwise.

The SL20 and Neutron gantry angle wrap from 359 to 0 as the gantry passes the home (top) position moving clockwise.

Table A.2 shows the relation between the Prism gantry angle and each machine's gantry angle, for four standard gantry angles.

A.2 Couch angle

Table A.3 lists the correspondence between the Prism couch angle scaling conventions and those of all the machines in use at the University of Washington.

For the couch, *Home* is the machine coordinate system value for the angle that puts the table long axis parallel to the axis of gantry rotation.

For the couch, *Dir* is the direction of increasing couch angle in the machine's coordinate system. It is clockwise (cw) or counterclockwise (ccw), seen from the isocenter looking down at the couch floor.

Couch rotation angle *Range* is expressed in each machine's coordinate system; for the Clinac 4, the second number is at the limit of counterclockwise rotation, and for the other machines it is at the limit of clockwise rotation.

The SL20 couch rotation angle wraps from 359 to 0 as the table passes the home position moving clockwise.

Table A.4 shows the relation between the Prism couch angle and each machine's couch angle for the four standard angles. Some couch rotation angles cannot be achieved by some machines. These inaccessible angles are indicated by asterisks (`**`). The Prism system does not prevent the dosimetrist from entering these angles, but the inaccessible angles are indicated on the chart by asterisks, just as they are in the table.

A.3 Collimator angle

Table A.5 lists the collimator angle ranges and motion conventions for all collimating systems in use in the treatment machines at the Radiation Oncology Department of the University of Washington Medical Center.

Home is the machine coordinate system value for the collimator angle that is favored when there are no other constraints (arising from wedge orientations, etc). Usually this is the rotation angle that is most convenient for loading and carrying the block tray.

The collimator is usually set at the home angle, or 90 degrees from home. If one of the two 90 degree angles is preferred, this is noted in the *Comment* column.

Machine	*Home*	*Dir*
Prism	0	cw
Clinac 4	180	ccw
Clinac 2500	180	ccw
Philips SL20	0	cw
CNTS Neutron	0	cw

Table A.1: Gantry angle machine scales

Prism g	0	90	180	270
Clinac 4	180	90	0	270
Clinac 2500	180	90	0	270
Philips SL20	0	90	180	270
CNTS Neutron	0	90	180	270

Table A.2: Prism gantry angle and machine gantry angles.

Dir is the direction of increasing collimator angle in the machine's coordinate system. It is clockwise (cw) or counterclockwise (ccw) seen from the isocenter looking into the collimator. (This is *not* a beam's eye view.)

Range is expressed in each machine's coordinate system. For the Clinac 2500 it is the maximum rotation in the counterclockwise direction; otherwise, it is the maximum in the clockwise direction.

Table A.6 shows the relation between the Prism collimator angle and each machine's collimator angle. Some collimator rotation angles cannot be achieved by some machines. These inaccessible angles are indicated by asterisks (`**`). The Prism system does not prevent the dosimetrist from entering these angles, but the inaccessible angles are indicated on the chart by asterisks, just as they are in the table.

A.4 Collimator jaws

This section lists the collimator jaw motion limits and describes the correspondence between Prism collimator jaw names and the names on each machine.

Width is the setting that opens the collimator across the width of the table (in the Prism patient X direction) when the machine is in its home position.

Length is the setting that opens the collimator along the length of the table (in the Prism patient Z direction) when the machine is in its home position.

For the Clinac 2500, when the upper jaw setting is symmetrical, the setting is a single number (the entire opening). When the upper jaws are set asymmetrically, two settings are needed. Each setting is the opening away from the central axis, usually a positive number. When an "overcentered" jaw crosses the central axis, its setting is a negative number.

Table A.7 lists the limits of collimator jaw motion for all machines, with and without wedges in place.

Machine	*Home*	*Dir*	*Range*	
Prism	0	ccw	0	360
Clinac 4	0	ccw	-90	90
Clinac 2500	180	cw	90	270
Philips SL20	0	cw	229	115
CNTS Neutron	180	cw	63	297

Table A.3: Couch angle machine scales

Prism	0	90	180	270
Clinac 4	0	90	180**	−90
Clinac 2500	180	90	0**	270
Philips SL20	0	270	180**	90
CNTS Neutron	180	90	0**	270

Table A.4: Prism couch rotation angle and machine couch angles.

Machine	*Home*	*Dir*	*Range*		*Comment*
Prism	0	cw	0	360	
Clinac 4	0	cw	−90	90	Differs from other Varians
Clinac 2500	180	ccw	79	283	
Philips SL20	0	cw	0	360	
CNTS Neutron	270	cw	75	284	270 and 180 are preferred

Table A.5: Collimator angle machine scales

Width and *Length* are the maximum collimator openings (in cm) across the couch and along the couch, respectively, when the collimator and couch are in their home positions.

Wedge Gradient is the direction of the wedge gradient when the collimator is in its home position. Neutron is the only machine where the wedge can be rotated to the 90 and 270 degree orientations to make an orthogonal gradient.

Wedge Limit is the maximum collimator opening (in cm) in the direction of the wedge gradient, when a wedge is present.

The Clinac 2500 independent jaws cannot be used when the wedge is present; wedged fields must be symmetrical.

Because of the collimator leaves, the Neutron field length can only be adjusted in 1.25 cm steps for lengths up to 12.5 cm and in 2.0 cm steps for larger fields. The SL20 X diaphragms enable its field length to be varied continuously.

The SL20 length can be the full 40 cm with the wedge in place, but can only be 30 cm wide with the wedge in place. (This is for the “Large Wedge,” which we have. For sites that have the “Standard Wedge” instead, the limits are 25 cm length and 20 cm width)

The Neutron limits with the wedge in place apply to the 45 degree wedge. The limits for the others are different (30 degree: 19 and 30, 60 degree: 14 and 29)

Prism	0	90	180	270
Clinac 4	0	90	180**	−90
Clinac 2500	90	0**	270	180
Philips SL20	0	90	180	270
CNTS Neutron	270	0**	90	180

Table A.6: Prism collimator rotation angle and machine collimator angles.

Machine	*Width*	*Length*	*Wedge Gradient*	*Wedge Limit*
Clinac 4	32	32	Length	15
Clinac 2500	40	40	Length	14.7
Philips SL20	40	40	Length	40 (along gradient)
				30 (across wedge)
CNTS Neutron	29	32.5	(both)	20 (along gradient)
				30 (across wedge)

Table A.7: Collimator limits

Table A.8 shows how the Prism beam panel collimator jaw setting names correspond to the machine names on the chart. The Prism X motion is the collimator lower set for the Clinac 4, but the upper set for the Clinac 2500.

There is a version of the SL20 data used when blocks, rather than the multleaf collimator, are used to shape the field. For this, the Prism variable jaw collimator models the Philips jaws. Philips' X and Y axes are reversed from Prism's.

The Neutron machine is really a leaf collimator machine, but (for now) is modelled in Prism as a variable-jaw collimator machine. The *width* $-$ setting printed on the chart for this machine is actually the maximum opening of leaves number 0 – 19 away from the central axis. The *width* $+$ setting is the maximum opening of leaves 20 – 39 away from the central axis. To increase the *height* $-$ setting, a larger number of leaves in the group 10 – 20 must be opened, and increasing *height* $+$ means opening more of the leaves numbered 0 – 9 and 30 – 39.

Machine	Collim type	Prism name	Machine name
Clinac 4	Symmetric	X	Lower
		Y	Upper
Clinac 2500	Combination	X inf	Jaw 1
	$(X_{inf} \neq X_{sup})$	X sup	Jaw 2
	$(X_{inf} = X_{sup})$	X	Upper
		Y	Lower
SL20 Blocks	Asymmetric	X inf	Y2
		X sup	Y1
		Y inf	X2
		Y sup	X1
Neutron Blocks	Asymmetric	X inf	width $-$
		X sup	width $+$
		Y inf	height $-$
		Y sup	height $+$

Table A.8: Collimator jaw names

Note that the Varian Clinac 2500 presents a complicated special case: it represents its independent jaw pair by a single setting named "Upper" when the opening is symmetric, and by two settings named “Jaw1” and “Jaw2” when the opening is asymmetric. Prism does not model this, but only provides the separate sliders for both symmetric and asymmetric settings.

No offsets or scaling constants are needed for collimator settings; the machine conventions are the same as in Prism: symmetric jaw settings are the width of the opening, and asymmetric settings are the opening of each jaw away from the central axis (overcentering is negative).

Prism does not check collimator jaw openings against any limits.

A.5 Multileaf (MLC) collimators

The collimator section on the EXTERNAL BEAM SETUP page shows four numbers for each MLC field. The *height* and *width* are the maximum dimensions of the collimator portal opening along and across the axis of gantry rotation, respectively. In the case where the collimator rotation is zero *in the Prism coordinate system*, these correspond to the number of open leaves and the maximum leaf opening, respectively.

For the SL20, *only when the collimator rotation angle is zero*, the four numbers correspond to the settings for the four SL20 jaws, as shown in Table A.9. Here again, Philips’ X and Y axes are reversed from Prism’s.

Prism chart	SL20 MLC
height	X field size
h offset	X offset
width	Y field size
w offset	Y Offset

Table A.9: Prism chart and SL20 jaw settings *when collimator rotation is zero*

A.5.1 Philips SL20 multileaf collimator

Fig. A.1 shows the SL20 multileaf collimator arrangement. This is a beam’s eye view; it shows the leaf numberings as seen *from* the source looking *out* through the leaves. The Prism chart should include a similar figure, by itself on an appropriately labelled page, for each SL20 beam in the plan.

When the collimator is in its home position (the collimator rotation angle is zero on the machine scale), the collimator is oriented so that the SL20 gantry protractor is at the *top* of the figure. When the SL20 couch is also at its home position (the couch couch rotation angle is 0 on the machine scale), opening the collimator leaves makes the field wider across the couch (parallel to the Prism patient coordinate system x axis), and opening more leaves makes the field longer along the couch (parallel to the Prism patient system z axis). All subsequent description refers to the collimator and couch in these home positions.

The SL20 machine scales call the direction of leaf motion the Y direction. The leaves on the right side of the figure are called the Y1 leaves and those on the left are the Y2 leaves.

The SL20 multileaf collimator has 80 leaves, each 1 cm wide. Each leaf is identified by the distance from the isocenter to the line of travel of the center of the leaf. Since the leaves are 1.0

cm wide and the isocenter is between leaves, all of these distances are odd multiples of 0.5 cm, ranging from -19.5 cm through 0.5 cm and up to 19.5 cm. Distances toward the gantry protractor are positive and distances away from the protractor are negative.

The setting of each leaf is the distance of the leaf end from the centerline. Leaf positions are positive when the leaf is retracted on its own side, zero on the centerline and negative when it is “overcentered” into the opposite side. The figure shows the settings for a 10×10 field; the settings of the open leaves are all positive.

Each leaf can open to $+20.0$ cm and can overcenter to -12.5 cm.

When all leaves are fully open the field size is 40×40 cm.

Opposing leaves cannot be closed together. A gap of at least 0.6 cm must be left between opposing leaves. In the figure, where opposed leaf settings are both shown as 0.0 cm, that means the leaf pair is hidden behind a *diaphragm*.

In addition to the 80 leaves, the SL20 collimator also has four *diaphragms* that are similar to conventional collimator jaws. The jaws are outside the leaves, nearer the patient. The diaphragms are named X1, X2, Y1 and Y2.

The Y diaphragms move in the same direction as the leaves. In the figure, the Y1 diaphragm is on the right, Y2 on the left.

The X diaphragms move perpendicular to the leaves. The X diaphragms allow continuous adjustment of the field size in this direction. In the figure, the X1 diaphragm is at the top, X2 at the bottom.

Diaphragm settings are a given as a *field size* and an *offset*. The field size is the separation between opposite diaphragms and is always positive. The offset is the distance from the isocenter to the midpoint of the separation between the opposite diaphragms. The offset is 0.0 if the diaphragms are symmetrical, positive if diaphragm number 1 is open wider, and negative otherwise.

The X diaphragms are *independent* with respect to the leaf settings. At the SL20 console, the therapist must first enter the X field size and offset. Then, the therapist is prompted to enter the settings of the leaves between the X diaphragms. All of the leaves between the X diaphragms, including leaves that are only partially covered by the X diaphragms, must be open.

The Y diaphragms are *dependent* with respect to the leaf settings. At the SL20 console, the therapist does not set the Y field size and offset. Instead, the SL20 console software computes these from the leaf settings that the therapist enters, so each Y diaphragm has the same setting as the leaf which is farthest open on its side.

The Y diaphragms can be overcentered past the central axis, but the X diaphragms cannot.

The SL20 wedge is fixed in the collimator; it cannot be rotated. The wedge gradient is perpendicular to leaf motion. In the figure, the toe of the wedge points toward the top (superior, toward the gantry protractor) and the heel of the wedge is toward the bottom (inferior).

```
X Field Size  10.0 cm,   X Offset    0.0 cm
Y Field Size  10.0 cm,   Y Offset    0.0 cm

Field
Length             X  Y2 Leaves                      X  Y1 Leaves

20              19.5        0.0                   19.5        0.0
19              18.5        0.0                   18.5        0.0
18              17.5        0.0                   17.5        0.0
17              16.5        0.0                   16.5        0.0
16              15.5        0.0                   15.5        0.0
15              14.5        0.0                   14.5        0.0
14              13.5        0.0                   13.5        0.0
13              12.5        0.0                   12.5        0.0
12              11.5        0.0                   11.5        0.0
11              10.5        0.0                   10.5        0.0
10               9.5        0.0                    9.5        0.0
 9               8.5        0.0                    8.5        0.0
 8               7.5        0.0                    7.5        0.0
 7               6.5        0.0                    6.5        0.0
 6               5.5        0.0                    5.5        0.0
 5               4.5        5.0                    4.5        5.0
 4               3.5        5.0                    3.5        5.0
 3               2.5        5.0                    2.5        5.0
 2               1.5        5.0                    1.5        5.0
 1               0.5        5.0         iso        0.5        5.0
                                         +
 1              -0.5        5.0                   -0.5        5.0
 2              -1.5        5.0                   -1.5        5.0
 3              -2.5        5.0                   -2.5        5.0
 4              -3.5        5.0                   -3.5        5.0
 5              -4.5        5.0                   -4.5        5.0
 6              -5.5        0.0                   -5.5        0.0
 7              -6.5        0.0                   -6.5        0.0
 8              -7.5        0.0                   -7.5        0.0
 9              -8.5        0.0                   -8.5        0.0
10              -9.5        0.0                   -9.5        0.0
11             -10.5        0.0                  -10.5        0.0
12             -11.5        0.0                  -11.5        0.0
13             -12.5        0.0                  -12.5        0.0
14             -13.5        0.0                  -13.5        0.0
15             -14.5        0.0                  -14.5        0.0
16             -15.5        0.0                  -15.5        0.0
17             -16.5        0.0                  -16.5        0.0
18             -17.5        0.0                  -17.5        0.0
19             -18.5        0.0                  -18.5        0.0
20             -19.5        0.0                  -19.5        0.0
```

Figure A.1: SL20 collimator leaf settings for 10×10 field

A.5.2 CNTS neutron multileaf collimator

Fig. A.2 shows the neutron multileaf collimator arrangement. This is a beam's eye view; it shows the leaf numberings as seen *from* the source looking *out* through the leaves. The Prism chart should include a similar figure, by itself on an appropriately labelled page, for each neutron beam in the plan.

```
 N  Setting                    Setting   N

 9      0.0                        0.0  39
 8      0.0                        0.0  38
 7      0.0                        0.0  37
 6      0.0                        0.0  36
 5      0.0                        0.0  35
 4      0.0                        0.0  34
 3     -5.0                        5.0  33
 2     -5.0                        5.0  32
 1     -5.0                        5.0  31
 0     -5.0          iso           5.0  30
                      +
10     -5.0                        5.0  20
11     -5.0                        5.0  21
12     -5.0                        5.0  22
13     -5.0                        5.0  23
14      0.0                        0.0  24
15      0.0                        0.0  25
16      0.0                        0.0  26
17      0.0                        0.0  27
18      0.0                        0.0  28
19      0.0                        0.0  29
```

Figure A.2: Neutron collimator leaf settings for 10×10 field

When the collimator is in its home position (the collimator rotation angle is 270 on the machine scale), the collimator is oriented so that the neutron gantry protractor is at the *top* of the figure. When the neutron couch is also at its home position (the couch couch rotation angle is 180 on the machine scale), opening the collimator leaves makes the field wider across the couch (parallel to the Prism patient coordinate system x axis), and opening more leaves makes the field longer along the couch (parallel to the Prism patient system z axis). All subsequent description refers to the collimator and couch in these home positions.

The neutron multileaf collimator has 40 leaves. The 20 central leaves are 1.25 cm wide and the outer leaves are 2.00 cm wide.

Leaves are identified by numbers 0 through 39 as shown in the figure. There are four quadrants of ten consecutive leaves; within each quadrant, leaf numbers increase moving away from the center. Therefore, consecutively numbered leaves are not always adjacent.

Settings for leaves whose ends lie in the right half of the figure have machine settings that are positive numbers; those in the left half have negative settings. Therefore, leaves 0 through 19 usually have negative settings and leaves 20 through 39 usually have positive settings. The setting changes

Wedge orientation	*Wedge heel*
0	right
90	top (superior)
180	left
270	bottom (inferior)

Table A.10: Neutron wedge orientation

sign when a leaf crosses the central plane. The figure shows the settings for a 10×10 field; note that the settings for the open leaves on the left are all -5.0.

Each leaf can open 14.5 cm and can overcenter 3.5 cm.

When all leaves are fully open the field size is 32.5×29.0 cm.

Opposing leaves can be closed together on the centerline by setting both leaves to 0.0. Some leaves at the ends are closed whenever the field is shorter than 32.5 cm. Central leaves can be closed to create the effect of midline blocks.

The neutron wedge can rotate to four different orientation angles within the collimator. In the figure, the wedge is oriented according to table A.10.

A.6 Wedge conventions

In the Prism system, when the *collimator rotation* is zero, the wedge rotation is zero when the wedge toe is pointed toward the gantry. Therefore, the Prism wedge rotation angle and neutron machine wedge rotation angle are related as shown in Table A.11[1].

Prism w	0	90	180	270
Neutron w'	270	0	90	180

Table A.11: Prism wedge rotation angle w and neutron wedge rotation angle w'

Table A.12 lists the wedge orientation conventions for all wedges and collimating systems in use in the treatment machines at the Radiation Oncology Department of the University of Washington Medical Center.

In the table, “left” and “right” refer to the *patient’s* left and right when the patient is supine with his/her head toward the gantry.

Most machines have a few preferred collimator rotation angles for use with wedges. This table only contains entries for those angles.

The Varian machines (Clinac 4, Clinac 2500) have a removable wedge tray with two possible orientations. These orientations do not have names; the therapists call the positions “heel superior” etc. as in the table headings. The position of the wedge tray that achieves these orientations depends on the collimator rotation angle.

---

[1] An earlier version of this table was incorrect: neutron wedge rotation angles 0 and 180 were backwards.

Machine	*Coll*	*Wedge Inf/Sup*		*Wedge Med/Lat*		*Comments*
	Rot	*Heel Inf*	*Sup*	*Heel Left*	*Right*	
Clinac 4	0	Yes				Collim rots are -90, 0, 90
	90				Yes	Only one wedge orientation
	-90			Yes		Rotate collim to orient wedge
Clinac 2500	180	Yes	Yes			Collim rots are 180, 90, 270
	270			Yes	Yes	Wedge gradient is parallel
	90			Yes	Yes	to independent jaw motion
Philips SL20	0	Yes				Only one wedge orientation
	90				Yes	Wedge gradient is
	180		Yes			orthogonal to leaf motion
	270			Yes		
CNTS Neutron	270	270	90	0	180	Collim rots are 270, 180
	180	0	180	90	270	Four wedge orientations

Table A.12: Wedge orientations and collimator angle machine scales

On the Clinac 4 only one wedge tray orientation is available when the block tray is in use.

On the Varian machines, therapists prefer to achieve rotated wedge orientations (e.g. for wedged parallel opposed pairs) by flipping the wedge tray, not rotating the collimator. On the Clinac 4 this is not possible, however; the collimator must be rotated to achieve the prescribed wedge orientation.

The Philips SL20 internal wedge is fixed in the collimator, so the collimator must be rotated to achieve the prescribed wedge orientation. The wedge gradient is perpendicular to the direction of leaf motion; the wedge is heel inferior when the collimator is at its home position.

The SL20 also has four external wedges that mount outside the collimator, and are used as alternates to the internal wedge when a plan requires them. These external wedges can each be used in only one wedge angle, as entered in the machine data files for the SL20 beams.

The CNTS Neutron machine wedge rotates within the collimator and can be set to its four orientation angles 0, 90, 270 and 180. The position of the heel in each orientation angle, at the two preferred collimator rotation angles, is shown in the table.

The Prism chart only shows the wedge rotation angle for the Neutron machine. The other machines do not have a wedge rotation angle setting; the wedge is either fixed, or placed by hand. For these machines the *Wedge Rot* row on the chart is left blank.

Table A.13 shows the wedge rotation angles for each machine. The Clinac 2500 is different from the other Varian machines because its Prism collimator rotation is defined to be zero when its asymmetrical jaw pair opens in the Prism x-direction.

Cl 4	0, 180
Cl 2500	90, 270
SL20 int	0
SL20 ext	90
Neutron	0, 90, 180, 270

Table A.13: Prism wedge rotation angles available for each machine