



# *Radixact*<sup>TM</sup>

## Physics Essentials Guide

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# Radixact™ Treatment Delivery System

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## Physics Essentials Guide

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### Prescription Device Statement



**Caution:** Federal law restricts this device to sale by or on the order of a physician.



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---

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# Radiation Safety

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In accordance with locally accepted practices and protocols for your facility, your Accuray Incorporated treatment system should be operated by appropriately educated and properly trained personnel only. In addition to the contents of this *Physics Essentials Guide*, trained medical physicists should also be familiar with the information, safety precautions and warnings provided in the following documentation:

- *Treatment Delivery Manual*
- *Treatment Planning Manual*
- *iDMS Manual*



**WARNING:** The treatment system is a radiation device, and improper use can result in serious injury or death.

- Only properly trained personnel should operate the treatment system.
- Always refer to the *Treatment Delivery Manual* and the *Treatment Planning Manual* for important instructions, safety information, and protocols for treatment planning and delivery.
- Make sure all signs required by local codes for the operation of a radiation device and the presence of radiation are posted.
- When operating the treatment system, always follow the procedures and monitoring requirements established by your facility's Radiation Safety Officer.
- Make sure all gantry enclosures are in place before you operate the treatment system.

Accuray Incorporated treatment systems, if misused, can emit lethal doses of radiation in a short period of time. It is imperative that system users carefully observe all safety precautions when operating or working with Accuray Systems. If you feel that your treatment system hardware components or associated software features or functions do not perform as expected, or they provide results that are inconsistent with your established clinical and research protocols, contact the Accuray Technical Solution Center.

## ◆ Use of the Treatment System

### Intended Use

The Radixact™ Treatment Delivery System is intended to be used for the delivery of radiation therapy, stereotactic radiotherapy or stereotactic radiosurgery to tumors or other targeted tissues. The megavoltage x-ray radiation is delivered using rotational, non-rotational, intensity modulated (IMRT), or non-modulated (non-IMRT/three dimensional conformal) treatment techniques and using image-guided (IGRT) or non-image-guided workflows in accordance with the physician approved plan.

### Indications for Use

The Radixact™ Treatment Delivery System is indicated for the delivery of radiation therapy, stereotactic radiotherapy or stereotactic radiosurgery to tumors or other targeted tissues anywhere in the body under the direction of a licensed medical practitioner.

## ◆ Safe Operating Conditions

Accuray Incorporated recommends that the safety elements described in the following paragraphs be incorporated into the institutional radiation safety program at each site. Accuray Incorporated customers are ultimately responsible for obtaining all local, state and national permits, licenses, or registrations, and satisfying any applicable requirements associated with site planning, shielding design, site preparation, vault construction, system installation, maintenance and use.

## ◆ Shielding and Accelerator Workload

The shielded barrier thickness requirements for Accuray systems will vary from site to site depending upon many factors including: local regulations, shielding design goals, exposure limits, adjacent area occupancy rates, and the weekly or yearly accelerator workload. It is highly recommended that a qualified radiation physicist estimates the anticipated clinical case workload at each specific facility, paying particular attention to the type, duration, and total number of treatments. Accuray customers are ultimately responsible for determining the proper shielding for their treatment room, performing shielding measurements, and ensuring compliance with all applicable local, state, and country regulations.

## ◆ Treatment Room Procedures

It is highly recommended that prior to energizing a radiation machine, the operator shall physically enter the treatment room to verify that no unauthorized persons are present within the shielded enclosure and that the area is in all respects safe to produce radiation.

## Emergency Procedures

Prompt and proper action is a prime consideration for limiting damage that may result from a radiation incident. A radiological emergency may involve exposure to radiation, contamination with radioactivity/nuclear substances, or both. Accuray systems do not contain or produce radioactive materials but such materials may be stored or used near Accuray system bunkers and potentially contribute to an incident. The following actions shall be immediately considered for applicability during an emergency/incident:

- Immediately terminate the machine generated radiation source
- Limit the radiation exposure to involved persons
- Limit the spread of radioactive contamination
- Seek assistance from experienced radiation safety professionals
- Evacuate the immediate area of the incident
- Control entry to the scene of the incident
- Identify and isolate persons who may have received significant radiation exposures
- Record all details of the event chronologically

## ◆ Engineering and Administrative Controls

The following engineering and administrative controls should be considered for applicability at each customer site.

Warning signs including: “Authorized Personnel Only”, “Caution: This Equipment Produces X-Rays When Energized”, and “Radiation Area” or “High Radiation Area” warning signs (or signs with similar wording and intent) as required by the regulations.

Entrances to the shielded enclosure may require one or more entry control devices (door interlocks) that will terminate the radiation source. For example, terminate high voltage to the pulse forming network, or otherwise terminate or prevent the generation of radiation upon entry to the area or actuation of the device.

The interior of the shielded enclosure may require a sufficient number of emergency power off (EPO) or emergency stop (E-Stop) devices, conveniently located and readily accessible, that will terminate or prevent the generation of radiation upon actuation. EPO and/or E-Stop devices shall also be located at the operator's controls. Additionally, it may be required that control devices that energize conspicuous visual indicators

whenever radiation is generated be located at the operator's controls, within the shielded enclosure, and in the general exterior area. All engineering and administrative controls should be function tested and verified to be in place periodically.

Personnel radiation exposure monitoring (dosimetry) is recommended and may be required by the applicable regulations for all personnel who operate radiation generating machines, perform other radiological work duties, frequent areas where radiation sources are in use, or otherwise have the potential to receive non-negligible occupational radiation exposure.

# System Interlocks and Safety Mechanisms

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## ◆ Safety Mechanisms

Refer to the "System Safety" and "Basic Tasks" sections of the *Treatment Delivery Manual* for the following information:

- General System Safety
- Use of Safety Mechanisms
- Resolve System Interruptions
- Resolve Status Alerts
- Manually Retract and Lower the Couch
- Operator Responsibilities
- Labels and Symbols



**WARNING:** Independent devices may not be safe, compatible, or acceptable for use with Accuray products. Prior to using any independent product with any Accuray product, contact Accuray Customer Support.

## ◆ Interlock Descriptions

### Entrance Interlock

At the time of system installation, provisions for the connection of an entrance interlock (treatment room barrier) are provided by Accuray Incorporated. Consequently, the type of entrance interlock installed is left to the discretion of the facility. Regardless of the type of entrance interlock used, its status is monitored continuously by the treatment system. It is independently wired and is not controlled by computer components.

### Hardware Interlock

The hardware interlock prevents or interrupts irradiation if the system experiences certain hardware conditions. It is independently wired and is not controlled by computer components.

### Software Interlock

The software interlock prevents or interrupts irradiation if there is a communication issue between computers mounted to the gantry.

## Jaw Interlock

For each jaw, there are two independent encoders. The absolute position encoder directly measures the jaw position for position feedback. A readhead with encoder scale is used at a large radius to meet accuracy requirements. The absolute position encoder measures the angle of the jaw, and a lookup table is used to convert this angle to a position at isocenter. The absolute position is monitored to ensure the jaw is in the right place at the right time. The tolerance for the primary encoder is 50 microns at isocenter.

The secondary encoder is a motor encoder used for both position feedback and velocity feedback. The motor encoder measures the jaw position based on the motor shaft position. A lookup table recorded during jaw calibration is used to convert this to the jaw position recorded by the absolute position encoder. Then the same lookup table used by the absolute position encoder to relate its position to isocenter is used by the motor encoder. The motor encoder position is monitored by the motion controller to ensure that the demanded position is met. Both position measurements must agree to within their respective tolerances, otherwise a fault is generated. The tolerance for the secondary encoder is 10% of the field width, with a maximum tolerance of 2 mm. Each jaw, front and back, uses one half of the field width tolerance. For example, for a field width of 10 mm, the tolerance for each encoder is 500 microns at isocenter.

## Multileaf Collimator Interlock

A multileaf collimator (MLC) interlock will interrupt a treatment if four or more MLC errors occur during one delivery fragment. A delivery fragment is a single TomoHelical™ fraction or an individual beam delivery within a TomoDirect™ fraction. The leaf positions are monitored by two optical position sensors as discussed in “Secondary Collimator (Multileaf Collimator)” (page 30). Any of the following causes a single MLC error:

- A leaf fails to start a leaf transition by the activation latency time
- A leaf fails to reach the final leaf state by the position latency time
- A leaf exceeds the over travel threshold
- A leaf exceeds the bounce threshold

For more information, see “System Level Properties” (page 100).

## Gantry Position Interlock

A gantry position interlock will occur if the gantry position is not maintained within  $\pm 0.286^\circ$  of the commanded position. An error of  $0.286^\circ$  corresponds to a 1 mm delivery discrepancy at 200 mm from isocenter. The error message GANTRY\_CHECK\_POSITION\_ERROR will be displayed.

## Couch Position Interlock

The absolute positioning accuracy of the treatment couch when moved from any point to any other point is  $\pm 1$  mm in IEC X,  $\pm 1$  mm in IEC Y, and  $\pm 2$  mm in IEC Z. In addition, if you image a patient and then treat the patient, the instantaneous couch position throughout the treatment is consistent with the instantaneous couch position for imaging within a 0.75 mm 3-dimensional vector, after accounting for any shifts applied during image registration.

The overall positioning accuracy of the couch is enforced by multiple interlocks on the couch position as monitored by the couch encoders. For example, when in Delivery Mode (Ready had been pressed), the couch encoders must maintain position within the following limits or an interlock will occur.

Direction	Position Limit
IEC X and IEC Z	+/- 0.5 mm
IEC Y (when couch is not moving)	+/- 0.5 mm

Direction	Average position over the total time that any given voxel is irradiated			Standard Deviation over the total time that any given voxel is irradiated
IEC Y (when couch is moving)	For couch velocity < 0.5 mm/s: +/- 0.100 mm	For couch velocity between 0.5 mm/s and 10 mm/s: +/- 0.250 mm	For couch velocity > 10 mm/s: +/- 0.500 mm	+/- 0.333 mm

There are additional interlocks on the couch encoder values, which are not listed here.

## High Voltage Interlock

A high voltage interlock prevents or interrupts irradiation when the **Stop** button on the **Status Console** is pressed or the barrier to the treatment room (entrance interlock) is opened. Certain hardware and software conditions can also cause a high voltage interlock. It is independently wired and is not controlled by computer components.

## Power Interlock

The power interlock shuts down power to the Radiation Delivery Subsystem. It prevents or terminates irradiation when any **Emergency Stop** button is pressed. Certain Power Distribution Unit (PDU) conditions can also cause a power interlock. It is independently wired and is not controlled by computer components.

## Dose Interlocks

Dose rate interlocks are based on raw chamber counts on Dose 1 and Dose 2. The monitor chamber hardware is described in “Dose Monitor Chambers” (page 27). The dose monitors will interrupt treatment if the raw counts of the Dose 1 and Dose 2 monitor chambers differ from the nominal count rate by:

For *TomoHelical* procedures:

- $\pm 5\%$  of the nominal count rate over any three consecutive, rolling 10-second periods, each starting 1 second later than the previous period started.
- $\pm 50\%$  of the nominal count rate over any three consecutive 1-second periods

For *TomoDirect* procedures:

- $\pm 3\%$  of the nominal count rate over any three consecutive, rolling 10-second periods
- $\pm 50\%$  of the nominal count rate over any three consecutive 1-second periods, each starting 1 second later than the previous period started.

As a verification of Dose 1 and Dose 2 performance and a gross verification of the transverse profile shape, treatment will also be interrupted if the ratio of Dose 2 to Dose 1 is outside of  $\pm 10\%$  of the nominal count rate over any three consecutive, rolling 10-second periods. In addition, Chambers A and B are monitored for gross movement of the beam. An interlock will occur if Dose A count rate, Dose B count rate, or the ratio of Dose B to A is outside of  $\pm 10\%$  of the nominal value over any three consecutive, rolling 10-second periods.

Three consecutive rolling 10-second periods are defined as:

- Sample average from 1st to 10th second
- Sample average from 2nd to 11th second

- Sample average from 3rd to 12th second. (Interruption would occur after the 12th second.)

## DCS Dose Interlock

In addition to the dose interlocks that define allowed ranges for Dose 1 and Dose 2 monitor chamber count rates, there are four software interlocks associated with the Dose Control System (DCS) that can occur once a procedure starts.

- Ion chamber bias voltage: The DCS interlocks if the monitor chamber bias voltage is out of range (allowed range is  $600V \pm 10\%$ ) for 2 consecutive seconds.
- PAC range: The DCS provides a limited range of freedom for adjusting PAC to maintain the desired set point for Dose 1. The PAC range corresponds to a Dose 1 range of  $\pm 10\%$  for treatment procedures, and  $\pm 20\%$  for imaging procedures. The DCS interlocks if PAC is outside of the range limits for 5 consecutive seconds.
- Injector Current range: The DCS provides a limited range of freedom for adjusting Injector Current to maintain the desired set point for Gun Current. The Injector Current range corresponds to a Gun Current range of  $\pm 5\%$ , which represents approximately a  $\pm 1\%$  change in the D20/D10 ratio. The DCS interlocks when Injector Current is outside of the range limits for 2 consecutive seconds.
- Consecutive number of dropped pulses: The system must not be permitted to attempt to account for dropped pulses by dramatically increasing the dose in subsequent pulses. In the event that a dropped pulse occurs, the DCS ignores the dropped pulse by inserting the nominal Dose 1 in its place into the running average. Thus, the feedback loop makes its correction using this substituted value. The DCS interlocks when there are 2 seconds of consecutively dropped pulses.

In the above scenarios, the on board computer software interlock is opened to stop radiation. Servo operation stops for the current procedure, and the system returns to initial servo conditions prior to running the next procedure.



## Chapter 2

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### System Overview

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## Machine Geometry

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## Coordinates and Movements

Refer to “Coordinates and Movements” in the *Treatment Delivery Manual* to identify coordinate systems used throughout this guide:

- The fixed X, Y, Z coordinate system (IEC f).
- Machine isocenter and virtual isocenter.
- Sagittal, transverse, and coronal planes.
- Sagittal, transverse, and coronal lasers.
- Positive and negative directions for pitch, roll, and yaw.



**NOTE:** At the zero degree gantry position, the LINAC points straight down. When viewed from the foot of the couch, the gantry rotates clockwise. The rotational coordinate system, IEC g, identifies the leading side (+Xg) and following side (-Xg) of the MLC. This information is used for specifying beam expansion (flash leaves) for TomoDirect™ plans.

## Jaw Numbers

Jaw positions for treatment are stored in the **Edit Machine** area of the Treatment Delivery Console (TDC), in the **Beam/DoseCom Twinnable/Jaw Field Specifications** section of the parameter tree. See “Machine Data” (page 99).

Jaw numbers are within an order of magnitude of, and have a roughly linear relationship to, the measured Full Width at Half-Maximum (FWHM) field width at isocenter. For example, "J42 [mm]" refers to jaw position settings of -21 mm for the front jaw and +21 mm for the back jaw, giving the nominal 50 mm field width. Jaw numbers in mm do not correspond exactly to physical measurements, so the jaw positions are sometimes listed without the mm or cm labels. Sometimes the nominal jaw numbers are compared to the projection of a light field through the jaws at isocenter. While the treatment delivery system has no light field, the idea is that a light field would show the position of the collimated field at isocenter, but measuring a light field with a ruler may not yield exactly the same result as a FWHM measurement of the radiation beam.

The actual FWHM field widths (specified at 850 mm SAD and 15 mm depth in water) differ slightly from the nominal values, and the FWHM field sizes also vary from one beam model to another.



**IMPORTANT:** To determine the actual FWHM fixed field widths in your beam model, please contact Accuray Customer Support, paying attention to the geometrical conditions described. Field sizes are measured in water at 850 mm SSD, 15 mm depth, but the quoted FWHM values may be divergence-corrected to isocenter (850 mm SAD, 835 mm SSD, 15 mm depth).

In the image below, note the following:

- On the left side of the image, for patient treatments on the TDC, the field size is displayed. These are real-time values from the machine, mapped to FWHM size at isocenter.
- On the right side of the image, the front jaw (1) position and back jaw position (2) may be viewed in the Auxiliary Data. The jaw positions in the Auxiliary data represent the jaw numbers.

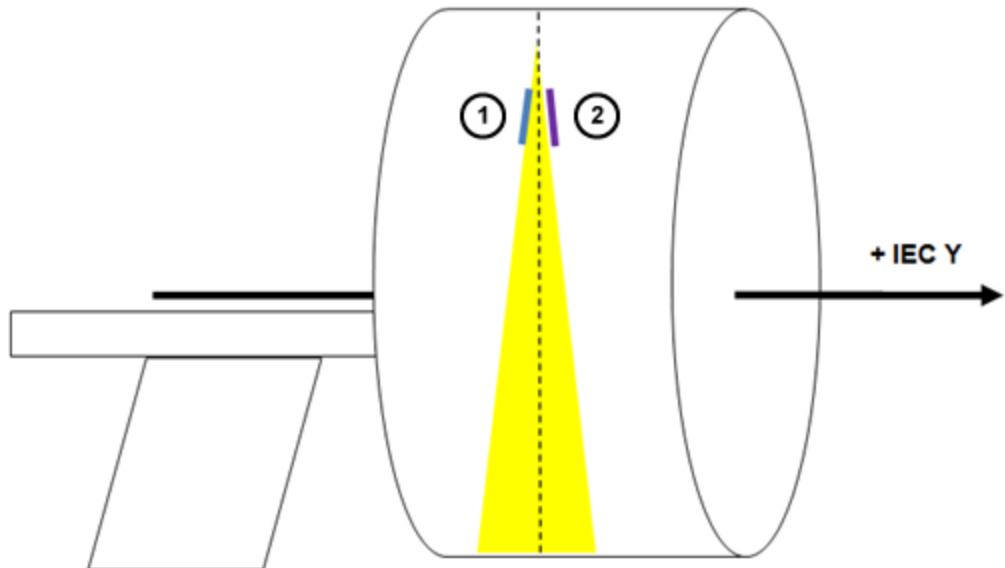
The screenshot shows two panels. The left panel displays "IEC Y Field (mm)" with the following data:

Mode:	Dynamic
Front:	-5.25
Back:	5.25
Width:	10.50

The right panel shows "Auxiliary Machine Data" with a "Show Data Selector" checkbox checked. Under "Select Auxiliary Data to View", "Front Jaw Position" and "Back Jaw Position" are selected. The "Viewed Auxiliary Data" table shows:

Auxiliary Data Element	Auxiliary Data Element	Value	Units
Power-on time	Front Jaw Position	-3.50	mm
Gantry revolutions	Back Jaw Position	3.50	mm
<input checked="" type="checkbox"/> Front Jaw Position			
<input checked="" type="checkbox"/> Back Jaw Position			
Dose A			
Dose B			

TDC Real-Time Measurements and Auxiliary Data View



Front Jaw (1) and Back Jaw (2)

The jaw positions for the available fixed field widths, as well as the imaging beam and J48 jaw opening, are listed in the table below. The mapping between the jaw numbers and the FWHM of the IEC Y profile at isocenter is stored in the beam model, and is verified by the site physicist during commissioning. The **backJaw** and **frontJaw** parameters may be set to other values for QA procedures, but fixed jaw treatment plans may only be generated for field widths for which commissioning data exists, i.e., 10 mm, 25 mm, or 50 mm fields. The FWHM field size of the scanning and J48 beams may vary among machines, as these are not used for treatments.

The sign of the jaw numbers is consistent with the IEC Y direction. Negative jaw positions indicate that a jaw is positioned on the -IEC Y side of the gantry, and positive jaw positions indicate that a jaw is positioned on the +IEC Y side of the gantry.

Nominal Field Size	Alias [mm]	Jaw position settings	
		frontJawIECMm	backJawIECMm
Imaging (~4 mm)	"J01"	-0.5	+0.5
10 mm treatment	"J07"	-3.5	+3.5
25 mm treatment	"J20"	-10	+10
50 mm treatment	"J42"	-21	+21
Fully open (~57 mm)	"J48"	-24	+24



## Major Components

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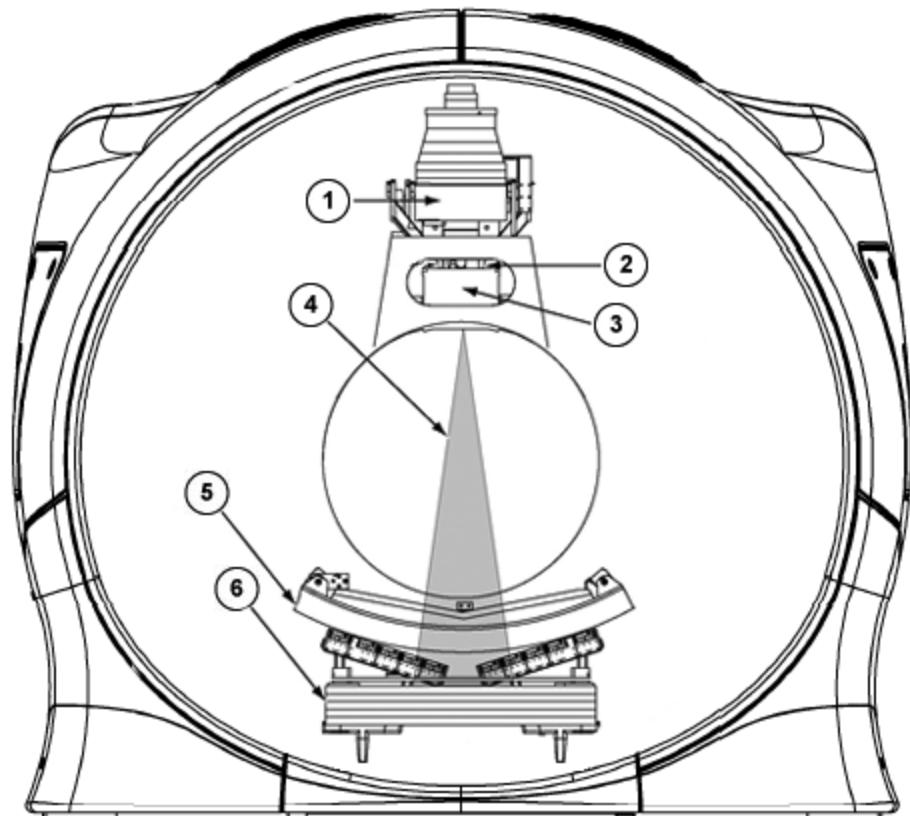
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## Treatment Beam Components

The treatment system features an enclosed gantry with fixed and rotating gantry assemblies that are connected via slip ring technology. The major components of the radiation delivery subsystem (RDS) (i.e., linear accelerator, primary collimator, multileaf collimator, MVCT imaging system, and beam stop) are mounted on the rotating gantry assembly.

The system gantry has an 85 cm source-to-axis distance (SAD), and an 85 cm bore diameter. The mechanical isocenter stability with rotation of the ring gantry is within 0.4 mm.

For TomoHelical™ treatments and CTrue™ imaging procedures, the gantry rotates continuously around the IEC Y axis. For *TomoHelical*/treatments, the speed of rotation varies and is determined by the TPS during planning. For systems equipped with the *TomoDirect* feature, treatments can also be delivered with static gantry angles.



Radiation delivery subsystem (RDS) hardware mounted on the rotating gantry assembly

Item	Name	Description
①	Linear Accelerator	The linear accelerator (linac) uses radio-frequency energy to accelerate electrons to very high (mega-voltage) energies. Acceleration occurs along a series of evacuated cavities filled with alternating electromagnetic fields. The linac directs the high-energy electrons to a target where they collide to produce high-energy photons.
②	Jaws	The jaws define a fan beam that is broad in the transverse direction (across the patient) and narrow in the longitudinal direction. Longitudinal extent depends on the jaw settings defined by the treatment plan. The fan beam defined by the jaws is modulated in the transverse direction by the MLC. The collimator jaws define the initial shape of the radiation beam before the beam is modified by the MLC.
③	Multi-leaf Collimator	The multi-leaf collimator (MLC) opens and closes 64 individual leaves to regulate the amount of radiation passing through to the patient at a transverse location corresponding to each leaf. This process is determined by patient plan information.
④	Beam	Photons emanating from the linac are collimated by the Jaws and MLC. The beam is collimated longitudinally by the Jaws to create the field width of the beam, and radially (laterally and vertically) by the MLC.
⑤	Detector	The detector reads the amount of exit radiation as the beam passes through the patient and the couch from each direction during gantry rotation. This data is used to create a <i>CT</i> True image.
⑥	Beam Stop	The beam stop provides shielding for the primary beam. The beam stop is aligned directly across from the primary beam source and beyond the bore, or positioned patient. As a result, the beam stop is always aligned with the primary beam source at any gantry position.

The following table lists the distances between the major system components:

#### Approximate Measurements; LINAC position at 0 degrees

Component	Distance along Central IEC Z axis from Virtual Source [mm]	Component Thickness in IEC Z [mm]
Jaw Pivot Focus	-43.5 (above the source)	

### Approximate Measurements; LINAC position at 0 degrees

Virtual Source	0	
MLC Focus	0.5	
Detector Focus	0.7 (varies)	
Target	4.6 (top surface)	0.89
Monitor Chamber	65.5 (top surface)	8.2
Jaws (closed position)	233.4 (tip of jaws distal from source)	117.7 (along collimation faces)
MLC Leaves (closed position)	350.4 (tip of leaves distal from source)	100.0
Isocenter	850	
Top of Centermost Collector in Detector	1371.5 (varies)	50.0
Top of Beam Stop	1593.5	127.0



**WARNING:** Avoid contact with the treatment system gantry when the covers are removed. Risk of serious injury or death exists due to exposed electrical components and potentially rotating parts. Do not operate the machine when the covers are removed unless specifically trained to do so. Do not touch an operating MLC. Pinch points exist that may cause serious injury. Do not touch any lead parts or leaking fluids on the machine without proper personal protective equipment.



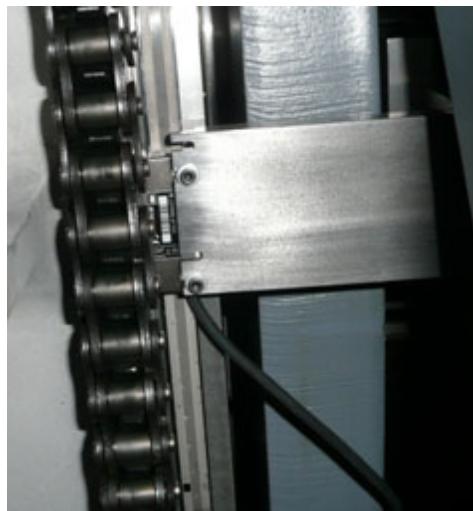
**IMPORTANT:** The gantry covers attenuate the primary beam by a small, but measurable amount. Thus, all beam measurements should be performed with the gantry covers in place.



**WARNING:** Do not place any tools or items inside the bore on the gantry covers. These items will attenuate the beam at certain angles, affecting the imaging and treatment accuracy.

## Gantry Positioning Hardware

The gantry positioning hardware includes a positioning tape with 550,000 marks that are read by an encoder (also called a read head), a motor drive controller, and a motor drive amplifier. The positioning tape is on the rotating side of the gantry and the read head is on the stationary side of the gantry. The gantry is only capable of rotating in the clockwise direction (when viewed from the foot of the couch). This hardware enables the system to set the gantry at 3,600 different positions ( $360^\circ / 0.1^\circ$ ).



Encoder tape and read head for gantry position monitoring

The RCS (Rotational Control System) controls the timing and monitoring of the radiation generation, collimation, and detection components of the interlock system.

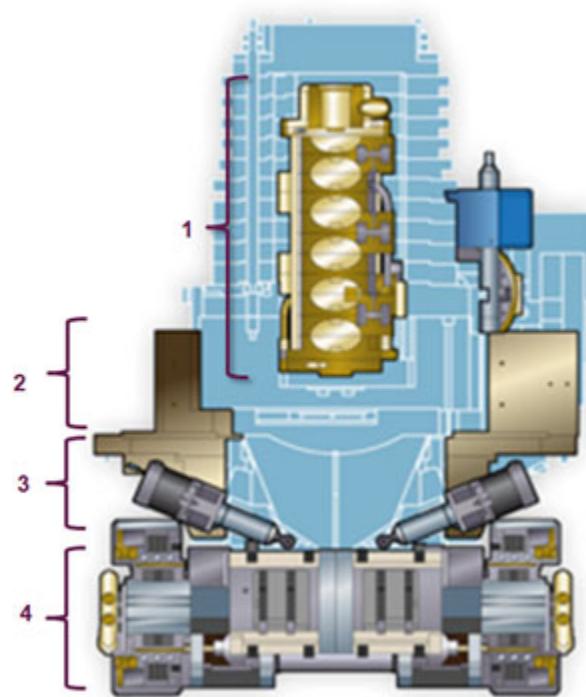
## Linear Accelerator

The treatment system uses a 6 MV, side coupled, standing wave LINAC to produce radiation. The LINAC accelerates electrons from cavity to cavity until they reach the target, where photons are produced via the bremmstrahlung effect.

The target and LINAC are one part. The target is a transmission-style tungsten target. Unlike some previous rotating target designs used on earlier systems, the target has a fixed position relative to the LINAC, and does not spin. The target is cooled by thermal conduction and not by direct contact with water.

After interacting in the target, the beam passes through hardening material. The treatment system does not have a flattening filter. The unmodulated fluence rate is higher in the center of the beam than on the edges. All patient treatment plans use the MLC to shape the beam intensity. The advantages of a system without a flattening filter include: higher fluence rate at isocenter, reduced scatter, and more uniform energy across the beam.

A magnetic shield is installed around the LINAC to reduce deflection of the electron beam in the LINAC by stray magnetic fields, thus improving source stability with gantry rotation.



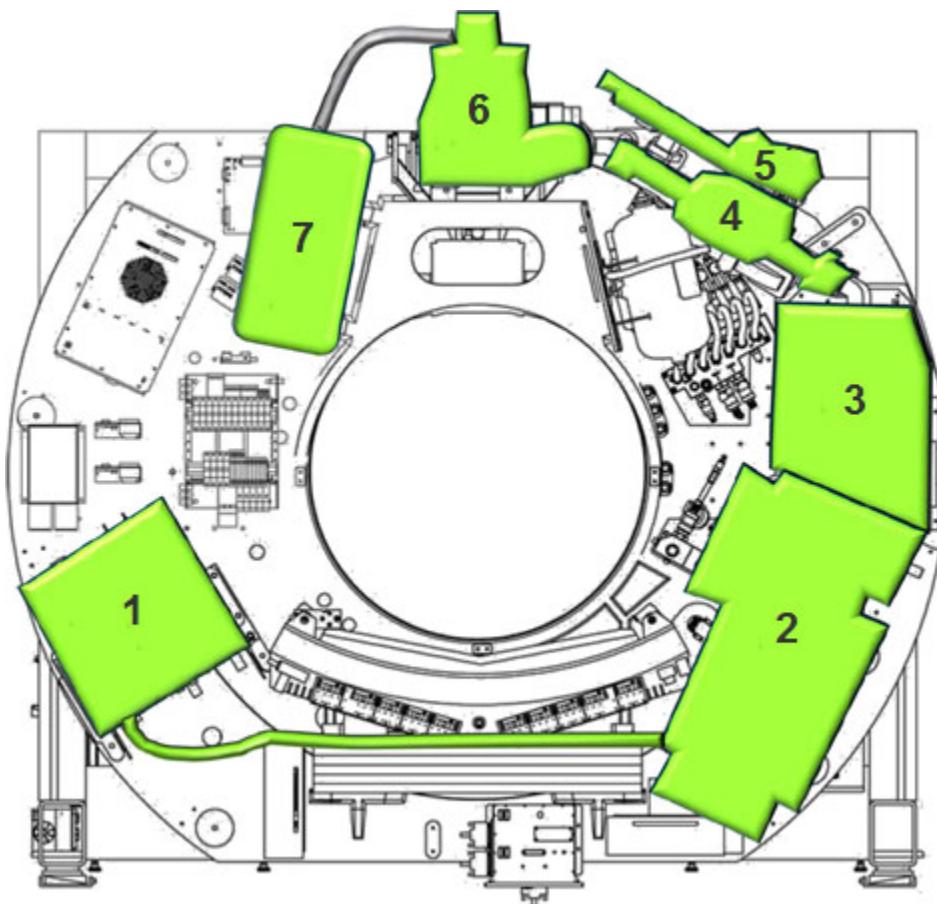
Depiction of beamline components

Item	Description
①	Extended Fixed Target LINAC
②	Fixed component of primary collimator
③	Jaws
④	MLC

# Radiofrequency (RF) Components

In addition to the LINAC, the treatment system uses various other RF components to produce high energy photons.

- ◆ High Voltage Power Supply (HVPS) ..... 25
- ◆ Solid State Modulator (SSM) ..... 25
- ◆ Magnetron (Mag) ..... 25
- ◆ Four Port Circulator (4-Port) ..... 25
- ◆ Automatic Frequency Controller (AFC) ..... 25
- ◆ Injector Assembly ..... 26



RF components involved in the production of high energy photons.

Item	Component
(1)	High Voltage Power Supply (HVPS) Assembly
(2)	Solid-State Modulator (SSM)

Item	Component
(3)	Magnetron (Mag)
(4)	4-Port Circulator (4-Port)
(5)	Automatic Frequency Controller (AFC)
(6)	Linear Accelerator (LINAC)
(7)	Injector Assembly

### ◆ High Voltage Power Supply (HVPS)

The High Voltage Power Supply creates DC high voltage used to charge the SSM.

### ◆ Solid State Modulator (SSM)

The Solid State Modulator acts as a switch and provides pulsed direct current (DC) high voltage to the magnetron.

### ◆ Magnetron (Mag)

The Magnetron uses high voltage pulses and strong magnetic fields to create the RF power used by the LINAC to accelerate electrons.

### ◆ Four Port Circulator (4-Port)

The Four Port Circulator directs the radiofrequency power from the magnetron to the LINAC and protects the magnetron from radiofrequency power reflected from the LINAC.

### ◆ Automatic Frequency Controller (AFC)

The Automatic Frequency Controller sends a signal to the magnetron tuning motor to adjust the operating frequency of the magnetron. This ensures that the magnetron frequency matches the needs of the LINAC despite temperature and load changes.

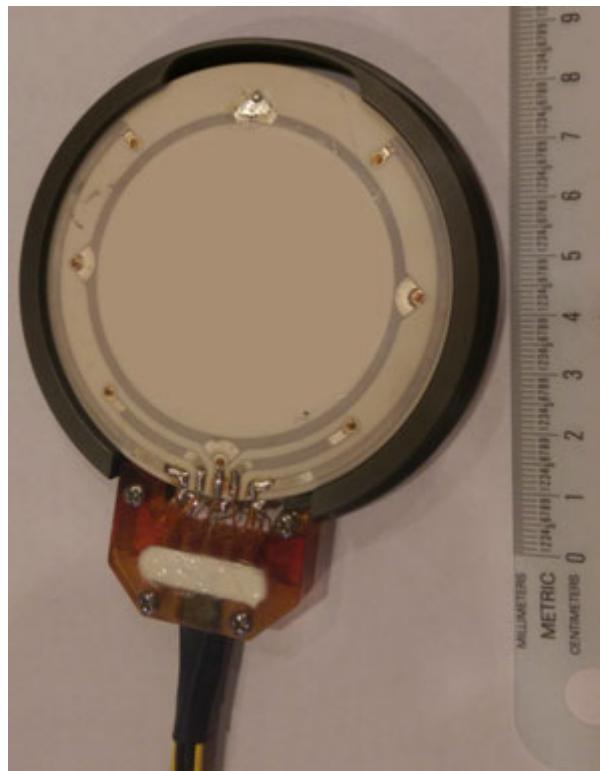
## ◆ Injector Assembly

The Injector Assembly accepts the parameters used to control the electron gun of the LINAC. Quantity, timing, and pre-injection velocity of the electrons into the LINAC can be controlled.

## Dose Monitor Chambers

The dose monitor chambers are located downstream of the LINAC and upstream of the jaws and MLC. They are ceramic parallel plate chambers with hermetically sealed cavities of Nitrogen at atmospheric pressure. The chambers are transmission chambers; the beam passes through the chambers before entering the collimation system.

The monitor chambers are composed of two layers of independently-sealed chambers (see the following image). The Dose1 signal pad is a large circle, and is located in the top signal plate. The Dose2 signal pad is a smaller circle, and is located in the bottom signal plate. Dose1 has a larger area than Dose2, and thus reads a higher raw count rate.



Monitor Chamber

# Primary Collimator

The primary collimator of the treatment system consists of both fixed and moveable components.

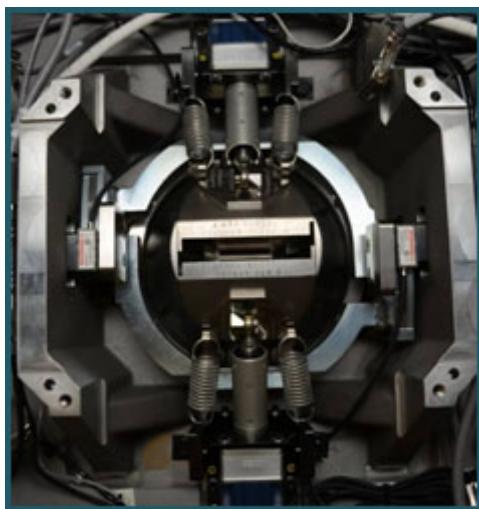
◆ Fixed Component . . . . .	28
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## ◆ Fixed Component

The fixed component of the primary collimator is a rectangular aperture in tungsten that is downstream of the LINAC and upstream of the jaws. Its main purpose is to shape the radiation cone beam produced by the LINAC and target into a fan beam. It also provides significant shielding, reducing the radiation leakage. The fixed component of the primary collimator cannot be adjusted.

## ◆ Moveable Components (Jaws)

The moveable component of the primary collimator is the set of jaws (see the following image). The jaws are downstream of the primary collimator fixed component and upstream of the multi-leaf collimator. There is only one set of jaws, which controls the width of the radiation beam in the IEC Y direction. The jaws are made of tungsten alloy.



Moveable Jaws

The jaws open and close in the IEC Y direction along an arc that is focused 43.5 mm above the source. The front jaw is on the negative IEC Y side of the gantry and the back jaw is on the positive IEC Y side of the gantry.

For treatments, the width of the jaws is set during treatment planning. Available treatment beams include (nominally at isocenter): 5.0 cm, 2.5 cm, and 1.0 cm.

For non-*TomoEDGE* licensed systems, treatments are delivered with the jaws fixed at the width selected during treatment planning.

For *TomoEDGE* licensed systems, treatments can be delivered with either fixed or moving (dynamic) jaws. Both the field width and jaw mode (fixed or dynamic) are selected during treatment planning. If dynamic is selected, the jaws will open and close around each target in a sliding window motion, improving the superior/inferior dose penumbra.

## ◆ Dynamic Jaws Hardware

Each dynamic jaw is powered using a servo motor and linear actuator. The servo motors are operated by a motion controller and servo amplifier.

To allow for controlled jaw motion during procedures, the hardware and software used for jaw positioning include:

- A motion controller quickly and precisely moves each jaw according to instructions from the Radiation Delivery System (RDS). The controller provides power to the servo motors and sends position updates to the RDS every 100 ms.
- One three-phase servo motor for each jaw enables precise static and dynamic positioning.
- A precision ball-screw actuator converts the rotary motion of the motor into linear motion.
- A load-side encoder provides absolute position feedback.

The maximum speed of the jaws is 25 mm/s, and the maximum acceleration is 250 mm/s<sup>2</sup> in jaw numbers (see “Jaw Numbers” (page 15) for a description of jaw numbers).

# Secondary Collimator (Multileaf Collimator)

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## ◆ MLC Hardware

The secondary collimator of the treatment system is the multileaf collimator (MLC). The MLC is downstream of the primary collimator and defines the radiation beam in the IEC X direction. The MLC provides the intensity modulation during treatment.

There are 64 binary, movable, interlaced leaves (tongue and groove design), arranged in banks of 32 leaves each. The bank of even numbered leaves retracts towards the positive Y side of the gantry, while the bank of odd numbered leaves retracts towards the negative Y side of the gantry. When the gantry is positioned at 0°, Leaf #1 is on the negative X side of the MLC bank.



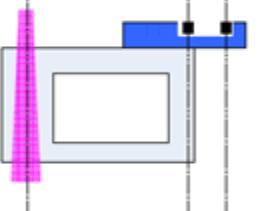
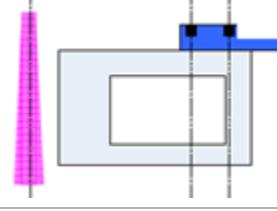
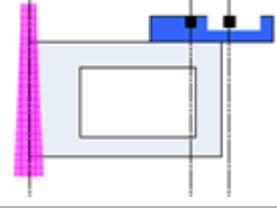
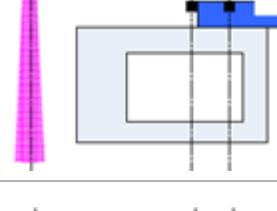
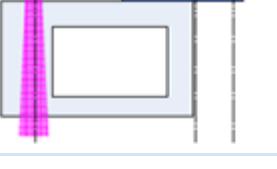
View of the MLC with all 64 leaves closed

The leaves are arranged on a curve with a focus near the x-ray source. Each leaf is made of tungsten and is ten centimeters thick in the in-beam direction. Each leaf is 2 mm wide (IEC X) on the LINAC side and 3 mm wide on the patient side, projecting to a width of 6.25 mm at isocenter.

The leaves are binary; they are always programmed to be open or closed. When open, the leaves are fully removed from the beam, and the fan beam shape is determined by the primary collimator. When closed, each leaf covers the full Y-extent of the beam.

The leaves are pneumatically driven. The leaf positions are continuously monitored by two optical position sensors that ensure the leaves open and close at the correct times. In the following images, several schematics of a single MLC leaf and its position sensors are shown. The gray rectangle is a

leaf, and the portion of the leaf that is colored blue in the diagram is the “sail.” The black squares represent the two position sensors that attempt to pass light through each leaf sail to determine its position. The pink column is the radiation beam.

Leaf Status	Example Image	Position Sensors
Closed		Sensor A: Open Sensor B: Open
Open		Sensor A: Blocked Sensor B: Blocked
Transition		Sensor A: Blocked Sensor B: Open
Overtravel		Sensor A: Open Sensor B: Blocked
Overtravel		Sensor A: Open Sensor B: Blocked

In the factory, an MLC leakage measurement is made on each machine using a film in the beam path positioned 18 cm above isocenter, with a gantry angle of 0°. A reference film is measured with the leaves open and the jaws open (J48 aperture) for 8 seconds. A leakage film is also measured with the leaves closed and the jaws open (J48 aperture) for 720 seconds. The film values are corrected for background and normalized to the

respective exposure times. The maximum rate in the MLC leakage film must not exceed 2% of the rate in the center of the reference image. The average rate in the MLC leakage film (calculated across the entire exposed region) must not exceed 0.5% of the average rate in the reference film (calculated across the entire exposed region). Planning dose calculations do not account for MLC leakage dose.

## ◆ Planning Considerations for the MLC

The planning system accounts for timing and geometrical properties of each MLC. These properties include:

- Minimum Leaf-Open Threshold: It takes about 12-17 milliseconds for a leaf to transition from closed to open, or from open to closed. As a result, the Treatment Planning System (TPS) will zero out (threshold) any planned leaf open times  $\leq$  18 milliseconds.
- Latency: There are small differences between how long the leaves are programmed to be open and how long they are actually open. The differences are measured and characterized by Accuray Incorporated service personnel, and input into the machine data used for planning. The treatment planning system corrects the MLC delivery instructions for the leaf latency.
- Leaf Fluence Output Factors (LFOFs): It takes more than one leaf to fully "uncover" the source, due to the source's finite spot size. As a result, the fluence through a leaf depends on the opened or closed state of the neighboring leaves. LFOFs are measured and characterized by Accuray Incorporated service personnel, and input into the TPS. The TPS adjusts leaf open times upward depending on the open or close state of neighboring leaves.
- Leaf Filters: While LFOFs represent the average fluence through a leaf opening, leaf filters represent the fluence distribution across the leaf opening, effectively modeling the leaf edges. Leaf filters are measured and characterized by Accuray Incorporated service personnel, and input into the TPS.

See "Beam Model" (page 412) for additional information on MLC latency, LFOFs, and leaf filters. See "Machine Data" (page 99) for information on additional parameters that impact the timing of leaf open commands in the delivery.

## MVCT Detector Array

The treatment system includes an on-board, single slice detector. The detector is an array of parallel plate ionization chambers (pressurized Xenon-filled cavities separated by stainless steel septa) housed in an aluminum case.

The detector consists of about 640 channels, 576 of which are connected to the Data Acquisition System. 520 of these channels are located in the imaging beam and are used for image reconstruction. The size of the detector channels is approximately 25 mm in IEC Y, and approximately 1.24 mm in the transverse direction.

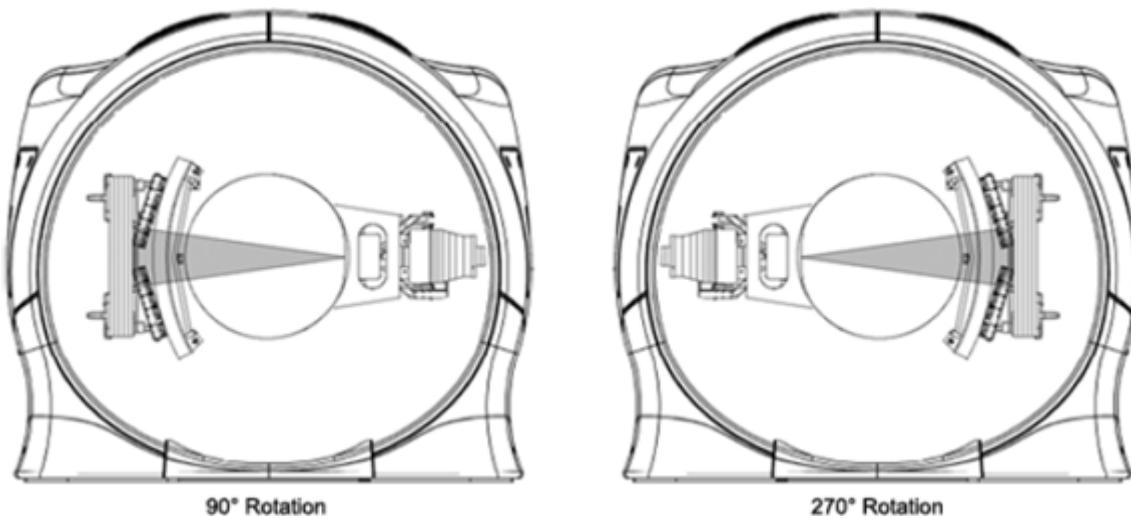
When a photon interacts in the detector, secondary electrons liberate additional electrons in the gas volume through ionization. Under the influence of an applied electric field (-200 V bias on every other plate), charges flow to the collecting electrode.

For a megavoltage beam, the detection efficiency is relatively low for photons that do not interact in the metallic septa. Photons that interact in the septa liberate secondary electrons that contribute to higher detection efficiency. The physics is described in Keller 2002 (although the detector has been updated since Keller's publication).

Current systems include a detector manufactured by Accuray Incorporated. The radius of curvature of the detector matches the source-to-detector distance; i.e., the detector is in focus with the radiation source. Thus, the detection efficiency is more uniform across all channels. The detector is installed with a slight tilt ( $< 1^\circ$ ) about the Y axis to prevent a straight path from the source between the septa.

## Beam Stop

The final component of the treatment system beam line is the lead beam stop (15.2 cm thick). The beam stop provides shielding for the primary beam. The beam stop is aligned directly across from the LINAC and beyond the bore, or positioned patient. As a result, the beam stop is always aligned with the primary beam source during gantry rotation (see the following image).



**Beam stop alignment during rotation.**

# Treatment Couch

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## ◆ Couch Hardware

The couch consists of a base that remains outside of the treatment field and is bolted to the floor, and a lower pallet and upper pallet that enter the treatment field. A pallet support ("catcher") at the rear of the gantry supports the weight of the couch as it enters the bore, significantly reducing couch sag.

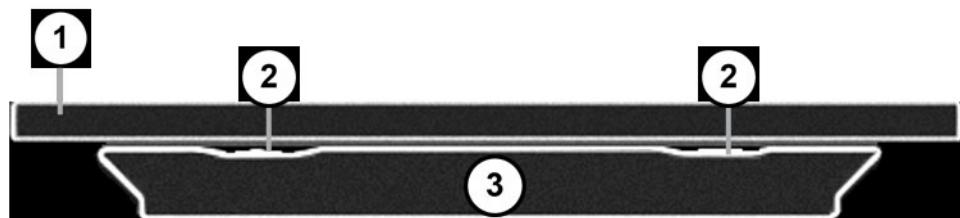


Couch, gantry, and catcher

The couch lower and upper pallets are composed of carbon fiber on the outside, and foam on the inside. The upper pallet has indexing holes that run all the way through the upper pallet. A very thin copper foil and optical cable assembly runs the length of the couch, connecting the Lateral Drive Assemblies (LDAs).



Cross-section of couch lower pallet



Upper and lower pallets of *Radixact* couch

CT Image Area	Description
① Top rectangle	Upper couch pallet (also known as the tabletop)
② Left and right channels	Flat flex circuits for Lateral Drive Assemblies (LDA)
③ Bottom trapezoid	Lower couch pallet

The couch attenuation is highest for beams that have a longer path length through the carbon fiber. Sample measurements were performed by placing couch components on top of a *Virtual Waterstack*, with ion chamber at 15 mm depth and 850 mm SAD. These sample measurements give a rough idea of the range of attenuation values through individual couch components as a function of beam angle and position on the couch. Daily variations in couch position or in beam angles (due to applied roll corrections) can change which parts of the couch the beam passes through. These changes contribute to delivery errors (higher or lower dose than

predicted for the couch position in the treatment plan). The measurements shown are only intended to give a rough idea of the couch attenuation. Actual delivery errors are plan-dependent.

## Sample Measurements of couch attenuation

Approximate Reduction of Ion Chamber Signal Compared to Air			
	Beam entrance perpendicular to couch	Beam entrance at 45° angle to couch	Beam entrance through couch edges
Lower Pallet	~2.75%	~4.4%	~7.6%
Upper Pallet	~1.4%	~2.6%	~3.5%
In addition, the copper foil attenuates the beam <1% more than air.			



**WARNING:** Serious injury may occur if any body parts obstruct the path of mechanical components that move the treatment couch or tabletop. Always verify that operators, patients, and any bystanders are positioned in safe locations and that the area is free of obstructing objects before moving the couch.



**CAUTION:** Damage to treatment couch, gantry covers, or other property may occur if any objects obstruct the path of the treatment couch or tabletop. Always verify that the area is free of obstructing objects, and that the couch is free to move through the entire range required for treatment before moving the couch or initiating a treatment procedure.



**WARNING:** The LDA density is not accounted for in dose calculations. To prevent under-dose to the patient, DO NOT position the patient target superior to the white line on the couch. See "Prevent LDA irradiation" in the *Treatment Delivery Manual* for more information.



**CAUTION:** To prevent unnecessary wear on the LDA, make sure that the LDA is out of the beam for all treatment, imaging, and QA procedures. See "Prevent LDA irradiation" in the *Treatment Delivery Manual* for more information.

## ◆ Couch Translation

The treatment couch is a three-dimensional couch, allowing adjustments in the X, Y, and Z directions. The Z axis is controlled by a screw drive, the Y axis by a belt drive, and the X axis by a combination of a belt and screw drive. Absolute magnetic encoders along each axis ensure that the couch has met its positions. While the machine is on, the couch servo continually makes corrections as needed to maintain the desired position.

During normal operation, the couch position may be controlled by the treatment system to set up or run a procedure. The couch position may also be adjusted by the user via the Positioning Control Panels on the gantry or the Couch Control Keypads (CCKs).

During normal operation, the **Unload** button on the Positioning Control Panels may be used to lower the couch to a height that allows a mobile patient to mount or dismount the couch. If the couch must be lowered manually, the user should use **Free Float** mode to first retract the couch from the bore in the Y direction. If an **Emergency Stop** has been pressed but the machine still has power, a button near the CCK can be used to lower the couch. In the event of a power loss the patient needs to dismount from the couch before power can be restored. Use a gurney, with the wheels securely locked, and carefully slide the patient off of the couch onto the gurney.

## ◆ Couch Translation in Y

During *TomoHelical* and *TomoDirect* treatments, the couch lower and upper pallets travel at a constant velocity in the +Y direction. For information on the maximum treatment length, see "Couch Specifications" (page 40).

Before a beam-on procedure can begin, the couch Y position must be far enough into the bore that it is beyond the limit switch on the rear of the couch base, and **Free Float** mode must be off. In addition, the user should verify that the couch position will not place the LDAs in the beam.



**TIP:** When setting up a patient or phantom for treatment, ensure that the couch is far enough into the bore that there is room for the couch to be shifted in the -IEC Y direction if necessary to accommodate registration offsets.



**NOTE:** The calibrated limits in the software prevent the couch from colliding with the bore when the couch is operated by the system. It is possible for the user to manually push the couch into the gantry covers using **Free Float** mode, if the couch height is below the bore opening. Do not use **Free Float** mode to push the couch into the gantry enclosures.



**WARNING:** The calibrated limits in the software do not ensure clearance between an object or patient on the couch and the gantry enclosures. Always check for sufficient clearance to prevent patient injury or damage to equipment.

## ◆ Couch Translation in X

For lateral setup adjustments, the upper pallet slides over the lower pallet. The upper pallet is equipped with  $\pm 25$  mm of motion range in the IEC X direction, to perform daily shifts as determined from the MVCT image.

The centering of the lower pallet depends primarily on how the base was bolted to the treatment room floor. The upper pallet is centered over the lower pallet when the X position on the **Positioning Control Panels** reads 0.0.

## ◆ Couch Translation in Z

The couch height (Z) can be adjusted prior to beam-on. The installer sets the limits of couch Z movement to prevent collision of the couch with the bore. The height of the pallet support is set during couch calibration by the installer, and automatically adjusts itself to match the height of the couch.

## ◆ Couch Specifications

The height of the pallet support adjusts automatically to the height of the couch.



**NOTE:** A system interruption will occur if the system encoder data indicates that the pallet support height does not match the couch height within tolerance.

The pallet support reduces but does not completely eliminate couch sag. The absolute positioning accuracy of the treatment couch when moved from any point to any other point is  $\pm 1$  mm in IEC X,  $\pm 1$  mm in IEC Y, and  $\pm 2$  mm in IEC Z. In addition, if you image a patient and then treat the patient, the instantaneous couch position throughout the treatment is consistent with the instantaneous couch position for imaging within a 0.75 mm vector, after accounting for any shifts applied during image registration.

The  $\pm 2$  mm absolute, point-to-point positioning specification in IEC Z includes positioning accuracy and mechanical deflection of the couch, such as sag. The specifications for absolute positioning accuracy apply to an unloaded couch, and also to a couch loaded with up to 200 kg of weight.

When the couch is out of the bore at the patient setup position, the treatment couch is not engaged with the pallet support. If you set up your patient inferior to the Lateral Drive Assembly (LDA) region, the couch will be engaged with the pallet support for the entire beam-on procedure. There may be a slight shift in the couch position at the moment of engagement with the pallet support, but this occurs before the image scan or treatment begins, and is included in the  $\pm 2$  mm absolute, point-to-point positioning specification in IEC Z.



**WARNING:** Do not rely on lasers alone for patient or phantom setup. Verify the setup inside the bore with an image prior to each patient or phantom treatment

For information on couch interlocks, see “Couch Position Interlock” (page 8).

## ◆ Indexing Holes

The couch has a column of indexing holes through the upper pallet on the left and right sides. The holes are labeled alternately with letters or numbers.

- The numbered indexing holes fit the Medical Intelligence indexing bars. The following image shows a Medical Intelligence iBEAM indexing bar, P10105-110. The distance between the metal knobs on the anterior side of the Medical Intelligence indexing bar is standardized, so for example, the indexing bars work with a Civco headholder or a MedTec breast board. The system comes with three Medical Intelligence iBEAM indexing bars.
- The letter-labeled indexing holes have different sizes on the left and right side of the couch, so they don't fit perfectly with the Medical Intelligence bars. The letter-labeled holes work for indexing bars made by other manufacturers that require a different size hole on the left versus right side of the couch.



Couch Indexing



**IMPORTANT:** To ensure safe and effective use of an accessory, verify that the indexing bar and the attached accessory are properly mounted to the couch. Refer to the instructions that accompany the accessory for additional information on the proper use of the device.

# General Specifications

This section gives operating conditions, equipment characteristics and specifications for the delivery subsystem.

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◆ Conditions for Normal Use . . . . .	43
◆ Gantry Specifications . . . . .	44
◆ Laser Specifications . . . . .	44
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## ◆ Conditions for Transport and Storage

- Relative Humidity: < 95%, non-condensing.
- Temperature: 4-50° C (40-120° F).
- Atmospheric Pressure: 600-800 mm Hg.
- Avoid direct sunlight.

## ◆ Conditions for Normal Use

### Treatment Room

- Temperature: 20-24° C (68-75° F).
- Relative Humidity: 30-60%, non-condensing.
- Atmospheric pressure: 600-800 mm Hg.

### Air Supplied to System

- Flow rate: 6 bar (90 psig) at 425 lpm at STP (15 scfm).
- Quality: water and oil free, filtered down to 0.5 microns. Dew Point of 1° C - 4° C (34° F - 40° F) at 90 psi.

### Power Supplied to System

- Nominal Input Range: 380-480VAC (3-phase), 60Hz, 60.4-76.3A/phase (76.3A/phase at 380VAC to 60.4A/phase at 480VAC).
- Unloaded Voltage Range: + 5% nominal voltage with no load

- Loaded Voltage Range: + 5% nominal voltage at full load.

## ◆ Gantry Specifications

### Machine Geometry

- Source-axis distance: 850 mm.
- Bore diameter: 850 mm.

### Rotations Per Minute (RPM)

Fixed for MVCT imaging:

- Clinical use:  $360^\circ/6$  seconds (10 rpm).

For *TomoHelical*/delivery:

- Minimum rpm:  $360^\circ/60$  seconds (1 rpm)
- Maximum rpm:  $360^\circ/11.8$  seconds (~5.08 rpm)

Gantry rotation is constrained within the following limits for point-to-point (non-continuous) positioning of *TomoDirect* beams, or for non-clinical quality assurance testing procedures:

- Minimum:  $360^\circ/60$  seconds (1 rpm).
- Maximum:  $360^\circ/6$  seconds (10 rpm).

## ◆ Laser Specifications

Stationary (Green) Laser	
Type	Diode
Wavelength	532 nm
Color	Green
Number of green lasers	Two a) one isocenter laser and b) one virtual isocenter laser
Maximum output power	$\leq 1$ mW
Projection and movement	
Isocenter laster	

### Stationary (Green) Laser

• Projection	• Projected from rear of gantry. Cross hair centered on machine isocenter with laser line projections coincident with the x-axis and z-axis.
• Movement	• Not applicable - laser does not move
Virtual isocenter laser	
• Projection	• Projected from above patient couch. Cross hair centered on virtual machine isocenter (fixed coordinate 0, -700, 0) with laser line projections coincident with the y-axis and parallel to the x-axis.
• Movement	• Not applicable - laser does not move

### Movable (Red) Laser

Type	Diode
Wavelength	635 nm
Color	Red
Number of red lasers	<p>Five</p> <ul style="list-style-type: none"> <li>• one sagittal plane</li> <li>• two transverse plane</li> <li>• two coronal plane</li> </ul>
Maximum output power	≤ 1 mW
Projection and movement	
Sagittal plane laser	<ul style="list-style-type: none"> <li>• Projection</li> </ul> <ul style="list-style-type: none"> <li>• Movement</li> </ul> <ul style="list-style-type: none"> <li>• Movement range</li> </ul> <ul style="list-style-type: none"> <li>• Movement speed</li> </ul>
Transverse plane laser	<ul style="list-style-type: none"> <li>• Projection from above the patient table. Line projection coincident with y-axis when at home position.</li> <li>• Plane moves in x-axis direction.</li> <li>• 400 mm</li> <li>• &gt; 100 mm/sec (to fix points)</li> <li>• 0.2-100 mm/sec (manually selectable)</li> </ul>

Movable (Red) Laser	
• Projection	• Projected from left and right sides of the patient couch. Line projection parallel with x-axis at -700 Yf when at home position.
• Movement	• Plane moves in the y-axis direction.
• Movement range	• 400 mm
• Movement speed	• > 100 mm/sec (to fix points) • 0.2-100 mm/sec (manually selectable)
Coronal plane laser	
• Projection	• Projected from left and right sides of the patient couch. Line projection coincident with y-axis when at home position.
• Movement	• Plane moves in the z-axis direction.
• Movement range	• 400 mm
• Movement speed	• > 100 mm/sec (to fix points) • 0.2-100 mm/sec (manually selectable)

## ◆ Photon Beam Specifications

The linear accelerator produces a single therapy energy spectrum of 6MV.  
This beam is not flattened.

### Dose and Energy

- Nominal energy: 6MV (single energy)
- Nominal dose rate at nominal Dmax\*: 850 cGy/min or 1000 cGy/min
- Nominal Dmax\*\*: 1.5 cm
- Percentage depth dose at 10 cm\*\*: 61.4%

\*Performance based on 5 cm x 40 cm field size at SSD = 85 cm

\*\*Performance based on 5 cm x 25 cm field size at SSD= 85 cm.

See "Dosimetry for the Treatment System" (page 97) for more information on nominal dose rate.

### Field Size at Isocenter

The treatment delivery system has two jaw modes:

- The first is called Fixed jaw where the collimator is at a fixed position throughout treatment. In this mode, geometric field widths (IEC Y) of 1 cm, 2.5 cm and 5 cm at isocenter are available.

- The second is called Dynamic jaw, where the collimator opens and closes around each target in a sliding window motion, with a field width that ranges from approximately 10 mm, up to the selected field size (nominal 25 mm or 50 mm).

## ◆ MLC Specifications

- Number of leaves: 64 binary interlaced movable leaves
- Leaf width projected to isocenter: 6.25 mm
- Leakage: ≤ 0.5 %
- Leaf transition time: ≤ 30ms
- Axis of travel: longitudinal direction (IEC Yf)
- Material and geometrical size of a single leaf:
  - Material, tungsten
  - X-axis (bottom of leaf), 2.374 mm
  - Y-axis, 132 mm
  - Z-axis, 100 mm
- Distance from lower end surface of multi-element beam limiting device to isocenter: 50.57 cm

## ◆ MVCT Specifications

- Spatial resolution: ≤ 1.6 mm (512 x 512 pixel, 39 cm FOV)
- Dose per MVCT image: 0.5 - 3 cGy (depending on acquisition pitch)
- Slice spacing available: 1 mm, 2 mm, 3 mm, 4 mm, 6 mm

## ◆ Radiation and Beam Characteristics

### Maximum Beam Field Size

With the jaws opened to the nominal 50 mm setting and all MLC leaves open, the maximum geometric beam field size is 50 mm (longitudinal) x 400 mm (transverse) at the machine isocenter.

### Treatment Volume

Maximum treatment volume is dependent on the plan image, couch height, and the physical installation of the system. In general:

- The MLC can deliver a 40 cm projection at isocenter, which allows irradiation of all target areas within a 40 cm diameter cylinder around

isocenter, throughout 360 degrees. Areas outside a 40 cm cylinder can be irradiated from a reduced, location-specific range of gantry angles.

- Actual maximum treatment length is dependent on couch height, but is typically up to 1350 mm (longitudinal) for typical patient set-up. Actual available treatment length may be 600 mm or 1350 mm, depending upon your specific license.



**NOTE:** Region of treatment used is determined by the planning CT image field of view (FOV). Provided the FOV is 800 mm or less and all patient anatomy is present in the planning image, the treatment system can import the image, plan, and treat.

## ◆ Couch Specifications

### Anti-collision Mechanisms

System software prevents the couch from hitting the bore of the gantry while it is advancing or retracting. A limit switch and hardware stop prevent the couch from being raised nominally above isocenter.

The *Radixact* couch features a catcher design, which minimizes any vertical couch deflection. Movement is not allowed in the longitudinal direction until the couch is at or above bore height.

### Couch Range of Motion

- Longitudinal: Approximately 0.0 mm to 2270 mm (manual range; obtainable after releasing couch tabletop).
- Vertical: Approximately 0 mm to 427 mm below isocenter (manual range; mechanical limits of travel).
- Lateral: 0.0 mm to  $\pm$  30 mm (mechanical limits of travel).
- Patient load capacity: 440 lbs / 200 kg.

See “Couch Position Interlock” (page 8) for information on positioning accuracy.

### Couch Speeds (Translation)

- Zero (0) speed during an air scan or other quality assurance procedure that does not require couch movement.
- The couch hardware is capable of moving at a velocity range of 0.010 mm/s to 100 mm/s in IEC Y. However, the planning system imposes a range of 0.0125 mm/s to 50 mm/s for treatment plans.

## Couch Treatment Length

For typical patient setup, the treatment couch may treat a longitudinal distance of up to 1350 mm. Refer to “Treatment Volume” (page 47) for additional information.

Actual available treatment length may be 600 mm or 1350 mm, depending upon your system’s specific license.

## ◆ Range and Resolution of Displayed Values

### Displayed Couch Values

Current couch positions are displayed at the Treatment Delivery Console (**Scan** and **Treat** tabs) and on the **Positioning Control Panel**:

- Display resolution: 0.1 mm.
- Vertical display range: 0.0 mm to +427.0 mm.
- Longitudinal display range: 0.0 mm to +2270.0 mm.
- Lateral range: 0.0 mm to  $\pm$  30.0 mm.

### Displayed Laser Values

The current laser positions are displayed on the **Positioning Control Panel**:

- Display Resolution: 0.5 mm.
- Range: 0-40 cm.

### Displayed Cumulative DMU Values

Cumulative Monitor Units (MU) are displayed throughout delivery at the Treatment Delivery Console (**Scan** and **Treat** tabs):

- Accuracy: the displayed value is within 3% of the actual delivery.
- Range: The Treatment Delivery Console starts counting from zero up to the delivered value.
- Resolution: integer MUs

## ◆ Electromagnetic Compatibility

The treatment system complies with the requirements for electromagnetic compatibility as specified in IEC 60601-1-2.





## Monitor Units

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# Time-Based Approach to Treatment Planning and Delivery

The treatment system plans and delivers treatments based on time:

- This approach is similar to a radioactive source treatment, where a constant dose rate is expected, and the patient is exposed to the source for a precisely determined amount of time.
- This approach is different from conventional LINAC-based systems, where the treatment plan indicates a specified number of monitor units, and the beam turns off when the full number of monitor units has been delivered.

The treatment system uses a timer to determine when the beam should be turned off at the end of the treatment. If the primary timer fails, there is also a back-up timer to terminate the treatment after 6 s additional time.

The time-based approach is suited to *TomoHelical* and *TomoDirect* treatments, for which the couch translates at a constant velocity, and targets are treated from the superior end to the inferior end. Each voxel within the target passes through the beam plane in a limited amount of time, and is affected only by the dose delivered while the voxel is in the beam plane (or within scatter's reach from the beam plane).

For example, if the treatment of a long target is interrupted halfway through, the superior end of the target will have received its full dose, but the inferior end of the target will not yet have reached the beam plane. The portion of the target in the beam at the time of the interrupt will have received a portion of the planned fraction dose.

During treatment, the raw counts on the monitor chambers are continually monitored. If the count rate falls outside the tolerances, an interlock will stop the treatment, as discussed in “System Interlocks and Safety Mechanisms” (page 6). A make-up procedure can then be delivered.

In the delivery report for a treatment fraction, the delivered time is expected to exactly equal the planned time, but the monitor units may fluctuate from their expected values, if the dose rate fluctuated within its allowed window during treatment. The total monitor units delivered to the patient each day can be compared to the value predicted by the TPS (see next section).



**NOTE:** The total number of monitor units delivered is not sufficient information to reconstruct the dose distribution in the patient. The dose to a voxel in the patient depends on the dose rate during the time that the voxel was in the beam, and on the leaf modulation.

# Monitor Unit Display Calculations

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## ◆ Measured Counts

The monitor unit display on the TDC is calculated as:

$$MU = (\text{raw counts} - \text{background counts}) * (\text{MU per chamber count})$$

where *MU per chamber count* values for Dose1 and Dose2 are recorded in the **Edit Machine** area, under **Beams > Controls**, and the background counts are determined just before the beam turns on.

The raw counts, not the calibration factor, are used for the Dose Control System (DCS) and to check the dose rate during treatment and initiate an interruption if the dose rate is out of tolerance. Thus, the calibration of the monitor unit display (*MU per chamber count*) has no direct impact on the patient treatment, but only impacts the numbers displayed on the TDC. Typically the monitor unit display is calibrated to display 1 cGy/MU at isocenter, for a 5 x 40 field at 1.5 cm depth in Virtual Water™, but the site physicist could choose to calibrate it differently.

For all patient procedures, leaves are closed for approximately the first 10 s, to allow the beam to stabilize. During this time, the primary beam does not reach the patient, so the monitor unit output of the machine is not of clinical interest. The **Cumulative (mu)** display does not increment during the warm-up for treatment or imaging procedures, but it does increment during the warm-up for Machine QA procedures.

The **Rate (mu/min.)** display is an average over the most recent 10 s, not including the warm-up period. No MU rate is displayed until after the warm-up has elapsed.

## ◆ Expected Counts

The *Accuray Precision* Treatment Planning System calculates the delivery in terms of leaf open times for each beamlet, and the total treatment time for the plan. The *Accuray Precision* Treatment Planning System then predicts the monitor units for the plan delivery by multiplying the treatment time (not including the 10-second warmup) by the TDC **Expected MU (MU/min)** parameter, which is located in the **Edit Machine** area. Depending on leaf modulation, plans that deliver the same number of monitor units could have very different patient dose distributions.

## Dose Control System

The Dose Control System (DCS) provides continuous, automatic control of the linear accelerator (LINAC) to achieve a stable output. This control is achieved by a closed loop control system, or servo. In the servo, the Dose Control System controls two critical parameters impacting dose:

- **The Injector Current** is the input to the electron gun. The Injector Current controls the **Gun Current**. The Gun Current is the rate of electrons injected into the acceleration field of the LINAC. The DCS software monitors the Gun Current using a Rogowski coil surrounding the injector cabling, and makes corrections to Injector Current. The Injector Current has the most prominent effect on the beam energy.
- The **Pulse Amplitude Control (PAC)** is the magnitude of the magnetron pulse, which excites the magnetron to create the radiofrequency power that establishes the acceleration field of the LINAC. The DCS software monitors the **Dose 1** monitor chamber and makes corrections to PAC to increase or decrease the output. The PAC signal has the most prominent effect on output dose rate.



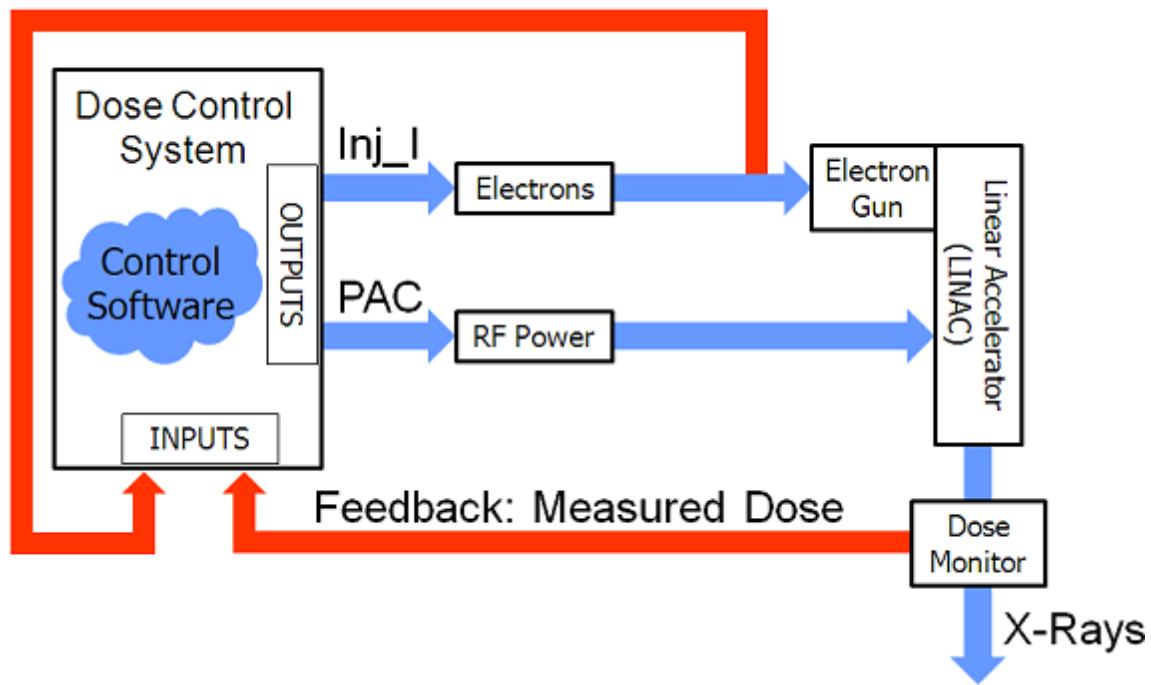
**IMPORTANT:** Gun Current is only one factor that can alter the energy of the radiation beam. Because the system does not directly monitor its own energy, a true energy servo is not possible. Energy QA should always be verified using a calibrated external ion chamber. Contact Accuray Customer Support for assistance in making energy adjustments.

Using both the Injector Current and the PAC signals, the Dose Control System can react to feedback obtained from the monitored Dose 1 and Gun Current signals to effectively control output dose and energy. The system must be properly calibrated so that the system knows how much to drive the magnetron and Injector Current. During the installation process and for any RF service thereafter, the system will be calibrated to obtain machine specific functions that relate PAC to Dose 1 and Injector Current to Gun Current.

The DCS is designed to not increase the rate of dropped pulses in a system. In the event that one occurs, the DCS ignores the dropped pulse by inserting the nominal **Dose 1** in its place into the running average. Thus, the feedback loop makes its correction using this substituted value.

The following figure is a simplified block diagram that illustrates the relationship between the DCS components.

## Feedback: Electron Gun Current



Block Diagram of Dose Control System





# Introduction to the Treatment System

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# Overview

This section introduces the basic delivery parameters for treatment plans, for the three modality selections of:

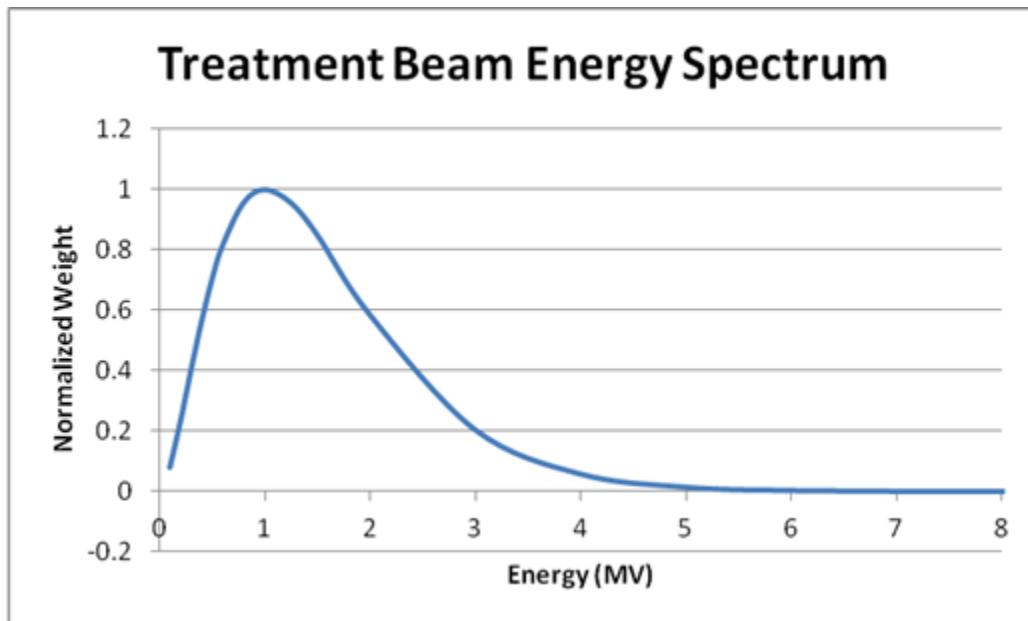
- *TomoHelical* or *TomoDirect*
- Fixed jaws or dynamic jaws
- IMRT, 3D Conformal (3DCRT), or Forward Planning

The user makes these three modality selections on the *Accuray Precision™ Treatment Planning System*. All combinations of the above delivery parameters are possible, except that Forward Planning is only available for *TomoDirect* plans. *TomoDirect* and dynamic jaws are purchasable features, and are discussed in subsequent sections of this chapter.

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◆ X Collimation (MLC) . . . . .	62
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## ◆ Treatment Beam

The system has only one treatment beam setting. The treatment beam is pulsed at 300 Hz and has a 6 MV energy spectrum. An example energy spectrum is shown (consult your beam model spreadsheet [TCOM spreadsheet] for machine-specific data).



Example Energy Spectrum for the Treatment Beam

Information on the dose rate is discussed in the Commissioning chapter. To allow time for the dose rate to stabilize before treatment begins, the treatment system adds at least 10 seconds of leaf-closed warm up to the beginning of each *TomoHelical* procedure or *TomoDirect* beam angle.

The Accuray Precision™ Treatment Planning System designates a **Planned Beam On Time** value for a treatment plan. This value differs from the actual Treatment Delivery treatment time, which includes the short warm up period.

Plan Name: translate_test
Plan Date: 28 Aug 2017, 08:45:46 AM
Fraction Dose: 1.80 Gy
Fraction Number: 4
Planned Beam On Time: 33.5 sec

## ◆ Couch Translation

During all patient treatments (both *TomoHelical* and *TomoDirect*), the couch travels at a constant velocity in the + Y direction. The velocity of the couch varies from one plan to another, and must be in the range 0.0125 mm/s to 50 mm/s for treatments.

Prior to running a procedure, the couch position may be adjusted in X, Y, and Z, to account for any shifts identified when registering the daily *CTrue* image to the planning image.

## ◆ Gantry Rotation

For *TomoHelical* treatments, the gantry rotates in the clockwise direction at a constant velocity, which may range from 11.8 s/rotation to 60 s/rotation. The combined effect of the couch translation and gantry rotation is a helical delivery pattern on the patient.

For *TomoDirect* treatments, the gantry is stationary at the user selected gantry angles, while the couch translates in the Y direction across the beam for each gantry angle.

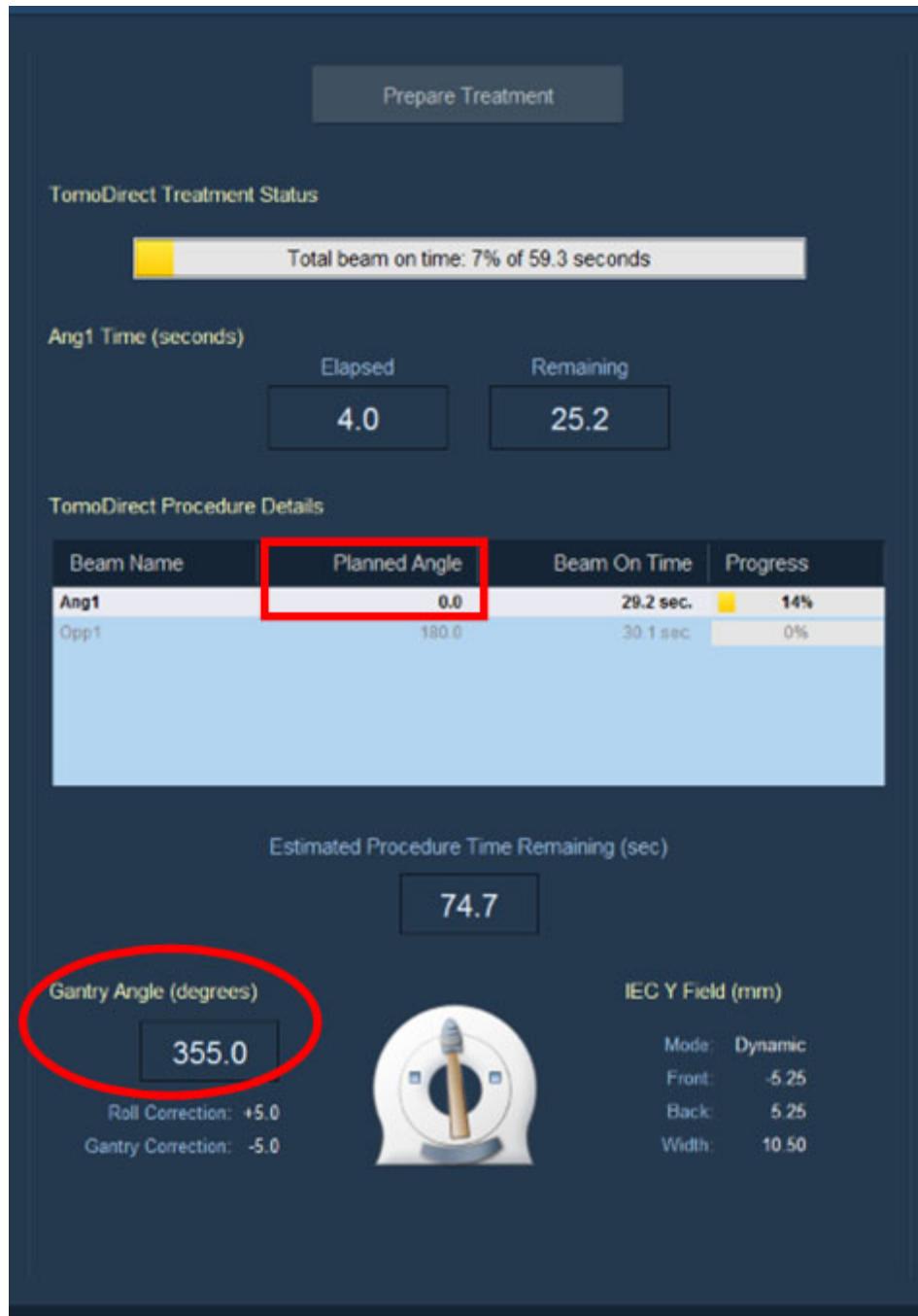
If a patient roll correction (rotation about the IEC Y axis) is accepted by the user on the **Register** tab, the system implements the correction automatically by adjusting the gantry start angle for a *TomoHelical* delivery, or by adjusting the gantry angle for each beam of a *TomoDirect* delivery. As discussed in the *Treatment Delivery Manual*, the Roll Correction and Gantry Correction have opposite signs; a clockwise correction to the gantry is equivalent to a counter-clockwise correction to the patient. See the following image for more information.



**IMPORTANT:** The TDC permits large roll adjustments to be applied to the gantry. However, roll adjustments can change the beam intersection with the couch, and thus the dosimetry. If image registration indicates that a large roll correction is needed, it is recommended to manually re-position the patient and take another setup verification image.



**WARNING:** If you accept a roll adjustment on the **Register** tab and apply the registration results on the **Treat** tab, the gantry angle will be adjusted automatically. Do not physically adjust the patient, or the beam angles will be inconsistent with the plan, which could cause bodily harm to the patient.



Treat Tab of the Treatment Delivery Console display for a TomoDirect treatment. The planned gantry angle is 0°. In the figure, a Roll Correction of +5° was accepted on the Register tab, so the Gantry Correction is -5°, and the current angle is 355°. In the case of a helical treatment, a similar adjustment is made to the gantry start angle, but the Roll Correction and Gantry Correction are not displayed on the Treat tab.

## ◆ Y Collimation (Jaws)

The field size in the Y direction is determined by the jaws. The commissioned fixed field sizes for treatment are nominally 1.0 cm, 2.5 cm, and 5.0 cm at isocenter. Consult your site-specific beam data for the exact field widths.

Systems with the dynamic jaws feature have the ability for the jaws to gradually open to the 2.5 cm and 5 cm field widths as the target enters the beam, and gradually close as the target exits the beam.

## ◆ X Collimation (MLC)

The intensity pattern in the transverse direction is determined by the MLC leaf open times. The maximum width of the beam is 40 cm at isocenter (all leaves open).

The MLC leaf open times may be determined by sophisticated IMRT optimization that allows the user to specify constraints, importances, and penalties for targets and sensitive structures. For simpler cases that do not require sophisticated IMRT optimization, the 3DCRT (3D Conformal Radiotherapy) planning mode may be used. The *TomoDirect* feature also has a Forward Planning option.

## ◆ Other

The system gantry is enclosed with gantry covers. It is not possible to attach an accessory to the linear accelerator. There is no light field or front pointer. Patients and phantoms are typically set up near the virtual isocenter outside the bore, then the couch advances into the bore for treatment.

# *TomoDirect* Treatments

Throughout this user guide, *TomoDirect* information is included along with *TomoHelical* information. For more information on the *TomoDirect* feature, see the *Treatment Planning Manual* and the *Treatment Delivery Manual*.

The *TomoDirect* feature enables planning and delivery of patient treatments with static beam angles and a moving couch. The number of beam angles for *TomoDirect* plans can range from two to twelve depending on the license purchased, with a minimum of two beam angles to treat each target.

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## ◆ *TomoDirect* Planning

*TomoDirect* plans may be created using IMRT, 3DCRT, or Forward Planning algorithms:

- In IMRT *TomoDirect* planning, the planner identifies the target and sensitive structure contours, sets the beam expansion as described in the following paragraph, and selects the *TomoDirect* beam angles. The planner does not set the MLC shape, but the leaf modulation is determined by the optimizer using the target contours, prescription, and dose constraints (if applicable). The planner also does not set the beam angle weights, since the leaf modulation is determined on a per-beamlet basis by the optimizer.

Patient motion during treatment, specifically breathing, causes the target to move relative to the static beam. Although the effects of motion are not included in dose calculations, the user may elect to open additional leaves beyond the target as **beam expansion** (also known as "flash") to improve target coverage.

- In 3DCRT *TomoDirect* planning, the planner identifies the target, and selects the *TomoDirect* beam angles and beam expansion. The planner does not set the MLC shape, but the MLC delivery pattern is determined by the software using the target contours and prescription. The planner also does not set the beam angle weights.
- In **Forward Planning**, the planner selects the beam angles, sets the field extent, and assigns the dose distribution as well as the beam weights. This information is used to produce a fluence map, from which the delivery plan is calculated.

## ◆ *TomoDirect Delivery*

After you turn the key to **Treat** and press **Start**, each of the beam angles is delivered in automatic sequence, without further interaction from the operator. The beam turns off for gantry and couch positioning between angles, then comes on automatically when the system is ready. Each beam delivery includes a warm-up of approximately 10 s.

The order of beam angles for delivery is determined for optimal efficiency: the system proceeds clockwise, starting from the gantry angle after the largest gap between gantry angles. (The gantry can only rotate clockwise. It is rare for the gantry to miss a position and need to make a second pass around the circle.)



**WARNING:** The patient must remain immobile from the time of the *CT* image until all beam angles have been delivered. If the patient moves out of their registered position, the dose distribution will be impacted, and this could result in harm to the patient. If the patient moves before all beam angles have been delivered, the operator should interrupt the treatment and verify the patient position. A make-up procedure can then be generated to deliver the remaining dose.



**IMPORTANT:** Entering the room or turning the status console key to **Program** before all beam angles have been delivered will cause a procedure interruption.

The Estimated procedure time remaining on the TDC **Treat** tab for a *TomoDirect* procedure includes time to re-position the couch and gantry between beams, as well as time to deliver the remaining beams. The estimated time  $T$ [seconds] for gantry positioning to the next beam is based on the distance  $A$  [degrees] to the next beam:

- If  $A \leq 5$ ,  $T = 2 + (A * 0.4)$
- If  $5 < A \leq 90$ ,  $T = 4 + (A * 0.125)$
- If  $A > 90$ ,  $T = 15.25 + ((A - 90) * 0.0462)$

This is only an estimate, since the time required to re-position the couch and gantry between beam angles can vary.

## TomoEDGE Dynamic Jaws Feature

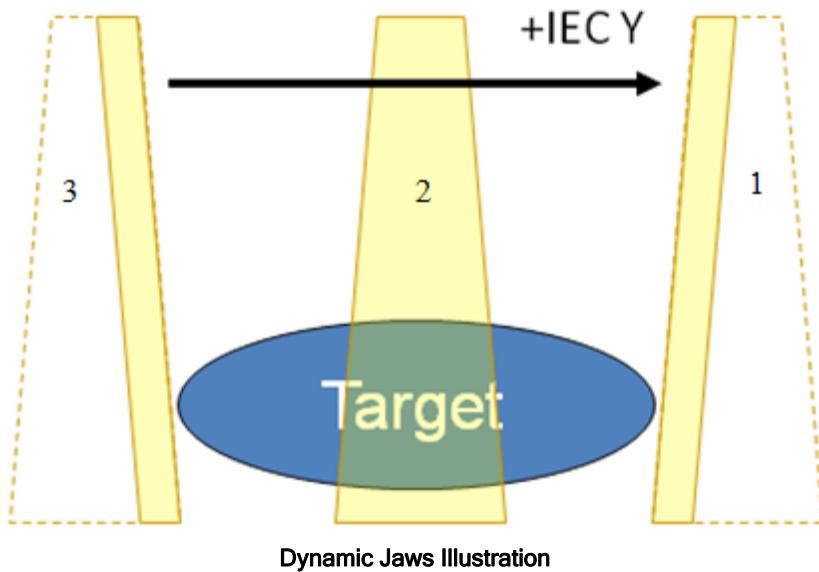
Throughout this user guide, dynamic jaws information is included along with fixed jaws information. For more information on the *TomoEDGE* dynamic jaws feature, see the *Treatment Planning Manual* and the *Treatment Delivery Manual*.

The *TomoEDGE* Dynamic Jaws open and close around each target in a sliding window motion (also known as running start and stop), to improve the superior/inferior dose penumbra for *TomoHelical* and *TomoDirect* deliveries (both IMRT and 3DCRT).

Beamlet selection is discussed in “Initial Beamlet Selection” (page 445). The optimizer opens beamlets superior and inferior to the target, where necessary to achieve a uniform target dose. The first beamlets available for optimization occur when the superior end of the target crosses the inferior edge of the beam, and the last beamlets available for optimization occur when the inferior edge of the target crosses the superior edge of the beam.

For systems that do not have the dynamic jaws feature, the smaller field widths are often selected to control the dose fall-off superior and inferior to the target. With dynamic jaws, the dose distribution inside the target is similar to a plan with the corresponding fixed field width, but the penumbra at the superior and inferior ends of the target is similar to a plan with the 1-cm field width, regardless of field size selection.

The dynamic jaw mode is available for the 2.5-cm and 5.0-cm treatment fields. The following diagram illustrates the dynamic delivery concept for the 5.0-cm field width. The target (blue shape) travels in the +IEC Y direction. The front jaw is on the - IEC Y side of the gantry, and the back jaw is on the +IEC Y side of the gantry. In stage 1, as the target first enters the beam, the jaws are asymmetrically closed to their minimum width. The minimum field width is J07 in jaw numbers; a jaw opening of J07 corresponds to the nominal 1-cm field width when the jaws are positioned symmetrically (see “Moveable Components (Jaws)” (page 28)). As the target continues to move into the beam, the back jaw moves ahead of the target until the jaws are fully opened. In stage 2, the central portion of the target is being treated, and the jaws are open to their maximum field size. As the target exits the beam, the front jaw follows behind the target until the minimum jaw width is reached. In stage 3, the target has moved beyond the beam and the treatment delivery is finished. Dynamic jaw plans also have leaf modulation, not pictured here.



**NOTE:** For the same field width, a plan with dynamic jaws will have a similar delivery time to a plan with fixed jaws. The significant time savings associated with dynamic jaws is due to the increased use of the larger field widths, since the sharpness of the superior/inferior dose fall-off is no longer the limiting factor for field width selection.



**TIP:** While many dynamic jaws plans can be created with the 5-cm field width, a smaller field size is sometimes needed for optimal critical structure sparing inside the target.

# Introduction to the Imaging System

The *CTrue* imaging system consists of a single slice CT detector mounted opposite the LINAC. The detector reads the exit radiation after the beam passes through the patient and the couch. This data is used by the treatment system to create 3D MVCT images.

The 3D MVCT images are acquired with all leaves open, typically just before each treatment fraction. (The system cannot reconstruct CT images during treatment delivery due to MLC leaf modulation.)

For information about testing image quality against specification see “*CTrue Image Quality Verification*” (page 243).

For information regarding image reconstruction see “*About Imaging Algorithms*” (page 473).

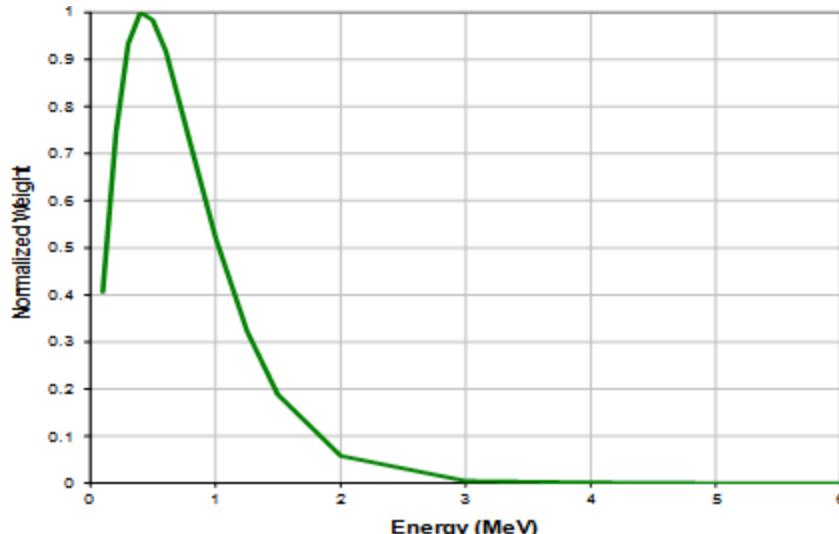
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## ◆ Imaging Beam

*CTrue* image acquisition uses the same radiation source as used for treatments. The LINAC parameters are adjusted for imaging to achieve a lower energy and fluence rate than the treatment beam. The figure below illustrates a sample energy spectrum for the imaging plan, with weights normalized to their peak value. The pulse rate of the LINAC for the imaging beam is 134 Hz.



**IMPORTANT:** The figure below is an example only. The imaging beam spectrum varies from machine to machine.



The patient imaging dose for a FINE scan is less than 3 cGy, when measured with an ion chamber near the center of the cheese phantom over a scan distance that spans the entire chamber collection volume. The imaging dose is not included in the dose calculated by the *Precision Treatment Planning System*. For more information about measuring the imaging dose see “CTrue Image Dose” (page 250).

To allow time for the dose rate to stabilize before imaging begins, six seconds (with all leaves closed) are added to the beginning of each imaging procedure.

## ◆ Gantry Rotation

Data is acquired helically with a six second gantry period, allowing for data collection for 804 LINAC pulses per gantry rotation.

## ◆ Couch Translation

The couch velocity is determined by the user selectable **Acquisition Pitch**. Couch speeds are 4 mm/rotation (**Fine**), 8 mm/rotation (**Normal**), and 12 mm/rotation (**Coarse**).



**NOTE:** For a given scan distance, a **Coarse** scan requires roughly one-third of the time and delivers roughly one-third of the patient imaging dose as compared to a **Fine** scan.

## ◆ Collimation

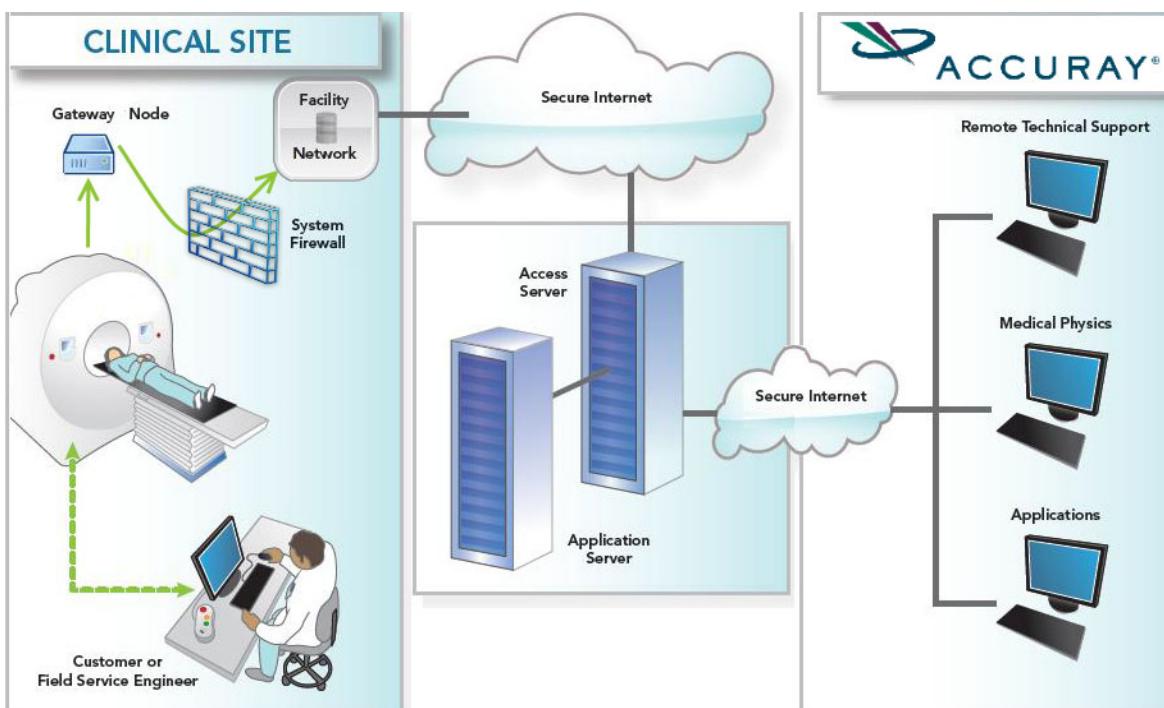
The jaw width for imaging is fixed at J1, which corresponds to a field width of approximately 4 mm projected to isocenter.

# Accuray Network Environment

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## ◆ iLink

iLink<sup>SM</sup> remote services provides a secure connection between your Accuray *integrated Data Management System* (iDMS) and the Accuray Customer Interaction Center, for efficient troubleshooting and improved system uptime. Installing *iLink* is optional, and requires cooperation with your clinic's IT department. Contact Accuray Customer Support to determine if your site is eligible for *iLink*.



## iLink Capabilities

*iLink* enables Accuray Incorporated to:

- Remotely view log files. This data includes error messages and records of machine use, such as a timestamp and basic delivery information for each procedure that was run on the machine.
- Log into *TQA* and review the module reports. *TQA* reports may assist your service representative to proactively address issues, should system performance migrate towards specification limits.

- With your permission, view your Treatment Delivery Console (TDC) Workstation or Precision Planning System screen in real time. Only verified Accuray Service Personnel can take control of the mouse.

Other actions can be completed through *iLink*, which are not listed here. Only verified Accuray Service Personnel can remotely control the *iDMS* and Gateway servers.



**TIP:** To provide your service representative with the best information for maintaining your system, run the **TQA Basic Dosimetry** or **Daily QA** module at least once per week.

## Data Protection

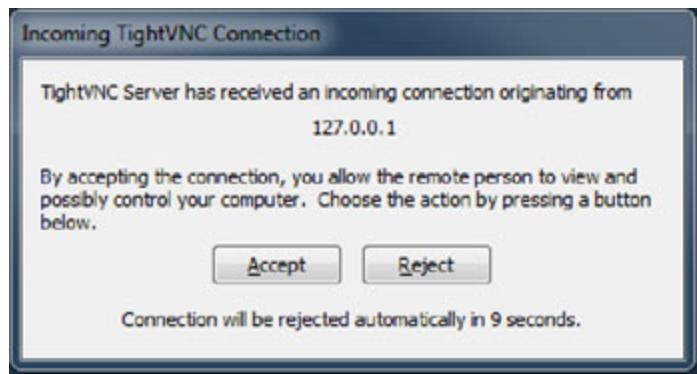
*iLink* is safe, secure, and based on Secure Socket Layer (SSL) encryption. *iLink* employs an end-to-end security strategy blanketing all layers, including networking, application, user and data security. *iLink* uses technology that meets the ISO 27001:2013 certification standards and is widely accepted and used in hospital settings worldwide.

The machine logs and *TQA* do not contain any patient identifying information, and can be viewed freely by Accuray if *iLink* is installed. If you want to share your screen, you will need to accept or reject the connection each time.

## Accepting Remote Access Request

Accuray Support may request remote access to your TDC or *Accuray Precision™* Treatment Planning System when working with you to resolve a problem. When the remote Accuray representative initiates a connection, a dialog box will appear on the monitor requesting that you **Accept** or **Reject** the remote connection.

Click the **Accept** button to allow remote access to your workstation. If you receive a request and do not wish to allow remote access to the workstation at the time, you can click the **Reject** button. If neither button is clicked within 60 seconds, the software will automatically reject the remote connection request.



Remote Permission Dialog

The shading of the icon located in the *Windows 7* system tray (click the double arrow to show hidden icons) will change when a remote connection is currently active.



**Left:** An icon with a white "V" and dark background indicates an active remote connection. **Right:** An icon with a dark "V" and white background indicates that the remote connection is not active.

## ◆ The Firewalls

The *iLink* system employs a single Security Appliance as its main point of connection to the hospital's network, and additional Security Appliances per connection to each system or vault. All Security Appliances come standard as part of your Accuray System, and are required for complete *iLink* functionality.

Each of the Security Appliances has its configuration tuned to the exact needs of each deployment location and its users. These configurations include providing product and location-specific access control rules and network address translation to each of the devices behind the Security Appliances. The access control rules and network address translations restrict incoming and outgoing traffic to a few select applications and programs approved by Accuray Incorporated.

## ◆ Delivering Data to Accuray using Customer Transfer Space

The customer transfer space is a secure web site for exchanging data with Accuray Incorporated. It is possible that you may be asked to provide data to Accuray Incorporated as a step in the problem resolution process. To exchange large or confidential data files with Accuray complete the following steps.

1. Right-click on the folder that you want to send to Accuray Incorporated, and choose **Send To > Compressed (zipped) folder**. Wait for the zip process to complete, before proceeding.
  - a) Copy your data to a PC that has access to the worldwide web.
  - b) Open the web browser on your PC and navigate to <http://go.accuray.com>.
  - c) Enter your username and password to access the customer transfer space. If you do not have your username and password, ask Accuray Customer Support for assistance.
  - d) In the **Realm** field, choose “Customer.”
  - e) Click on **Transfer Space**.
  - f) Click on the folder for your machine serial number and site name
  - g) Click **Upload Files**.
  - h) Click **Browse**, then choose your file.
  - i) Click **Open**.
  - j) Type the file name in the “Save as” field.
  - k) Click **Upload** to upload the file.
2. Inform Accuray Customer Support when the upload is complete. Accuray Customer Support will not receive automatic notification of newly uploaded data, so you need to inform Accuray Incorporated after you have uploaded your data.



**NOTE:** Your customer transfer space account may expire after one year of inactivity. If your account expires, ask Accuray Customer Support to reactivate it.





## Basic Procedures

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## System Startup

Prior to performing any beam-on tests, do the following to help achieve a stable beam output and optimal *CTrue* image reconstruction:

- Turn the system on.
- Wait until the machine water temperature is above 39°C.
- Run a 5-minute warm up procedure.
- Run an air scan.

See "Basic Tasks and Information" in the *Treatment Delivery Manual*.



**IMPORTANT:** If the system is restarted immediately after an unrecoverable interruption, a few minutes will be required for the system to prepare internal components.

## Standard Safety Checks

System interlocks and stop buttons are introduced in "Use of Safety Mechanisms" in the *Treatment Delivery Manual*.

Instructions for standard safety checks are also available in the *Treatment Delivery Manual*:

- "Check entrance interlock and indicators"
- "Safety mechanisms on the status console"
- "Facility installed safety mechanisms"

# Scan, Position, and Treat

Refer to the *Treatment Delivery Manual* for more information about generating a *CT*True image, registering the *CT*True image to the planning image, and treating a patient.

## ◆ Default Scan Settings

You can set or modify the default scan settings for all treatment plans. On the Treatment Delivery Console navigate to **Tools > Edit Scan Default Settings**. Set the following fields to the desired defaults:

- Scan Viewer Plane
- Pitch
- Reconstruction Interval
- Window Level Center Point
- Window Level Width

During normal treatment workflow a user can override the default site scan settings by changing any of these fields. If a user changes the scan settings on the **Scan** tab, that plan will retain the updated setting for future sessions.



# Manage Treatment Interruptions

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## ◆ Introduction to Make-up Procedures

The *Treatment Delivery Manual* includes instructions for resolving system interruptions, delivering make-up procedures, and verifying the make-up procedure duration.

If the **Stop** button is pressed, or a machine interrupt occurs during a treatment, only the superior portion of the target(s) was treated with the current procedure (*TomoHelical* Treatment Delivery) or current beam angle (*TomoDirect* Treatment Delivery). The system keeps track of where and when the interrupt occurred. If the machine lost power, the Uninterruptible Power Supply (UPS) maintains power to the SCS (Stationary Control System) computer to ensure that data in the volatile memory specifying where the procedure was interrupted is safely stored.

Before **Ready** is pressed for a make-up procedure, the patient must be at the registered setup position outside the bore. The setup-to-ready distance for the make-up procedure will generally exceed that of the original procedure, so that after the make-up procedure's approximately 10 s warm up, the couch is at the desired IEC Y position for treating the remaining (inferior) portion of the target(s).



**IMPORTANT:** Check the couch position carefully before running a make-up procedure.

- After pressing **Ready** for a make-up procedure, observe in the room that the correct anatomy is in the beam region.
- Record the Y position of the couch where the interrupt occurred. After pressing **Ready** for the make-up procedure, verify that the Y position of the couch is close to the interrupt position (the couch will move into the bore during the 10 s warmup, and should reach the interrupt position at the end of the 10 s warmup).
- If the patient has moved, or if there is any doubt about the correct couch position, verify the patient position with a *CTrue* image before running the make-up procedure.

It is recommended to verify the make-up procedure time before delivering a make-up procedure. The following section explains the theory of make-up procedure time calculations.

## ◆ Equation for Make-up Procedure Time

The following equation may be used to verify the make-up procedure time for *TomoHelical*/treatment procedures or individual *TomoDirect* beams:

$$\text{Make-up time} = (\text{planned delivery time} - \text{elapsed time} + \text{warm up}) \pm (\text{s per proj} + 0.2 \text{ s})$$

There are two exceptions to the make-up procedure equation:

- If the procedure was interrupted before the warm up was completed, make-up time is equal to the planned delivery time for the *TomoHelical* procedure or the interrupted *TomoDirect* beam. (For a *TomoDirect* procedure, the total make-up procedure time is then equal to the sum of the planned time for all beams that have not yet been delivered.)
- If the procedure was interrupted in the final projection of the procedure, in some cases no make-up procedure is necessary/possible.

The following images indicate where you can find the planned delivery time, elapsed time, warm up, and seconds per projection for an interrupted treatment:

- The planned delivery time and elapsed time for the procedure may be determined from the procedure list on the left side of the screen. For the planned delivery time and elapsed time of individual *TomoDirect* beams, see the **Procedure Beam Details** area below the procedure list for the selected fraction.
- The warm-up time (10 s rounded up to the nearest integer number of projections) and time per projection may be determined from the **Procedure Details** information that appears below the procedure list for the selected fraction.

The screenshot shows a software interface for managing medical treatments. At the top, there's a table listing treatment steps:

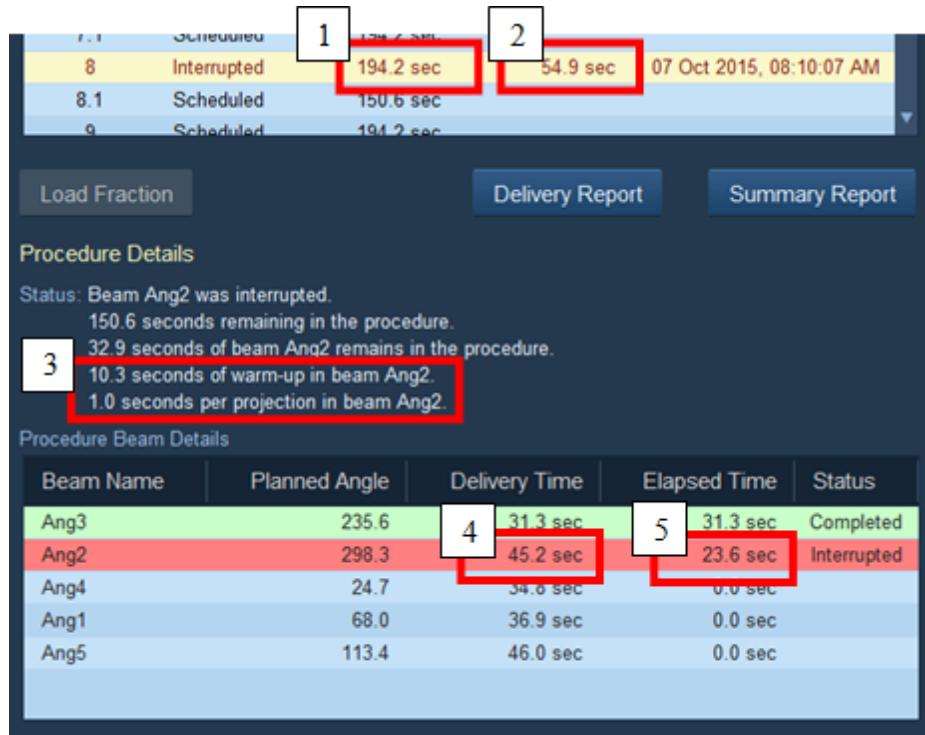
Step	Status	Time	Date
59	Performed	1 112.6 sec	02 Oct 2015, 08:19:59 AM
60	Interrupted	112.6 sec	07 Oct 2015, 07:57:49 AM
60.1	Scheduled	75.9 sec	
61	Scheduled	112.6 sec	

Below the table are three buttons: "Load Fraction", "Delivery Report", and "Summary Report".

In the "Procedure Details" section, the status is listed as "Procedure was interrupted." It also displays the remaining time: "75.9 seconds remaining in the procedure." Below this, there's a box containing the following text:

3 10.0 seconds of warm-up.  
0.3 seconds per projection.

Interrupted *TomoHelical*/procedure



**Interrupted *TomoDirect* procedure**

Item	Description
①	Planned Delivery Time for the entire procedure.
②	Elapsed beam-on time at the point of interruption.
③	Warm-up time and projection time.
④	Planned Delivery Time for the interrupted <i>TomoDirect</i> beam.
⑤	Elapsed beam-on time for the interrupted <i>TomoDirect</i> beam, at the point of interruption.



**IMPORTANT:** When determining the elapsed time for the make-up procedure equation, refer to the status indicators on the left side of the **Treat** tab of the TDC (i.e., in the **Procedures** list). Elapsed times in the **Procedures** list are based on actual data from the Radiation Delivery System. The elapsed time in the **Treatment Status** area in the center of the screen is an estimate, based on the Treatment Delivery Console counting independently from the machine after a start signal is received. In the case of an unrecoverable interrupt, the system may need to be restarted in order to update the elapsed time on the interrupted procedure from the Radiation Delivery System.

The treatment system delivers procedures in integer numbers of sinogram projections. The time per projection is fixed throughout a procedure (for *TomoHelical* Treatment Delivery) or throughout a beam angle (for *TomoDirect* Treatment Delivery). Thus, partially delivered projections will need to be delivered from the start of the projection. Leaf open times within the projection will be scaled to account for fluence already delivered before the interrupt.

If the procedure was interrupted during a projection, such that no leaf has open time remaining in that projection, the make-up procedure time will be shortened by one projection. If this happens in the final projection, the interrupted procedure (*TomoHelical*) or beam (*TomoDirect*) will be marked as **Complete**, and there is no opportunity (or need) for creating a make-up procedure.

In the make-up procedure equation, the tolerance of  $\pm$  s per proj accounts for the possibility of adding less than one projection to the make-up procedure if it needs to start at the beginning of a projection that was partially delivered, or subtracting less than one projection from the make-up procedure if no leaf open time remains in the projection that was interrupted. The additional 0.2 second accounts for rounding of the numbers used in the calculations.



**NOTE:** Make-up procedures for multi-target treatments are handled the same way as make-up procedures for single-target treatments. If an interruption occurs in a closed-leaf gap between targets, the make-up procedure will start with the next undelivered projection, regardless of whether or not that projection has open beamlets. This is in contrast to previous software versions, where the make-up procedure "skipped" the gap between targets and started with the first projection after the interruption that included open beamlets.

# Manage Machine QA Procedures

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## ◆ Introduction to Machine QA Procedures

A procedure is a single fraction of machine instructions to be delivered on the treatment system. Machine QA procedures may be saved to external media or loaded onto the data server as **.xml** (Extensible Markup Language) files that list parameters and their definitions (e.g., **nominalGantryPeriod**: 20 s). Additionally, **.xml** files reference other files (e.g., to specify the planning image and the MLC delivery instructions).



**WARNING:** Treating a patient with a QA procedure can cause serious injury to the patient. Patient treatments include: dose calculation in the patient, control over the number of available fractions, a record of delivered fractions, ability to create a completion procedure if there is an interrupt, safeguards to prevent procedure modification, machine safety checks and warnings, and patient-specific laser positions. Each type of QA procedure (Machine QA, Patient QA, Phantom Plan) lacks several of these important safety features.

## ◆ Create a Machine QA Procedure

Using the **Basic Create Tool** on the TDC (Treatment Delivery Console), you can create your own machine QA procedures and specify the motion of the gantry, couch, leaves, jaws, etc. See “Create Machine QA” (page 525) for more information.

For your convenience, pre-made **.xml** files are available from Accuray Incorporated for most common tasks:

- *TQA* **.xml** files can be downloaded from the *TQA* application.  
See the *TQA Manual* for more information.
- Additional **.xml** files are available from Accuray Customer Support.

To load **.xml** files on the TDC:

1. Unzip the procedure files if necessary.
2. Place the files in the appropriate directories:
  - Place the **.xml** on the TDC in  
**C:\accuray\tdc\calibrationData\Treatment  
Procedures\TreatmentProcedure Templates**

- Place any provided sinograms (.bin files) in:  
**C:\accuray\tdc\calibrationData\sinograms**
  - Place any provided dynamic jaw profiles (.txt files) in:  
**C:\accuray\tdc\calibrationData\JawProfiles**
  - Place any provided images in: **C:\accuray\tdc\calibrationData\CTs**
3. From the TDC home screen, click the **Create Machine QA** task.
  4. Click **Create**.
  5. Click **Load File**.
  6. Browse to the folder location of the .xml files mentioned in Step 2. Select the desired file and click **Open**.
  7. Right-click in the blank space on the screen to **Expand** the data tree and review the .xml file.
  8. If you want the default couch position to be out of the bore (so that the **Setup** button can be used to bring the couch out of the bore), navigate to **Couch and Laser Setup** in the data tree, and set the **Use Default Setup Positions** parameter to **True**.



**TIP:** After typing new values for any parameter, press the Enter key and ensure that your new entry has turned yellow. If the entry is still white, the parameter has not been successfully changed.



**NOTE:** When the **Use Default Setup Positions** parameter is set to **True**, the **Couch Setup Y Position** and **Couch Setup Z Position** parameters in the .xml file will be ignored. The system will use the default couch positions specified in the **Edit Machine** area.

9. You may want to double-check that all **File Name** paths in the .xml tree are valid. If they are invalid you will receive errors.
10. Click **Save to Data Server** to load the procedure on the data server. (The **Save XML File** button only saves the procedure to your hard drive or external media.)



**NOTE:** If you wish to save to an .xml file for your records, don't forget to check **Save Binaries**. Binaries includes the sinogram and jaw position files. The machine instructions are not complete without the binaries.

11. Review the messages on the screen and click **Close**.



**TIP:** If a procedure file with the same **Name** parameter already exists on the data server, you will get an error message. Change the **Name** parameter and try again.



**TIP:** If the system cannot find any of the files in their correct paths, you will get error messages when you attempt to save the .xml to the data server. Ensure that all paths point to existing files, and try again.



**TIP:** If the message "Unable to find matching jaw spec" appears, your jaw settings do not match one of the commissioned treatment field widths. This is OK as long as you did not intend to use one of the commissioned treatment field widths.

12. After the procedure is successfully created, the procedure may be opened from the **Machine QA** task on the home screen of the TDC.
13. If you wish to delete the older procedure, you may do so by clicking **Create Machine QA** from the home screen of the TDC, then click **Delete** to select the procedure that you want to delete.

## ◆ Edit a Machine QA Procedure

It is not possible to edit a **Machine QA** procedure that is currently on the data server. However, you can edit a copy of the procedure and re-submit it to the data server.

1. From the home screen of the TDC, click **Create Machine QA**.
2. Click **View**.
3. Click **Query**.
4. Select the desired procedure.
5. Edit the procedure as desired and update the **Name** parameter to assign a new name. See “Using the Create XML Interface” (page 552) for parameter definitions.
6. Click **Save to Data Server**.
7. After confirming that the above steps were completed successfully, you can delete the older machine QA procedure. From the TDC dashboard, click **Create Machine QA**, then click **Delete** to select the procedure you want to delete.

## ◆ Access Sinogram Values for a Patient Plan



**NOTE:** The workflow described in this section is not part of the recommended QA tasks, but it may be used for research or troubleshooting purposes.

The following workflow may be used to view the leaf-open times in the sinogram for an authorized patient plan:

1. From the home screen of the TDC, click **Create Machine QA**.
2. Click **Create From Patient Plan**.
3. Select the desired plan to open from the patient database.
4. Save the procedure to the TDC C:\ drive, making sure to use the checkbox to save binaries (the MLC sinogram is a binary file).
5. Press **Cancel** to close the .xml file.
6. To view the sinogram you just saved, from the TDC **Create Machine QA** task, click **Basic Create**.
7. Set the sinogram mode to **Dynamic**.
8. **Browse** to locate the sinogram that you saved in Step 4 (the file is named **ProcedureSinogram1.bin**).
9. Click **Edit** to view the sinogram in the sinogram editor.
10. Hover the mouse over the beamlets in the sinogram editor, and the percentage open time for each beamlet is displayed on the bottom of the sinogram editor.
11. To convert the percentage open time values to seconds, multiply by the projection time. For a helical procedure,  $\text{projection time} = \text{gantry period}/51$ .



**NOTE:** The MLC delivery instructions accessed by this method include latency corrections to achieve the planned leaf open times. Planned leaf open times are slightly different from the MLC delivery instructions.



**WARNING:** Never use the workflow in this section to create a procedure for treating a patient. Machine QA procedures lack important safeguards that may result in injury or death if delivered to patients:

- No dose calculation is available for Machine QA procedures.
- If a Machine QA procedure is interrupted, it is not possible to create a completion procedure.
- Patient treatment plans require plan approval on the planning system in order to be run on the machine, but Machine QA procedures do not need to be accepted.
- Patient treatment plans use a checksum to prevent modification, but Machine QA procedures can be easily modified.
- There is potential for a Machine QA procedure to be delivered on a machine other than what it was planned on, with no accounting for beam model and MLC differences.
- Patient delivery records are not available for Machine QA procedures.
- There is no control over the number of fractions in a Machine QA procedure.
- Treatment procedure delivery uses couch position checks, machine data consistency checks, warning messages and other safety restrictions that are not applied to Machine QA procedures.

# Set up the *Tomo-Electrometer*

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- ◆ Plot the Tomo Electrometer Data Using TEMS Software ..... 89

1. Set up the *Standard Imaging Tomo Electrometer* outside the treatment room, near the Treatment Delivery Console.
2. Connect the triax cables to the desired channels in the back of the *Tomo Electrometer*.



**TIP:** Triax cable connections must be kept clean to reduce drift and leakage. Use the provided caps to cover the connectors when they are not in use. If drift or leakage is noted, try cleaning the triax cable connections with a dry and oil free compressed air source (do not blow on the connectors with your mouth).

3. Connect the *Tomo Electrometer* to a power source, to ensure it does not run out of batteries while you are collecting data.
4. Turn the *Tomo Electrometer* on, and wait for it to complete the 5 minute warm-up cycle.



**WARNING:** Minor shock or damage to equipment may occur if electrometer ports are charged when connecting or disconnecting components. To prevent this, remove the electrometer charge (zero bias) before connecting or disconnecting components.

## ◆ Measure the Integrated Charge

1. Press **Measure**.
2. Dial in the Bias to +300 V, for consistency with the calibration conditions.



**NOTE:** The displayed bias typically differs by about 2 Volts from your selected value.

3. Select the channels that will be used for measurement.
4. Zero the electrometer when the beam is off and the current rate is stable (wait at least one minute after setting the bias).
5. Set the Timer to **Free Run** to ensure that the data collection is not interrupted.
6. Press **Start** to begin collecting data.
7. While the beam is off, verify that the leakage is not excessive.

## ◆ Plot the *Tomo* Electrometer Data Using TEMS Software

1. Connect the *Tomo* Electrometer to the Physics Workstation using the RS485 cable with RS232 converter.
2. Open the TEMS software and click **Control > Initialize Electrometer**. (Or, if you also have the water tank connected, click **Control > Initialize All**.)
3. Verify that the message at the bottom of the screen is green, indicating a successful connection. If the connection is not successful:
  - Ensure that the *Tomo* Electrometer is plugged into the electrical outlet, and that it is turned on.
  - Ensure that the cable connection to the Physics Workstation is secure.
  - Ensure that the *Tomo* Electrometer is not currently measuring dose (press **Stop** on the electrometer if necessary).
  - Ensure that only one instance of TEMS is running on the Physics Workstation.
  - Check the configuration of TEMS and the *Tomo* Electrometer as indicated in the *Dosimetry Analysis Guide*.
4. Set the bias to -300 V, so that positive charge will be collected and the graph will not be inverted.
5. Select the desired channel(s) for measurement.
6. Set the time sampling to 100 ms.
7. Zero the electrometer when the beam is off and the current rate is stable (wait at least one minute after setting the bias).
8. Press **Sample** to begin sampling data.
9. Press **Sample** to stop the sampling after a few seconds, since sometimes the first sample contains a spike at the beginning of the sample.
10. Press **Sample** to begin sampling data for measurement purposes.

# Account for Couch Sag

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- ◆ Correct for Couch Sag in Phantom Set Up ..... 91

## ◆ Explanation of Couch Sag

A CT-style couch typically sags as it moves into the bore, according to the physics of a cantilevered beam (diving board). The couch sag depends on the weight distribution on the couch, and the distance from the end of the supporting base of the couch outside the bore to the beam plane.

The only aspect of couch sag that is relevant for patient images and treatments is the couch sag at the plane of the treatment beam. Couch sag superior to the beam plane is not clinically relevant.

Couch sag should be taken into clinical consideration whenever there is a difference between the sag of the planning image and the sag of the treatment delivery:

- In the hypothetical case of a perfectly level treatment couch, sag inherent in the planning image could still cause discrepancies between planning and treatment.
- Ideally, CT simulation and treatment would be performed on the same couch and with consistent couch coordinates - then the amount of couch sag would not be clinically relevant because the planning geometry would match the treatment geometry. (Planning and treating on the same couch is possible using the *CTrue* images, but most patients are planned on kVCT images received from another system.)

The pallet support structure at the rear of the gantry supports the weight of the couch and substantially reduces (but may not completely eliminate) couch sag. Accuray Incorporated specifies that the couch may not sag more than 2 mm at the beam plane.

The room lasers are set to be level with gravity; the room lasers do not account for couch sag.

Two types of differences in the couch sag should be considered:

1. Any net difference in couch height from the setup position outside the bore to isocenter should be accounted for by acquiring a daily MVCT setup verification image, registering to the planning image, and adjusting the couch height.



**IMPORTANT:** Always verify the daily patient setup with a *CTrue* image to account for couch sag differences between the planning image and the treatment.

2. As a long target advances into the bore, the amount of couch sag at the beam plane may vary from the superior end to the inferior end of the target.

The treatment system only allows you to make one couch height adjustment that applies to the entire treatment. Differences in couch sag from one end of a long target to the other end (planning image versus treatment geometry) may be visualized using MVCT, but cannot be corrected for all positions in the long target. The couch height adjustment in this case is a clinical decision.

## ◆ Correct for Couch Sag in Phantom Set Up

### Option 1: Acquire a CT image

One way to account for couch sag in a phantom setup is to acquire a setup verification image, as you would do for a patient. Register the *CTrue* image to the planning image (or to the isocenter lasers on the **Register** tab of the TDC if you are using a phantom). Then, apply the shifts to the couch.

### Option 2: Use green bore lasers to determine sag correction

Alternatively, here is a workflow for setting up a phantom to the green bore lasers to correct for couch sag:



**NOTE:** This workflow is not suitable for patient set up. Patients are set up to the red lasers, and you cannot see the red lasers inside the gantry bore.

1. Ensure that the couch is not too far out of the bore.
2. Place the phantom on the couch near virtual isocenter.
3. If you are using the *Tomo*-phantom, rotate the phantom on its base so that it is level with the green bore lasers.
4. Adjust the height of the couch so that the phantom is appropriately aligned with the green bore laser at virtual isocenter, according to the requirements of your QA test.
5. Set the phantom X and Y positions to the green overhead lasers at virtual isocenter.
6. Use the **Step Move** function to send the couch into the bore +700 mm in Y, to the radiation isocenter. Adjust the couch height to correct for sag. The phantom is now properly aligned at isocenter.



**TIP:** You may need to walk to the back side of the gantry to view the intersection of the green bore lasers on the phantom and determine if a couch sag correction is needed.



**TIP:** To set the surface of a *Virtual Water* stack to 850mm SSD, attach a small piece of masking tape to the -Y surface of the block, and let it stick up above the *Virtual Water* (see the following image). This will allow you to visualize the distance from the surface of the *Virtual Water* to the laser without walking behind the gantry.



**Tape Trick**

7. If the QA procedure will move the couch into the bore when **Ready** is pressed, use the **Step Move** function to return the couch to the virtual isocenter (-700 mm in Y).



## Chapter 3

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### Commissioning

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## Commissioning Overview

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# Introduction to Commissioning

The system comes with a pre-installed beam model. In the factory, the machine output, energy, and beam profiles are adjusted to match standard beam model data. Machine-specific MLC properties are measured and entered on your system.

The facility should make arrangements with the installers to perform a radiation survey as soon as possible after the system is able to produce radiation.

Following installation, qualified personnel will verify that your system meets Accuray Incorporated tolerances, as outlined in the Acceptance Test Procedures document, including but not limited to:

1. Alignment:
  - LINAC aligned in IEC X with MLC
  - LINAC aligned in IEC Y with jaws
  - Beam pointed in plane of gantry rotation
  - Lasers and couch aligned with beam line and gravity
  - Detector aligned in IEC Y with jaws

2. Beam characteristics for each licensed field size:
  - Longitudinal and transverse profiles
  - Percent depth dose
  - Output calibration using helical IMRT measurements (Establish baseline for future static output/energy constancy checks)

3. MVCT dose

Machine procedure files used during specification conformance verification are made available to the site physicist for future use. The site physicist will also receive a copy of the reference and measured data, spreadsheets summarizing tests performed, and a test patient for IMRT dose calibration.

After Accuray Incorporated has completed the specification conformance verification and acceptance testing, the site physicist can proceed with the remaining commissioning tasks. TG 148 recommends that prior to the start of patient treatments, all daily, monthly, quarterly, and annual QA tests should be performed. Before creating treatment plans, the site physicist will also need to prepare a Density Model for each CT scanner in the facility that provides images for treatment plans.

The site physicist makes the final decision of when the machine is ready to treat patients.

## Dosimetry for the Treatment System

Dose may be calculated for the treatment beam using a modified version of the TG-51 protocol, as described by TG-148.

The TG-51 protocol is not directly applicable to the treatment beam because the 100 mm x 100 mm field width is not achievable. The 850 mm SAD and 850 mm diameter bore opening of the system do not allow sufficient space for measurements at 1000 mm SSD and 100 mm depth, as prescribed by TG-51. Also, because the system has no flattening filter, the beam quality spectrum is different than for a conventional 6 MV system.

TG-148 prescribes modifications to the TG-51 protocol to accommodate the unique aspects of the delivery: a "machine-specific-reference" factor is included in the TG-51 dose calculation to account for the differences in geometry and beam quality from a conventional system, and a "plan-class specific reference" factor is included for IMRT treatment plans. The combined scaling effect of the beam quality factor, machine-specific reference factor, and plan-class specific reference factor is very close to 1.0.

Accuray recommends converting ion chamber charge measurements to dose using the formalism described in TG-148. However, when Accuray Incorporated personnel determine dose from the A1SL ion chamber measurements, a simplified formula is used:

$$D = M N_{D,w}^{60Co} P_{elec},$$

where  $D$  is the calculated dose,  $M$  is the charge reading that has been corrected for pressure and temperature (the A1SL arrives calibrated by a US accredited standards lab at 22 C and 760 mm Hg absolute pressure),  $N_{D,w}^{60Co}$  is the ion chamber calibration factor, and  $P_{elec}$  is the electrometer calibration factor. Dose measurements with the *Tomo* Electrometer are made at +300 V to match the calibration conditions.

Dose calculations using the simplified formula are very close to the TG-148 calculations. The simplified formula helps to reduce the risk of gross errors by reducing the number of factors.

The treatment beam is calibrated to achieve agreement between planning dose calculations and IMRT ion chamber measurements. Depending on how the various system parameters fall within their tolerance ranges, the static open-field output of the system may vary from one machine to another.

The machine-specific static output rate of your system will be determined during commissioning and used henceforth as a constancy check:

- A typical static output rate for a system with the standard dose rate configuration is  $850 \pm 30$  cGy/min at 850 mm SSD, 15 mm depth in *Virtual Water*, and 50 mm x 400 mm field size.
- A typical static output rate for a system with the high dose rate configuration is 1025 cGy/min at 850 mm SSD, 15 mm depth in *Virtual*

*Water*, and 50 mm x 400 mm field size. As with the standard dose rate, the machine-to-machine variation in the nominal output rate is expected to be a few percent.

# Machine Data

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The beam model and other machine parameters may be accessed by users with appropriate permissions from the Treatment Delivery Console. From the **Tools** menu, click **Edit Machine**. From here you can look at the data tree, which contains system level properties, as well as properties for the treatment and image beams.

Some parameters in the **Edit Machine** area are used by the system for plan calculations, while other parameters control various aspects of beam delivery and image reconstruction. A few parameters are labels that do not control anything, or are not used at all. Several of the parameters describe basic system characteristics that are not intended to be changed from their default values.

The parameters accessible from the machine data area are intended to be maintained by the service representative. Permission to access the **Edit Machine** area of the Treatment Delivery Console is assigned from the **User Administration** task of the Treatment Planning System system. It is recommended that the site physicist not change any parameters in the machine data area, except that the site physicist may calibrate the monitor unit display, as discussed in “Monitor Unit Display Calibration” (page 257).

Several of the parameters contain lists of numbers, and are not organized in a human-readable way. The service representative has special software tools for populating these data fields. The data that was provided to your site by Accuray Customer Support at the completion of Acceptance Testing includes reference longitudinal and transverse profile data, PDDs, and energy spectrum data in a spreadsheet format.



**TIP:** If you need a copy of the beam model data that was installed on your system and cannot find your ATP data, contact Accuray Customer Support for assistance.



**WARNING:** Do not change the **Edit Machine** data unless you are fully trained by Accuray in the consequences of changing a particular parameter:

- Inappropriate changes may result in discrepancies between plan calculation and delivery that could cause death or serious injury.
- Inappropriate changes may cause unnecessary wear on system components, causing system downtime for repairs.
- The Dose Control System (DCS) is calibrated by the service representative in a separate software program. Some **Edit Machine** changes will trigger interlocks that render the system unable to run the beam, until the service representative recalibrates the DCS.



**WARNING:** The only two parameters that the site physicist could have legitimate reason to adjust are the **Expected MU (MU/min)** and the **MU per chamber count**. These two parameters influence the monitor unit display and reporting, but do not impact the beam delivery (see “Monitor Unit Display Calibration” (page 257)). Changing machine parameters (other than the **Expected MU (MU/min)** and **MU per chamber count**) may put the system in a state where it cannot be used until the service representative performs calibration, destroy machine components, or cause a mismatch between beam properties for delivery versus planning.

## ◆ System Level Properties

This section describes some of the data components that are included in the System Level portion of the **Edit Machine** tree.

### Machine Settings

The **Helical start angle (deg)** parameter is not currently used.

The **Bore size (mm)** is the diameter of the opening in the bore through which the patient enters, and is 850 mm.

The **Max jaw speed** is expressed in millimeters (jaw numbers) per second, and is used during End of Planning to ensure that the dynamic jaw movement does not exceed the maximum speed.

The **Water Temperature Minimum Threshold** and **Water Temperature Maximum Threshold** determine the color of the **Water Temperature** indicator in the upper left corner of the home screen of the TDC, and do not control the machine.

The **Facility lights mode** applies to the indicator lights outside the bunker (power, radiation, etc.) In **MutuallyExclusiveMode**, only one light will be illuminated at a time. In non-exclusive mode, multiple applicable lights can be illuminated at the same time.

- **Dose Control:** References calibration files set by the service representative to define the relationship between Dose1 and PAC, and between injector current and gun current.
- **Couch Settings:** Includes limits on the couch speed, as well as parameters that control couch insertion for treatment planning and indicates the file location of the couch image used for treatment planning.

The **Out of bore setup** parameters set the default couch position for Machine QA procedure creation to bring the couch out of the bore (when the **useDefaultCouchSetupPosition** parameter in the **.xml** file is set to **true**). This default couch position is also used as the **Expected Couch Position** for images and treatments when there is no pre-defined

or stored couch position available. The **Out of bore setup** position is determined at the time the procedure is delivered. If you change the **Out of bore setup** position, a Machine QA procedure will use the new one next time it runs.

- **MVCT Settings:** Contains parameters related to image acquisition and reconstruction.
- **Airscan Settings:** Contains parameters related to acquisition and analysis of air scan data.
- **Linearity Settings:** Contains parameters for automated analysis of the CT number calibration results.
- **Detector Settings:** Provides basic information on the detector geometry, and allows the service representative to identify bad channels that should not be used for image reconstruction.
- **Gantry Settings:** References configuration files for gantry calibration by the service representative.
- **Jaw Settings:** The service representative adjusts these values to ensure that the beam is pointed in the plane of gantry rotation, and to control the width of the longitudinal profiles (one set of jaw encoder values controls all the field widths).
- **Monitored Signals:** Indicates the allowed bias range on the dose monitor chambers.

**MLC Settings:** Contains settings for the MLC related to planning and delivery.

The **Minimum time per projection (ms)** is 230 ms.

The **Number of projections per rotation (proj/rot)** is 51 for all helical treatment plans created on the Treatment Planning System.

The **Maximum active leaf cycles per second** is the maximum number of leaf transitions (open to close or close to open) that an MLC may perform per second. This is enforced at End of Planning to avoid positioning errors in the pneumatically driven leaves due to low facility-supplied air pressure. The number of leaf transitions per second is calculated as a moving average over the **Leaf cycles buffer time (s)**.

The **Leaf threshold (ms)** is set to 18. At End of Planning, leaf open times less than or equal to 18 ms are discarded from the plan.

The **Open latency activation (ms)** is the expected time delay from when a leaf open command is issued until the leaf actually begins to open. The **Open latency transit (ms)** is the expected time required for the leaf to finish opening. These parameters are used to adjust the timing of when leaf open commands are issued in the delivery.

The **Leaf Bounce Tolerance (ms)** indicates the amount of time that a leaf can stay in the bounce state before counting a leaf error.

**MLC Settings:** Contains settings for the MLC related to planning and delivery.

The **Leaf Overtravel Tolerance (ms)** indicates the amount of time that a leaf can stay in the overtravel state before counting an overtravel error.

## ◆ Beam Level Properties

Each system contains two beams: a treatment beam and an imaging beam. If any additional custom beams exist (e.g., for a research collaboration with Accuray Incorporated), they are not available for treatment planning.

As described in the System Overview chapter, the pulse rate, energy spectrum, and output rate of the treatment beam are higher than the imaging beam, requiring different machine settings to control the beam producing components. The **Controls** and **Monitored Signals** settings are maintained by your service representative for the imaging and treatment beams to ensure that the machine is operating with settings that will not damage machine components, and with oversight from the customer physicist to ensure that the treatment beam is performing consistently with the beam model used by the planning system.

The **Beams** section for the scan beam also includes a **Measurements** section with information specific to *CTrue* acquisition and image reconstruction. The treatment beam does not contain a **Measurements** section.

The **Beams** section for the treatment beam also contains the beam model. The beam model is used by the planning system to perform dose calculations. The scan beams do not have a beam model, since no dose calculations are performed for the scan beam.

The beam model includes a combination of standardized (**DoseCom Twinnable**) and machine-specific (**DoseCom Non-Twinnable**) parameters. For more details on the beam model data, see “Beam Model” (page 412) in the Algorithms chapter.



**IMPORTANT:** The parameters on the Treatment Delivery Console should be maintained to achieve consistency between delivery and planning (which is based on the beam model data). Contact Accuray Customer Support for assistance if changes to the machine data are needed.

# Physics Considerations for *TomoDirect* Treatments

In this section, additional physics considerations for proper use of the *TomoDirect* treatment modality features are discussed.

- ◆ Patient and Couch Positioning ..... 103
- ◆ Potential for Hot Spots ..... 105

## ◆ Patient and Couch Positioning



**TIP:** Use the beam angles display on the **Register** tab of the Treatment Delivery Console to check daily target coverage. Set the **Balance** slider to **Plan** to see the planned coverage, or to **Scan** to see the expected daily coverage. Similar to the **Entire Treatment** option on the Planning Station **Beam Angles** tab, the **Register** tab beam display on each slice shows the beam coverage on all slices, and includes any beam extension due to flash.

In any given treatment, beams may enter through the treatment couch. During the treatment planning process, the couch in the planning CT image is replaced with an image of the *Radixact* couch. In this way, the dose calculator accounts for the attenuation and scatter of beams that pass through the couch.

For a *TomoHelical*treatment, minor discrepancies in the way that the couch image accounts for the position and attenuation of the couch tend to average out due to the large number of beam angles.

With only a few beam angles in *TomoDirect*treatments, more attention is needed to ensure acceptable agreement between calculations and measurements.



**IMPORTANT:** The delivered dose can be sensitive to the daily couch setup position for beams that enter through the couch, especially for plans with few beam angles. A gantry roll adjustment can also change the intersection of the beam with the couch and thus the dose distribution in the patient.

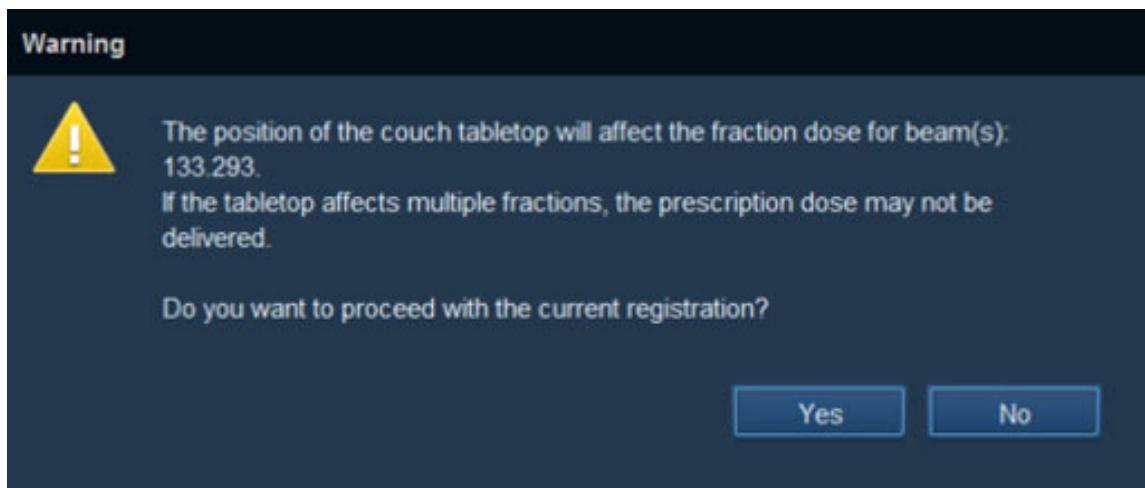
The *Precision* Treatment Planning System calculates dose in the geometry of the patient planning image. The *Radixact* system does not adjust the dose calculation to account for daily setup variations. The *Precision* Treatment Planning System and *Radixact*Treatment Delivery Console call attention to the importance of consistent daily setup for *TomoDirect* plans.

On the **Beam Angles** tab of the Planning System, a **Notice** lists any beams that pass through the couch before reaching the target. The dosimetry in the target for these beams will be sensitive to the path of the beam through the couch.



Tools tab Notice During *TomoDirect* Planning

On the **Register** tab of the Treatment Delivery Console, if the accepted registration results would cause a difference between planning and delivery in how the beam intersects the couch, a warning may be displayed.



Couch Position Warning During Patient Setup

1. To determine if the warning will be displayed, the upper and lower pallets of the couch are each represented by a rectangular bounding box. The beam edge is defined by the two most distal open leaves in each slice.
2. In each slice of the planning CT image and in the daily registration result, the software checks whether or not the beam edges intersect each of the four sides of the two bounding boxes. If there are any changes in this result from the planning CT image to the daily registration, the warning will be displayed.
3. A record of acceptance of this warning is included in the delivery report.



**IMPORTANT:** A change in the intersection of the beams with the couch can result in overdose or underdose. Consider the following:

- Indexing patients for simulation and treatment can help to reduce the need for couch adjustments and gantry roll corrections that may change the intersection of the beams with the couch.
- When selecting *TomoDirect* beams, avoid beam angles that pass within 2.5 cm of the edges of the couch, since the intersection of these beams with the couch will be very sensitive to daily couch shifts.
- If there are more beams entering from below the couch than above the couch, prepare an action plan in case the warning in the previous image appears on the Treatment Delivery Console.



**NOTE:** To check if daily registration results have changed the amount of beam intersection with the couch for the warning, the software must relate the X and Z couch position values displayed on the **Positioning Control Panel** to isocenter. See “Couch Alignment Tests” (page 166) for details on the parameters **Lateral Offset** and **Couch height at isocenter (mm)**.

## ◆ Potential for Hot Spots

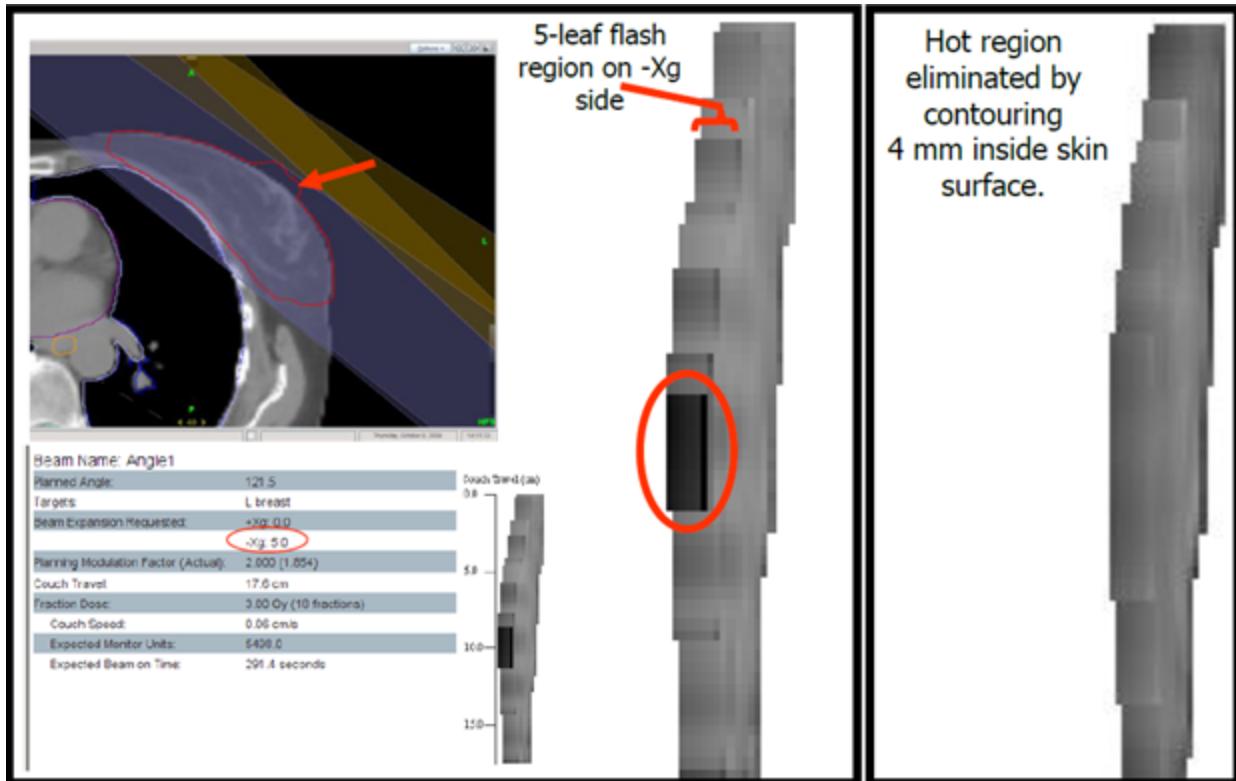
*TomoDirect* treatments may have high fluence regions near the beam edges. This section describes how appropriate contouring may reduce high fluence regions, and how to check for high fluence regions.

Beamlet selection for optimization is discussed in “Initial Beamlet Selection” (page 445). The initial beamlet selector uses a transverse beamlet projection for each individual beamlet that is 0.4 leaf widths wider than the geometrical leaf projection on both the +Xg and -Xg sides of the MLC. Beamlets are considered available for optimization if any part of the beamlet projection passes through a target, and if no part of the beamlet projection passes through a blocked structure. If only the edge of a beamlet projection intersects with the target, the optimizer would need to increase the beamlet weighting significantly to have an effect on the target voxels, since most of the beamlet contribution is from scatter. If there are heavily weighted beamlets at the edge of the target, additional leaves that the user has opened for *TomoDirect* flash (beam expansion) may also be heavily weighted.

The following image illustrates the concept. On the left side of the figure, a *TomoDirect* plan with five flash leaves on the -Xg side was created. The contour is too close to the skin surface, and there is an exaggerated contouring error with the contour extending into air (indicated by the red arrow). Where target contours extend near the patient border or into air, the optimizer can assign high fluence values to edge leaves and also to flash leaves. The circled dark region in the sinogram represents hot flash leaves due to the exaggerated contouring error. (With fewer flash leaves and/or a

less exaggerated contouring error, hot leaves may appear less obvious in the sinogram than shown here.) On the right side of the figure, the hot region was eliminated by contouring 4 mm inside the skin surface.

For both helical and *TomoDirect* plans, the planner should avoid contouring targets next to the surface of the patient. If the optimizer is trying to fill in some dose, it needs more fluence if the beamlet is being transported mostly through air. When the target contour has tissue around it, the resulting higher dose will be visible in the isodose plots and the DVH plots (if the patient has contours there). This helps make the higher fluence regions more detectable and less likely to be severe.



Contouring and Sinogram Samples



**IMPORTANT:** Check your *TomoDirect* plans for high fluence values near the beam edges:

- Contour targets a few mm inside the patient surface.
- Check the sinogram in the plan report for high-fluence leaves on the edge of the sinogram.
- Check the **Beam's Eye View** display.
- Patient QA measurements should include measurements in the target, at the edge of the beam and in any flash region beyond the target.



**WARNING:** Failure to verify the patient position may result in bodily harm to the patient. *TomoDirect* Treatment Delivery plans may have high-gradient regions. It is especially important to confirm the patient setup with an MVCT image and registration prior to delivering a *TomoDirect* procedure (also important for *TomoHelical* Treatment Delivery procedures).





## Equipment

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## System QA Accessories

Your system includes the following QA tools:

- Three (3) 18-meter ion chamber triaxial cables. These cables have BNC connectors and can be used with the A1SL or A17 chambers, and with the *Tomo-Electrometer*. (30-meter cables are available by special purchase order.)
- The TQA™ (Total Quality Assurance) Software package *TQA Essentials*. This software consists of the **Basic Dosimetry**, **Air Scans**, and **System Monitor** modules described in the *TQA Manual*.

See your purchase agreement for additional items.

# Customer Site QA Equipment

The equipment listed in this section should not be considered complete, and is meant only as a starting point for decision making. It is the responsibility of the clinic to provide the equipment required for commissioning and ongoing QA activities.

There is more than one way to perform some operations. Equipment requirements may vary with individual Medical Physicists and the specific environment. Equipment is constantly being released, changed and discontinued. If you have questions about specific equipment, please contact Accuray Customer Support, and ask to speak with a physicist.

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- ◆ Additional Equipment Requirements ..... 118

## ◆ Equipment Available through Accuray

The following paragraphs list the basic QA tools available for purchase through Accuray Incorporated, and necessary for system commissioning. This list does not show all the product options, and it does not take into account equipment that may already exist at your site.

### Standard IMRT QA Package

#### Cylindrical Water-Equivalent Tomo-Phantom

- **Make & Model:** Med-cal *Virtual Water* or Sun Nuclear *Solid Water*

TIP: Med-Cal Virtual Water is red and Sun Nuclear Solid Water is blue.



- **Description:** 300 mm diameter; 180 mm long. Contains cavities for ion chambers and density plugs. Splits in half to receive a film.
- **Use:** Density Model; IMRT dose calibration; image quality; MVCT number calibration; laser alignment; patient QA; rotational output.
- **Equipment Compatibility:** *Tomo-phantom* is required for use with dose calibration plans and the CT Number Calibration procedure provided by Accuray Incorporated. Cavities fit A1SL ion chambers and Gammex density plugs.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	X	X	X	X	X

## Density Plug Set

- **Make & Model:** Selected density plugs from Gammex 467 Tissue Characterization Phantom set. Phantom not included.
- **Description:** LN-300, LN-450, Inner Bone, CB2-30% Mineral, CB2-50% Mineral, SB3 Cortical Bone, two *True Water* plugs, and two resolution plugs. Density plugs labeled with mass density.
- **Use:** Density model; image quality.
- **Equipment Compatibility:** Gammex plugs fit *Tomo*-phantom.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	X	N/A	N/A	N/A

## Rectangular Water-Equivalent Stack

- **Make & Model:** Med-Cal *Virtual Water* or Sun Nuclear *Solid Water*



**NOTE:** Throughout the document where procedures require Virtual Water, Sun Nuclear Solid Water may be substituted. When substituting with Sun Nuclear Solid Water, small differences in density HU and depth dose values must be taken into account.

- **Description:** Each block (set of ten blocks) is 55 cm x 15 cm x (0.5 to 5 cm). Some blocks have holes for an ion chamber. See “Virtual Water and Step Wedge” (page 116).
- **Use:** Static output and PDD consistency; monthly longitudinal profiles, build-up for film tests.
- **Equipment Compatibility:** *Virtual Water* stack holes fit A1SL chambers.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	X	X	X	X	N/A

## Ion Chambers

A calibration certificate is included, which reports the absorbed dose to water calibration coefficient  $N_{D,w}^{60Co}$  (Gy/C), as per the TG 51 protocol of the AAPM, and corrected to 22°C and 101.325 kPa, along with the calibration uncertainty.

- **Make & Model:** Two Standard Imaging Exradin A1SL ("Calibrated Mini-Ion Chamber")

- **Description:** 0.053 cc collecting volume. Waterproof. Initial calibration traceable to NIST standards and accredited to the ISO/IEC 17025:2005 standard.
- **Use:** Static output and PDD consistency; beam profiles; completion procedure check; MVCT dose; TG-51 calibration; patient QA.
- **Equipment Compatibility:** An A1SL chamber was used to collect data for the beam model installed on your system. A1SL chambers fit in *Tomo*-phantom and *Virtual Water* stack (can be helpful to purchase more than two).
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	X	X	X	X	X

### Large Volume Ion Chamber

A calibration certificate is included, which reports the Air Kerma Calibration Coefficient  $N_K$  (Gy/C) and Exposure Calibration Coefficient  $N_X$  (R/C), as per the TG 21 protocol of the AAPM, and corrected to 22°C and 101.325 kPa, along with the calibration uncertainty.

- **Make & Model:** Standard Imaging Exradin A17 in build-up cap ("Calibrated CT Slice Ion Chamber and Buildup Cap")
- **Description:** 1.91 cc collecting volume. Uniform response within  $\pm 1.5\%$  over 8 cm length. Initial calibration traceable to NIST standards and accredited to the ISO/IEC 17025:2005 standard.
- **Use:** Y-jaw alignment; *TQA Jaw Sweep- Dynamic Jaws* module; reference chamber during water tank data collection.
- **Equipment Compatibility:** N/A
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	X	N/A	X	N/A

### Beam Measurement and QA Package

#### Water Tank

- **Make & Model:** Standard Imaging Water Tank with detachable scan arm, scan arm controller box and associated cables. See "Types of Water Tanks" (page 485) for more information on water tanks.

- **Description:** 2D tank. Fits inside system bore. Accommodates water depth > 250 mm. Tank width appropriate for the system beam (max field size 50 mm x 400 mm at isocenter).
- **Use:** Transverse profiles, longitudinal profiles, PDDs.
- **Equipment Compatibility:** The Standard Imaging water tank was used to collect data for the beam model installed on your system. Accuray Incorporated provides procedure files and step-by-step instructions specific to this tank.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	N/A	N/A	X	N/A

### Electrometer

A calibration certificate is included, which reports the calibration coefficients for each electrometer channel (Ampere/reading and Coulomb/reading), along with the calibration uncertainty.

- **Make & Model:** Standard Imaging *Tomo*-Electrometer
- **Description:** 8 channels. Rate mode and integrate mode. Display range is set automatically according to the amount of charge present. Channels 1-7 have a rate range of 0.001 pA to 4.9 nA. Channel 8 has a rate range of 0.01 pA to 19.6 nA. Channels 5-8 are fast response channels. Initial calibration traceable to NIST standards and accredited to the ISO/IEC 17025:2005 standard.
- **Use:** See "Ion chambers" and "Large volume ion chamber" above.
- **Equipment Compatibility:** Works with TEMS.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	X	X	X	X	X

### PC with Software Installed to Run Water Tank

- **Make & Model:** Windows PC with *Tomo*-Electrometer Measurement System (TEMS) software
- **Description:** Interfaces with Standard Imaging water tank and *Tomo*-Electrometer to plot scanning data. Can determine profile FWHM. Data files can be saved in .csv format.
- **Use:** Water tank data collection; also plots data as a function of time while the couch travels across the beam, or the jaws move for *TQA Field Width* or *Jaw Sweep- Dynamic Jaws* modules.

- **Equipment Compatibility:** Works with *Standard Imaging* Water Tank and *Tomo-Electrometer*.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	X	N/A	X	N/A

## RITg148+ Film Digitizer Kit

### Scanner

- **Make & Model:** Vidar DosimetryPRO Red Scanner
- **Description:** Medical quality scanner appropriate for digitizing EDR2 film and/or EBT film.
- **Use:** Completion procedure check; synchronization films; alignment films; patient QA.
- **Equipment Compatibility:** If using film for patient QA, consider the need for patient QA film analysis software. RITg148+ does not analyze patient QA films, but RIT Complete does analyze patient QA films. If analyzing patient QA films outside of RIT, you will need software to drive the Vidar and save the film as a .tif file.

RITg148+ V6.6 or RIT Complete V6.6 can drive the Vidar and save film files in .tif format. Versions of RITg148+ or RIT Complete older than V6.6 can drive the Vidar to scan a film, but can only save films in a proprietary format that cannot be read outside of RIT.

If your RIT software is older than V6.6 and you want to analyze your patient QA film outside of RIT, you will need to upgrade to RIT V6.6 or provide other software to drive the Vidar to save a .tif file of your patient QA film. See “Film Analysis” (page 511).

- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	X	X	X	X

## Film Analysis Software

- **Make & Model:** RITg148+
- **Description:** Includes analysis modules for all TG 148 film alignment tests.
- **Use:** Completion procedure check; alignment films; synchronization films.

- **Equipment Compatibility:** See “Overview of RIT Analysis Software” (page 515).
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	N/A	X	X	X	N/A

## *Advanced TQA Package*

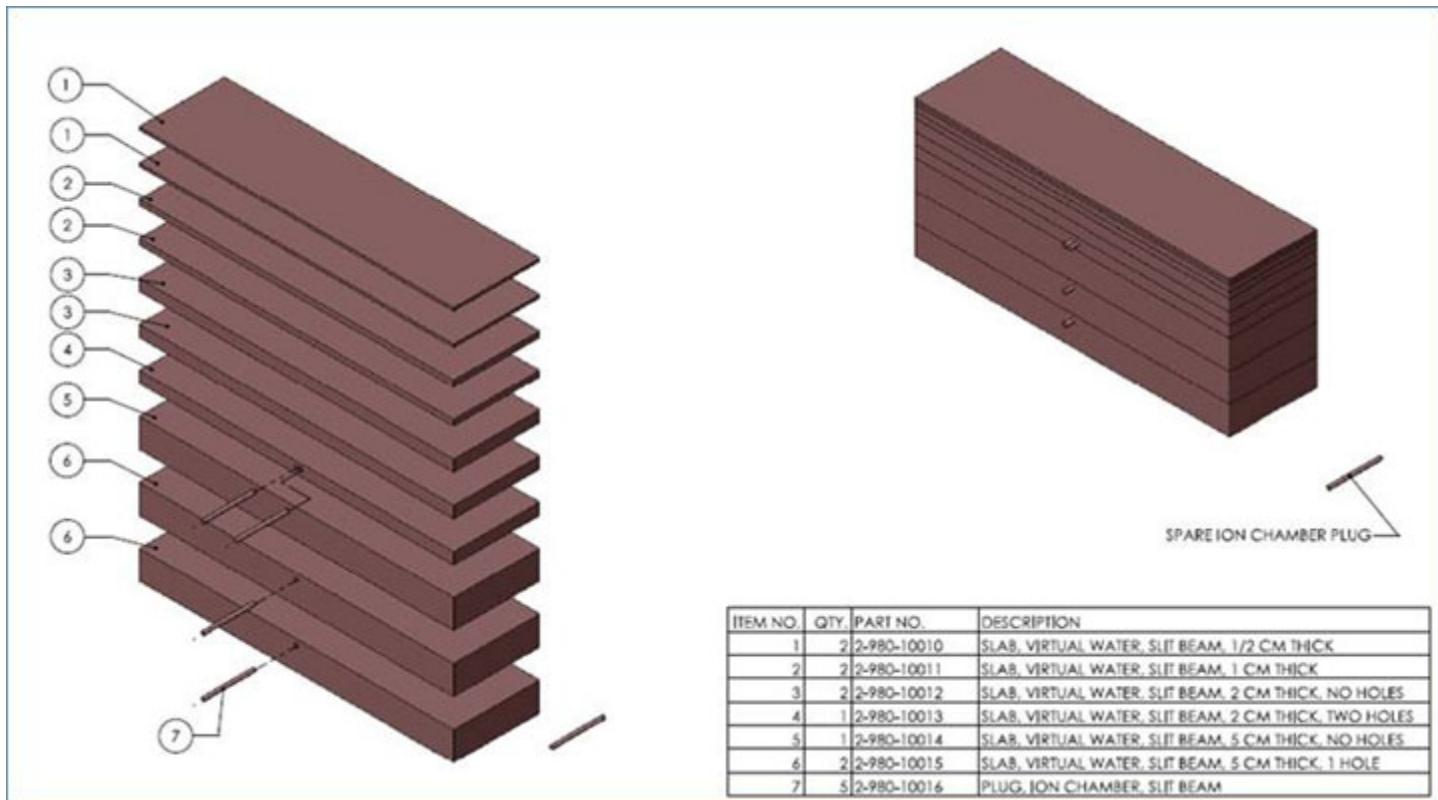
### Software Licenses and Step Wedge

- **Make & Model:** Accuray Incorporated software. See “Virtual Water and Step Wedge” (page 116) for the step wedge.
- **Description:** Includes all *TQA* modules. Provides automated analysis and reporting of machine data through the on-board MVCT detector and monitor chambers, and analysis of some ion chamber data.
- **Use:** Constancy checks of an extensive range of system parameters; see *TQA Manual* for details.
- **Equipment Compatibility:** Some modules require equipment from the Standard System QA package, *Tomo-Electrometer*, and TEMS.
- **Frequency of Use:**

Commissioning	Daily / Weekly	Monthly	Quarterly	Annually	Patient QA
X	X	X	X	X	N/A

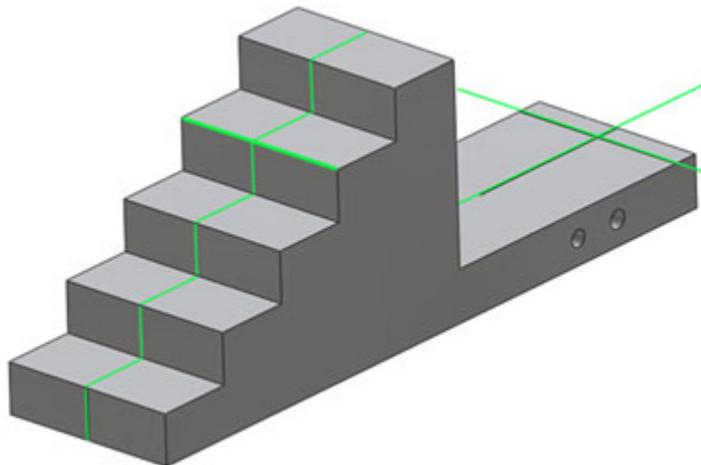
## **Virtual Water and Step Wedge**

In the following water stack image, circled numbers correspond to item numbers in the table. The quantity of each block is listed in the "QTY" column of the table



**Virtual Water Stack**

The step wedge comes with the *TQA* Advanced Package. The step wedge is 270 mm long, 97.5 mm high, and 69.7 mm wide. Each step is 19.5 mm high.



**Aluminum *TQA* Step Wedge**

## ◆ Additional Equipment Requirements

The following are not available from Accuray Incorporated but will be needed for QA:

- Computer with *Microsoft Excel*.



**IMPORTANT:** The reference data spreadsheets provided by Accuray Customer Support are written in *Excel*. Because of the embedded calculations, it is not recommended to use other software to open these spreadsheets.

- Digital level, approximately 530 mm long. This will be used for monthly verification of treatment couch leveling, and annual verification of room lasers.
- Barometer.



**IMPORTANT:** Do not use pressure that has been corrected to sea level.

- Hand-held thermometer.
- Film. See “Appendix B” (page 511) for film specifications.
- Patient QA tools.

If you will perform patient QA with ion chambers and film in the *Tomo-phantom*, you will need third party software to drive your film scanner to digitize the film, and to compare the calculated dose distribution (exported from the software) with the measured film dose distribution. Note that RITg148+ software does not perform this function.

Some sites choose to purchase an array device for patient QA. The *Accuray Precision™ Treatment Planning System* software can calculate the dose distribution on any phantom for which a CT image is available. Choose a device that has isotropic response to radiation. Accuray Incorporated acknowledges the benefit of third-party array devices, but does not provide training or support for third-party devices.



**TIP:** Before purchasing an array device, talk with other users about their experience with the device and with the transfer of data from the software.



**NOTE:** Array devices typically do not have the sub-millimeter resolution required for alignment QA and profile measurements.



## Alignment Tests

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# Introduction to Alignment Tests

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## ◆ Summary of Alignment Tests

This chapter introduces the beam alignment tests of the treatment system. These tests, shown in the table below, are also described in TG-148 Section V.B.1.

Alignment Tests	Test Purpose
MLC Tongue & Groove	LINAC aligned in IEC X with MLC
Jaw Shift	LINAC aligned in IEC Y with jaws
Beam Planarity	Beam pointed in plane of gantry rotation
Stationary Laser Alignment	Green lasers aligned with beam line and gravity
Moveable Laser Alignment	Red lasers aligned with green lasers in “home” position
Couch Alignment	Couch motion is aligned with green lasers and consistent with digital display, and level and sag are within tolerances
MLC Center of Rotation (COR)	MLC leaves evenly divided about center of gantry rotation
Field Center vs. Jaw Setting	Centers for different field sizes are consistent in IEC Y



**IMPORTANT:** Before performing QA tasks, warm up the system and run an air scan as described in “System Startup” (page 76) to help achieve a stable beam and optimal image quality.

## ◆ XML Files for Film Alignment Tests

The following .xml files are available from Accuray Customer Support for the film alignment tests:

- GAF TG148 Film Alignment Tests-MultiFragment.xml
- TG148 Film Alignment Tests-MultiFragment.xml

For several of the tests, the GAF (EBT) versions of the procedures use longer beam-on times, since EBT film is less sensitive than EDR.

The "multi-fragment" .xml files take advantage of a feature that allows for combining gantry fields at different angles or jaw positions into a single QA-MACH procedure.

The following procedures are included within each .xml:

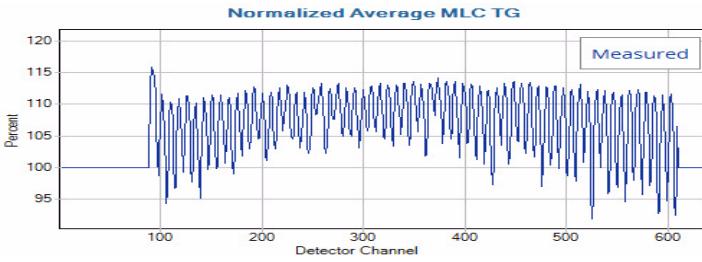
- Beam planarity
- Overhead laser
- MLC center of rotation
- Field center v jaw setting
- Couch translation
- Static star shot
- Helical star shot

In addition to the film alignment QA .xml that includes several of the tests in one .xml, Accuray Incorporated provides individual .xml files for several of the non-film tests; see the individual test instructions on the following pages.

# MLC Tongue and Groove (MLC TG)

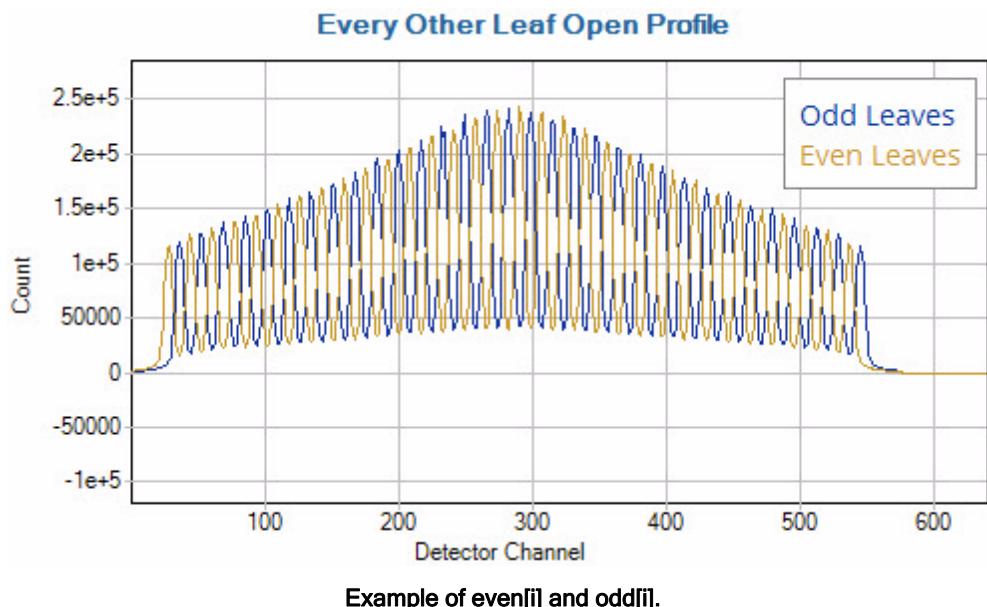
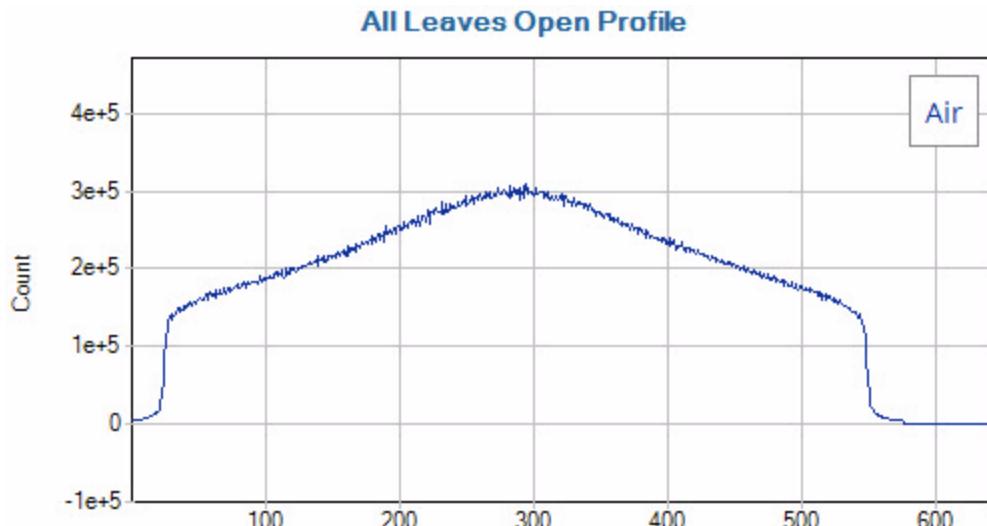
- ◆ Overview of MLC Tongue and Groove Test (MLC TG) ..... 122
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## ◆ Overview of MLC Tongue and Groove Test (MLC TG)

<b>TG-148 Reference:</b>	<i>x-alignment of source</i> (V.B.1.b)
<b>Other names for this test:</b>	LINAC transverse alignment
<b>Purpose:</b>	Verify that the radiation source is laterally centered over the MLC.
<b>Method:</b>	Calculate the TG profile from on-board CT detector data for three different MLC configurations. The symmetry of the TG profile is empirically correlated with the lateral position of the source.
<b>Accuracy specification:</b>	MLC TG Percent Out of Focus $\leq 2.0\%$ (indicates that the radiation source is laterally centered over the MLC within $\pm 0.34$ mm.)
<b>Sample result image:</b>	 <p>The graph is titled "Normalized Average MLC TG". The vertical axis is labeled "Percent" and ranges from 95 to 120. The horizontal axis is labeled "Detector Channel" and ranges from 100 to 600. A blue line represents the measured data, showing a high-frequency noise pattern centered around the 100% mark.</p>
<b>Equipment needed:</b>	TQA software

## ◆ Theory of MLC Tongue and Groove Test (MLC TG)

The LINAC alignment with the MLC is most readily tested using the on-board CT detector array. Detector data is measured for three different MLC configurations, and plotted as a function of detector channel  $i$ . The three MLC configurations include: all leaves open ( $\text{air}[i]$ ), even-numbered leaves open, and odd-numbered leaves open ( $\text{even}[i]$  and  $\text{odd}[i]$ ).



The Tongue and Groove profile is determined as:

$$\text{TG}[i] = (\text{odd}[i] + \text{even}[i])/\text{air}[i]$$

The image below shows an example of the Tongue and Groove profile. If the source is properly centered over the MLC, the Tongue and Groove profile will have a symmetrical shape. The symmetry of the Tongue and Groove profile is represented by a parameter called the *Percent Out of Focus*. The derivation of the *Percent Out of Focus* is provided in the appendix to the *TQA Manual*.

The *Percent Out of Focus* has been empirically related to the lateral source position as:

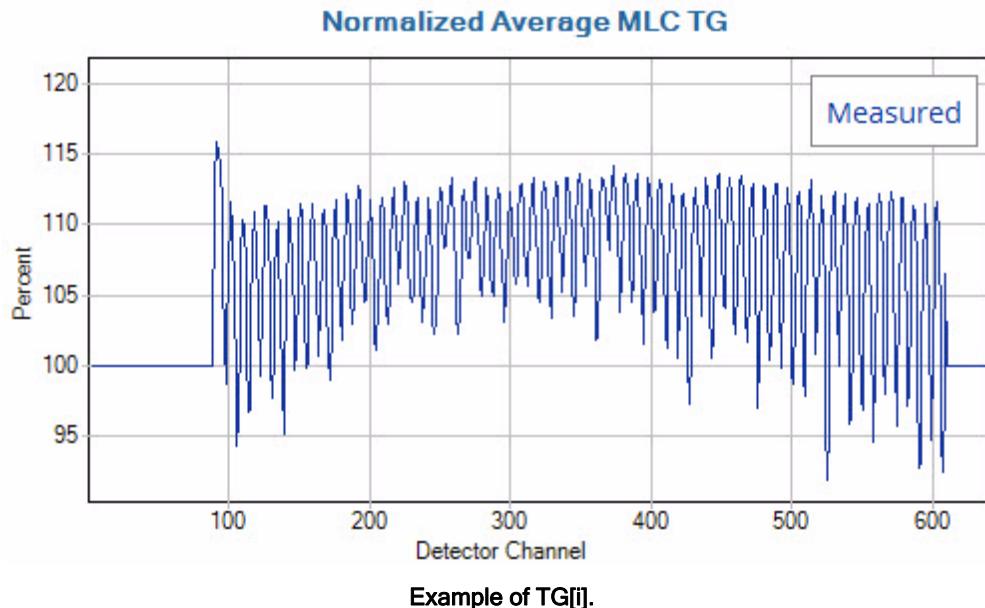
Source offset in mm  $\approx 0.17 \times$  Percent Out of Focus.

Thus, if the magnitude of the *Percent Out of Focus* is 2% or less, the source lateral position is centered over the MLC within  $\pm 0.34$  mm.

The measurements can be performed with a static or rotating gantry.

Performing the procedure with a rotating gantry provides additional verification of the stability of the relative positions of the source and MLC with gantry rotation.

If an adjustment is needed, the Accuray service representative will use the LINAC fine adjustment plate to move the source with respect to the MLC. (The MLC is bolted to the gantry, and its position is not adjustable.)



## ◆ XML Description

### MLC Tongue and Groove (MLC TG): Static Version

Where to get the .xml:

This .xml can be downloaded from the **LINAC Transverse Alignment** module of the *TQA* software.

### MLC Tongue and Groove (MLC TG): Static Version

Patient Name	zzzzz TQA LINAC Transverse Alignment (MLC TG)
Procedure Description	STATIC_0deg_35s_J7mm_0cm translation
Couch movement in IEC Y when Ready is pressed	None
Couch translation during the procedure	None
Gantry	Fixed at 0°
Jaws	J07 (nominal 1-cm field size)
MLC	<ul style="list-style-type: none"> <li>First 25 s: all leaves open</li> <li>Next 5 s: odd numbered leaves open</li> <li>Next 5 s: even numbered leaves open</li> </ul>
Beam-on time	35 s

### MLC Tongue and Groove (MLC TG): Rotating Version

Where to get the .xml:	This .xml can be downloaded from the <b>LINAC Transverse Alignment</b> module of the <b>TQA</b> software.
Patient Name	zzzzz TQA LINAC Transverse Alignment (MLC TG)
Procedure Description	ROTATIONAL 10 20-sec rots MLC TG J7mm
Couch movement in IEC Y when Ready is pressed	None
Couch translation during the procedure	None
Gantry	10 rotations at 20 s/rotation
Jaws	J07 (nominal 1-cm field size)
MLC	<ul style="list-style-type: none"> <li>First 4 rotations: all leaves open</li> <li>Next 3 rotations: odd numbered leaves open</li> <li>Next 3 rotations: even numbered leaves open</li> </ul>
Beam-on time	200 s

## ◆ Set Up and Deliver the Test

Follow the instructions in the *TQA Manual* to run the **LINAC Transverse Alignment** test.



**NOTE:** The **LINAC Transverse Alignment** module should be run with no couch or object in the bore. *TQA* automatically analyzes the detector data and generates a report.

## ◆ Analyze the Result

Look at the report in *TQA* and verify that the **IECx LINAC Shift** is within  $\pm 0.34$  mm. If using the procedure with a rotating gantry, also verify that the TG Percent Variation range displayed on the **Misc** tab does not include values greater than 2.0.

## ◆ What to Do if the Test Fails

Contact Accuray Customer Support to adjust the LINAC position and repeat the test.

# Jaw Shift

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- ◆ Theory of Jaw Shift ..... 128
- ◆ Alternate Methods for Performing this Test ..... 130
- ◆ XML Description ..... 131
- ◆ Set Up and Deliver the Test ..... 132
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## ◆ Overview of Jaw Shift Test

<b>TG-148 reference:</b>	<i>y-jaw centering</i> (section V.B.1.a)
<b>Other names for this test:</b>	LINAC longitudinal alignment
<b>Purpose:</b>	Verify that the radiation source is longitudinally centered over the jaws.
<b>Method:</b>	Irradiate a long chamber (with a constant signal response over its length) with multiple asymmetric jaw settings. Use a curve fit to determine the jaw settings that produce the maximum signal, and use geometry to determine the source offset.
<b>Accuracy specification:</b>	For systems with dynamic jaws, the source should be centered over the jaws in IEC Y within $\pm 0.2$ mm. For systems without dynamic jaws, the source should be centered over the jaws in IEC Y within $\pm 0.3$ mm.
<b>Sample result image:</b>	<p>Data (normalized)</p> <p>%max</p> <p>mm</p> <p>Site</p> <p>Bunker</p>

**Equipment needed:**

- A17 ion chamber
- *Tomo-Electrometer*
- *Microsoft Excel* or TQA software
- TEMS software (optional for use with TQA and dynamic jaws)

## ◆ Theory of Jaw Shift

To ensure optimal output and penumbral symmetry, the radiation source must be centered over the jaws in the longitudinal direction.

This test is performed by irradiating a long ion chamber (with a relatively constant signal response over its length) with multiple asymmetric jaw settings, using a narrow jaw opening. If the source is properly centered over the jaws, the highest signal will be measured when the jaws are centered over isocenter.

The figure below demonstrates the concept, and the results sample shows the response of an A17 ion chamber obtained by irradiating through the jaws (set to a width of J02 in jaw numbers), centered at -24, -20, -15, -10, -5, 0, 5, 10, 15, 20, and 24 mm. These positions are in jaw numbers, which are considered sufficiently similar to actual jaw positions projected to isocenter for the purpose of this test (see “Jaw Numbers” (page 15) for a discussion of jaw numbers).

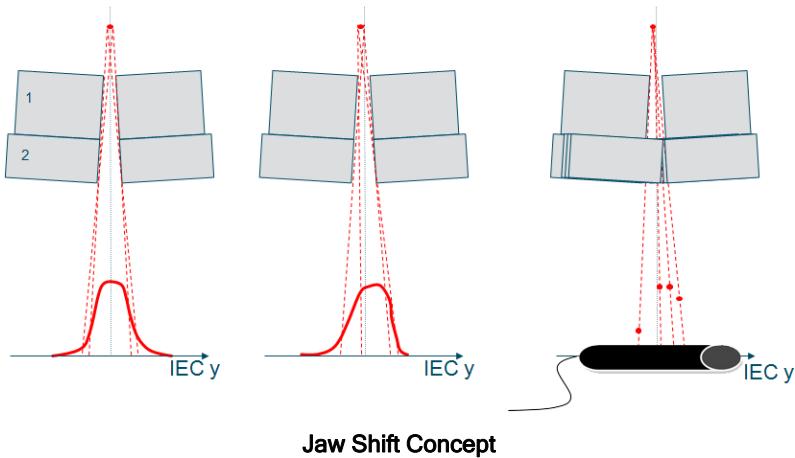
The location of the maximum of the jaw shift profile in the results sample can be determined by fitting a quadratic to the curve ( $f(y) = ay^2 + by + c$ ), setting the derivative to zero ( $\frac{df}{dy} = 2ay + b = 0$ ), and solving for  $y$ , giving

$$y_{\text{isocenter}} = -\frac{b}{2a}.$$

$y_{\text{isocenter}}$  is an estimate of the jaw position projected to isocenter that gives the maximum signal at the ion chamber. The actual shift in the source position is much smaller than  $y_{\text{isocenter}}$ . The jaws move on a circular arc that is focused 43.5 mm above the source. Historically, this distance was approximated as 5 cm. Utilizing this distance with the source-to-isocenter distance of 85cm, the source offset is approximated using similar triangles:

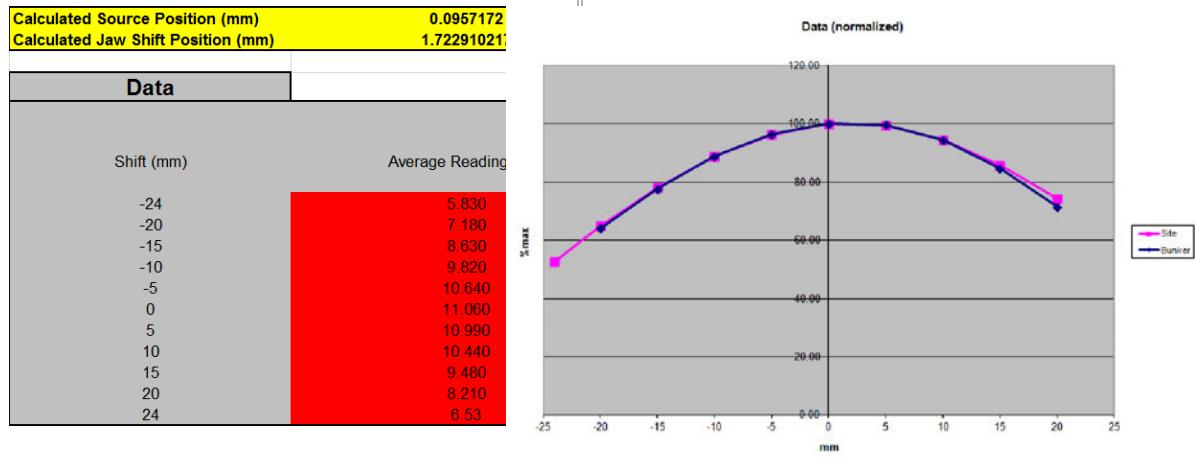
$$\text{Source Offset(IEC } Y, \text{mm}) = y_{\text{isocenter}} \times \left( \frac{5}{5+85} \right) = \frac{y_{\text{isocenter}}}{18}$$

This equation is approximate, as the actual jaw focus distance is 43.5 mm, and the value of  $y_{\text{isocenter}}$  is reported in jaw numbers, not millimeters. The tolerance for the source offset, as calculated by this approximate equation, has been tested to verify that it results in beam profiles that are an acceptable match to the model data.



The following list describes the Jaw Shift Concept figure. A side view of the gantry illustrates the Jaw Shift test. The source is illustrated by the red dot at the top of each diagram. The top square (1) indicates the primary collimator, and the bottom square (2) indicates the jaws.

- At Left: The source is centered in the Y direction over the jaws. If you measured the longitudinal profile at isocenter, it would have a symmetrical shape.
- At Center: The source is not properly centered over the jaws. If you measured the longitudinal profile at isocenter, it would have an asymmetrical shape.
- At Right: A series of procedures is run with narrow jaw slit openings centered on different IEC Y locations. Charge is measured with an A17 ion chamber.



**Sample data for the jaw shift test.** The physicist runs a series of procedures with known jaw positions ("shift" values). Ion chamber measurements are recorded in the red box. These measurements are plotted as a function of jaw position. The spreadsheet fits the data to a curve, and reports the "calculated jaw position" and "calculated source position" in the yellow box.

## ◆ Alternate Methods for Performing this Test

The jaw shift test can be performed with or without TQA:

- Without *TQA*: Manually enter the charge readings for a series of procedures with different jaw positions into a *Microsoft Excel* spreadsheet provided by Accuray Incorporated. The spreadsheet reports the **calculated source position**.
- Two modules within *TQA* can be used to determine the jaw shift result:

Module	Description
Jaw Sweep - Dynamic Jaws	This module collects all data in a single procedure. It requires dynamic jaws and access to TEMS software for plotting data from the <i>Tomo-Electrometer</i> . Upload the .csv file to <i>TQA</i> to determine the <b>IECy Source Position</b> .
LINAC Longitudinal Alignment	Manually enter the charge readings for a series of procedures with different jaw positions into the provided .csv file. Upload the .csv file to <i>TQA</i> to determine the <b>IECy LINAC Shift</b> .



**NOTE:** The calculated source position, IECy LINAC Shift, and IECy Source Position are three different names for the same parameter. They should be within  $\pm 0.3$  mm for a system that does not have dynamic jaws, or  $\pm 0.2$  mm for a system that has dynamic jaws.

## ◆ XML Description

### Jaw Shift: Manual Data Entry Version

<b>Where to get the .xml:</b>	The Jaw Shift .xml file may be requested from Accuray Customer Support. <b>Jaw Shift.xml</b> can be used interchangeably with <b>zzzzz_TQA_Jaw_Shift.xml</b> . You can download the <b>zzzzz_TQA_Jaw_Shift.xml</b> from the <b>LINAC Longitudinal Alignment</b> module of the <b>TQA</b> software.
<b>Patient Name:</b>	ZZZ Jaw Shift, or <b>zzzzz TQA LINAC Longitudinal Alignment (Jaw Shift)</b>
<b>Procedure Descriptions:</b>	<ul style="list-style-type: none"><li>• Static_0deg_30s_0mm shift_0cm translation</li><li>• Static_0deg_30s_+5mm IECY shift_0cm translation</li><li>• Static_0deg_30s_+10mm IECY shift_0cm translation</li><li>• Static_0deg_30s_+15mm IECY shift_0cm translation</li><li>• Static_0deg_30s_+20mm IECY shift_0cm translation</li><li>• Static_0deg_30s_+24mm IECY shift_0cm translation</li><li>• Static_0deg_30s_-5mm IECY shift_0cm translation</li><li>• Static_0deg_30s_-10mm IECY shift_0cm translation</li><li>• Static_0deg_30s_-15mm IECY shift_0cm translation</li><li>• Static_0deg_30s_-20mm IECY shift_0cm translation</li><li>• Static_0deg_30s_-24mm IECY shift_0cm translation</li></ul>
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static 0°
<b>Jaws:</b>	Narrow opening of J02 in jaw numbers, centered on the shift position in jaw numbers listed in the procedure description
<b>MLC:</b>	All leaves open
<b>Beam-on time:</b>	30 seconds at each jaw position

Jaw Shift: TQA Dynamic Jaws	
Where to get the .xml:	This .xml file can be downloaded from the <b>Jaw Sweep - Dynamic Jaws</b> module of the <i>TQA</i> software.
Patient Name:	zzzzz TQA Jaw Sweep Dynamic Jaws
Procedure Description:	Jaw QA
Couch movement in IEC Y when Ready is pressed:	700 mm
Couch translation during the procedure:	None
Gantry:	Static 0°
Jaws:	Jaws move dynamically to perform several different tests. See the <i>TQA Manual</i> for details. During the part of the procedure used to determine the IECy source position, jaws are open to a narrow J02 width in jaw numbers, centered on a series of positions: [24, 20, 15, 10, 5, 0, -5, -10, -15, -20, -24] mm in jaw numbers.
MLC:	All leaves open
Beam-on time:	600 s

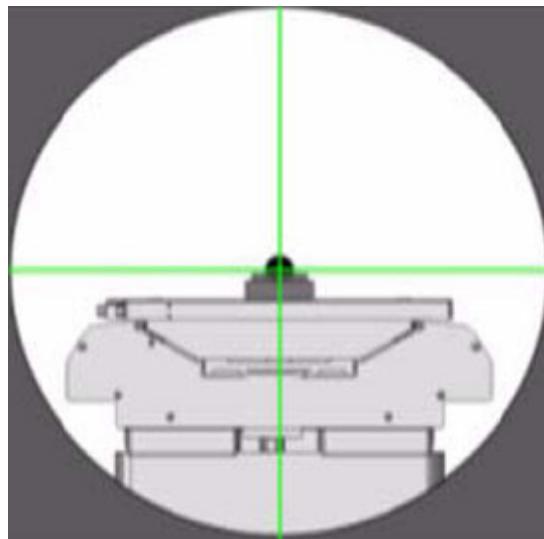
## ◆ Set Up and Deliver the Test

Instructions for running the jaw shift test in *TQA* (using the LINAC **Longitudinal Alignment** module or **Jaw Sweep - Dynamic Jaws** module) can be found in the *TQA Manual*. This section provides instructions for running the jaw shift test without *TQA*.

### Set Up the Jaw Shift Test

1. Set up an electrometer outside of the treatment room. See “Set up the Tomo-Electrometer” (page 88).
2. Place the A17 chamber in its buildup cap, along with the foam base from the box, on the couch. The long axis of the chamber should be parallel to the Y axis, and the chamber cable should face away from the gantry. If the ion chamber is not fully inserted into the buildup cap, it may cause a setup misalignment.
3. Connect the ion chamber to the electrometer using the triaxial cable. Tape the cable to the couch tabletop.

4. Adjust the couch height so that the chamber is centered on the green bore laser. Adjust the X and Y position of the chamber so that it is centered on the green overhead laser at virtual isocenter.
5. Bring the couch 700 mm into the bore, and correct for couch sag. See the following image for reference. When finished with setup, leave the chamber inside the bore.



View from behind the gantry of the A17 chamber in its foam base, centered on the green bore lasers.

### Deliver the Jaw Shift Test

1. Load the .xml file (**Jaw Shift.xml** or **zzzzz\_TQA\_Jaw\_Shift**) on the Treatment Delivery Console.
2. Open the patient via the Machine QA task on the Treatment Delivery Console.
3. Navigate to the **Run** tab.
4. Select the procedure with a jaw shift of 0 mm.
5. Set the electrometer to begin collecting charge.
6. Deliver the procedure. The couch will not move when **Ready** is pressed.
7. Record the charge in the *Excel*/spreadsheet as described in the next section.
8. Repeat Steps 3-7 for jaw shift positions of  $\pm 5$  mm,  $\pm 10$  mm,  $\pm 15$  mm,  $\pm 20$  mm, and  $\pm 24$  mm.

## ◆ Analyze the Result

If you are using the **TQA LINAC Longitudinal Alignment** module, follow the instructions in the *TQA Manual* to upload your **.csv** file, then check the **IECy LINAC Shift** in the *TQA* report.

If you are using the **TQA Jaw Sweep - Dynamic Jaws** module, follow the instructions in the *TQA Manual* to upload your **.csv** file, then check the **IECy Source Position** in the *TQA* report.

If you are not using *TQA* for this test:

1. Obtain a copy of the *Microsoft Excel*/jaw shift spreadsheet. This spreadsheet may be found with the data provided by Accuray Incorporated at the time of ATP, or you may request a copy from Accuray Customer Support.
2. Open the **Site** worksheet and clear out any existing data. Enter the **Gantry Serial Number**, **Date** and **Physicist Name**.
3. For each jaw shift position, enter the absolute value of the electrometer charge (nC) as shown in Label 1 of the following figure.



**NOTE:** Since the test involves a relative comparison of readings, temperature/pressure corrections and calibration factors are not needed if all data was acquired in the same session.



**TIP:** Normalizing to the displayed Monitor Units is unlikely to be necessary for a system with dose control system. If desired, you may optionally record the displayed Monitor Units (MU's) for each run in an adjacent column, in case you find it necessary to factor out run-to-run output fluctuation.

4. The spreadsheet calculates the **jaw shift position** of maximum reading. These positions are along the axis of gantry rotation; there is a magnification factor of 18 compared to the source position. See Label 2 in the following figure.

The spreadsheet calculates the **source position** by dividing by 18; see Label 3 in the following figure. Verify that the **Calculated Source Position** is within  $\pm 0.3$  mm for a system without dynamic jaws, or  $\pm 0.2$  mm for a system with dynamic jaws.

5. In the spreadsheet, check the plots to ensure that the shape of the curve looks reasonably smooth.



**TIP:** All the available jaw shift positions should be measured, so that you can verify that the curve is smooth.

C		D	
JAW/SOURCE ALIGNMENT - SITE DATA			
Site:	T 3 Customer Training Bunker		
Date:	6/8/2011		
Physicists:	SM, RC		
Notes:			
Temperature	23.6		
Pressure	727.71		
SAD	85		
Build up (cm)	1.0		
Phantom	cylindrical black plastic cap		
3	Source-to-isocenter distance Point-to-isocenter distance Collimator width (mm) Ion Chamber Used Electrometer Used Time for rad (sec)	850 900 2 A17 Tomo 20	
	Calculated Source Position (mm)	-0.0898792	
	Calculated Jaw Shift Position (mm)	-1.617824773	
Data			
2	Shift (mm)	Average Reading (nC)	
	-24	6.890	
	-20	8.340	
	-15	9.710	
	-10	10.750	
	-5	11.300	
	0	11.400	
	5	10.990	
	10	10.140	
	15	8.860	
	20	7.320	
	24	5.9	

Sample of Jaw Shift Excel/Spreadsheet provided by Accuray Incorporated

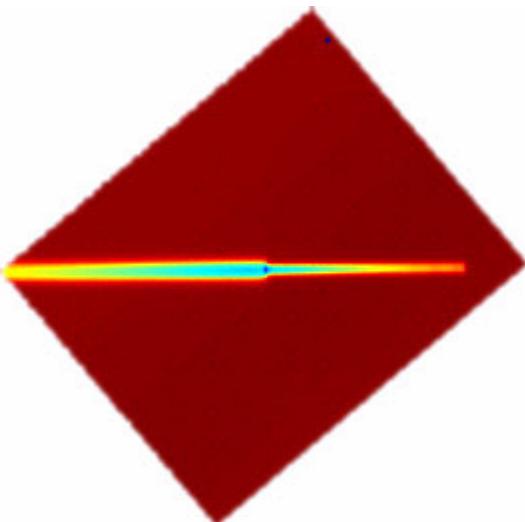
## ◆ What to Do if the Test Fails

Contact Accuray Customer Support to adjust the LINAC, then repeat the test.

# Beam Planarity

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- ◆ Theory of Beam Planarity Test ..... 137
- ◆ XML Description ..... 138
- ◆ Set Up and Deliver the Test ..... 138
- ◆ Analyze the Result ..... 139
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## ◆ Overview of Beam Planarity

<b>TG-148 reference:</b>	y-jaw divergence/beam centering (section V.B.1.c) and y-jaw/gantry rotation plane alignment (section V.B.1.d)
<b>Other names for this test:</b>	Central axis/y-divergence (CAX-Y)
<b>Purpose:</b>	Verify that the beam is parallel to and in the plane of gantry rotation.
<b>Method:</b>	Expose a film to a slit beam from gantry angles of $0^\circ$ and $180^\circ$ . Verify that exposures are mutually parallel and centered.
<b>Accuracy specification:</b>	Jaw offset within $\pm 0.5$ mm, and $ \text{jaw twist angle}  < 0.5^\circ$
<b>Sample result image:</b>	

**Equipment needed:**

- Two (2) 2-cm blocks of *Virtual Water* (55 cm x 15 cm x 2 cm)
- 1 EDR or EBT film (recommended minimum size 20 cm x 25 cm)
- Pin for marking EDR film, or medium-point permanent marker for EBT film
- Analysis software (RITg148+), film scanner, computer

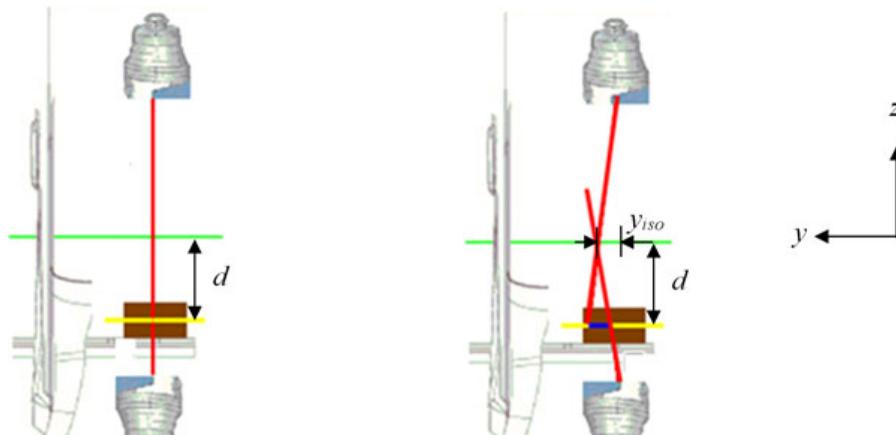
## ◆ Theory of Beam Planarity Test

A film that is vertically offset from isocenter is exposed to a slit beam from gantry angles of  $0^\circ$  and  $180^\circ$ , with leaves 1-32 open. The two exposures are mutually parallel and centered, if the beam is pointed in the plane of gantry rotation. The offset of the beam at isocenter,  $y_{iso}$ , is also known as the jaw offset and is determined as:

$$y_{iso} = \frac{85}{2d} y_{film}$$

where  $y_{film}$  is the distance between exposures on the film, and  $d$  is the distance of the film below isocenter. The vertical offset of the film from isocenter enables the jaw offset to be detected. If the film were located at isocenter, the exposures would share the same center even if the beam diverged from the plane of gantry rotation. The jaw twist is determined as half the angle between the exposures.

The following image represents the theory of the beam planarity test. A side view of the gantry is shown. The film is sandwiched between two blocks of *Virtual Water*, at a distance  $d$  below isocenter. At left, the beam is properly aligned with the plane of gantry rotation. At right, the beam diverges from the plane of gantry rotation, and the blue region on the film represents  $y_{film}$ .



Beam Planarity Theory

## ◆ XML Description

Beam Planarity Test	
<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" .xml package. See "XML Files for Film Alignment Tests" (page 120).
<b>Machine QA Name:</b>	<b>ZZZ TG148 Film Alignment Tests-MultiFragment</b> <b>ZZZ GAF TG148 Film Alignment Tests-MultiFragment</b>
<b>Procedure Description:</b>	<i>Beam Planarity</i>
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static 0° and static 180°
<b>Jaws:</b>	J07 (Nominal 1-cm field size)
<b>MLC:</b>	Leaves 1-32 are open
<b>Beam-on time:</b>	<ul style="list-style-type: none"><li>At gantry angle 0°, the beam is on for 45 s for EDR film, or 70 s for EBT film.</li><li>At gantry angle 180°, the beam is on for 15 s for EDR film, or 40 s for EBT film.</li></ul>

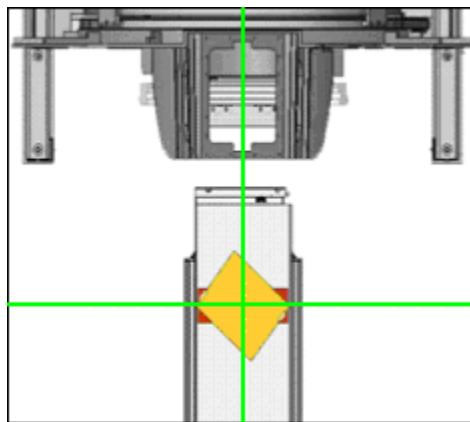
## ◆ Set Up and Deliver the Test

1. Position a 20-mm block of *Virtual Water* on the couch top so it is centered under the overhead laser (at virtual isocenter).
2. Adjust the couch height so that the green bore laser skims the surface of the *Virtual Water*.
3. Move the couch 700 mm in the +IEC Y direction into the bore and account for couch sag. The surface of the *Virtual Water* should be at isocenter height.
4. Use the **Step Move** function to lower the couch in the IEC Z direction by approximately 230 mm.



**NOTE:** The minimum couch height in the bore is set by your installer to prevent a collision of the couch with the bore. If 230 mm cannot be achieved, 220 mm may be used.

5. With the couch still in the bore, use a ruler to verify the distance from the surface of the *Virtual Water* to the bore laser. Record this value, as it will be needed for the analysis.
6. Bring the couch back out of the bore to virtual isocenter, centering the *Virtual Water* block under the overhead laser in Y.
7. Place a piece of film on top of the *Virtual Water*. Optionally, rotate the film to allow for maximum exposure length in the transverse direction, as in the following figure.



Set up for beam planarity test. Film in coronal plane, rotated to capture maximum possible exposure length.

8. Mark a dot in the corner of the film that is closest to the +IEC X and +IEC Y direction, approximately 1 cm from the film edge. Do not make any other marks on the film.
9. Place another 20-mm *Virtual Water* block on top of the film. (The film is now sandwiched between the 20-mm *Virtual Water* blocks.)
10. Bring the couch into the bore exactly 700 mm.
11. Run the procedure. The procedure delivers the 0° and 180° beams in automatic sequence.

## ◆ Analyze the Result

The beam planarity film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.



**IMPORTANT:** For successful analysis in the RITg148+ software:

1. Never use the ROI tool to cut off part of the beam. The entire beam, and some empty space around the beam, is needed for accurate alignment of the film.
2. Enter the “Film Setup Distance (cm) to Isocenter (IEC Z).” This value is used in the jaw offset calculation and impacts the results.
3. The sign of the jaw offset determines the needed direction of adjustment if the test fails. Prior to accepting the results, check the Aligned Image to ensure that the exposure is in the horizontal orientation, the alignment mark is in the upper right corner, and the wider exposure is on the left side.
4. Prior to accepting the results, check the Analyzed Image to ensure that the software properly identified the analysis regions:
  - Dashed horizontal green lines mark the exposure centers.
  - A solid blue line marks the junction between the two exposures. (It is OK if the junction is not centered left/right in the Analyzed Image window. However, the junction must be visible, and correctly marked by the solid blue line.)
  - The dashed blue lines bound the two analysis regions. One analysis region passes through the wider exposure, and one analysis region passes through the narrower exposure.

## ◆ What to Do if the Test Fails

Adjustments to correct for an offset are often needed following a LINAC, target, or jaw actuator change. Contact Accuray Customer Support for assistance. To correct a jaw offset, a service representative adjusts the zero position of the jaws in the software. A service representative may adjust or replace jaws to correct for a twist condition.



**IMPORTANT:** After a service representative adjusts the zero position of the jaws, it is recommended to verify the longitudinal field widths. See “Longitudinal Profiles in Virtual Water” (page 362).

# Stationary Laser Alignment

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## ◆ Overview of Stationary Laser Alignment

<b>TG-148 reference:</b>	Axial and sagittal/coronal green laser (section V.B.4.b)
<b>Other names for this set of tests:</b>	Overhead and bore laser alignment
<b>Purpose:</b>	Verify that the green lasers are properly tilted/rotated with respect to gravity and the beam plane, and that they accurately mark the virtual isocenter (-700 mm in Y from the machine isocenter).
<b>Methods:</b>	<p>Step 1: Adjust the overhead laser.</p> <ol style="list-style-type: none"><li>Use a level to verify that the overhead laser points straight down with gravity.</li><li>Use a film to verify that the transverse component of the overhead laser is parallel to the beam plane, and -700 mm in IEC Y from the beam plane.</li></ol>
	<p>Step 2: Adjust the bore laser.</p> <ol style="list-style-type: none"><li>Use a level to verify that the bore laser is level along the X and Y axes.</li><li>Tilt the bore laser so that its sagittal component is parallel to the sagittal component of the overhead laser.</li><li>Use an MVCT image to verify that the bore laser marks the radiation isocenter (translate in X and Z).</li></ol>
	<p>Step 3: Translate the overhead laser in X so that its sagittal component overlaps the sagittal component of the bore laser.</p>
<b>Accuracy specifications:</b>	<p>Step 1: Overhead laser.</p> <ol style="list-style-type: none"><li>Divergence in X and Y from vertical level &lt; 1 mm over 550 mm vertical displacement.</li><li>Transverse component of overhead laser is 700 mm <math>\pm</math> 1 mm from the center of the radiation plane, and parallel to the radiation plane within 1 mm over 550 mm lateral displacement (0.1°).</li></ol>

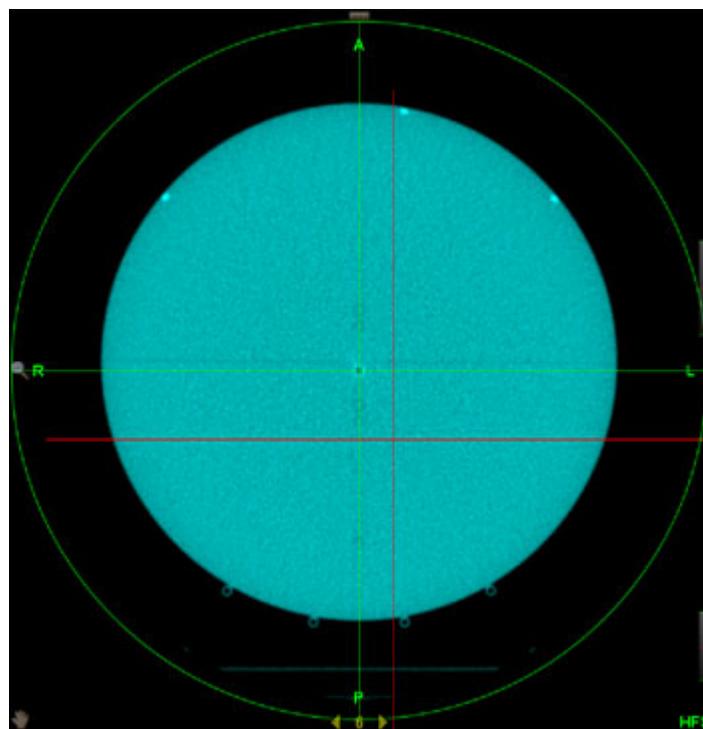
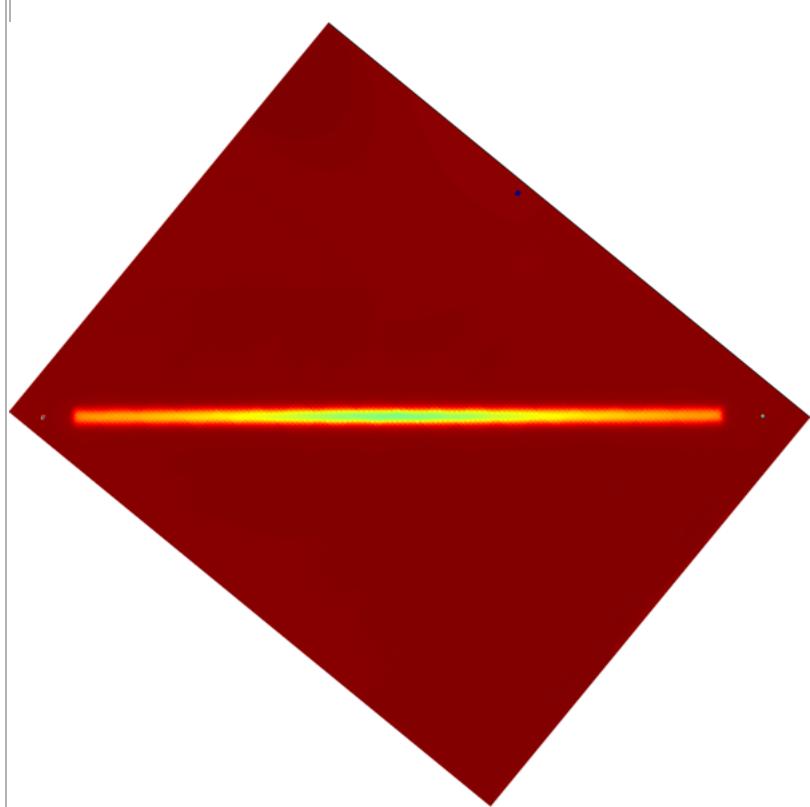
**Step 2: Bore laser.**

- a. Bore laser is level within 1 mm over 550 mm displacement in X and Y.
- b. Sagittal component of bore laser is parallel to sagittal component of overhead laser within 1 mm over 700 mm displacement.
- c. Bore laser passes within 1 mm of isocenter in X and Z directions.

---

**Step 3: Sagittal component of bore laser overlaps sagittal component of overhead laser.**

Sample result  
images:



<b>Equipment needed:</b>	<ul style="list-style-type: none"> <li>• Digital level (approximately 55 cm long; calibrated according to manufacturer's instructions)</li> <li>• One 5-cm block of <i>Virtual Water</i> (55 cm x 15 cm x 5 cm)</li> <li>• Two 2-cm blocks of <i>Virtual Water</i> (55 cm x 15 cm x 2 cm)</li> <li>• 1 EDR or EBT film (recommended minimum size 32 cm x 43 cm)</li> <li>• Pin for marking EDR film, or medium-point permanent marker for EBT film</li> <li>• Masking tape</li> <li>• Ruler</li> <li>• <i>Tomo</i>-phantom</li> <li>• Green laser remote control</li> <li>• Film scanner, computer, Analysis software</li> </ul>
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## ◆ Theory of Stationary Laser Alignment Tests



**NOTE:** The bore laser and the overhead laser each project a green cross hair with two perpendicular components. Laser components are referred to by the planes they define. The overhead laser projects a cross hair that defines a transverse plane and a sagittal plane. The bore laser (gantry isocenter laser) projects a cross hair that defines a coronal plane and a sagittal plane. See "Axes, Planes, and Lasers" in the *Treatment Delivery Manual*.

Accurate laser alignment is important both for QA setup and patient treatments. TG-148 recommends maintaining the laser alignment to the same standards as for other imaging and treatment units used for radiation oncology.

To prevent test errors and rework, pay careful attention to the order of the tests and adjustments provided in the Methods portion of the test overview.

- Align the green lasers before you align the red lasers.
- Align the overhead green laser before you align the bore green laser. (After aligning the bore laser, you may need to translate the overhead laser in X.)
- In most cases, rotational alignment is verified prior to translational alignment.



**IMPORTANT:** If you have accidentally adjusted any parameter that was verified in a previous step, you will need to start over with the laser alignment tests.

## Step 1a: Verify that the overhead laser points straight down with gravity

Step 1a could be accomplished by more than one method. Accuray Incorporated suggests setting up a reference vertical surface that runs parallel to gravity, then checking the distance from the vertical surface to the lasers over a distance of 550 mm in IEC Z.

A reference vertical surface may be achieved by setting a *Virtual Water* block on end on the treatment couch, as shown in the following image. The couch might not be perfectly level and the block might not be perfectly square, so use a calibrated digital level to check the angle of the vertical surface, and shim the block if necessary.



**Step 1a of stationary laser alignment.** A reference vertical surface is set up near virtual isocenter, so that you can check the distance from the vertical surface to the lasers over a range of Z positions.

Start by setting the block surface a few mm from virtual isocenter in the Y direction, to check the rotation of the overhead laser about the X axis (pitch). Then, rotate the block 90 degrees and place it a few mm from virtual isocenter in the X direction, to check the rotation of the overhead laser about the Y axis (roll). See the following image for reference.

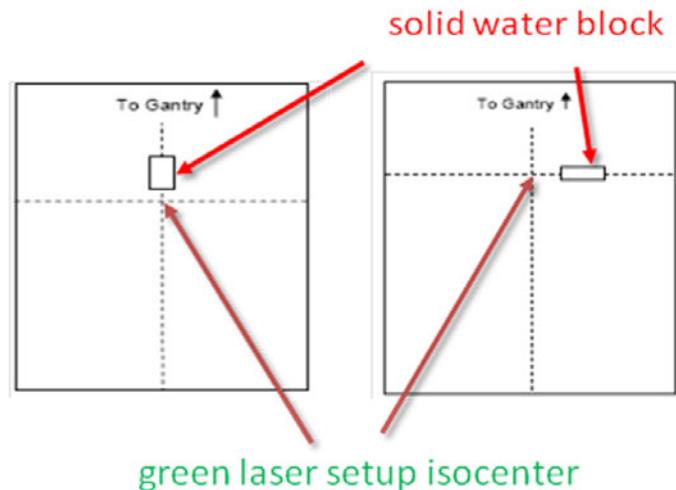


Diagram of Step 1a of stationary laser alignment, viewed from above the couch. Left image: Set the block on end in the indicated position on the couch to check laser tilt about the X axis. Right image: Set the block on end in the indicated position on the couch to check laser tilt about the Y axis.

### Step 1b: Verify that the transverse component of the overhead laser is parallel to the beam plane, and -700 mm in Y from the beam plane

This is the only laser alignment test that requires a film. With the film at isocenter height, center the film on virtual isocenter, and mark the transverse component of the overhead laser on both sides of the film. The couch moves 700 mm into the bore and then irradiates a narrow field from the 0° gantry position. Verify that the laser marks on the film correspond to the center of the exposure.

This test confirms both the distance from the virtual isocenter to the radiation isocenter, and the rotation of the overhead laser about the Z axis (yaw).



**NOTE:** The two components of the overhead laser are always perpendicular to each other (they form a cross). If the transverse component of the overhead laser is parallel to the beam plane, the sagittal component of the overhead laser is perpendicular to the beam plane.



**NOTE:** Optionally, you can mark the sagittal component of the overhead laser on the film. However, the overhead laser film is not suitable for determining the X position of virtual isocenter. This is because the entire MLC is allowed to be offset by up to 1.5 mm in the transverse direction (see “MLC Center of Rotation (COR)” (page 176) for details). The X position of the green lasers will be verified in Step 2c, using an MVCT image of the *tomo*-phantom.

## **Step 2a: Verify that the bore laser is level along the X and Y axes**



**NOTE:** The lasers in the treatment room should be adjusted so they are level with gravity.

To verify that the bore laser is level along the X and Y axes, you can use a reference horizontal surface along the X and Y axes, respectively.

A reference horizontal surface may be achieved by setting a long calibrated digital level on the treatment couch, with the top of the level several mm below isocenter height. Shim the level until it reads 0°. Compare the distance from the level to the laser on both ends of the level, over a range of 550 mm in X and Y.

## **Step 2b: Tilt the bore laser so that its sagittal component is parallel to the sagittal component of the overhead laser**

The overhead laser and bore laser both have a sagittal component. The rotation of the overhead laser was verified in Step 1b. Now, adjust the bore laser so that it is parallel to the overhead laser, over 700 mm distance in Y. It is most straightforward to simply adjust the bore laser to overlap the overhead laser for now. (In Steps 2c and 3, you may need to translate the bore and overhead lasers, together, in the X direction.)

## **Step 2c: Verify that the bore laser marks the radiation isocenter**

Use a *CTrue* image of a phantom to check the IEC X and Z translation of the bore laser. The *Tomo*-phantom or other phantom could be used.

Set up the phantom so that it has a distinct feature aligned to the lasers (or at a known distance from the lasers). You will need to correct for any couch sag. Scan the phantom, and check if this distinct feature appears in the center of the *CTrue* image (or at the expected known distance from the center).

## **Step 3: Translate the overhead laser in X so that its sagittal component overlaps the sagittal component of the bore laser.**

The overhead laser and the bore laser have a common sagittal component. The X translation of the bore laser was verified in step 2c. Now, translate the overhead laser in X to match the bore laser.



**TIP:** After completing the laser alignment, consider marking the laser positions on the walls and floor. Marks on the walls and floor are not a substitute for laser QA, but they can be helpful for noticing a change in laser positions.

## ◆ XML Descriptions

### Stationary Laser Alignment: Overhead Laser Film Test (Step 1b)

<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" .xml package. See "XML Files for Film Alignment Tests" (page 120).
<b>Machine QA Name:</b>	<ul style="list-style-type: none"><li>• ZZZ GAF TG148 Film Alignment Tests-MultiFragment</li><li>• ZZZ TG148 Film Alignment Tests-MultiFragment</li></ul>
<b>Procedure Description:</b>	Overhead Laser
<b>Couch movement in IEC Y when Ready is pressed:</b>	700 mm
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	J05 (smaller than the nominal 1-cm field width)
<b>MLC:</b>	All leaves open
<b>Beam-on time:</b>	The beam is on for 30 s (including 10 s warm up) for EDR film, or 60 s (including 10 s warm up) for EBT film.

- To scan a phantom from the Treatment Delivery Console you can either use the **Acquire Planning Image** workflow accessible from the **Tools** menu, or scan from an existing plan. In the present context, it is better to scan from an existing plan so that you can access the image registration tools. Any patient or procedure can be used to acquire a phantom image from the **Scan** tab.

The Superior/Inferior extent of the planning image determines the available scan length for slice selection on the **Scan** tab (you can scan approximately  $\pm 9$  slices beyond the planning image).

- The Y resolution of the patient planning image impacts the image display on the **Register** tab (MVCT image is interpolated to slice positions of planning image).

### Stationary Laser Alignment: Tomo Phantom Scan (Step 2C)

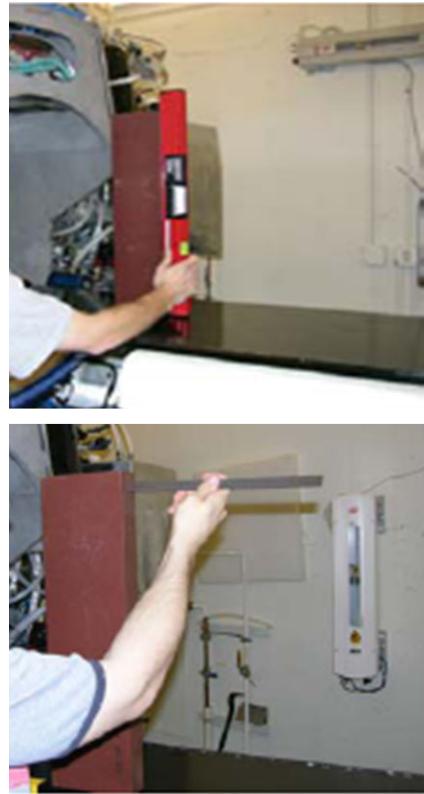
<b>Where to get the .xml:</b>	The TransversePlaneXZLaserLocalization.xml file may be requested from Accuray Customer Support.
<b>Machine QA Name:</b>	<b>ZZZ Transverse Plane (X-Z) Laser Localization</b>
<b>Procedure Description:</b>	<i>CT</i> True Image (run from the <b>Scan</b> tab of the <b>Machine QA</b> task)
<b>Planning Image Content:</b>	Synthetically created cross hair located at isocenter
<b>Planning Image Dimensions:</b>	256 x 256 x 10 voxels
<b>Planning Image Resolution:</b>	0.0705 cm x 0.0705 cm x 0.1905 cm

## ◆ Set Up and Deliver the Tests

### Step 1a: Verify that the overhead laser points straight down with gravity

1. On the patient table, place a 50-mm *Virtual Water* block upright on its short edge. Position the block a few millimeters in Y from the virtual isocenter.

Place a digital level along the -Y surface of the block as shown. Shim the block to ensure it is level.



Reference Vertical Surface



**IMPORTANT:** Use a calibrated level. A calibrated level will give a consistent reading when the level is rotated 180° about its long or short axis, and placed against the same surface.



**IMPORTANT:** Do not rest the end of the level on the couch as you are determining if the block is level.

2. Use a ruler to compare the distance in Y from the block to the overhead laser near the top and bottom of the block. If measurements at the top and bottom of the block differ by  $\geq 1$  mm, go to “What to Do if the Tests Fail” (page 159).

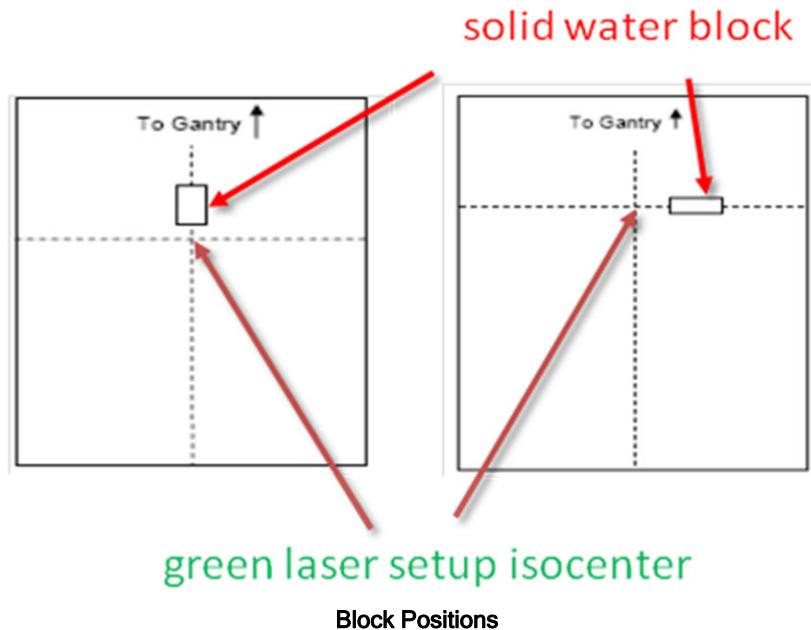


**IMPORTANT:** The angle of the ruler impacts the measurement. Hold the ruler perpendicular to the block.



**IMPORTANT:** For optimal sensitivity, measurement positions should span the full length of the *Virtual Water* block (550 mm).

3. Rotate the block 90° and position it a few millimeters in X from the virtual isocenter (right side of the Block Positions figure).



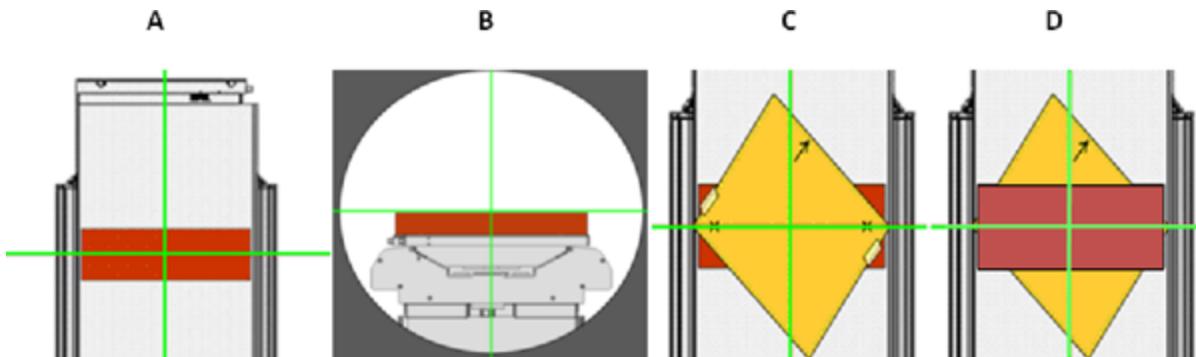
4. Place a digital level along the -X surface of the block. Shim the block to ensure it is level.
5. Use a ruler to compare the distance in X from the block to the overhead laser near the top and bottom of the block. If measurements at the top and bottom of the block differ by  $\geq 1$  mm, go to "What to Do if the Tests Fail" (page 159).



**IMPORTANT:** Ensure that this test passes in both orientations in the Block Positions figure before proceeding to Step 1b.

## Step 1b: Verify that the transverse component of the overhead laser is parallel to the beam plane, and -700 mm in Y from the beam plane

- With the couch pulled out of the bore, position the 20-mm block of *Virtual Water* on the couch at virtual isocenter, as shown in part A of the following image. The green bore laser should skim the top of the *Virtual Water* block.



Overhead Laser Setup (A, C, and D) show the view from above the couch. Part B shows the view from the back side of the gantry through the bore. C and D show an arrow in the corner and "x" for laser marks, but a small dot is sufficient.

- Move the couch 700 mm into the bore and account for the couch sag (part B of the aforementioned image), to ensure 850 mm SSD to the *Virtual Water* block.
- Move the couch out of the bore until the block is centered under the overhead laser at virtual isocenter.
- Place a large-format film ( $\approx 320 \times 430$  mm) on the *Virtual Water* block diagonally so the maximum width of beam can be captured (part C of the aforementioned image). Use tape to secure the film to the block.



**TIP:** It may be convenient to push the block against a couch indexing bar to help prevent the block from slipping during setup.

- Mark the overhead transverse laser at two positions beyond the ends of the 400 mm field using two small dots at locations denoted by the X in Part C of the previous figure. Ensure that the dots are more than 220 mm from isocenter, so that they will not appear in the 400 mm wide exposure. Laser marks should be at least 10 mm from the outer edge of the film.
- Make an alignment mark (dot) near the +IEC X, +IEC Y edge of the film. It is not necessary to mark the Sagittal laser on the film.
- Place another block of *Virtual Water*, 20-mm thick, on top of the film (part D of the aforementioned image).
- Deliver the overhead laser procedure.
- Remove the upper block.

10. If necessary, develop the film.
11. Place the film back on the lower block and align the film so that the marks on the film go through the lasers. If a visual inspection indicates that the transverse laser is parallel to and centered on the exposure, scan and analyze the film (see “Analyze the Results” (page 156)). If a visual inspection indicates that the transverse laser is not parallel to or centered on the exposure, proceed to “What to Do if the Tests Fail” (page 159).



**IMPORTANT:** Ensure that this test passes before proceeding to Step 2a.

### **Step 2a: Verify that the bore laser is level along the X and Y axes**

1. Place a digital level on the couch laterally and slightly below the bore laser (see the left side of the following image). Shim the level until it reads 0.0 degrees.
2. To check for laser rotation about the IEC Y axis, use a ruler to compare the distance from the top edge of the level to the laser on the far left side of the level and the far right side of the level. If measurements at the ends of the level differ by > 1 mm, go to “What to Do if the Tests Fail” (page 159).



**IMPORTANT:** The angle of the ruler impacts the measurement. Hold the ruler perpendicular to the block.

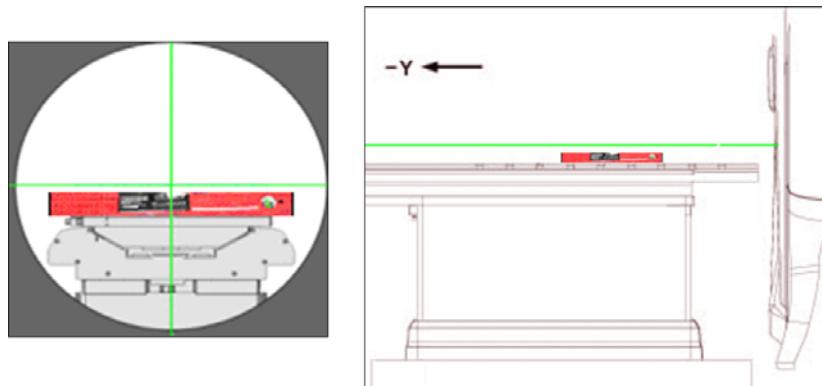


**TIP:** For optimal sensitivity, measurement positions should span the full length of the level (tolerance is defined over 550 mm lateral displacement).

3. Rotate the level 90° so that it is parallel to the Y axis (see the right side of the following image), and repeat the test to check for rotation about the IEC X axis.
4. If measurements at the ends of the level differ by > 1 mm, go to “What to Do if the Tests Fail” (page 159).



**IMPORTANT:** Ensure that this test passes before proceeding to Step 2b.



**Left side:** Check bore laser rotation about the Y axis (roll). **Right side:** Check bore laser rotation about the X axis (pitch).

### Step 2b: Tilt the bore laser so that its sagittal component is parallel to the sagittal component of the overhead laser

1. Set the couch height several cm below isocenter.
2. Place a white piece of paper on the couch near isocenter.
3. Lift the -Y end of the paper off the couch a bit, so the paper is at an angle.
4. Hold your finger above the paper to block a portion of the overhead laser. You should now be able to distinguish between the sagittal component of the overhead laser and the sagittal component of the bore laser on the paper.
5. Check the overlap of the sagittal component of the bore laser and the sagittal component of the overhead laser over a Y distance of 700 mm.
6. If the bore laser and overhead laser are not parallel and overlapping within 1 mm over a distance of 700 mm in Y, go to “What to Do if the Tests Fail” (page 159) to adjust the bore laser.

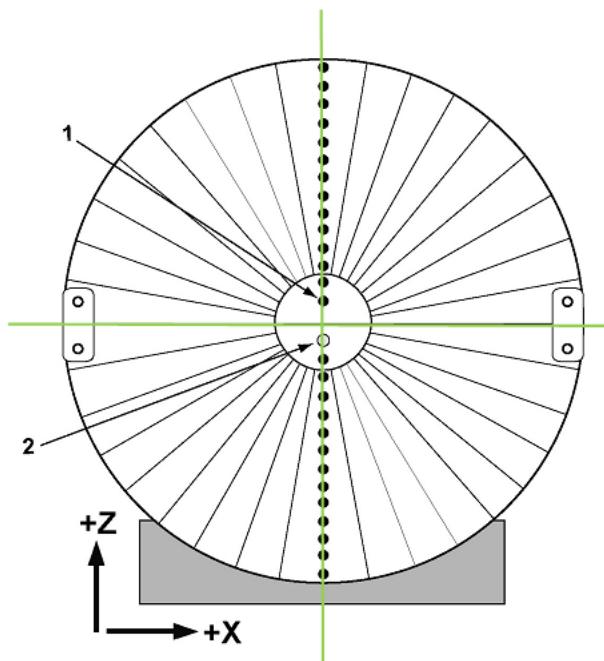


**IMPORTANT:** Ensure that this test passes before proceeding to Step 2c.

### Step 2c: Verify that the bore laser marks the radiation isocenter

1. Place the *Tomo*-phantom on the couch, with the small ion chamber holes on the -Y side of the gantry.
2. Rotate the phantom so that the 10 mm plug is above the center of the phantom, as shown in the following image. Use the bore laser as a guide to ensure the phantom is level.
3. Center the phantom on the green lasers in X, Y, and Z.

4. Send the phantom into the bore and account for couch sag. The green lasers should run through the center of the phantom (where the phantom splits in half).
5. Move the couch out of the bore and center the phantom on the green lasers in Y.
6. Remove a plug from the phantom to create a “fiducial” mark located 5 mm below the isocenter (position 2 in the following image).



Tomo phantom centered on green lasers, as viewed from behind the gantry. Label 1 is the dowel 10 mm above isocenter. Label 2 is the empty cavity at -5mm.

7. From the home screen of the Treatment Delivery Console, click **Machine QA** and open the **ZZZ Transverse Plane (X-Z) Laser Localization** procedure described for Step 2c.
8. From the **Scan** tab, select **Fine** slices and the 2 mm reconstruction interval. Zoom in on the image so you can clearly see the slices. Select three (3) slices on both sides of the green overhead laser line. The total number of selected slices is seven (7).
9. Acquire a *CTrue* Image Scan.
10. Proceed to “Analyze the Results” (page 156).



**IMPORTANT:** Ensure that this test passes before proceeding to Step 3.

### **Step 3: Translate the overhead laser in X so that its sagittal component overlaps the sagittal component of the bore laser.**

The tilt of the bore laser was already set in Step 2b. If you translated the bore laser in Step 2c, you will need to translate the overhead laser to overlap the bore laser. Step 2b describes how to check the overlap of the sagittal components of the bore and overhead lasers.

## ◆ **Analyze the Results**

### **Step 1a: Verify that the overhead laser points straight down with gravity**

If measurements at the top and bottom of the *Virtual Waterblock* differ by < 1 mm, the test passes. If an adjustment is needed, proceed to “What to Do if the Tests Fail” (page 159). Ensure that the test passes in both orientations of the Block Positions figure before proceeding to Step 1b.

### **Step 1b: Verify that the transverse component of the overhead laser is parallel to the beam plane, and -700 mm in Y from the beam plane**

The overhead laser film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions. Verify that the Offset from center of exposure to transverse laser line (IEC Y) does not exceed  $\pm 1$  mm, and that the Rotation of transverse laser line with respect to exposure does not exceed  $\pm 0.1$  deg. If an adjustment is needed, proceed to “What to Do if the Tests Fail” (page 159).

**IMPORTANT:** Observe the following for analysis in the RITg148+ software:



- For most accurate analysis, use an image filter to reduce noise. However, sometimes the image filter can hide small pin pricks. If the pin pricks can't be located, try reducing the filter to “Median 3x3,” or set the **Filter Type** to “None.” If you can see the pin pricks, you can enhance them with the **Image Erase/Pin Prick Tool**.
- If the pin pricks can't be located, start over with a new film. Never try to estimate or “guess” their positions.
- If the laser marks on the film are too large to identify their precise position, start over with a new film.
- The laser marks on the film should be located beyond the beam. If the laser marks are at the very ends of the beam, the analysis may be incorrect. Start over with a new film.

- The sign of the results is important to determine the appropriate direction of adjustment. Check the **Aligned Image** to ensure that the exposure is in the horizontal orientation and the alignment mark is in the upper right corner.
- Check the **Analyzed Image** to ensure that the ends of the red lines mark the laser pin pricks (use the **Zoom** tool in the **Analyzed Image** window if necessary), and ensure that the green line indicates the center of the exposure.
- The offset from center of exposure to sagittal laser line is only provided if you included an optional sagittal pin prick or two on the film. This value should not be used to adjust the lasers.

## **Step 2a: Verify that the bore laser is level along the X and Y axes**

If measurements at the ends of the level differ by  $\leq 1$  mm, the test passes. If an adjustment is needed, proceed to “What to Do if the Tests Fail” (page 159). Ensure that the test passes in both orientations before proceeding to the Step 2b.

## **Step 2b: Tilt the bore laser so that its sagittal component is parallel to the sagittal component of the overhead laser**

If the bore laser and overhead laser are parallel and overlapping within 1 mm over 700 mm distance in Y, the test passes. If not, proceed to “What to Do if the Tests Fail” (page 159) to adjust the bore laser. Ensure that the test passes before proceeding to Step 2c.

## **Step 2c: Verify that the bore laser marks the radiation isocenter**

1. **Optional step:** As a quick second check of the Y position of the green overhead laser, zoom in on the *CTrue* image on the **Scan** tab, and find the small metal balls embedded in the surface of the phantom. These metal balls are located in the IEC Y center of the phantom. The metal balls should show up most clearly in the central slice that has been imaged (4th of 7 slices,  $\pm 1$  slice), if the slices are symmetrical about the green lasers.



**IMPORTANT:** Regarding the optional second check of the Y position of the green overhead laser:

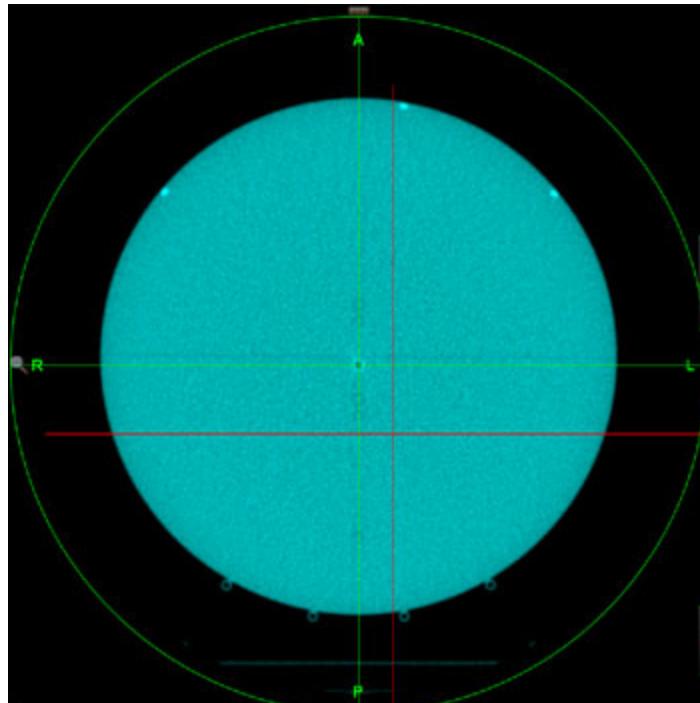
- The optional check is not as robust as the overhead laser film test, so it should not be used to adjust the laser.
- The optional check must be done on the **Scan** tab. (On the **Register** tab, the slices of the *CTrue* image are interpolated for display at the slice positions of the planning image.)

- The 2-mm reconstruction interval is recommended for the scan. If you use the 1-mm interval, the metal balls show up in several slices, making it difficult to perform the optional check.
2. At the Treatment Delivery Console, click the **Register** tab.
  3. Use manual registration to align the empty ion chamber cavity in the *CTrue* image (black circle) with the planning image (cross-hair).



**TIP:** The cross hair of the planning image is located at the radiation isocenter. Alternatively, you can turn on the display of the green lasers, and align the empty ion chamber cavity to the intersection of the green lasers.

4. Verify that a vertical adjustment of 5 mm ( $\pm 1$  mm) and a lateral adjustment of no more than  $\pm 1$  mm is necessary to align the images. See the following image for reference. If the test fails, go to “What to Do if the Tests Fail” (page 159). Ensure that the test passes before proceeding to Step 3.



Analyze Bore Laser

### Step 3: Translate the overhead laser in X so that its sagittal component overlaps the sagittal component of the bore laser.

If the bore laser and overhead laser are parallel and overlapping within 1 mm over 700 mm distance in Y, the test passes. If not, proceed to “What to Do if the Tests Fail” (page 159) to translate the overhead laser.

## ◆ What to Do if the Tests Fail

Observe the following for laser adjustments:

- If any step fails, resolve the failing step, before going on to the next step.
- Verify that you completed the steps in the correct order. Refer to the Overview and Theory sections for details.
- Instructions for using the remote control may be found in the next section.
- Contact Accuray Customer Support if you need assistance.

### Step 1a: Verify that the overhead laser points straight down with gravity

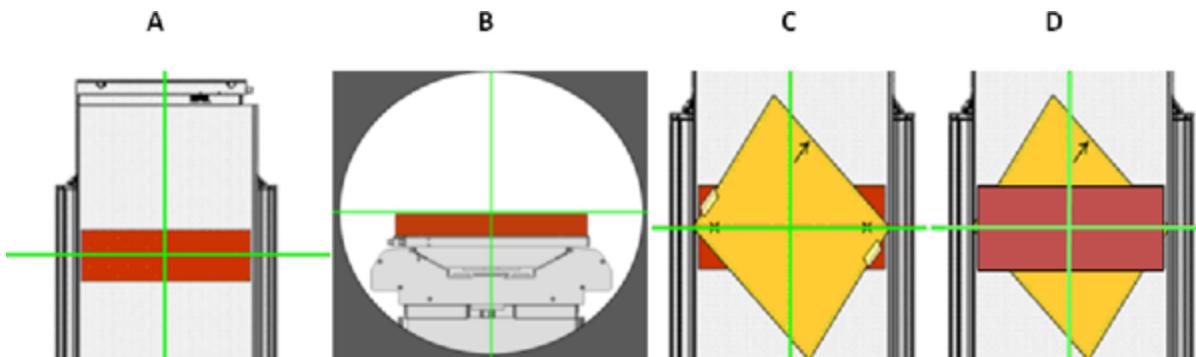


**TIP:** You may find it helpful to mark the initial laser position so that adjustments can be tracked and reversed.

Use the **Tilt** function on the laser remote to make any corrections. Repeat the test to ensure that it passes.

### Step 1b: Verify that the transverse component of the overhead laser is parallel to the beam plane, and -700 mm in Y from the beam plane

1. Place the exposed film back in position at virtual isocenter, to use as a visual guide for your adjustment. Retain the same setup (couch height and lower block of virtual water) that was used to expose the film. Carefully align the marks on the film to the lasers at virtual isocenter. Tape the film in place, as in part C (below). Do not cover the film with the upper block of virtual water.



2. Before adjusting the lasers, mark the current laser position on the couch with a piece of tape.

3. Use the remote control to **Translate** in IEC Y and/or **Rotate** the overhead green laser to the center of the exposure. Use the tape mark to ensure that the X position of the laser was not disturbed.
4. Repeat the overhead laser test with a new film until a passing result is achieved.
5. Use the **Tilt** button on the remote to adjust the sagittal component of the bore laser so that it overlaps the overhead laser.



**IMPORTANT:** In Step 1b, use the **Rotate** and **Translate** buttons for the overhead laser, and use the **Tilt** button for the bore laser. If you **Tilt** the overhead laser at this stage, you will need to start over with all the laser alignment tests.

### **Step 2a: Verify that the bore laser is level along the X and Y axes**

Use the **Rotate** function on the laser remote to rotate the bore laser about the Y axis (roll). Use the **Tilt** function on the laser remote to rotate the bore laser about the X axis (pitch). Repeat the test to ensure that it passes.



**IMPORTANT:** In Step 2a, adjust the bore laser only. If you adjust the overhead laser at this stage, you will need to start over with all the laser alignment tests.

### **Step 2b: Tilt the bore laser so that its sagittal component is parallel to the sagittal component of the overhead laser**

Use the **Tilt** and/or **Translate** function on the laser remote to adjust the bore laser so that it is overlapping the overhead laser along the Y axis. When finished, if the **Tilt** function was used, repeat Step 2a to ensure that it still passes.



**IMPORTANT:** In Step 2b, adjust the bore laser only. If the overhead laser was adjusted at this stage, all the laser alignment tests will need to be repeated from the beginning.

### **Step 2c: Verify that the bore laser marks the radiation isocenter**

1. Adjust the phantom setup, re-scan, and repeat until the phantom is in a position that achieves a passing result.
2. Return the phantom to isocenter, plus 700 mm into the bore.

3. **Translate** the bore laser to coincide with the center of the phantom in X and Z.
4. Before adjusting the overhead laser in X, mark the current Y position of the laser on the couch with a piece of tape.
5. **Translate** the overhead laser to coincide with the bore laser in X. Use the tape mark to ensure that the Y position of the laser is not disturbed.



**IMPORTANT:** In Step 2c, **Translate** the lasers only. If you use the **Rotate** or **Tilt** buttons at this stage, all the laser alignment tests will need to be repeated from the beginning.

### Step 3: Translate the overhead laser in X so that its sagittal component overlaps the sagittal component of the bore laser.

1. Before adjusting the overhead laser, mark the current Y position of the laser on the couch with a piece of tape.
2. Use the **Translate** button on the remote to translate the sagittal component of the overhead laser to align with the bore laser. Use the tape mark to ensure that the Y position of the overhead laser is not disturbed.



**IMPORTANT:** In Step 3, **Translate** the overhead laser in X only. If you adjust the bore laser at this stage, or if you **Rotate** or **Tilt** any laser, all the laser alignment tests will need to be repeated from the beginning.

## ◆ Use the Remote Control to Adjust the Green Lasers



**WARNING:** The lasers should only be adjusted by qualified personnel following a structured laser alignment workflow. Incorrect laser adjustments, or adjustments of individual laser components without consideration of the workflow, may result in contradictions between lasers, and poor setup for patients and QA, which could lead to bodily harm to the patient. Consider storing the laser remote in a place that is only accessible to your service representative and clinical staff who are qualified to adjust the lasers.

The green laser position can be adjusted using the remote control:

1. Aim the remote control at the laser box of interest.
2. Press **Select** on the remote control twice, then enter the number of the laser source (usually 1 or 2). The selected laser should now be blinking (flashing).



**TIP:** If the laser cannot be selected, ensure that nothing is blocking the path from the remote control to the laser receptor (if the laser is housed in a cabinet, you will need to open the cabinet). Also, try replacing the batteries in the remote control.

3. Hold down the appropriate arrow button to **Translate**, **Rotate**, or **Tilt** the lasers:

- **Translate** shifts the laser in a plane perpendicular to the direction of laser travel.
- **Rotate** rotates the laser in a plane perpendicular to the direction of laser travel.
- **Tilt** rotates the laser in a plane parallel to the direction of laser travel.



**NOTE:** The green lasers stay where you set them using the **Translate**, **Rotate**, and **Tilt** buttons. The green lasers do not have a revert or save button.



**TIPS** for performing laser adjustments:

- Be sure the intended laser is selected (overhead laser or bore laser) before pressing **Translate**, **Rotate**, or **Tilt**.
- Avoid using the **Tilt** button unless it is necessary. If the tilt is misaligned, the translation and tilt functions will have to be used repeatedly in order to visualize and restore the laser alignment.
- Depending on how the lasers are mounted to the ceiling and walls, a translation motion along one axis may unintentionally introduce some translation along the perpendicular axis. Always mark the current laser position (e.g., using a piece of tape on the couch) prior to translating the lasers. This will provide a guide for restoring the laser position along the secondary axis if it is disturbed.

# Moveable Laser Alignment Tests

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- ◆ Theory of Moveable Laser Alignment Tests..... 163
- ◆ XML Description ..... 164
- ◆ Set Up and Deliver the Test ..... 164
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## ◆ Overview of Moveable Laser Alignment Tests

<b>TG-148 reference:</b>	Red laser initialization (section V.B.4.b) and red laser movement (section V.B.4.b)
<b>Purpose:</b>	<ol style="list-style-type: none"><li>1. Verify that the red lasers coincide with the green lasers in the "home" position.</li><li>2. Verify that the red lasers move to their expected positions for a plan.</li></ol>
<b>Method:</b>	<ol style="list-style-type: none"><li>1. Visual observation in the treatment room.</li><li>2. Use a ruler to measure red laser shifts and compare against programmed values.</li></ol>
<b>Accuracy specification:</b>	When homed, the moveable lasers overlap the fixed lasers at virtual isocenter within $\pm 1$ mm, and the moveable lasers diverge from the fixed lasers $< 1$ mm over 550 mm displacement.
<b>Equipment needed:</b>	Ruler

## ◆ Theory of Moveable Laser Alignment Tests



**IMPORTANT:** Finish the stationary (green) laser alignment before attempting the moveable (red) laser alignment.

In their "home" position, the red lasers should overlap with the green lasers, in the region near virtual isocenter where the red lasers may be used for patient setup (e.g., within 550 mm of virtual isocenter).



**NOTE:** It is normal for the red lasers to diverge from the green lasers far away from virtual isocenter (e.g., at the walls of the treatment room). This does not impact patient setup, as long as the lasers are aligned within tolerances near the virtual isocenter.

The programmed positions of the red lasers are used for initial patient setup. The distances and directions of the offsets from the green lasers should be checked using a ruler. Measurements should be compared against the programmed laser positions, which are displayed on the **Main** screen of the Positioning Control Panel on the gantry, in the **Current Laser Position** area.

## ◆ XML Description

To perform these tests, you will need two plans:

- Any plan for which the red lasers are known to be in their "home" position, such as the AIRSCANS procedure that is built into your TDC.
- Any plan for which the red lasers are programmed to move away from the green lasers in the X, Y, and Z directions. For example, the **ZZZ Transverse Plane (X-Z) laser localization** patient (introduced in the stationary laser alignment test) is programmed to shift the lasers by +2.0 cm in X, +8.0 cm in Y, and -4.0 cm in Z.

For the moveable laser alignment tests, you will not need to run these plans. However, you will need to open the **Machine QA** plan, click **Prepare Scan** or **Prepare Treatment**, and work through all the messages on the screen. The red lasers begin to move to their programmed positions about the time that the **Ready** button becomes available and you hear the MLCs performing their pre-procedure exercise.

## ◆ Set Up and Deliver the Test

**Verify that the red lasers coincide with the green lasers in the "home" position**

1. Restart the machine, or open the **AIRSCANS** patient and prepare a scan to send the red lasers to their "home" position.
2. Verify that the **current laser position** displayed on the **main** screen of the **Positioning Control Panel** is 0.0 in X, Y, and Z.
3. Check the red and green laser overlap near virtual isocenter.



**NOTE:** There are five red laser sources in the treatment room, and two green laser sources.

4. If the red lasers overlap the green lasers within  $\pm 1$  mm, and if the red lasers diverge from the green lasers  $< 1$  mm over a distance of 550 mm, the test passes. If the test fails, continue to “What to Do if the Test Fails” (page 165).

**Verify that the red lasers move to their expected positions for a plan**

1. Open a **Machine QA** plan that contains programmed red laser movement, such as the **Transverse Plane (X-Z) laser localization** patient. Prepare a scan or treatment to cause the red lasers to move.
2. Read the **current laser position** on the **main** screen of the **Positioning Control Panel**.
3. Use a ruler to measure the distances from the green lasers to the red lasers in X, Y, and Z. Also compare the direction of the offsets against the sign of the values indicated on the **Positioning Control Panel**.
4. Check that red laser movement matches the **Positioning Control Panel** display within 1 mm (Accuray does not have an official tolerance for this test, but TG-148 recommends a tolerance of 1 mm). If the test fails, continue to “What to Do if the Test Fails” (page 165).

## ◆ What to Do if the Test Fails

The red laser tests rely on accurate calibration of the green lasers. Refer to “Stationary Laser Alignment” (page 141) for instructions for checking the green lasers.

If your green laser alignment is correct, and if the red lasers do not overlap the green lasers, or if the red laser motion is incorrect, contact Accuray Customer Service to adjust the lasers. (Red laser alignment involves using a remote control to adjust the translation home position, and using Allen wrenches that come with the lasers to remove the laser cover and adjust the rotations. The process works best with two people.)

# Couch Alignment Tests

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## ◆ Overview of Couch Alignment Tests

TG-148 reference:	Treatment couch (V.B.4.c)
Purpose:	<p>Verify that:</p> <ol style="list-style-type: none"><li>1. The couch does not stray in the X direction while it moves in Y or Z.</li><li>2. The couch travels the programmed distance in the Y direction.</li><li>3. The couch Y position is accurately maintained as the couch is translated in Z.</li><li>4. When completely withdrawn from the bore, the couch is horizontally level.</li><li>5. The couch maintains its IEC Z position within tolerance when it travels in the IEC Y direction.</li><li>6. The couch is appropriately centered in the X direction.</li></ol>

<b>Method:</b>	<ol style="list-style-type: none"> <li>1. Mark the lasers on the couch. Move the couch in the IEC Y and Z directions, and check that the couch travels parallel to the lasers.</li> <li>2. Use a ruler to verify the couch travel distance.</li> <li>3. Mark the overhead laser on the couch. Step Move the couch in -20mm increments in Z, over the range of allowed couch heights in the bore. After each movement, check for consistency in the couch Y position on the digital display, and compare the mark on the couch to the overhead laser.</li> <li>4. Use a level to verify that the couch is level.</li> <li>5. Set a <i>Virtual Water</i> block on the couch at virtual isocenter, with the surface of the block skimming the green bore lasers. Send the block into the bore, and compare the height of the block against the green bore lasers.</li> <li>6. Use a ruler or <i>CTrue</i> image to verify couch centering.</li> </ol>
<b>Accuray specification:</b>	<ol style="list-style-type: none"> <li>1. The couch travel diverges &lt; +/- 1mm over the entire IEC Y couch displacement. The couch travel diverges &lt; 2 mm in X over the Z range of motion allowed by the bore limits.</li> <li>2. The <b>Positioning Control Panel</b> and ruler should agree within <math>\pm 0.5</math> mm over 200 mm couch travel.</li> <li>3. Over the available vertical range of couch motion, the Positioning Control Panel maintains its Y position within +/- 1 mm, and the couch stays on its laser mark within +/-2 mm in Y.</li> <li>4. When completely withdrawn from the bore, the couch is horizontally level within <math>0.2^\circ</math> in the IEC X and Y directions.</li> <li>5. The couch is expected to maintain its IEC Z position within <math>\pm 2</math> mm, for any point-to-point move in IEC Y, with or without weight on the couch.</li> <li>6. The overhead laser bisects the couch to within <math>\pm 2</math> mm when the X couch position is zeroed.</li> </ol>

<b>Equipment needed:</b>	<ul style="list-style-type: none"> <li>• Calibrated digital level</li> <li>• Ruler</li> <li>• Masking tape</li> <li>• <i>Virtual Water</i> block (55 cm x 15 cm x 5 cm)</li> </ul>
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## ◆ Theory of Couch Alignment Tests



**IMPORTANT:** The couch alignment tests use the green lasers as a reference for the IEC X, Y, and Z directions. Verify the green laser alignment before checking the couch alignment. A couch adjustment requested with poorly-aligned green lasers will probably result in an incorrect couch alignment.

1. The couch does not stray in the X direction while it moves in Y or Z.  
If the couch strayed to the left or right as the Z position of the couch was adjusted, patient setup could be impacted. If the couch strayed to the left or right as it moves in Y, the treatment delivery could be impacted. The couch Y position should be far enough into the bore that it engages with the pallet support for all couch positions included in the test, because the couch may shift slightly when it first engages with the pallet support.
2. The couch travels the programmed distance in the Y direction. See “Couch Position Interlock” (page 8) for information on couch positioning accuracy.



**NOTE:** For procedures with a moving couch, when **Ready** is pressed on the Positioning Control Panel, the couch moves into the bore slightly less than indicated in the .xml, to allow space for couch acceleration to the programmed velocity before the beam turns on:

*Distance traveled before irradiation in mm = v\*(2-0.01\*v)+0.005v<sup>2</sup>*, where *v* is the procedure velocity in mm/s. (For example, if *v* = 1 mm/s, the distance the couch will travel before irradiation is 1.995 mm. If the couch setup to ready distance is 700 mm, the couch will move  $698.005 \pm 0.5$  mm when **Ready** is pressed, and then the couch will accelerate over an additional 1.995 mm just prior to beam-on.)

3. The couch Y position is consistent as the couch travels in Z.  
The digital couch position display reports the Y position consistently, regardless of the couch height.
4. When completely withdrawn from the bore, the couch is horizontally level.  
The couch will sag under the weight of a patient. However, the couch should be level when it is withdrawn from the bore and there is no weight on the couch.

5. The couch maintains its IEC Z position within tolerance when it travels in the IEC Y direction.

The tolerance for this test should account for the couch positioning specification of  $+/ - 2$  mm in IEC Z, as well as the bore laser leveling. A properly aligned bore laser is level within 1 mm over 550 mm displacement in IEC Y.

6. The couch is appropriately centered in the X direction

For a new machine, the couch should be installed so that it is laterally centered in the bore (centering of  $0 \pm 2$  mm). The centering of the couch can be compared against the green isocenter lasers using a ruler.

The **Couch Settings** folder of the **Edit Machine** area (accessible from the Treatment Delivery Console) contains a parameter to indicate the lateral position of the couch installation with respect to isocenter. This feature enables more accurate insertion of the treatment couch image for planning.

The **Couch Settings** folder of the **Edit Machine** area also includes a parameter to relate the vertical couch Positioning Control Panel position to isocenter. This enables the Treatment Delivery Console to warn the user if daily registration results have caused a change in *TomoDirect* beam intersection with the couch. This parameter is also used in the PreciseART workflow, to replace the full couch at the appropriate daily location in the CTrue images before performing dose calculations.



**IMPORTANT:** If the "Couch Height at Isocenter (mm)" is not set correctly, the accuracy of PreciseART calculations will be affected.

To determine the lateral offset in the couch installation, an Accuray Incorporated representative positions the couch so that the Positioning Control Panels display 0.0 in X. The Accuray Incorporated representative then acquires a *CTrue* image of the couch. Using the Registration panel, the *CTrue* image is compared against an image of a centered couch to determine the lateral offset. The Accuray Incorporated representative enters this **Lateral Offset (mm)** value in the **Couch Settings** folder of the **Edit Machine** area. It must be within  $0 \pm 2$  mm.

The **couch height at isocenter (mm)** relates the vertical couch position displayed on the positioning control panel to isocenter. As with the **Lateral Offset**, the **couch height at isocenter** is determined from a *CTrue* image of the couch.

This chapter provides a procedure to verify the calibration position of the couch using a *CTrue* image of the couch.

## ◆ XML Description

The only couch alignment test that requires an **.xml** file is Test #6, to verify that the couch is properly centered in the X direction using a *CTrue* image.

The couch calibration **.xml** file is available by request from Accuray Customer Support. The procedure file contains a default “planning” image of a centered couch, for comparison against a *CTrue* image of your couch on the OS **Register** tab.



**IMPORTANT:** The **.xml** file must point to reference image data that is consistent with the couch installed in your treatment room.

## ◆ Set Up and Deliver the Tests

### 1. The couch does not stray in the X direction while it moves in Y or Z

#### **Couch does not stray in X while it moves in Y**

1. Set the couch height to a vertical position of 350 mm (Z). Ensure that the couch is engaged with the pallet support.
2. Set a Virtual Water block on the couch near virtual isocenter, with a piece of tape sticking up above the block.
3. Make a vertical mark on the tape to record the X position of the bore laser.
4. Place two additional pieces of tape on the couch, inferior to the Virtual Water block. Separate these two pieces in IEC Y as much as possible, over the range that you can see the overhead laser on the couch. Mark the X position of the overhead laser on these two pieces of tape.
5. Move the couch into the bore the entire range in Y; keep X and Z couch coordinates at the initial setup value. As the couch moves into the bore, the tape mark should remain aligned with the green bore laser within < +/- 1 mm in X. The inferior two tape marks should remain aligned with the green overhead laser within < +/- 1 mm in X.

#### **Couch does not stray in X while it moves in Z**

1. Lower the couch to its minimum allowed height inside the bore.
2. Bring the couch out of the bore.
3. Place a piece of tape on the couch at virtual isocenter, and mark the sagittal component of the overhead laser position on the tape.
4. Raise couch to maximum height. As the couch is being raised up, the tape mark on the couch should remain aligned with the green overhead laser within < 2 mm in X.

## **2. The couch travels the programmed distance in the Y direction**

1. With the couch at an appropriate height for patient treatments, bring the couch out of the bore.
2. Use a piece of tape to mark the virtual isocenter on the couch.
3. Use the **Step Move** function on the **Positioning Control Panel** to introduce a +200 mm translation in Y. Use the ruler to verify that the distance from the mark on the couch to the virtual isocenter is  $200.0 \pm 0.5$  mm.

## **3. The digital display of the couch Y position is consistent as the couch travels in Z**

1. Raise the couch to its maximum height in the bore.
2. Place a piece of tape on the couch at the virtual isocenter and mark the position of the green overhead lasers on the tape.
3. Record the Y position of the couch as displayed on the **Positioning Control Panel**.
4. Use the **Positioning Control Panel Step Move** function to lower the couch 20 mm (-Z).
5. After each step move, compare the mark on the couch to the lasers and check the Y value on the **Positioning Control Panel**. The Positioning Control Panel should maintain its Y position (recorded in Step 3) within +/-1 mm, and the couch should stay on the laser mark within +/-2 mm in Y.
6. Repeat steps 4-5 until you reach the minimum couch height inside the bore allowed by the software.

## **4. When completely withdrawn from the bore, the couch is horizontally level**

1. Pull the couch out of the bore, and remove all items from the couch top.
2. Place a digital level on the couch in the positions shown in the following image.
3. Verify that the digital level reads  $0.0 \pm 0.2^\circ$  at each of the six positions shown in the following image.

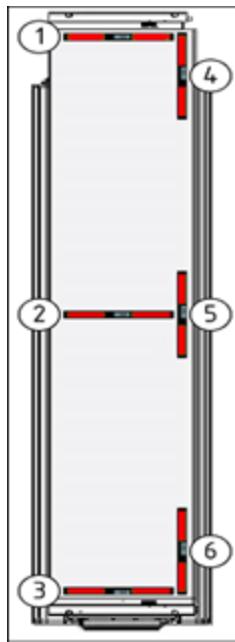


Figure [CouchLevel].

## 5. Couch sag for an unloaded couch is within specifications

1. Remove all items from the couch, except for a single *Virtual Waterblock* at virtual isocenter.
2. Set the couch height so that the surface of the *Virtual Waterblock* skims the green lasers at virtual isocenter.
3. Move the couch 700 mm into the bore.
4. Use a ruler or the **Step Move** function on the Positioning Control Panel to determine the couch sag.



**TIP:** Attach a small piece of masking tape to the -Y surface of the block, and let it stick up about 1 cm above the *Virtual Water*. This will allow you to visualize the distance from the surface of the *Virtual Water* to the laser while standing on the couch side of the gantry. Refer to the tape trick figure in "Account for Couch Sag" (page 90).

## **6.a. The couch is appropriately centered in the X direction: Ruler Test**

1. Set the couch lateral position to 0.0 mm. (One way to do this is to press the **Unload** button on the Positioning Control Panel, then raise the couch up to isocenter height.)
2. Use a ruler to determine the lateral center of the couch (the couch is 530 mm wide). Verify that the overhead laser is within 2 mm of the lateral center of the couch.

## **6.b. The couch is appropriately centered in the X direction: Image Test**

### **Prepare the Procedure**

1. From the Treatment Delivery Console, open the **Machine QA** task, and select the couch calibration procedure.
2. Navigate to the **Scan** tab, and select the **Fine Acquisition Pitch** and **1 mm Reconstruction Interval**. In the **Slice Selector**, select at least five slices. Include the slice that the green laser passes through, plus two slices superior and two slices inferior to the green laser.
3. Click **Prepare Scan** and **OK**.

### **Position the Couch**

1. In the treatment room, remove all objects from the couch.
2. Set the couch lateral position to 0.0 mm. One way to do this is to press the **Unload** button.
3. Adjust the couch height so that the top of the couch is near isocenter height.
4. Record the vertical (IEC Z) **Current Couch Position** coordinate on the **Positioning Control Panel**.
5. On the **Positioning Control Panel**, press **Main > Ready > Yes**.
6. Ensure that the sensitive lateral drive assembly region of the couch is beyond the beam area after you press **Ready**. (The beam area is indicated approximately by the marks on the gantry covers).
7. Exit the treatment room and secure the entrance interlock.

### **Acquire the Image**

1. At the Treatment Delivery Console, turn the mode switch on the **Status Console to Image**, and press the **Start** button.
2. When the scan is complete, turn the mode switch on the **Status Console to Program**.

## Determine the Registration Result

1. Select the **Register** tab. The **Scan** and **Plan** couch images are displayed.
2. Use the manual registration controls to align the new image to the reference image.
3. Record the lateral and vertical registration offsets.

## Review Couch Settings

1. Click the **Edit Machine** tab.



**TIP:** The **Edit Machine** tab may be accessed from the **Machine QA** task, or from the **Tools** menu on the home screen of the Treatment Delivery Console.

2. Open the **Couch Settings** folder and check that the measured values match the **Lateral offset (mm)** and **Couch Height at Isocenter (mm)** as follows:
  - The **Lateral offset (mm)** should match the lateral registration offset within  $\pm 2$  mm.
  - The **Couch Height at Isocenter (mm)** field should match the sum of the vertical registration offset and the vertical (IEC Z) value of the current couch position displayed on the **Positioning Control Panel**, within  $\pm 2$  mm.

## ◆ What to Do if the Test Fails

First, verify that the green laser alignment is within tolerance (see “Stationary Laser Alignment” (page 141)). Then, contact Accuray Customer Support to perform tests and make appropriate adjustments. After a service representative adjusts the couch, repeat the couch alignment tests.



**IMPORTANT:** If the **Lateral Offset** in the **Couch Settings** folder of the **Edit Machine** area is changed, understand the following:

- Inaccurate values may affect treatment accuracy.
- At the Treatment Delivery Console, each time you open a *TomoDirect* plan that was approved with the previous values, a message will notify the user that the calibrated lateral position of the couch has changed.
- On the Treatment Planning System, unapproved plans will be required to replace the couch in the image volume. The user must also cancel and restart the plan calculation process for any calculations that were in progress.

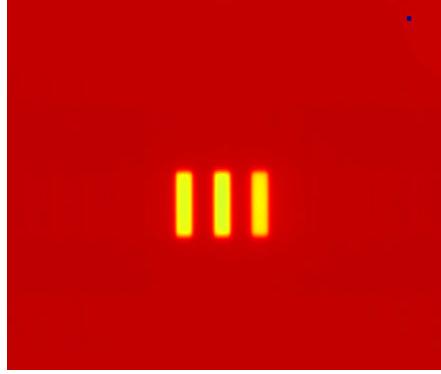


**NOTE:** **Plan Transfer** does not account for differences in the **Lateral Offset** from one machine to another.

# MLC Center of Rotation (COR)

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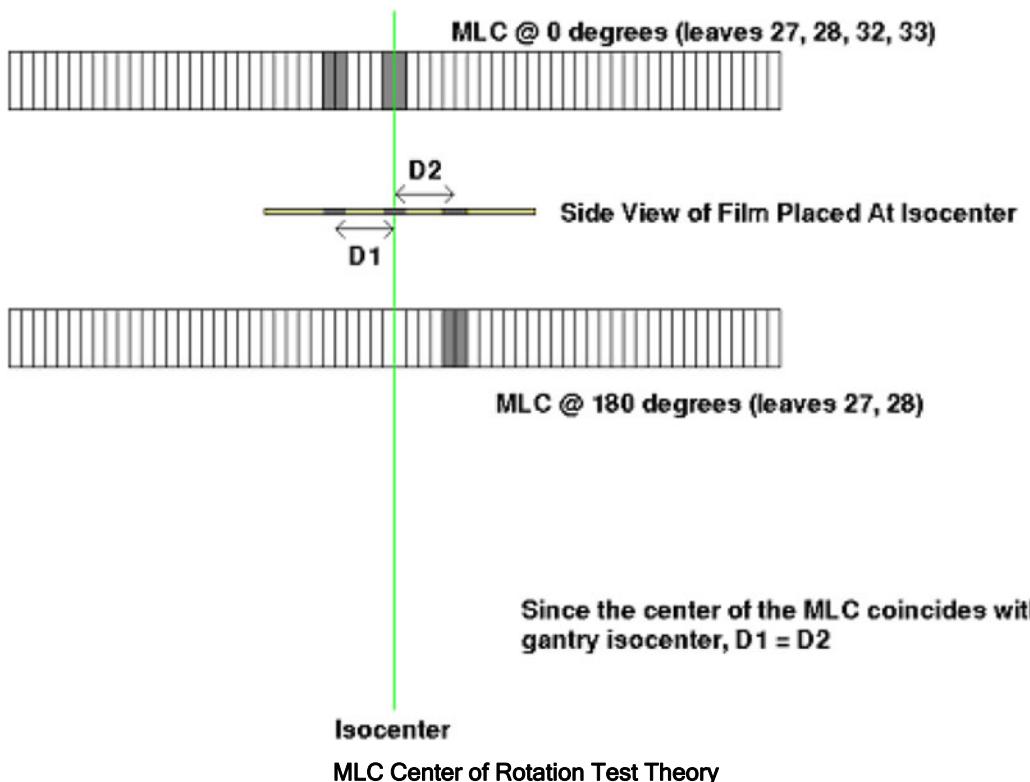
## ◆ Overview of MLC COR Test

<b>TG-148 reference:</b>	MLC lateral offset and MLC twist (section V.B.1.f)
<b>Other names for this test:</b>	MLC center gantry isocenter
<b>Purpose:</b>	Verify that MLC is parallel to the beam plane, and that the center of the MLC bank (between leaves 32 and 33) corresponds to the gantry isocenter.
<b>Method:</b>	At gantry angle 0°, expose a film in the coronal plane at isocenter with leaves 27-28 and 32-33 open. At gantry angle 180°, expose the same film with leaves 27-28 open. Check that the three exposures are parallel and equidistant.
<b>Accuracy specification:</b>	MLC offset is $0 \pm 1.5$ mm; MLC twist < 0.5 deg
<b>Sample result image:</b>	
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• Two 2-cm blocks of <i>Virtual Water</i> (55 cm x 15 cm x 2 cm)</li><li>• 1 EDR or EBT film (recommended minimum size: 20 cm x 25 cm)</li><li>• Pin for marking the EDR film, or medium-point permanent marker for EBT film</li><li>• Film scanner, computer, and Analysis software</li></ul>

## ◆ Theory of MLC COR Test

The beam model contains a parameter to represent the centering of the MLC with respect to the gantry center of rotation. This parameter is determined by your installer, using the same on-board detector data that is collected for leaf filter measurements. The customer film test is not used to update the value in the beam model, but it does check that the MLC center (between leaves 32 and 33) corresponds to gantry isocenter within +/- 1.5 mm, and that the leaves are parallel to the Y axis. If the test fails the MLC may be improperly bolted to the gantry.

To perform the test, the film is placed in the coronal plane at isocenter and exposed at 0° and 180° angles, without moving the film between exposures. For the 0° exposure, leaves 27, 28, 32, and 33 are open; for the 180° exposure, leaves 27 and 28 are open. For the 0° exposure, leaves 27 and 28 are on the -X side of isocenter, and for the 180° exposure, leaves 27 and 28 are on the + X side of isocenter. If the MLC is perfectly centered above isocenter, the three exposures on the film will be parallel and equidistant. The MLC offset is half the difference between the distance from the right exposure to the central exposure and the distance from the left exposure to the central exposure. The MLC twist is half the angular difference between the exposures.



## ◆ XML Description

MLC COR Test	
<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" .xml package. See "XML Files for Film Alignment Tests" (page 120).
<b>Machine QA Name:</b>	<b>ZZZ TG148 Film Alignment Tests-MultiFragment</b> , or <b>ZZZ GAF TG148 Film Alignment Tests-MultiFragment</b>
<b>Procedure Description:</b>	<i>MLC center of rotation</i>
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0 deg and 180 deg
<b>Jaws:</b>	J50 (maximum possible field size; a little larger than the nominal 5-cm beam)
<b>MLC:</b>	<ul style="list-style-type: none"><li>At gantry angle 0°, leaves 27, 28, 32, and 33 are open (also leaves 1 and 64 for the EDR .xml only, although these leaves are not used in the analysis).</li><li>At gantry angle 180°, leaves 27 and 28 are open (also leaves 2 and 63 for the EDR .xml only, although these leaves are not used in the analysis).</li></ul>
<b>Beam-on time:</b>	At each gantry angle, the beam is on for 40 s for EDR film (including a 20 s warm up), or 60 s for EBT film (including a 20 s warm up).

## ◆ Set Up and Deliver the Test

1. Position a 20 mm block of *Virtual Water* on the couch top so it is centered under the overhead laser (at virtual isocenter). The surface of the *Virtual Water* should be at isocenter height.
2. Move the couch exactly 700 mm in the IEC Y direction into the bore and account for couch sag using the **Step Move** function. The bore green laser should be aligned with the film plane. When finished adjusting for couch sag, do not bring the couch out of the bore.

3. Position a film on the *Virtual Water* block in **Portrait** or **Landscape** orientation (it is not necessary to mark the lasers for this test).
4. If desired, place a mark (dot) in the +IEC X, +IEC Y corner of the film.
5. Place a 20 mm block of *Virtual Water* over the film.
6. Run the procedure. The procedure delivers the 0° and 180° beams in automatic sequence.

## ◆ Analyze the Result

The MLC COR film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.



**TIP:** The sign of the result is not important for this test, so it is not critical that the film alignment mark is in the upper right corner.



**IMPORTANT:** Prior to accepting the RIT results, check the **Aligned Image** to ensure that the exposures are in the vertical orientation, and the top crop lines separate the exposures from any markings (change the **Top Crop Percentage** in the MLC COR Settings to adjust the position of the lines).



**IMPORTANT:** Prior to accepting the RIT results, check the **Analyzed Image** to ensure that the center of each exposure is correctly identified by the blue dots.



**IMPORTANT:** Never use the ROI tool to cut off part of the beam. The entire beam, and some empty space around the beam, is needed for accurate alignment of the film.

## ◆ What to Do if the Test Fails

The most likely cause of failure is an incorrect source-to-film distance. If the SSD for your setup is correct and the test still fails, contact Accuray Customer Support for assistance. In extremely rare cases, the MLC may not be properly bolted to the gantry.

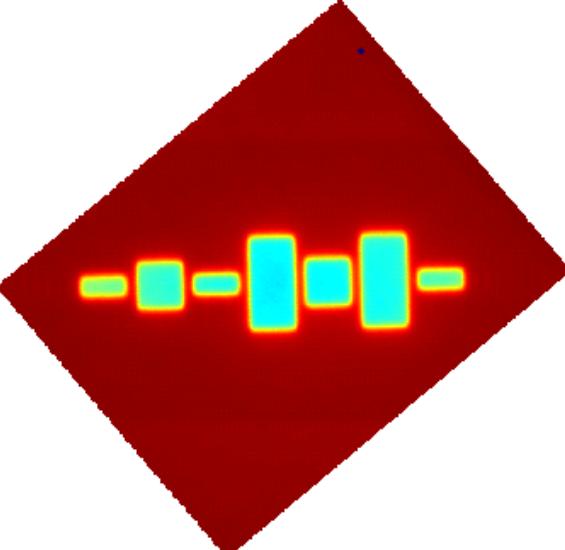


**IMPORTANT:** The three exposures on the film should be the same size. Although Accuray Incorporated has no specification about the size of the exposures, RITg148+ will issue a warning if the **Largest Area Difference** exceeds 20%. If a warning appears, check the source-to-film distance, then contact Accuray Customer Support to check that the MLC is properly attached to the gantry.

# Field Center vs. Jaw Setting

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## ◆ Overview of Field Center vs. Jaw Setting Test

<b>TG-148 reference:</b>	Treatment beam field centering (section V.B.1.e)
<b>Other names for this test:</b>	FC v. JS
<b>Purpose:</b>	Verify that the jaws open and close symmetrically about the central axis, so that the centers for different field sizes are consistent in the IEC Y direction.
<b>Method:</b>	Expose a film in the coronal plane at isocenter to the three different field widths. Compare the IEC Y center positions of the exposures.
<b>Accuracy specification:</b>	Individual exposure centers differ from the average center by < 0.5 mm.
<b>Sample result image:</b>	

**Equipment needed:**

- Two 20 mm blocks of *Virtual Water* (55 cm x 15 cm x 2 cm)
- 1 EDR or EBT film (recommended minimum size: 200 mm x 250 mm)
- Pin for marking the EDR film, or medium-point permanent marker for EBT film
- Film scanner, computer, Analysis Software

## ◆ Theory of Field Center vs. Jaw Setting Test

A film is placed in the coronal plane at isocenter and exposed to the three commissioned fixed treatment field widths, without moving the film between exposures. The MLC is used to limit the transverse extent of each exposure. The IEC Y center positions of the exposures should be consistent for all field widths.

## ◆ XML Description

### Field Center vs. Jaw Setting

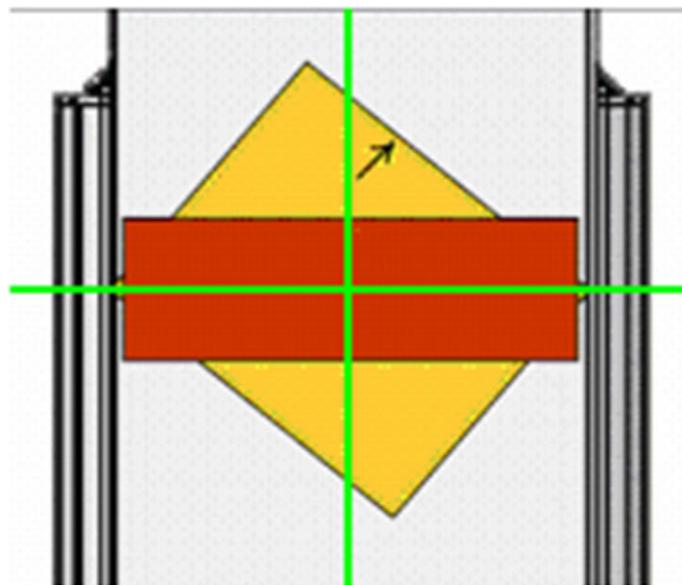
<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" .xml package. See "XML Files for Film Alignment Tests" (page 120).
<b>Patient Name:</b>	ZZZ TG148 Film Alignment Tests-MultiFragment, or ZZZ GAF TG148 Film Alignment Tests-MultiFragment
<b>Procedure Description:</b>	Field Center v jaw setting
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0 deg
<b>Jaws:</b>	J42 (nominal 5 cm), J20 (nominal 2.5 cm), and J07 (nominal 1 cm)

## Field Center vs. Jaw Setting

<b>MLC:</b>	The pattern of open and closed leaves spans from leaf number 16 to leaf number 49 (approximately 21 cm in the transverse dimension): <ul style="list-style-type: none"><li>• When the jaws are set to the 5-cm field, leaves 31-34 and 41-44 are open.</li><li>• When the jaws are set to the 2.5-cm field, leaves 21-24 and 36-39 are open.</li><li>• When the jaws are set to the 1-cm field, leaves 16-19, 26-29, and 46-49 are open.</li></ul>
<b>Beam-on time:</b>	For each field size, the beam is on for 25 seconds for EDR film, or 75 seconds for EBT film.

## ◆ Set Up and Deliver the Test

1. Position a 20 mm block of *Virtual Water* on the couch top so it is centered under the overhead laser (at virtual isocenter). The surface of the *Virtual Water* should be at isocenter height.
2. Move the couch exactly 700 mm into the bore and account for couch sag. When finished adjusting for couch sag, leave the couch in the bore (setup to ready couch movement is 0 for this test).
3. Position a film on the *Virtual Water* block. Landscape orientation is preferred for the RIT analysis. However, the film can be placed at an angle if needed to achieve sufficient width for the measurement. Ensure that the film is wide enough to accommodate the transverse width of the exposure (more than 210 mm).



Film in Coronal Plane on Couch in a Diagonal Orientation

4. It is not necessary to mark the lasers for this test. If desired, place a mark (dot with a permanent marker) in the +IEC X, +IEC Y corner of the film.
5. Place a 20 mm block of *Virtual Water* over the film.
6. Run the procedure. The procedure delivers three field widths in automatic sequence.

## ◆ Analyze the Result

The field center vs. jaw setting film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.



**TIP:** The sign of the result is not important for this test, so it is not critical that the film alignment mark is in the upper right corner.



**IMPORTANT:** Prior to accepting the RIT results, check the **Aligned Image** to ensure that the exposures are in the horizontal orientation, and the top crop lines separate the exposures from any markings (you can change the **Top Crop Percentage** to adjust the position of the lines).



**IMPORTANT:** Prior to accepting the RIT results, check the **Analyzed Image** to ensure that it identifies the exposure centers.



**IMPORTANT:** This test includes two or three exposures of each field width, at different IEC X positions in the row of exposures. The field center results for each instance of the same field size in the row of exposures are expected to be very similar. If they do not agree, the software may have done a poor job aligning the film.



**IMPORTANT:** Never use the ROI tool to cut off part of the beam. The entire beam, and some empty space around the beam, is needed for accurate alignment of the film.

## ◆ What to Do if the Test Fails

This test does not have a history of failure. If it fails, first check for a setup issue. Then ask Accuray Customer Support to troubleshoot the jaws.





## Measuring Beam Profiles

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# Overview of Beam Profiles

<b>TG-148 reference:</b>	Beam quality (section V.B.2.a), Transverse profile (section V.B.2.b), and Longitudinal profiles (section V.B.2.c)
<b>Other names for this test:</b>	The transverse profile is sometimes referred to as the "cone" profile within Accuray Incorporated software (but this usage is avoided to prevent confusion with a LINAC accessory, since none is used). The longitudinal profile is sometimes referred to as "penumbra."
<b>Purpose:</b>	Verify that the PDDs, longitudinal profiles, and transverse profiles agree with the gold standard data
<b>Method:</b>	Measurements in a water tank
<b>Accuray specification:</b>	<ol style="list-style-type: none"> <li>1. Longitudinal profiles at 15 mm depth:           <ul style="list-style-type: none"> <li>• Symmetric profiles: FWHM is within 1% of the reference FWHM. Gamma &lt; 1 over a range of three times the field width (gamma criteria: 2% dose difference and 1% of the field width for the distance to agreement (DTA))</li> <li>• Asymmetric profiles for systems with the <i>TomoEDGE</i> feature: Gamma &lt; 1 over a range of three times the field width (gamma criteria: 3% dose difference and 0.5 mm DTA)</li> </ul> </li> <li>2. PDDs for all fixed field widths within 2% of gold standard data, from 10 mm to 200 mm depth</li> <li>3. Transverse profiles for all fixed field widths at 15 mm depth: FWQM (full-width at 25% max) is within 1% of the reference FWQM. Gamma &lt; 1 over a range of 400 mm (gamma criteria: 2% dose difference and 1 mm DTA)</li> </ol>
<b>Equipment needed:</b>	<ul style="list-style-type: none"> <li>• Water tank and scan arm</li> <li>• Waterproof ion chamber</li> <li>• Reference chamber</li> <li>• Electrometer</li> <li>• PC and software to drive the tank and plot data</li> <li>• Associated cables and electronics</li> <li>• PC with <i>Microsoft Excel</i></li> <li>• TQA™ Advanced (optional)</li> </ul>

# Theory of Beam Profile Measurements

This section provides instructions for collecting profiles in the water tank. Absolute dose calibration for the system is not performed in the water tank, but is performed via helical IMRT treatment plan calculations and delivery in a solid phantom such as the *Tomo*-phantom; see “Absolute Dose Calibration” (page 211).

TG-148 recommends an annual dose measurement in a water tank. This measurement is only a constancy check and is not used to adjust the machine (see “Annual QA” (page 371) ). If desired, perform a dose measurement when the water tank is set up for profile measurements. However, if subsequent IMRT dose calibration measurements lead to machine adjustments, your water tank dose measurement will be invalidated and will need to be redone.

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## ◆ Explanation of Accuray Incorporated Tolerances

Longitudinal profiles, transverse profiles, and PDDs should be collected for all fixed field widths. The fixed field widths include the nominal 50 mm, 25 mm, and 10 mm field widths, plus the intermediate 18 mm field width for machines with dynamic jaws.

The Accuray Incorporated tolerance for symmetric longitudinal profiles includes both a FWHM requirement and a gamma requirement. TG-148 does not include the gamma analysis requirement. The gamma analysis method is described in Low 1998.

Systems with dynamic jaws include six asymmetric profiles in the beam model. The asymmetric profiles are only used briefly at the beginning and end of treatments with dynamic jaws, as interpolation points for the dose calculator. As such, there is no FWHM requirement for the asymmetric profiles. Accuray Incorporated applies gamma criteria of 3% dose difference and 0.5 mm DTA. The 0.5 mm DTA criterion corresponds to 1% of the nominal 50 mm fixed field width. All asymmetric profiles share one field edge with the 50 mm beam.

The Accuray Incorporated specification for PDD measurements is agreement with the gold standard within 2%, for depths ranging from 10 mm to 200 mm. Surface depths are ignored due to the use of a cylindrical A1SL ion chamber for the gold standard data collection. Because the 10-mm PDD is very sensitive to water tank alignment, it is recommended to collect both a regular PDD and a "serpentine" (snake-like) PDD for the 10-mm field width. A serpentine PDD involves taking a small longitudinal profile at each depth to ensure that the maximum value is identified.

Accuray Incorporated criteria for the transverse profiles includes a gamma measurement and a FWQM (full width at quarter max) measurement. The 25% max is used because it is a stable position to measure the field size; the half-max is too close to the "corners" of the transverse profile.

## ◆ Equipment and Setup Considerations

Because the data used to derive the beam model was collected with an A1SL ion chamber and Standard Imaging Water Tank it is recommended that the site physicist compare their data against the Accuray Incorporated reference data if the same equipment is used.

Measurements using other chamber models (which will have different response functions) are not directly comparable to Accuray Incorporated reference data. If using different equipment, the site physicist will need to determine and account for the response function of the chamber in use [see "Chamber Response Function" (page 191)] or create a secondary standard data set with your current equipment shortly after Accuray Incorporated finishes verifying the beam profiles in the water tank at ATP. For more information about using other water tanks see "Appendix A" (page 483).

For information on the recommended procedures to acquire secondary reference data and perform comparisons with other water tanks or ion chambers, contact Accuray Customer Support.

If a two-dimensional water tank such as the Standard Imaging tank is used, it will be necessary to rotate the tank to switch between the longitudinal/PDD orientation and the transverse orientation. It is recommended to start with the longitudinal/PDD orientation, since this orientation is most likely to reveal a need for beam adjustments. The transverse profiles usually pass if the longitudinal profiles and PDDs pass. Since the transverse width of the beam is determined by the fixed collimation system, if the beam width does not match the reference data, it usually indicates a setup error (such as incorrect SSD).

A reference chamber may be used to monitor the constancy of the output while collecting water tank data. The reference chamber must be placed in a location where it does not interfere with the beam's path to the measurement chamber and the measurement chamber does not interfere with the beam's path to the reference chamber.

For the Standard Imaging Water tank, an A17 chamber may be placed in the moat outside the water tank, along the long edge of the tank. The signal at this position will be low for some setups.



**NOTE:** For example, in the transverse orientation of the SI water tank, placing the A17 chamber in the moat means it will only collect beam scatter.

In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio and should not be necessary if the reference chamber data shows that the beam output is stable during the delivery.

TG-51 notes that the effective point of measurement for a cylindrical chamber is upstream from the actual chamber position, due to the mainly forward direction of the secondary electrons. Accuray Incorporated accounts for the effective depth by collecting all water tank profiles with the cylindrical A1SL chamber physically shifted 1.2 mm deeper than the stated depth of measurement ( $r_{cav} = 2.025 \text{ mm}$ ;  $0.6 r_{cav} = 1.215 \text{ mm}$ ).

## ◆ Analysis Method

*TQA* can be used to verify transverse profiles, non-serpentine PDDS, and longitudinal profiles. See the Accuray TQA software manual for more information regarding profile analysis.

If *TQA* is unavailable, the following alternative methods of profile analysis can be used instead.

The TEMS software that comes with the Beam Measurement and QA package (Standard Imaging water tank kit) may be used to determine the FWHM or FWQM size of the profiles. It also includes processing features (shift on FW%M, interpolate, etc.) to allow for further comparison in *Excel*, but does not include tools for automatic comparisons between measured and reference profiles.

You can use your own gamma profile comparison tool or plot the measured and reference data together in the *Microsoft Excel*/spreadsheet provided by Accuray Incorporated, for visual comparison.

The Microsoft *Excel*/spreadsheet provided by Accuray Incorporated is called the TCOM (Treatment Commissioning) spreadsheet. The TCOM spreadsheet includes the reference water tank data as well as the corresponding calculated dose profiles generated using the beam model installed on your system. This includes the PDD, transverse, and longitudinal profiles for all commissioned treatment beams.



**IMPORTANT:** There are several different beam models in the field. Use the spreadsheet provided by Accuray Incorporated that is appropriate for your beam model.

## ◆ Chamber Response Function

The data for the beam model was measured using a Standard Imaging water tank and an A1SL ion chamber. Therefore,

$$\text{Measured Profile} = \text{Actual Profile} \otimes \text{Detector Response}$$

Detector response can have a significant impact on profile measurements in the high gradient regions. This was taken into consideration in the reference water tank profiles:

- The longitudinal fluence profiles in the beam model were deconvolved from the A1SL response, to make them independent of the A1SL chamber characteristics.
- The transverse profile data was not deconvolved from the detector response, because the high gradient regions of the transverse profile (penumbra region) are modeled by the leaf filters, not the transverse profile data.
- The PDD data was not deconvolved from the detector response, because the high gradient (build up) region of the PDD data is outside the comparison range of Accuray Incorporated. See “Explanation of Accuray Incorporated Tolerances” (page 189).

A set of reference data provided by Accuray Incorporated and corresponding to the beam model of your system consists of longitudinal profiles (already convolved with the A1SL ion chamber response and labeled as "convolved calculated"), transverse profiles, and PDDs. This data may be appropriately compared with your measurements using an A1SL chamber.

If a different ion chamber is used for QA measurements and if you intend to compare the longitudinal profile measurements against the beam model data, you can perform the following tasks.

1. Determine the chamber response function. (Accuray Incorporated does not provide tools to assist in determining the chamber response function.)
2. Locate the de-convolved longitudinal profiles in the TCOM spreadsheet provided by Accuray Incorporated. These profiles were generated using the beam model installed on the system.
3. Convolve the de-convolved model profiles from Step 2 with the chamber response function determined in Step 1, to facilitate comparison against longitudinal water tank data measured with your ion chamber.

# XML Description

The .xml files listed in this section include procedures for measuring water tank data on machines that have dynamic jaws, and are suitable for measuring water tank data on machines that do not have dynamic jaws. The .xml files contain the same machine settings that were used for the reference data collection when Accuray Incorporated created the beam model. All water tank scans are run from the **Machine QA** task of the TDC.



**NOTE:** If the machine does not have dynamic jaws, use the .xml files listed below, and ignore the J14mm procedure and all the asymmetric procedures.



**NOTE:** The water tank .xml files have all leaves open for the transverse profile measurements, but only the central 40 leaves open in the longitudinal tank orientation, due to the limited width of the Standard Imaging water tank along its shorter dimension.

## Longitudinal Profile and PDD Measurements

<b>Where to get the XML:</b>	The WaterTankLongitudinal.xml file may be requested from Accuray Customer Support or downloaded from <i>TQA</i> .
<b>Patient Name:</b>	ZZZ Water Tank Longitudinal (Mid40 leaves)
<b>Procedure Descriptions:</b>	<ul style="list-style-type: none"><li>• J42mm Mid40leaves</li><li>• J20mm Mid40Leaves</li><li>• J14mmMid40Leaves</li><li>• J7mm Mid40Leaves</li><li>• J20mm +IECY Mid40Leaves</li><li>• J14mm +IECY Mid40Leaves</li><li>• J7mm +IECY Mid40Leaves</li><li>• J20mm -IECY Mid40Leaves</li><li>• J14mm -IECY Mid40Leaves</li><li>• J7mm -IECY Mid40Leaves</li></ul>
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	See procedure descriptions

### Longitudinal Profile and PDD Measurements

<b>MLC:</b>	Leaves 13-52 open (40 central leaves)
<b>Beam-on time:</b>	1000 s (the procedure may be interrupted when finished collecting data)

### Transverse Profile Setup

<b>Where to get the XML:</b>	The <b>WaterTankTransverseSetup.xml</b> file may be requested from Accuray Customer Support or downloaded from <i>TQA</i> .
<b>Patient Name:</b>	ZZZ Water Tank Transverse Setup Topo
<b>Procedure Description:</b>	Topo_FW10_AllLeavesOpen_Couch_40sec
<b>Couch movement in IEC Y when Ready is pressed:</b>	30 mm
<b>Couch translation during the procedure:</b>	1.0 mm/s
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	J07 (nominal 1 cm field width)
<b>MLC:</b>	All leaves open
<b>Beam-on time:</b>	40 s

### Transverse Profile Measurements

<b>Where to get the XML:</b>	The <b>WaterTankTransverse.xml</b> file may be requested from Accuray Customer Support or downloaded from <i>TQA</i> .
<b>Patient Name:</b>	ZZZ Water Tank Transverse (All Open)
<b>Procedure Description:</b>	<ul style="list-style-type: none"> <li>• J42mm All Open</li> <li>• J20mm All Open</li> <li>• J7mm All Open</li> <li>• J14mm All Open</li> </ul>

### Transverse Profile Measurements

<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	See procedure descriptions
<b>MLC:</b>	All leaves open
<b>Beam-on time:</b>	1000 s (the procedure may be interrupted when finished collecting data)

# Set Up and Deliver the Test

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**NOTE:** This section contains general instructions for water tank data collection. Instructions specific to the Standard Imaging equipment and TEMS software may be found in the appendix “Appendix A” (page 483).



**IMPORTANT:** Before performing QA tasks, warm up the system and run an air scan as described in “Basic Procedures” (page 75) to help achieve a stable beam and optimal image quality.

## ◆ Initial Tank Setup: Longitudinal Orientation

1. Set the water tank on the couch at virtual isocenter. If it is a 2D tank, start with the orientation that will be used to collect longitudinal profiles and PDDs.
2. Align the yaw rotation of the tank with the green overhead lasers (it may be easier to do this with an empty tank).
3. Fill the tank with water to a depth of at least 215 mm.
4. Place the measurement chamber in the scan arm holder.
5. Place the reference chamber in the appropriate position.
6. While you are still in the treatment room, use the scan arm controller to send the chamber around the entire perimeter of the tank. Ensure that:
  - The limit switches prevent the chamber from colliding with the tank walls or compressing the ion chamber cable against the tank walls.
  - The setup allows the signal cable to move freely in the tank.
  - The measurement chamber cable does not interfere with the beam path to the measurement chamber.
  - The reference chamber does not interfere with the beam's path to the measurement chamber, and the measurement chamber does not interfere with the beam's path to the reference chamber.



**CAUTION:** If the measurement chamber cable intercepts the beam path to the chamber, it will cause anomalies in the signal.

7. With the tank out of the bore at virtual isocenter:
  - Align the yaw rotation of the tank ( $\pm$  IEC Y) so that the chamber travels parallel to the overhead sagittal laser.
  - Move the chamber to the approximate center of the tank in Y. Then, adjust the tank so that the chamber collection volume is centered on the green overhead lasers in X and Y.
8. Send the tank 700 mm into the bore.



**IMPORTANT:** Check for sufficient clearance as the couch moves into the bore.

9. With the tank in the bore at isocenter:
  - Adjust the couch height so that the surface of the water corresponds to the green bore lasers (850 mm SSD).
  - Adjust the leveling of the tank or scan arm (pitch) so that the chamber travels parallel to the surface of the water.



**IMPORTANT:** The pitch of the tank must be adjusted with the couch in the bore, to account for the effects of couch sag.

- Adjust the leveling of the tank or scan arm (roll) so that the vertical travel of the chamber is parallel to the Z axis.
  - Adjust the depth of the chamber so that it is half-submerged.
10. Re-check the tank setup to ensure that all parameters in Steps 7-9 pass (some parameters are inter-dependent).
11. Send the cylindrical chamber  $0.6 r_{cav}$  deeper into the tank, to account for the effective depth of measurement. In the software, mark this chamber position as the origin (zero position).
12. If desired, bring the couch out of the bore 700 mm and acquire a *CTrue™* image to verify the setup (water at 850 mm SSD, chamber at 1.2 mm physical depth). Adjust the setup if needed, then send the couch 700 mm into the bore.

## ◆ Alignment Verification: Longitudinal Orientation

Prior to measuring water tank profiles, check the Y position of the chamber and the rotational alignment of the tank about the X axis (pitch) by collecting alignment profiles:

1. Open the **ZZZ Water Tank Longitudinal (Mid40 leaves)** patient, and run a **J7mm Mid40Leaves** procedure.
2. After the beam has been on for at least 10 seconds, use the water tank software to collect longitudinal profiles at depths of 15 mm and 200 mm. Collect data in steps of 0.5 mm over a 30 mm range.
3. Use the water tank software to find the centers of the profiles (based on their FWHM), relative to the center position of the chamber.
4. If the centers of the profiles at different depths differ by more than 2 mm, adjust the leveling of the tank in the room, reset the depth of the chamber, and run the scans again until it passes.

If the profiles at different depths agree within 2 mm, the rotation of the tank about the X axis (pitch) is acceptable. With the chamber in its zero position (origin; 1.2 mm physical depth), adjust the Y position of the chamber according to the average of the results for the two profiles, and reset the origin in the software.



**NOTE:** Although the chamber was aligned in the Y position to the lasers when it was outside the bore, a small Y adjustment is typically required when the chamber is inside the bore, due to the effect of the couch sag pitch on the Y position of the chamber.

## ◆ Symmetric Longitudinal Profiles

Collect longitudinal profiles for all the symmetric field widths. The specification is based on the 15 mm depth, but it is recommended to collect data at depths of: [15, 50, 100, 150, and 200] mm. A time sampling resolution of 100 ms may be used. The recommended minimum scan distances and couch speeds are listed in the following table.

Field Width (mm)	Total Scan Distance (mm)	Scan Speed (mm/s)	Scan Depths (mm)
FW10 (J07)	100	1	15,50,100,150,200
FW18 (J14)	150	2	15,50,100,150,200
FW25 (J20)	150	2	15,50,100,150,200
FW50 (J42)	200	2	15,50,100,150,200

## ◆ PDDs

Collect PDDs for all symmetric field widths. Measure the PDD at depths of 0 to 19 mm in steps of 1 mm, and 20 to 220 mm in steps of 10 mm. Also, perform a serpentine PDD for the 10 mm field (longitudinal profiles at 2 mm/s scan speed over a distance of 20 mm in Y at each depth).

## ◆ Asymmetric Longitudinal Profiles

Asymmetric longitudinal profiles must be collected with precise longitudinal positioning. They are typically only measured at 15 mm depth.

To verify the setup for the asymmetric profiles, repeat the alignment profile at depth 15 mm as described in “Alignment Verification: Longitudinal Orientation” (page 198), and adjust the Y reference position until the symmetric 1 cm profile is centered within  $\pm 0.05$  mm of isocenter at depth 15 mm.

Collect the longitudinal asymmetric profiles at 15 mm depth in 1.0 mm steps over at least 100 mm scan distance, for all the asymmetric field widths.

## ◆ Initial Tank Setup: Transverse Orientation

1. With a 2D tank, bring the tank out of the bore and rotate the tank 90° to collect the transverse profiles. Use the scan arm controller to send the chamber around the entire perimeter of the tank to ensure that the cables have sufficient slack and do not get in the way of the measurement.



**TIP:** Mark the transverse and sagittal overhead lasers with tape on the tank prior to rotating it. These marks can be used as a guideline to achieve a 90° rotation from the previous setup in the longitudinal orientation.

2. With the tank out of the bore at virtual isocenter:
  - a) Align the yaw rotation of the tank so that the chamber travels parallel to the overhead transverse laser.
  - b) Move the chamber to the approximate center of the tank in X. Then, adjust the tank so that the chamber collection volume is centered on the green overhead lasers in X and Y.
3. Send the tank 700 mm into the bore.
4. With the tank in the bore at isocenter:
  - a) Adjust the couch height so that when the tank is in the bore, the green bore laser skims the surface of the water (850 mm SSD).
  - b) Re-level the setup to account for couch sag in the new orientation. When the tank is in the bore, the chamber should travel parallel to the

- surface of the water. Also when the tank is in the bore, the pitch of the scan arm will need to be adjusted for couch sag using a level.
- c) Adjust the depth of the chamber so that it is half-submerged.
  - 5. Re-check the tank setup to ensure that all parameters in Steps 2-4 pass (some steps are inter-dependent).
  - 6. Send the cylindrical chamber  $0.6 r_{cav}$  deeper into the tank, to account for the effective depth of measurement. In the software, mark this chamber position as the origin (zero position).
  - 7. If desired, bring the tank out of the bore and acquire a *CTrue™* image to confirm the setup. Adjust the setup if needed, then send the couch 700 mm into the bore.

## ◆ Alignment Verification: Transverse Orientation

Prior to measuring water tank profiles, check the rotational alignment of the tank by collecting alignment profiles:

1. Bring the couch 50 mm out of the bore and run a set of 3 setup verification scans using the **WaterTankTransverseSetup.xml** patient. For each scan, use a different chamber position: 1) X = -150 mm, depth = 15 mm; 2) X = +150 mm, depth = 15 mm; 3) X = 0, depth = 200 mm. Start the profile measurement before the beam turns on.



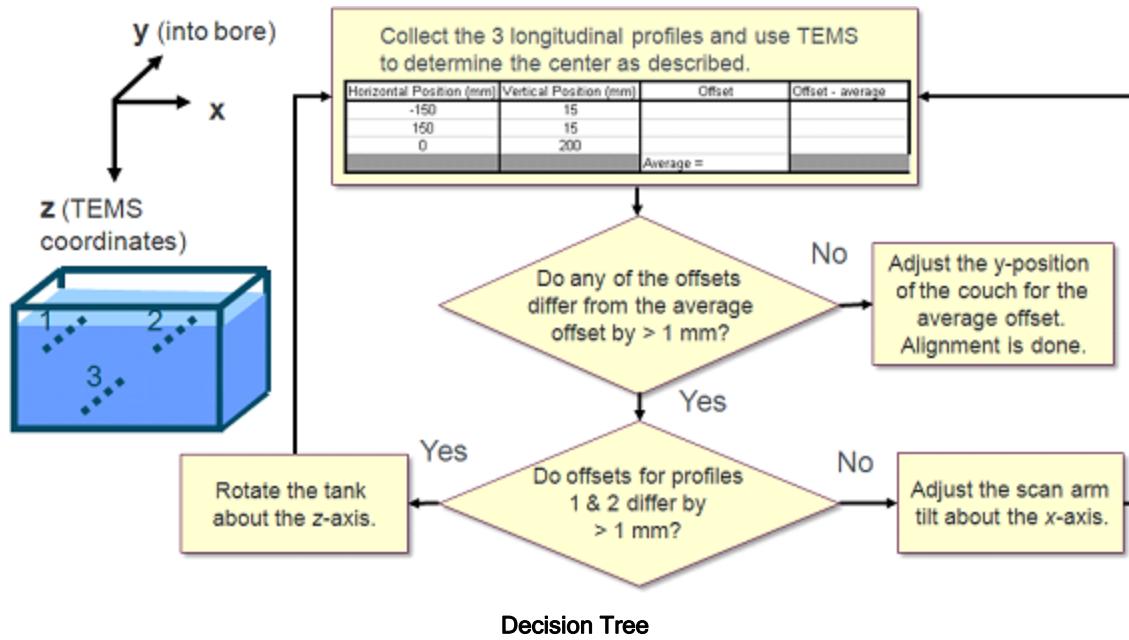
**NOTE:** Each **WaterTankTransverseSetup.xml** procedure sends the couch 30 mm into the bore (setup to ready distance). During beam-on, the couch travels in the Y direction to collect a longitudinal profile over 40 mm distance (scanning a range of [-20 mm, 20 mm] in Y with respect to isocenter). When the procedure is finished, the couch returns to the position just before **Ready** was pressed.

2. Since the profile measurement is started before turning the beam on, the beam-on and beam-off corners can be identified in the profiles by the sudden increase in the chamber signal. Check the FWHM centering of each profile relative to the beam-on and beam-off positions. Determine the average centering result. See the following image for more information.

If the individual profiles differ from their average by more than 1 mm, adjust the leveling of the tank in the room (pitch or yaw), reset the depth of the chamber, and run the scans again until it passes.

If the individual profiles are within 1 mm of their average, the rotation of the tank about the X and Z axes (pitch and yaw) is acceptable. Adjust the Y position of the couch to correct for the average center position in your 3 scans.

3. Bring the couch 50 mm into the bore (to isocenter).



## ◆ Transverse Profiles

Transverse profiles for all symmetric field widths should be collected. Although the specification is based on the 15 mm depth, it is recommended to collect transverse profiles at depths of [15, 50, 100, 150, 200] mm. Accuray Incorporated uses a horizontal velocity of 6 mm/s, and a scan distance of 510 mm for the transverse profile scans.

# Analyze the Result

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## ◆ General Notes Regarding the TCOM Spreadsheet



**NOTE:** See the TQA Guide for instructions on analyzing the profiles in TQA. This section discusses use of the TCOM spreadsheet for analysis.

Disregard any worksheets labeled for Helical data. All other worksheets contain measured and calculated beam profile data, or plots comparing the measured and calculated profile data. The yellow shaded cells are cells in which measured *processed* data should be copied. See “Appendix A” (page 483) for information on processing the data with TEMS.

When the spreadsheet is first provided, the **Measured Data** columns contain the reference water tank data that was averaged over ten production machines. This ten-machine average data was used to derive the beam model, but it is not identical to the beam model. The measured profile data in the TCOM spreadsheet can be overwritten with site specific measured data for comparison purposes.

By convention, when Accuray Incorporated personnel use internal non-commercial software for gamma comparison between measured and reference data, the reference data is the original ten-machine average data from the yellow **Measured Data** columns of the spreadsheet. However, for visual comparison in the TCOM spreadsheet, data calculated from the beam model is typically plotted as the reference for comparison against the site's measured A1SL data (see descriptions of **Scaled Convolved Calculated Data** and **Scaled CalcData** below). Comparing against the beam model data is more strictly correct than comparing against the ten-machine average.

### For Longitudinal Profile (LONG\_DATA\_##) Worksheets:

- The **Calculated Data** columns contain position and dose information for beam profiles generated by performing a dose calculation using the beam model installed on your system. This data is de-convolved from ion chamber response.



**NOTE:** If a chamber other than an A1SL is used, the calculated data can be convolved with the chamber's response to be compared with the measured data.

The de-convolved dose profiles can be found in the Calculated Data columns (A - J) of the LONG\_DATA\_## worksheets. Sample rows from a LONG\_DATA\_10 worksheet are presented in the following image. Two columns of data exist for each dose profile at a given depth: one column for position and one column for dose.

	Calculated Data (Gy/min)									
1	A	B	C	D	E	F	G	H	I	J
2	D15mm	6.877693	D50mm	5.41687	D100mm	3.800239	D150mm	2.684361	D200mm	1.905475
3	135	0.005726	135	0.007521	135	0.010544	135	0.011412	135	0.012188
4	134.5	0.00575	134.5	0.007556	134.5	0.010571	134.5	0.011439	134.5	0.012385
5	134	0.00586	134	0.007665	134	0.010727	134	0.011616	134	0.012484
6	133.5	0.005891	133.5	0.007855	133.5	0.01103	133.5	0.011772	133.5	0.012703
7	133	0.005913	133	0.008087	133	0.011065	133	0.011944	133	0.012925

De-Convolved Calculated Data from sample LONG\_DATA\_10 worksheet

- The **Convolved Calculated Data** columns contain the position and dose information from the Calculated Data columns convolved with the A1SL ion chamber response.
- The **Measured Data** columns contain position and dose information for measured beam profiles. This data is plotted on the corresponding plot worksheet.
- The **Scaled Convolved Calculated Data** columns contain the position and dose information from the Convolved Calculated Data columns scaled to the Measured Data maximum. This data is plotted on the corresponding plot worksheet.



NOTE: The **Scaled Convolved Calculated Data** can be used for comparison with longitudinal beam profile measurements that are collected using the A1SL ion chamber.

### For PDD Profile (PDD\_DATA\_##) Worksheets:

- The **Calculated Data** columns contain position and dose information for beam profiles calculated using the beam model installed on your system. The energy spectrum used by the Planning System was determined to make the calculated PDD very close to the gold measured PDD (average of 10 machines).
- The **Measured Data** columns contain position and dose information for measured beam profiles. This data is plotted on the corresponding plot worksheet.
- The **Scaled CalcData** column contains the dose information from the Calculated Data column scaled to match the Measured Data at depth 100mm.

## For Transverse Profile (TRAN\_DATA\_##) Worksheets:

- The **Calculated Data** columns contain position and dose information for beam profiles calculated using the beam model installed on your system.
- The **Measured Data** columns contain position and dose information for measured beam profiles. This data is plotted on the corresponding plot worksheet.
- The **Scaled Calculated Data** columns contain the position and dose information from the Calculated Data columns scaled to the Measured Data maximum. This data is plotted on the corresponding plot worksheet.

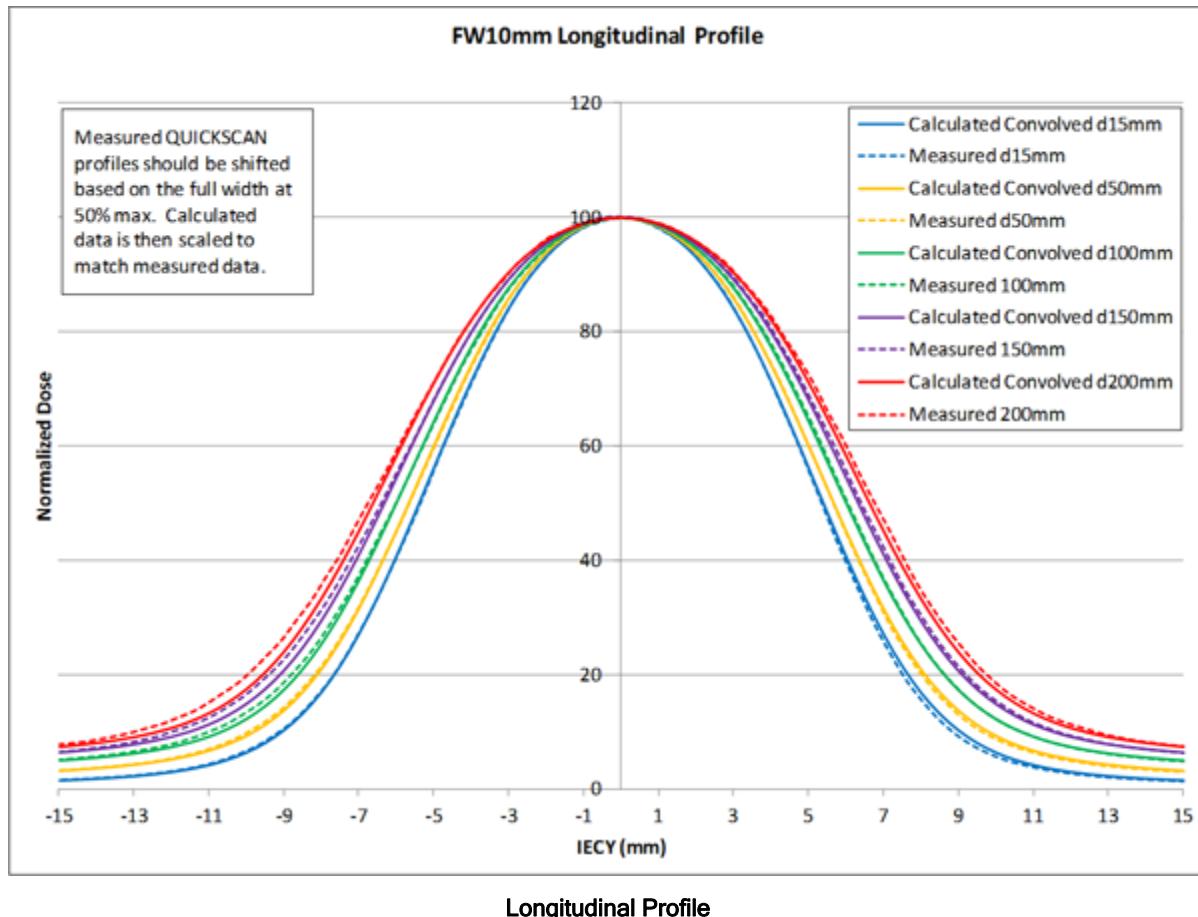
### ◆ Analyze Transverse (IECX) and Longitudinal (IECY) Data

1. If data is measured using the TEMS software, the data format is stored as a comma-separated value (.csv) file that can be opened in *Microsoft Excel*. Open the processed measured data in *Microsoft Excel* (see “Appendix A” (page 483) for processing instructions), and copy the **position** and **value** columns for each depth. A sample TEMS file can be seen in the following image.
2. Paste the measured processed data into the appropriate yellow shaded columns of the TCOM spreadsheet using **Paste Special > Values**.
3. Visually compare the measured and calculated data, or use your own (non-Accuray) analysis tools.

The following image is a sample longitudinal profile plot from the TCOM spreadsheet. Column C represents the chamber position (whether the scanning axis is X or Y depends on the orientation of the tank). Column D represents the chamber depth. Column E represents the measured data in Channel 1. Column F is the reference channel in this example. Note that in this example, Channel 1 was not normalized to the reference channel.

	A	B	C	D	E	F	G
7	*abs time	delta time	iec x/y	iec z	tt1	tt2	tt3
8	172	172	24.656	15	150.4439	35648.86	-
9	359	187	24.282	15	150.6657	35672.17	-
10	547	188	23.906	15	153.7706	35689.31	-
11	734	187	23.532	15	157.7746	35656.97	-
12	922	188	23.156	15	160.7356	35653.66	-
13	1109	187	22.782	15	165.4169	35633.16	-
14	1297	188	22.406	15	168.6297	35652.79	-
15	1484	187	22.032	15	167.9104	35651.69	-
16	1672	188	21.656	15	171.0813	35638.06	-
17	1859	187	21.282	15	174.7316	35625.47	-
18	2047	188	20.906	15	177.0453	35602.57	-
19	2234	187	20.532	15	179.5688	35651.94	-
20	2422	188	20.156	15	185.401	35653.68	-
21	2609	187	19.782	15	188.9974	35629.99	-
22	2797	188	19.406	15	193.6907	35635.7	-
23	2984	187	19.032	15	199.5948	35593.11	-
24	3172	188	18.656	15	206.8416	35648.9	-
25	3359	187	18.282	15	213.1413	35613.85	-
26	3547	188	17.906	15	218.2542	35642.3	-
27	3734	187	17.532	15	228.8456	35594.78	-
28	3922	188	17.156	15	233.7308	35619.6	-

Example of longitudinal profile data measured in TEMS and opened in *Microsoft Excel*

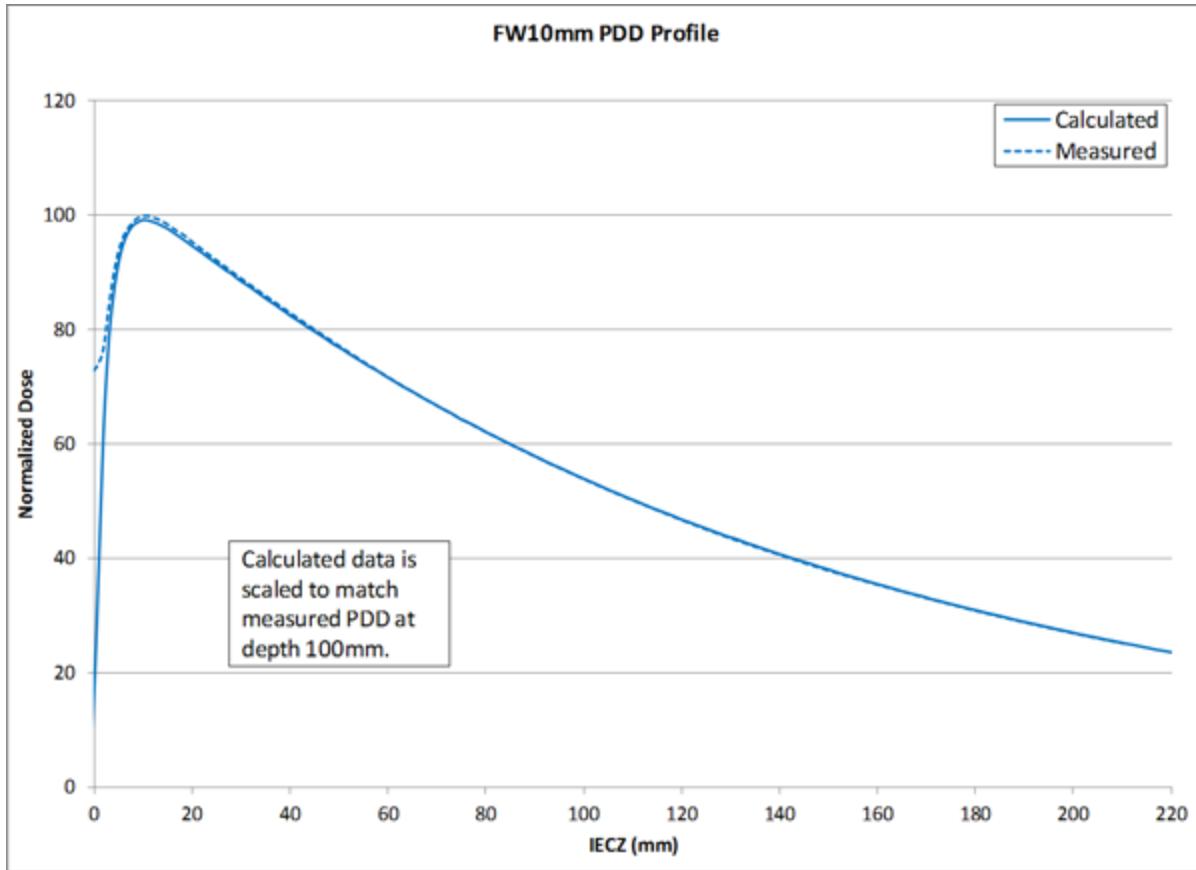


**Longitudinal Profile**

## ◆ Analyze PDD (IECZ) Data

1. If you measured your data using TEMS, copy the relevant depth and value data from the measured, TEMS-processed data files:
  - TEMS groups the profile data by depth. When you **Translate PDD** in TEMS, the algorithm created an artificial depth of 900 mm for grouping all the PDD data into one set.
  - Ignore rows in the measured processed spreadsheet where IEC Z < 900.
  - The rows labeled with depth 900.1 should be copied if the data channel was channel 1, and the rows labeled 900.2 should be copied if the data channel was channel 2. For non-serpentine profiles, 900.1 and 900.2 contain the same data.
2. Paste in the measured data in the yellow columns of the TCOM spreadsheet using **Paste Special > Values**. Depths are in mm.
3. Visually compare the measured and calculated data, or use your own (non-Accuray) analysis method. The spreadsheet scales the calculated

PDD to match your measured data at 10 cm depth. The following image is a sample PDD profile plot from the TCOM spreadsheet.



Sample PDD Profile Plot

## ◆ Results Summary

This table can be used to keep track of your results.

Field Width	PDD	Longitudinal (symmetric)	Longitudinal -IECY (asymmetric)	Longitudinal +IECY (asymmetric)	Transverse
FW10mm (J07)	PASS / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL
FW18mm (J14)	PASS / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL

<b>Field Width</b>	<b>PDD</b>	<b>Longitudinal (symmetric)</b>	<b>Longitudinal -IECY (asymmetric)</b>	<b>Longitudinal +IECY (asymmetric)</b>	<b>Transverse</b>
<b>FW25m m (J20)</b>	PAS S / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL	PASS / FAIL
<b>FW50m m (J42)</b>	PAS S / FAIL	PASS / FAIL	NA	NA	PASS / FAIL

## What to Do if the Test Fails

- Check the setup (tank leveling, SSD, depth and position of chamber). Go into the room to ensure that the chamber is in the expected position as reported by the scanning software.
- Ensure that the ion chamber cable is not intercepting the beam's view of the chamber at shallower depths.
- Ensure that the scan arm does not bounce or vibrate excessively during scanning.
- Ensure that the scan arm axes are square with each other.
- If you use the Standard Imaging tools, try collecting and comparing the longitudinal and transverse profiles at 15 mm depth in **Quick Scan** mode versus in **Step Profile** mode. (**Step Profile** mode eliminates chamber position uncertainties associated with scan arm acceleration.)
- Try analyzing the data without normalizing to the reference channel, since the reference channel may introduce noise to the data.
- If you have questions about interpreting the results, contact Accuray Customer Support.
- If you have determined that an adjustment is necessary (e.g., energy or field widths), contact Accuray Customer Support to perform the adjustment. After the adjustment, re-measure the water tank data to ensure that it passes. Also, follow up with IMRT dose verification.



**NOTE:** Your service representative is not trained in measuring water tank data, but is able to adjust the energy by a specified percentage, or address failing longitudinal profiles via measurements in *Virtual Water*.





## Absolute Dose Calibration

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# Overview of Absolute Dose Calibration

<b>TG-148 reference:</b>	Dosimetric verification (IV.B.3)
<b>Other names for this test:</b>	<i>TomoHelical</i> -phantom, <i>TomoDirect</i> -phantom
<b>Purpose:</b>	Verify that the dose delivered by the machine is consistent with predictions of the dose calculator.
<b>Method:</b>	For a set of IMRT plans in the <i>Tomo</i> -phantom, measure dose with an ion chamber and compare against calculated dose.
<b>Accuracy specification:</b>	Measured dose matches calculated dose to within $\pm 3\%$ of the target dose ( $\pm 3\%$ of 2 Gy is $\pm 0.06$ Gy) and $\pm 3$ mm for <i>TomoHelical</i> and <i>TomoDirect</i> plans.
<b>Sample result image:</b>	<p>The screenshot shows a Microsoft Excel spreadsheet with two main sections. The top section is a table with columns for Position, Value, Frac Dose (Gy), Ion Chamber #, IC Serial #, Electrometer (Cp), IC Cal (nGy/C), and various offsets and scaling factors. The bottom section is a graph titled "Calculated &amp; Delivered Dose: 50mm Beam, Non RSS" showing Dose (Gy) on the y-axis (0 to 2.0) versus Distance (cm) on the x-axis (-20 to 20). It displays a blue curve for calculated dose and red squares with error bars for measured dose, showing a sharp peak at 0 cm and a drop-off at +/- 10 cm.</p>
<b>Equipment needed:</b>	<ul style="list-style-type: none"> <li><i>Tomo</i>-phantom</li> <li>One or more A1SL ion chambers</li> <li>Electrometer</li> <li>Microsoft Excel</li> </ul>

# Theory of Absolute Dose Calibration

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## ◆ IMRT Dose Calibration Method

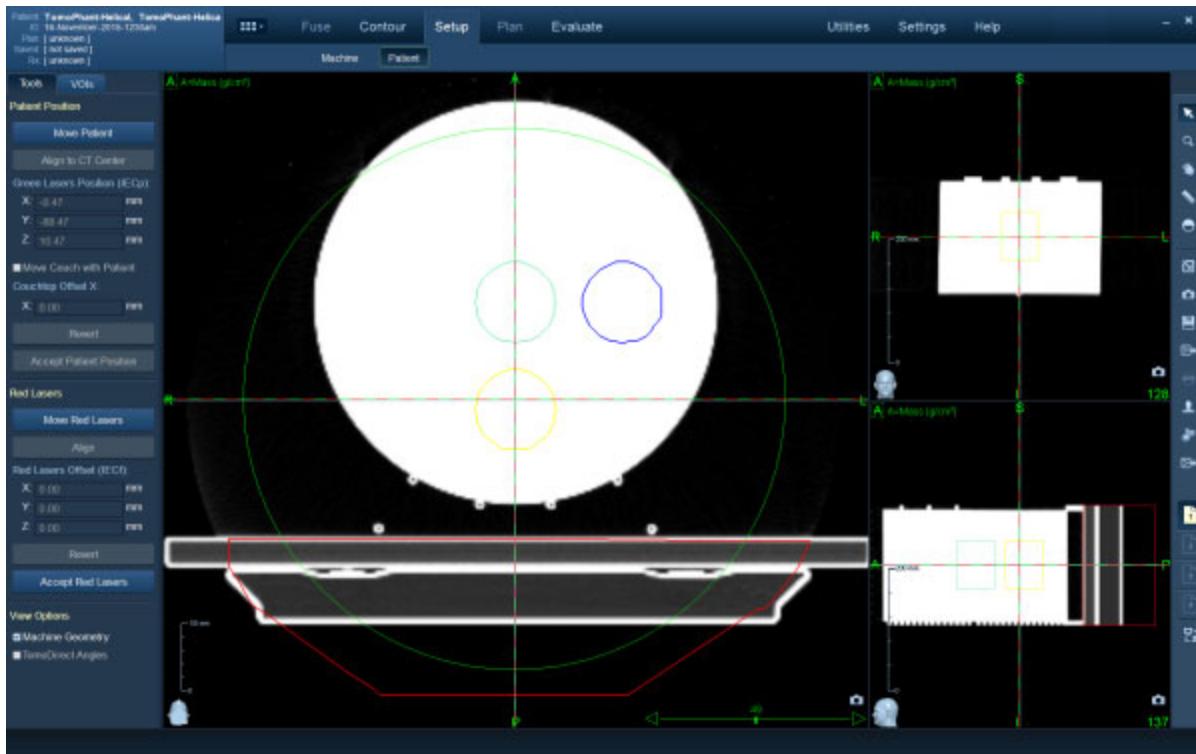
The dose output of a treatment system is calibrated by comparing dose calculations for helical IMRT plans in the *Tomo*-phantom to ion chamber measurements. This method of dose calibration is used because it simulates a generalized patient treatment, and because the dose calculator reports the expected dose only for plans created on the planning system (all plans created on the planning system have couch motion and leaf modulation).



**NOTE:** Measurements with static open fields are an important part of daily and monthly QA, serving as a constancy check against site-specific references established at the completion of commissioning. The *Accuray Precision™* Treatment Planning System does not calculate the expected dose for static open fields, so they are not used for absolute dose calibration.

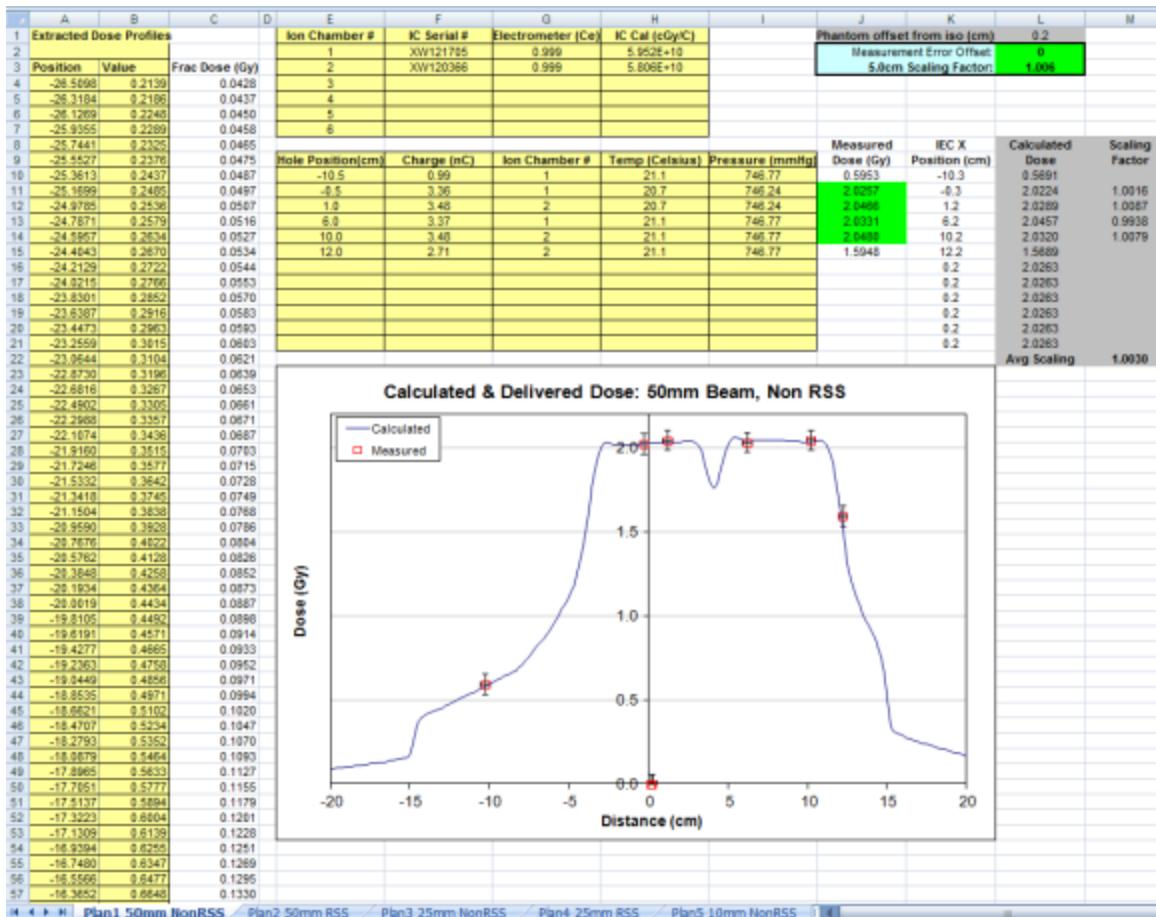
The calibration requires a set of plans in the *Tomo*-phantom. Accuray Incorporated provides an example set of plans and an accompanying spreadsheet that contains calculated dose profiles for use in Acceptance Testing. The same planning image and planning parameters are applied for all machines, but the optimization results and calculated dose profiles are particular to the beam model and MLC data of each machine. For customer commissioning and ongoing QA, a similar set of plans should be generated by the Site Physicist. The Site Physicist may choose to use their own phantom scan and density model to account for the density of their particular phantom serial number. The Site Physicist should perform their own plan calculations on the *Accuray Precision™* Treatment Planning System to ensure that the most recent beam model and MLC data are used for the calculations (service events may involve updates to the beam model and MLC data).

In the following *Tomo*-phantom plan VOIs figure, the dark blue structure and the aqua structure are targets, and the yellow structure is an avoidance structure. Two targets are used to exercise a wider range of leaves. The phantom setup is offset from isocenter in the IEC Z direction.



**Tomo-phantom Plan VOIs**

In the following Sample *Tomo-Phantom Calculation Spreadsheet*, the blue line in the plot represents the calculated dose profile. *Tomo-phantom* calculated profiles are machine-specific; this figure is for illustrative purposes only. The red points in the plot are ion chamber measurements with error bars of  $\pm 3\% / 3 \text{ mm}$  (the red point at (0,0) has not been measured and can be ignored). Worksheets labeled "RSS" (Running Start and Stop) are used for dynamic jaws plans, and worksheets labeled "NonRSS" are used for fixed jaws plans.



Sample Tomo-Phantom Calculation Spreadsheet

## Workflow Overview

The following steps are incorporated to generate the IMRT dose calibration plans used at acceptance testing. Accuray Incorporated initially plans the *Tomo*-phantom structure set on a standard kVCT image of *Tomo*-phantom and accompanying standard density model used in factory testing. All plans are created with the same contour sets and the same planning protocol.

1. The *Tomo*-phantom patient kVCT and structure set are imported by Accuray Incorporated via DICOM as a standard test plan at installation.
2. The *Accuray Precision* Treatment Planning System is used to optimize the various *Tomo*-phantom plans. The *Accuray Precision* Treatment Planning System performs dose calculation using the site-specific beam model, which includes the machine-specific MLC parameters and JFOF's.
3. The calculated dose values are written to an Excel/spreadsheet.
4. The plans are delivered to the *Tomo*-phantom, and ion chambers are used to measure dose at designated positions. The measurements are entered

in the *Excel*/spreadsheet for dose calculation and comparison against the calculated data.

5. The measurement results are used to inform machine adjustments.

The Site Physicist may implement a similar workflow for commissioning and routine IMRT dose calibration.

## ◆ Output and JFOF Adjustments

In the commissioning workflow, IMRT dose calibration is one of the last steps, after ensuring that the alignment, profiles, and energy are within tolerance. At this point, any discrepancy between calculated and delivered dose can be appropriately addressed by adjusting the machine output or the planning Jaw Fluence Output Factors (JFOFs) with assistance from Accuray Customer Support. *TomoDirect*-phantom plans should be measured to ensure that they meet specifications, but they are not used to inform output adjustments.



**IMPORTANT:** Accuray Incorporated recommends that output adjustments are based on measurements for helical plans only.

## ◆ Phantom Considerations

All *Tomo*-phantom plans generated by Accuray Incorporated are based on the same universal kVCT planning CT image of the Med-Cal *Tomo*-phantom (which can be distinguished by its red color). There is an accompanying Factory Test density model, which is applicable for the scanner used to acquire this particular phantom image only. The Site Physicist may choose to use the Accuray CT image and Factory Test density model with a Med-Cal *Tomo*-phantom or create similar plans using a scan of a different phantom with the accompanying density model.

### Phantom Density

The Med-Cal *Tomo*-phantom most closely matches formulation "G" of *Virtual Water*, as described by McEwen and Niven 2006.

The material of the phantom is designed to mimic the radiation attenuation properties of water. Compton interactions (the dominant interactions in megavoltage beams, and the dominant interactions in kilovoltage beams for water-like materials) are proportional to electron density. The nominal electron density of the Med-cal *Tomo*-phantom relative to water is 1.013. The electron density of the Sun Nuclear *Solid Water Tomo*-phantom HE relative to water is specified by the manufacturer as 1.000 +/- 0.005.

The relative electron densities of all soft tissues within the human body are numerically within 1% of their mass densities. In this regard, the *Tomo*-phantom is not very similar to human soft tissue. The specification for the mass density of the Med-Cal *Tomo*-phantom is  $1.047 \text{ g/cm}^3 \pm 0.01 \text{ g/cm}^3$ . The mass density of the Sun Nuclear *Solid Water Tomo*-phantom HE is specified by the manufacturer as  $1.032+/-0.005 \text{ g/cm}^3$ .

When creating a density model, do not use plastic plugs in the range of  $0 \pm 100 \text{ HU}$ . Plugs in the range of  $0 \pm 100 \text{ HU}$  may have CT numbers and electron densities very similar to the corresponding human tissue, but the mass densities may be a few percent different. Instead, scan real water to obtain a density model point at  $1.0 \text{ g/cm}^3$  and about  $0 \text{ HU}$ . This will maintain the human tissue-like feature of the numerical similarity of mass density and relative electron density, for materials with density near water.

When scanning your *Tomo*-phantom (using an MVCT or KVCT scanner) and applying a density model that was measured according to Accuray instructions, the mass density of the *Tomo*-phantom in the TPS will be numerically similar to its relative electron density. That is, the density of your Med-Cal *Tomo*-phantom in the TPS should be close to  $1.013 \text{ g/cm}^3$  and the density of your Sun Nuclear *Tomo*-phantom HE in the TPS should be close to  $1.000$ .

In the *Accuray Precision™ Treatment Planning System*, when the Factory Test density model is applied to the universal Med-Cal *Tomo*-phantom image, the average phantom density is  $1.023 \text{ g/cm}^3$ . This is about 1% different from the nominal expected density of the phantom. (While the water point in the density model could have been adjusted to achieve a density consistent with the nominal value of  $1.013 \text{ g/cm}^3$ , Accuray Incorporated chose to maintain consistency with the currently installed systems in the field by keeping the value at  $1.023 \text{ g/cm}^3$ .)

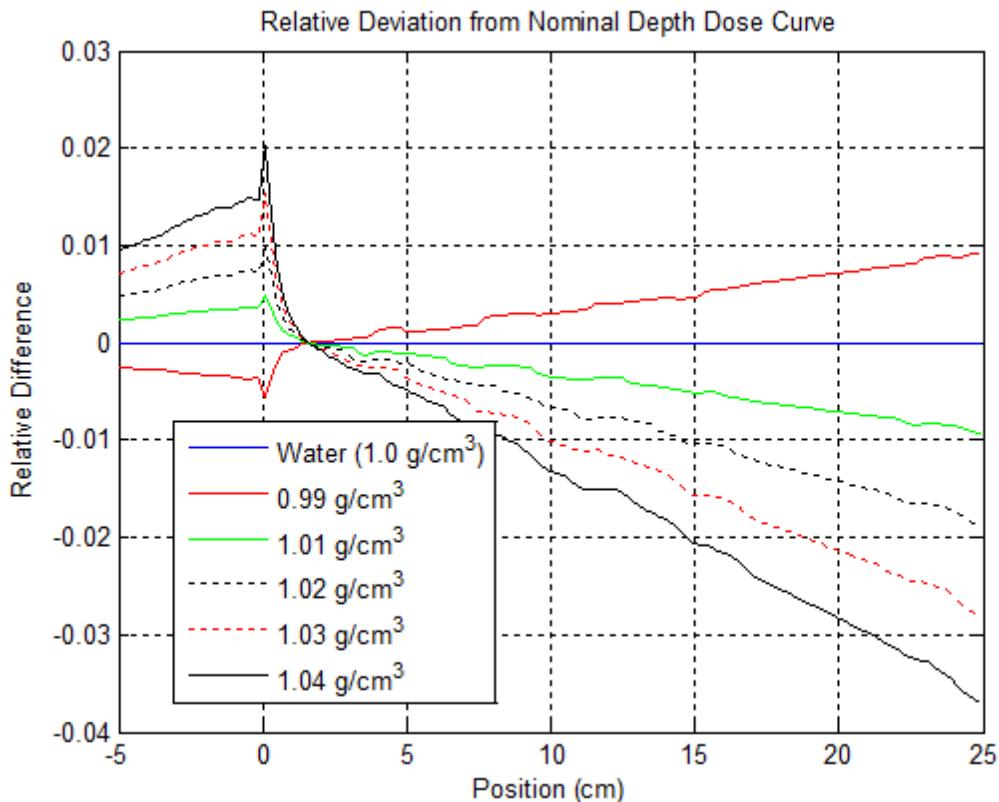
The IMRT dose calibration method rests on the assumption that the relative electron density of your phantom matches the relative electron density of the universal phantom image in the Med-Cal *Tomo*-phantom patient. If the density of your phantom differs significantly from the density in the plan calculations, the dose calibration will be incorrect.



**IMPORTANT:** The factory IMRT dose calibration plans are based on the Med-Cal *Tomo*-phantom (red color). Due to phantom density differences, do not use the Accuray-provided IMRT dose calibration plans in the Sun Nuclear *Tomo*-phantom (blue color). If you do not have the Med-Cal *Tomo*-phantom or if your Med-Cal *Tomo*-phantom has a different density from the factory IMRT dose calibration plans, you should create similar IMRT dose calibration plans on your own phantom and apply a density model that was measured on your CT scanner.

As an example of the magnitude of dose errors associated with incorrect density values, the following graph shows the deviation from the nominal depth dose curve for a  $5 \text{ cm} \times 40 \text{ cm}$  beam impinging on a water tank. If the true density is  $1.0 \text{ g/cm}^3$ , but the dose calculator uses a density of  $1.02 \text{ g/cm}^3$  as an input, the dose difference at  $15 \text{ cm}$  depth will be about -1%.

Therefore, in this example, a mis-representation in the density of 2% corresponds to a 1% dose error at 15 cm depth. In clinical situations, the amount of dose error associated with a mis-represented density will depend on the exact delivery sinogram (MLC delivery pattern) and the phantom or patient geometry, as well as the beam model.



**Example of Dose Error in Relative Deviation from Nominal Depth Dose Curve**



**IMPORTANT:** Before using the Med-Cal *Tomo*-phantom patient for dose calibration, the site physicist should determine if the relative electron density of your own *Tomo*-phantom is within 2% of the relative electron density of the universal Med-Cal *Tomo*-phantom planning image. To test this, scan your Med-Cal *Tomo*-phantom on your CT scanner with the uniform density plugs in place, and also perform another scan with the variable density plugs in place to create a density model following the recommendations of Accuray Incorporated. Apply the site-specific density model you measured to your site-specific phantom image. Verify that the density of your Med-Cal *Tomo*-phantom image is  $1.023 \pm 0.020 \text{ g/cm}^3$ . If the density of your phantom is outside this range, do not use the universal Med-Cal *Tomo*-phantom planning image. Create your own dose calibration patient by scanning your own phantom.

## Phantom Position



**NOTE:** This section is only applicable to *Tomo*-phantom plans created with the universal Med-Cal “TomoPhant” image.

When the original, universal kVCT planning image of the Med-Cal *Tomo*-phantom was acquired, the phantom was set up with a slight yaw and a lateral offset of approximately 2 mm in the center of the phantom with respect to isocenter. For calibration measurements, the phantom should be set up to match the planning image position. Use an MVCT image for setup verification. It is not necessary to replicate the slight yaw of the planning image, but the center of the phantom (where the measurement chambers are) should be well aligned to the planning image. The *Excel*/spreadsheet used by Accuray Incorporated accounts for the 2 mm lateral offset.

# Tomo-Phantom Plan Description

*Tomo*-phantom plans are optimized and calculated on the *Accuray Precision™* Treatment Planning System, with an image of the *Tomo*-phantom as the planning image volume.

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## ◆ Tomo-Phantom Patient Plans

Dose should be verified for both static jaw and dynamic jaw plans, and for *TomoDirect* and *TomoHelical*/plans. Two targets are used in each plan: one "on-axis" target and one "off-axis" target.

### *TomoHelical*-Phantom Patient

Jaw Mode	Field Width	Plan Description
Static	5 cm	<i>TomoHelical</i> static jaws plan
Dynamic	5 cm	<i>TomoHelical</i> dynamic jaws plan
Static	2.5 cm	<i>TomoHelical</i> static jaws plan
Dynamic	2.5 cm	<i>TomoHelical</i> dynamic jaws plan
Static	1 cm	<i>TomoHelical</i> static jaws plan

### *TomoDirect*-Phantom Patient

Jaw Mode	Field Width	Plan Description
Static	5 cm	<i>TomoDirect</i> static jaws plan
Dynamic	5 cm	<i>TomoDirect</i> dynamic jaws plan
Static	2.5 cm	<i>TomoDirect</i> static jaws plan
Dynamic	2.5 cm	<i>TomoDirect</i> dynamic jaws plan
Static	1 cm	<i>TomoDirect</i> static jaws plan

## ◆ When to Re-Plan the *Tomo*-Phantom Set

The *Tomo*-phantom patients should be re-calculated if there is a beam model change or MLC replacement, to account for the new latency data and leaf filters.

For example, a major system upgrade may have been performed, involving the installation of a new beam model. Or, the beam model may have been updated due to an MLC replacement. You need to update your *Tomo*-phantom IMRT calibration plans to use the new or updated beam model data.



**WARNING:** If you do not re-calculate *Tomo*-phantom plans after a beam model change, absolute dose testing tolerances may be less accurate, possibly resulting in lower quality patient treatments.



**IMPORTANT:** Re-calculating the plans will change the expected dose. Be sure to compare your measurements against expected dose values for the current plans.

# Tomo-Phantom Verification Spreadsheet

This section introduces the *Tomo*-Phantom Verification Spreadsheet used by Accuray Incorporated. If you create *Tomo*-phantom plans on your own phantom scan or if you recalculate the plans to account for beam changes, the *Tomo*-Phantom Verification Spreadsheet cannot be used. Instead, use the *Accuray Precision™* Treatment Planning System to determine the dose values at each ion chamber position. The same planning image and optimization protocol are used for all *Tomo*-phantom plans, but the optimized results are dependent on the beam model installed on the machine. Accuray Incorporated has an internal tool that extracts the plan-specific calculated dose profile through the center of the phantom from a patient archive. Accuray Incorporated uses this data to populate the site-specific *Tomo*-Phantom Verification Spreadsheet.

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- ◆ Determining the Measured Dose ..... 223
- ◆ Calculated Versus Measured Dose ..... 223



**IMPORTANT:** The *Tomo*-Phantom Verification Spreadsheet used by Accuray Incorporated has been validated for use with *Microsoft Excel*. If you use a different software program, ensure that the formulas are calculated correctly.



**IMPORTANT:** Do not use the Accuray *Tomo*-Phantom Verification Spreadsheet with the Sun Nuclear *Tomo*-phantom HE. The Sun Nuclear *Tomo*-phantom HE is blue.

## ◆ Calculated Profile Data

The calculated profile data is stored in columns A and B of the worksheet. Column C lists the per-fraction data from column B (column C = column B/50, since there are 50 fractions in the plan). The profile data is plotted as a blue line in the graph.

## ◆ Phantom Offset from Isocenter

The same kVCT planning image of the Med-Cal *Tomo*-phantom is used on all machines for both the *TomoEDGE* and static jaws systems. This phantom was set up with a slight yaw and a lateral offset of approximately 2 mm in the center of the phantom with respect to isocenter. For calibration measurements, the phantom should be set up on the couch to match the

planning image; an MVCT verification scan is recommended. In cell L1, the *TomoHelical*-phantom and *TomoDirect*-phantom spreadsheet includes a built-in, 2-mm correction called **Phantom offset from iso** to convert the coordinates of ion chamber positions in the phantom to positions with respect to isocenter. This shift is necessary and should not be modified by the user, assuming that the Accuray provided universal phantom image is used.

For example, the spreadsheet sample provided earlier showed that the first ion chamber was collected at a hole position of -105 mm from the center of the phantom (cell E10). Because cell L1 indicates the standard phantom offset of 2 mm, the position of the hole with respect to isocenter is -103 mm, as indicated in cell K10. Thus, the spreadsheet looks up the dose value at a position of -103 mm with respect to isocenter (in columns A and C), and reports the calculated dose value in cell L10.

In addition, cell L2 lists the **Measurement Error Offset**, which should be left at 0. The purpose of this cell is to shift the data to evaluate a possible lateral setup error. Entering a non-zero value in this cell introduces an arbitrary shift in the data.

## ◆ Determining the Measured Dose

When the measured data is entered in the spreadsheet, the spreadsheet determines the measured dose value in Column J of the worksheet. The dose is approximated as the product of the charge measurement, ion chamber calibration factor, electrometer calibration factor, and temperature/pressure correction for chambers calibrated at 22 C.

The measured dose points are plotted in red on the graph, with error bars of  $\pm 3\%$  of 2 Gy =  $\pm 0.06$  Gy, and  $\pm 3$  mm.

## ◆ Calculated Versus Measured Dose

Column J indicates the measured dose. Column L indicates the calculated dose from the plan. For each point in the plateau region of the delivery (dose > 1.9 Gy), a scaling factor is also listed in column M as the ratio of the measured to calculated dose. Ideally, this factor would be 1.0. In cell M22, an average scaling factor is listed for all points in the plateau region. In cell L3, an average scaling factor for all plans of the same field width (dynamic jaws and non-dynamic jaws) is reported. If your system is not equipped with the *TomoEDGE* feature, use only worksheets labeled "nonRSS" (non-Running Start and Stop = fixed jaws). For "nonRSS" systems, cell L3 will display the average scaling factor for the "nonRSS" plan. The scaling factors in column M and in cell L3 are calculated metrics to quantify the agreement between planned and calculated point doses. They are not arbitrary shifts, but results. The values in these boxes are not intended to be manually adjusted (if they are manually adjusted, it will not scale the results displayed in the spreadsheet).

# Create *Tomo*-Phantom Patients

This section provides an example of how to create dual-target plans using the Accuray Incorporated Med-Cal *Tomo*-phantom image, contours, and density model. You will create one *TomoHelical*-phantom patient for helical plans, and one *TomoDirect*-phantom patient for static beam plans. The steps in this section should be implemented in the event of an MLC data or beam model update as discussed in “When to Re-Plan the Tomo-Phantom Set” (page 221). If you already have *Tomo*-phantom patients and accompanying calculated dose information based on the beam model and MLC data currently installed on your system, skip this section and proceed to “Set Up and Deliver the Test” (page 232).

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## ◆ Prepare the Files

If you choose to use the Accuray provided universal Med-Cal phantom image and accompanying density model, the Med-Cal *Tomo*-phantom data to create the necessary test plans is located on the disc you received during installation. It is commonly referred to as the “ATP CD.” The disc contains DICOM data of the kVCT image and structures to optimize test plans on your system. The disc also contains an analysis spreadsheet based on your treatment machine beam model at the time it was produced in the factory.



**NOTE:** The *Accuray Precision™* Treatment Planning System only permits one copy of each patient with the same medical record number, so you must input a unique ID each time you create a new patient. Use the current date and time as part of the ID to ensure it is unique.

## Create Factory Density Model



**IMPORTANT:** Use the density model specifications provided by Accuray Incorporated with the Med-Cal *Tomo*-phantom, unless you have acquired your own kVCT image of the *Tomo*-phantom. If you use a different phantom, use a density model that is appropriate for the imaging device that the phantom image was acquired on.

1. To create the Accuray Incorporated factory density model, open the Treatment Planning System software and click the **Plan Parameters** button.
2. Click the **Planning Parameters** tab. Is an Accuray Incorporated Factory density model available in the **Density Models** drop-down?
  - If yes, select it and verify its numbers against the table below. Continue to step 3.

- If not, create this model with the following entries

Index	HU	Relative Electron Density	Mass Density (g/cm <sup>3</sup> )
1	-1024	*	0.000
2	-1000	*	0.001
3	-726	*	0.300
4	-562	*	0.450
5	-117	*	0.941
6	0	*	1.000
7	206	*	1.153
8	430	*	1.334
9	823	*	1.560
10	1237	*	1.824
*			

3. Click the **Set Default** button to set the Accuray Incorporated Factory density model as the default for the duration of absolute dose calibration testing.



**WARNING:** The Accuray Incorporated Factory density model should not be used for patient planning, because it is not specific to your CT simulator and could result in incorrect patient dose calculations. Reset the default density model when you are finished planning the *Tomo*-phantom patients.

## Enter Patient Data

1. From the Treatment Planning System dashboard, click **Image Review and Import** to load the *Tomo*-phantom kVCT and ROI structure set.



**IMPORTANT:** If you prefer to use a different phantom, or a different kVCT image of your *Tomo*-phantom, modify the patient and plan creation steps according to your needs.

2. Click the **Load DICOM Series From Disk** icon and browse to the **TomoPhant 2mm CT** image folder. Click **OK**.
3. Repeat the previous step for the **TomoPhant RTStruct** folder.
4. Click the **Refresh** icon and wait for the hourglass icon to disappear. The imported TomoPhant data appears.
5. Right-click on the imported *Tomo*-phantom CT image and select **Manage Selected DICOM Series**. Click **OK** on any messages that display.
6. Click the **Associate with New Patient** button. The **Create New Patient** dialog appears.
7. Enter the following data into the **Create New Patient** dialog:
  - **Medical ID:** Enter today's date and time in your preferred local format.

- **Last Name and First Name:** Enter “*TomoHelical*-phantom” or “*TomoDirect*-phantom,” depending on the type of plans you are creating.
- **Type:** Select **Phantom**



**IMPORTANT:** The default **Medical ID** must be changed to today's date and time as a precaution against unique ID collisions.

8. Click **OK**. The **Image Review** screen appears.
9. Click the **Import DICOM Series** icon. A **Warning** dialog appears.
10. Enter your password and click **OK** to override the image series width restriction.
11. Close the *iDMSSystem* window to return to the Treatment Planning System dashboard.

# Create *Tomo*-Phantom Plans

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## ◆ Create a Base Plan

The base plan is a partially completed plan which saves you time. To create each of the five required *TomoHelical*-phantom plans, you can load the base plan, make minor modifications, and save a copy of the base plan with an appropriate name.



**NOTE:** The *Accuray Precision™* Treatment Planning System software also has a Template feature that allows you to save a list of plan parameters that can be applied to similar plans on different patients. However, since all the *TomoHelical*-phantom plans use the same image and the same patient, it is easier just to create copies of the base plan by saving them with new names.

1. From the Treatment Planning System dashboard, click the **New Plan** button.
2. From the patient list, select *TomoHelical*-phantom and click the **Next >>** button.
3. Under **Modality**, select **CT** and click **Select Exam**.
4. Click **Finish**. A dialog box appears.
5. Under the **Setup task > Machine step > Tools** tab, select the appropriate density model, **Treatment Machine**, **Delivery Mode**, **Plan Mode**, and **Jaw Mode** for the plan you wish to create. You need one of each of the ten plans listed under “Tomo-Phantom Patient Plans” (page 220).
6. Right-click in the image. Under **Window Level Presets**, select **Couch**.
7. Click near the surface of the couch in the image, and click the **Replace Couch** button.
8. If the former couch was accurately replaced with your couch image, click the **Accept** button. If not, repeat the previous step.
9. Under the **Setup task > Patient step > Tools** tab, click **Accept Red Lasers**.
10. Under the **Plan task > Optimize step > Tools** tab, enter the following settings:
  - Select a **Field Width** according to the plan type you are creating. Refer to “Tomo-Phantom Patient Plans” (page 220) for a list of the ten plan types you need to create.

- **Pitch** = 0.287 for *TomoHelical* plans. For *TomoDirect* plans, a **Pitch** value is automatically provided based on your **Field Width** selection. Do not modify the **Pitch** for *TomoDirect* plans.
- **Modulation Factor** = 1.800.
- **Optimization Resolution** = Medium.
- Select **Initiate Final Dose After** 20 iterations.
- **Final Dose Resolution** = High.

11. On the same screen, enter the settings provided in the following tables:

Prescription	
% Volume	
Target	
95.00%	
100.00 Gy	
50 Fractions	

Target Objectives	Target	ROI_1
Priority	1	2
Use	Yes (select)	Yes (select)
! (Importance)	100	100
Max Dose (Gy)	100	100
Max Penalty	100	100
DVH Vol (%)	95	95
DVH Dose (Gy)	100	100
Min Dose (Gy)	100	100
Min Penalty	100	100

Critical Constraints	couch	ROI_2
Priority	1	2
Beam Intersection	Allowed	Allowed
Use	No (empty)	Yes (select)
! (Importance)	N/A	2
Max Dose (Gy)	N/A	100
Max Penalty	N/A	10
DVH Vol (%)	N/A	15
DVH Dose (Gy)	N/A	30
DVH Penalty	N/A	10

12. Click the **Save** icon on the center-right side of the screen and save the current settings as “thphant” for future re-use.



**TIP:** Use the settings in the base plan "thphant" to create additional *Tomo-phantom* plans based on the pre-optimization settings entered in the previous steps. Some changes to **Delivery Mode**, **Jaw Mode**, and **Field Width**, will be required before optimizing each plan, but this base plan will save time in the creation of all ten absolute dose calibration plans.

13. Continue to “Optimize a Plan” (page 229).

## ◆ Optimize a Plan

- Under the **Plan** task > **Optimize** step, click the **Start** button to begin plan optimization.
- Wait for the optimization to complete.
- Under the **Evaluate** task > **Review** step > **Standard** tab, click the **Save Plan** button, The **Save Plan** dialog box appears.
  - In the **Plan Name** field, enter an appropriate descriptor for the plan type.
  - Click the **Make Deliverable** option.
  - Click **Save**, and continue to “Create the Remaining Tomo-Phantom Plans” (page 230).

## ◆ Create the Remaining *Tomo*-Phantom Plans



**TIP:** Use the settings in the base plan "thphant" to create additional *Tomo*-phantom plans based on the pre-optimization settings entered in the previous steps. Some minor modifications to **Delivery Mode**, **Jaw Mode**, and **Field Width**, will be required before optimizing each plan, but this base plan will save time in the creation of all ten absolute dose calibration plans.

### Create *TomoHelical*-Phantom Plans

1. From the Treatment Planning System dashboard click the **Load Plan** button.
2. In the **Load Plan** list, select the *TomoHelical*-phantom patient.
3. Under **Select Plan**, select "thphant". Use this base plan to create additional *Tomo*-phantom plans based on the pre-optimization settings.
4. Modify **Delivery Mode**, **Jaw Mode**, and **Field Width** settings depending on the plan you want to create. Refer to "TomoHelical-Phantom Patient" (page 220) for a list of required plans.
5. Repeat the steps under "Optimize a Plan" (page 229) to optimize and save each plan.
6. Repeat steps 1 - 4 to create all five *TomoHelical*-phantom plans required for absolute dose testing.

### Create *TomoDirect*-Phantom Plans

1. Follow the steps under "Enter Patient Data" (page 225) to create a *TomoDirect*-phantom patient.
2. Follow the steps under "Create Tomo-Phantom Plans" (page 227) to create a *TomoDirect*"tdphant" base plan. At the **Plan** task > **Beam Angles** step, add four *TomoDirect* beam angles at 0, 90, 180, and 270 degrees.
3. From the Treatment Planning System dashboard click the **Load Plan** button.
4. In the **Load Plan** list, select the *TomoDirect*-phantom patient.
5. Under **Select Plan**, select "tdphant". Use this base plan to create additional *Tomo*-phantom plans based on the pre-optimization settings.
6. Modify **Delivery Mode**, **Jaw Mode**, and **Field Width** settings depending on the plan you want to create. Refer to "TomoDirect-Phantom Patient" (page 220) for a list of required plans.
7. Repeat the steps under "Optimize a Plan" (page 229) to optimize and save each plan.

8. Repeat steps 3 - 7 to create all five *TomoDirect*-phantom plans required for absolute dose testing.

## Reset the Default Density Model



**WARNING:** The Accuray Incorporated Factory density model should not be used for patient planning, because it is not specific to your CT simulator and could result in incorrect patient dose calculations. Reset the default density model when you are finished planning the *Tomo*-phantom patients.

1. From the Treatment Planning System dashboard, click the **Planning Settings** button.
2. Click the **Planning Parameters** tab.
3. Under the **Density Models** drop-down, select a density model that is representative of the imaging device you normally use for treatment planning.
4. Click the **Set Default** button to set the selected density model as the default for treatment planning.

## Determine Calculated Dose

If new *Tomo*-phantom plans were created because of a machine change, you will need to determine the new calculated dose values. There are several methods to accomplish this:

- Check the dose statistics for contoured ion chamber positions
- Use the dose readout tool for point dose information
- DICOM export the calculated dose information, and read it in third-party software

# Set Up and Deliver the Test

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◆ Analyze the Results . . . . .	238



**IMPORTANT:** Before performing QA tasks, ensure that warmup and airscan procedures were run to achieve a stable beam and optimal image quality.

## ◆ Set Up the Phantom

1. On the Treatment Delivery Console, click the **Treat Phantom Plan** icon, select the desired *Tomo*-phantom patient and plan.
2. Acquire an MVCT scan of the phantom to verify the phantom position and correct for couch sag. Click the **Scan** tab, set the **Acquisition Pitch** to **Fine**, and select several slices near the center of the phantom.
3. Click **Prepare Scan**. After acknowledging the on-screen messages, the red lasers will move to the position stored in the plan.



**TIP:** Because the phantom planning image used by Accuray has a slight yaw, slices in the center of the phantom should be selected to verify the setup in the central portion of the phantom where dose is measured.

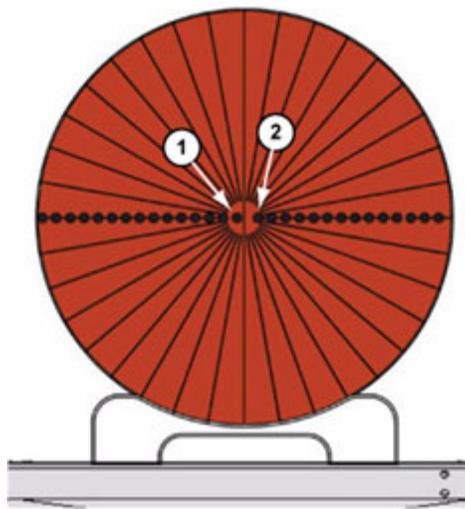
4. Set up the *Tomo*-phantom on the treatment couch:
  - The ion chamber holes should face the foot end of the couch.
  - If you are using the universal phantom image provided by Accuray, the phantom is centered on the green lasers in IEC X and IEC Y, approximately 7.2 cm above isocenter in IEC Z.



**WARNING:** Prior to rotating the phantom, ensure that the two halves of the phantom are securely attached to each other to prevent the phantom halves from separating and falling onto the floor. If the phantom is dropped, it can cause injuries or break.

- If you are comparing measurements against calculated profiles such as those in the Accuray analysis spreadsheet that run from left to right along the IEC X axis through the center of the phantom, the phantom should be rotated so that the row of holes is in the horizontal orientation (i.e., row of holes runs parallel to the IEC X axis). Use a small level or the green bore lasers to ensure proper rotation of the phantom about the IEC Y axis.

- The ion chamber holes in the phantom are 1 cm apart. As shown in the *Tomo*-phantom setup image below, from the break line in the middle of the phantom, the first hole on one phantom half is 0.5 cm from the center of the phantom, and the first hole on the other phantom half is 1 cm from the center of the phantom. Set up the phantom so that the holes on the left half of the phantom are at positions of -0.5 cm, -1.5 cm, -2.5 cm ... and the holes on the right half of the phantom are at positions of 1 cm, 2 cm, 3 cm ... (It is also acceptable to mirror the setup left/right, as long as you enter the actual measurement positions in the spreadsheet.)
- Insert at least one chamber in the phantom so that it will appear in the *CTrue* image. Tape the chamber in place so that it does not slide out of the phantom.
  - Ensure that the uniform density plugs are inserted in the phantom, not the CT contrast plugs.



*Tomo*-phantom Setup

The phantom pictured above has the ion chamber holes in the horizontal orientation. 1) On the -IEC X side of the phantom, the first hole is 0.5 cm from the break in the phantom. 2) On the +IEC X side of the phantom, the first hole is 1.0 cm from the break in the phantom.

- Acquire the *CTrue* image. When the scan is completed, register the MVCT image to the planning image. The registration result should include translations only (no roll, pitch, or yaw).

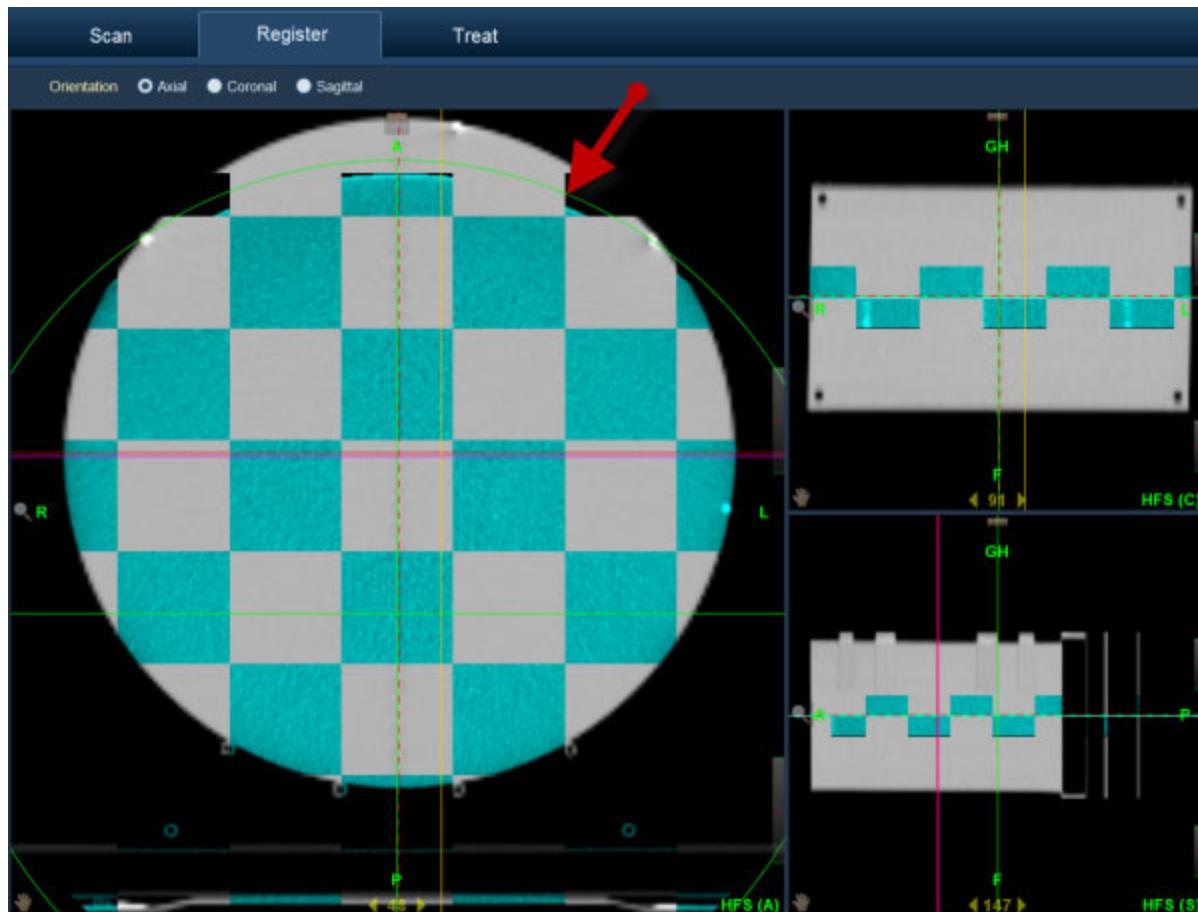


**TIP:** The phantom does not have much contrast in the IEC Y direction, so it will be necessary to perform manual (not automatic) image registration.

- After completing the manual registration, accept the registration results.



**NOTE:** Phantom measurements should be collected with the line of ion chamber holes in the horizontal orientation. However, in the Accuray planning image, the phantom is rotated so that the line of ion chamber holes runs parallel to the IEC Z axis (vertical orientation of holes). This difference does not impact the dose delivery because the phantom is homogeneous and cylindrically symmetric.



Transverse Phantom Registration



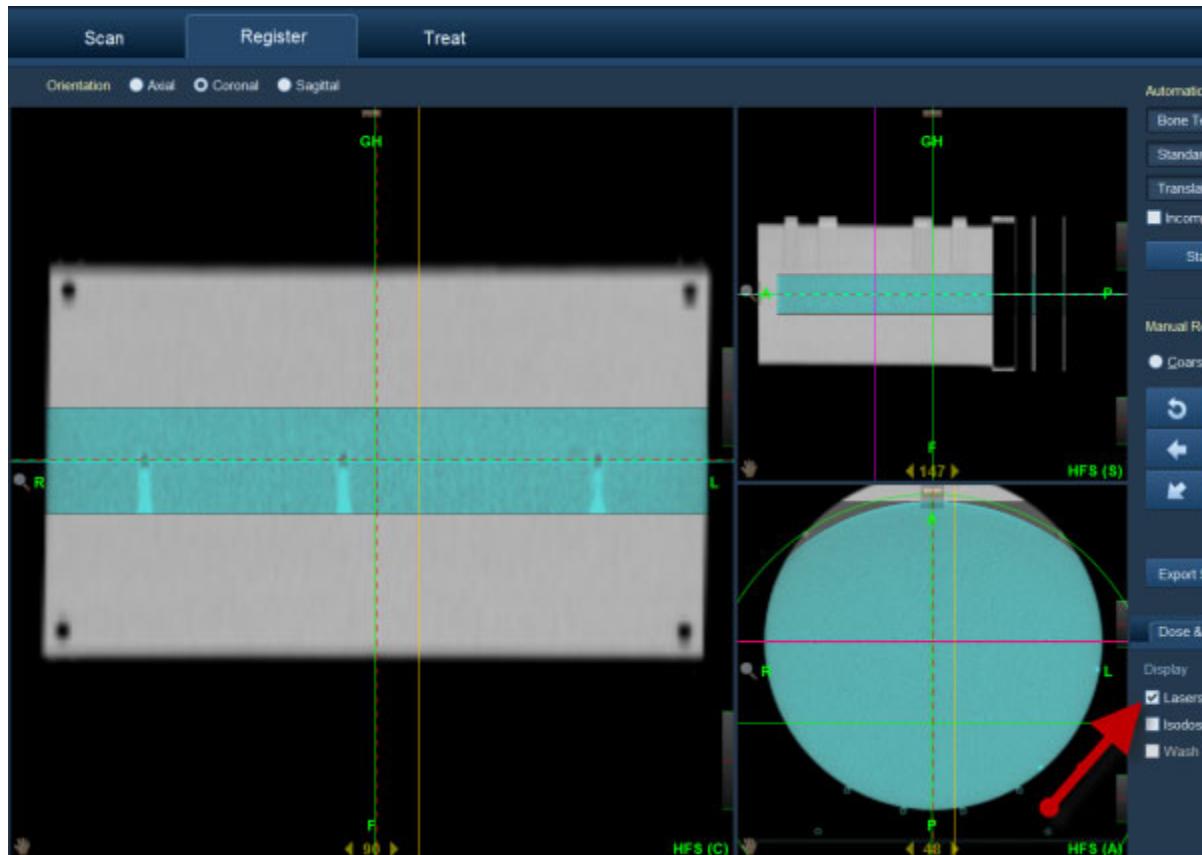
**NOTE:** Register the MVCT image to the planning image in IEC X and IEC Z by aligning the lower edges of the phantom. The arrow indicates the top portion of the phantom, where the MVCT image is cut off by the 39 cm field of view.



**TIP:** The collection volume of the ion chamber in the phantom should be aligned with the green lasers in IEC Y (but not in IEC X, since the hole positions are offset from the center of the phantom).



**TIP:** If you cannot find the ion chamber in your image, ensure that the CT artifact correction checkbox is unselected in the **CTTrue Image Filter** portion of the **Register** tab controls.



Longitudinal Phantom Registration

## ◆ Collect Data

1. Set up the ion chambers in the desired positions. Plug unused holes with *Virtual Watersticks*. Tape the chamber cables to the couch so that they will

not slide out of the phantom, and label them to avoid confusing the channel numbers.



**NOTE:** Accuray Incorporated recommends placing an A1SL ion chamber in the phantom to verify the dose at six different points along the dose profile for each of the absolute dose calibration plans:

- Two locations in each of the two plateau regions of each plan (e.g., positions of -0.5 cm, 1 cm, 6 cm, and 10 cm relative to the center of the phantom).
- One location in a high-gradient region (e.g., position of 12 cm relative to the center of the phantom).
- One location in a low-dose region (e.g., position of -10.5 cm relative to the center of the phantom).

The desired positions of the ion chambers may be determined by examining the profiles.



**TIP:** With ten plans and six phantom measurement points per plan, the total number of recommended data collection points is 30 for the *TomoHelical*-phantom plans and 30 for the *TomoDirect*-phantom plans. If you have more than one A1SL ion chamber and the multi-channel *Tomo* Electrometer, measurement points in the same plan may be collected simultaneously to speed up the data collection.



**NOTE:** To reduce perturbations that may impact dose measurements, avoid measurements with several ion chambers along the same line from the source through the phantom, especially for static beam angles. In the Accuray universal phantom image, the phantom is raised 7.2 cm above the central axis, so even for the 90° and 270° *TomoDirect* beams, a ray from the source through the phantom does not pass through multiple ion chambers. Ensure that the ion chamber positions measured simultaneously are not very close together.

2. Set up the electrometer for measuring integrated dose (+300 V bias). For instructions on setting up the *Tomo*-Electrometer, see “Set up the *Tomo*-Electrometer” (page 88).
3. Record the temperature, pressure, ion chamber calibration factors, and electrometer calibration factors.
4. Proceed to the **Treat** tab and select a fraction for delivery.
5. Click **Prepare Treatment** and click **Apply** to apply the registration results.
  - If you have just accepted the image registration results on this plan without closing the TDC or opening any other plan, press the **Setup** button on the TDC couch control or **Positioning Control Panel** on the gantry to move the couch to account for the registration results. Then,

record the couch position from the **Positioning Control Panel** for reference.

- If you have not just completed the MVCT image registration on the current plan, do not press **Setup**, but simply check that the couch coordinates displayed on the TDC match the registered position that you recorded previously.



**TIP:** All *Tomo*-phantom plans generated by Accuray use the same phantom position. Once you have confirmed the setup with one *CTrue* image, you can use the same position for all the other plans.

6. Press the **Ready** button to move the couch into the bore for treatment delivery.
7. Start the electrometer integrating.
8. Run the treatment and record the charge measurement.
9. Repeat Steps 1-8 for additional points and additional plans.

## ◆ Enter Data in the Spreadsheet



**IMPORTANT:** These instructions are specific to the Accuray provided spreadsheet that is based on the universal Med-Cal phantom image and the beam calculation data installed on your system at the time of factory testing. Ensure that you are using a spreadsheet that was generated from the same *Tomo*-phantom plan set that is delivered on the machine. If the *Tomo*-phantom plans were re-calculated, do not use the Accuray provided spreadsheet. Instead, use the VOI dose statistics, dose readout, or DICOM export tools on the *Accuray Precision™ Treatment Planning System* to determine the calculated dose.

1. If the spreadsheet currently has data in it, make a copy of the spreadsheet and delete all measurement data in yellow boxes of columns F-I on all worksheets. Do not delete the column headings. Do not delete data in yellow boxes of columns A-B (this is the calculated dose profile).
2. Navigate to the worksheet for the plan you just ran.



**TIP:** On the TDC, the plans may be distinguished by the plan number, which corresponds to the labeling on the analysis spreadsheet.

3. In cell 2F, enter the serial number for ion chamber #1 (do not change the numbers or order of the numbers 1 through 6 in cells E2 through E6). In cell 2G, enter the electrometer calibration factor (usually close to 1.0 for the

*Tomo* Electrometer). In cell 2H, enter the ion chamber calibration factor in cGy/C. Repeat in rows 3 and following for any additional ion chambers.

4. In Column E, rows 10-21, enter the hole positions for the ion chambers you will use. The spreadsheet will use columns A and C to determine the expected dose value for the hole positions you enter. The dose value calculated by the Treatment Planning System will be displayed in column L.
5. In Column G, rows 10-21, enter the ion chamber number used. The spreadsheet will use the number you enter to determine the appropriate row in the ion chamber table, to get the ion chamber and electrometer calibration factors.
6. In Column H, enter the temperature in degrees C.
7. In Column I, enter the absolute pressure in mm Hg.



**WARNING:** Absolute pressure must be entered. The units in the Accuray spreadsheet are in mm Hg. Do not use a pressure that has been corrected to sea level, or the dose calculations will be incorrect.

8. In Column F, enter the charge reading from the electrometer in nC. Since the bias is +300 V, the charge reading will be negative. Enter the absolute value in the spreadsheet (do not enter a negative sign).

## ◆ Analyze the Results

Check that the measured dose points match the calculated dose within  $\pm 3\%$  and  $\pm 3$  mm. Determine the average scaling factor for each field width for measurements in the target regions.

If tests do not produce passing results, refer to “What to Do if the Test Fails” (page 239).

# What to Do if the Test Fails

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## ◆ Verify the Test Setup

If the measurements indicate a discrepancy between planned and calculated dose, the setup should be verified before requesting a machine adjustment.

- Ensure that you are using an appropriate phantom. The Accuray-provided plans and spreadsheet are not appropriate for use with the Sun Nuclear Tomo-phantom HE
- Confirm phantom setup with an MVCT image
- Confirm that ion chambers were placed in the intended holes in the phantom, and that chambers and electrometer channels are not mixed up
- Ensure that measurement equipment is functioning properly

## ◆ Rule Out Other Sources of Error

*Tomo*-phantom or patient QA measurements are a composite check that all system components (linac, MLC, jaws, gantry, and couch) are working together. Thus, IMRT dose calibration should be the culminating QA activity, after the system alignment, beam profiles, and energy are individually verified.



**IMPORTANT:** Perform QA tests in an order that helps to isolate individual sources of error. The output rate of the system should not be adjusted until other sources of error are ruled out.

For example, if the current machine settings produce a longitudinal jaw width that is larger than the longitudinal profiles in the beam model, the rotations of a *TomoHelical* delivery will have more overlap than predicted by the *Accuray Precision™* Treatment Planning System. This can result in high IMRT measurements. The solution in this case would not be to lower the machine output, but to request that your Field Service Engineer adjust the machine jaw settings in order to match the field widths in the beam model.

## ◆ Consider Overall System Performance

This sub-section applies only to a machine that is already treating patients on the current beam model. *Tomo*-phantom measurements are the standard method for checking the system output. Often, the need for an output adjustment can be supported by other measurements, such as *TQA Basic Dosimetry* or *Daily QA* results, static open-field output consistency checks in the rectangular *Virtual Waterstack*, or patient-specific QA results.

If there is a discrepancy between the *Tomo*-phantom results and *TQA*, patient QA, or static QA results, extra care should be taken to look for other sources of error, prior to adjusting the machine output to get the *Tomo*-phantom test results to pass. This could include:

- Measuring beam profiles and energy in a water tank.
- Verifying the density model applied to the phantom.
- Verifying system alignment, especially the beam planarity result.
- Asking Accuray Customer Support to analyze beamline health by evaluating the most recently performed *TQA Basic Dosimetry* or *Daily QA* procedure.
- Asking Accuray Customer Support to double-check the MLC data installed on the system.

After a thorough investigation, if discrepancies still remain, *Tomo*-phantom results should be regarded as the standard for calibrating the machine output. In some cases the secondary baseline data (*TQA* and static output consistency checks) may need to be reset.

## ◆ Request Dose Adjustment



**NOTE:** *TomoDirect*-phantom plans should be measured to ensure that they meet specifications, but only *TomoHelical*-phantom plans are used to inform output adjustments.

If the average scaling factor for the *TomoHelical* plans is consistently high or low for all field widths, the Site Physicist may contact Accuray Customer Support to adjust the machine delivery output by a certain percentage. After the output adjustment, the Site Physicist should perform QA to ensure that the output adjustment was achieved as desired.



**IMPORTANT:** Contact Accuray Customer Support to perform the machine adjustment. A service representative can check that beamline components are operating within system specifications, that interlocks are set correctly, and that the Dose Control System is properly calibrated to keep the dose servo aiming at the desired setpoint.



**NOTE:** An adjustment to the machine delivery output does not impact the dose calculations performed by the *Accuray Precision™* Treatment Planning System, so there is no need to re-calculate plans in this case.

## ◆ Request JFOF Adjustment



**NOTE:** *TomoDirect*-phantom plans should be measured to ensure that they meet specifications, but only *TomoHelical*-phantom plans are used to inform JFOF adjustments.

If the average scaling factor for the helical *Tomo*-phantom plans varies with field size, the site physicist should contact Accuray Customer Support to help assess the situation. Since the machine has no field size-dependent output adjustment parameter, this kind of discrepancy would need to be addressed by adjusting the relative Jaw Fluence Output Factors (JFOF's) in the beam model. This will effectively adjust the dose calculation to match the delivery of the machine. After initial commissioning of a new beam model, adjustments to the JFOF's should be very rare.



**IMPORTANT:** Following an adjustment to the relative JFOF's, the *Tomo*-phantom plans should be re-optimized on the *Accuray Precision™* Treatment Planning System, and the *Tomo*-phantom dose points should be re-measured on the machine and compared against dose values from the re-optimized plans.



**IMPORTANT:** The new relative JFOF's will be applied to new plans. Fixed jaw plans created prior to the relative JFOF adjustment should be put through self transfer if they use the affected field size. All dynamic jaw plans created prior to the adjustment should be put through self transfer.



**NOTE:** For fixed jaw plans, there is only one relative JFOF that affects each plan. For dynamic jaws plans, several different relative JFOF's are used during the running start and stop portion of the delivery, as the jaws gradually open and gradually close. Thus, if any JFOF value is changed, all dynamic jaw plans should be updated with the self-transfer process.



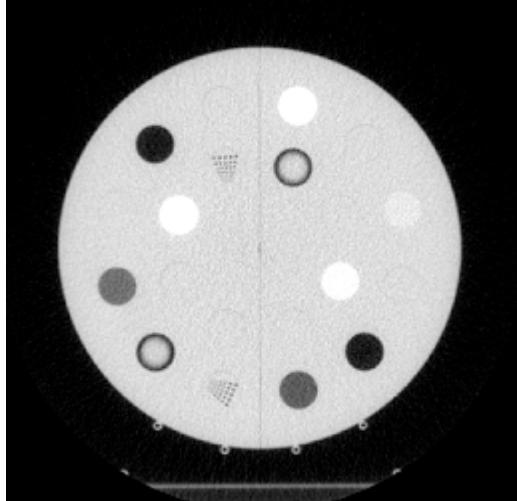


## *CTrue* Image Quality Verification

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# Overview of *CTrue* Image Quality

<b>TG-148 reference:</b>	MVCT Geometric distortions (section VI.B.1.a), Noise (section VI.B.2.a), Uniformity (section VI.B.2.b), Spatial resolution (section VI.B.2.c), Contrast (section VI.B.2.d), Dose (section VI.B.3)
<b>Purpose:</b>	Verify that the image quality is acceptable.
<b>Method:</b>	<ul style="list-style-type: none"><li>• Perform an Air Scan and CT number calibration.</li><li>• Scan the <i>Tomo</i>-phantom with density plugs and spatial resolution plug in place. Make subjective observations, and compare the image dimensions against the actual object dimensions.</li><li>• Export the image to third party software for numerical evaluation of image noise and uniformity.</li><li>• Scan the phantom with an ion chamber in place to determine the CT dose.</li></ul>
<b>Accuracy specification:</b>	There are no significant artifacts in the image. The largest three rows of holes in the CT resolution plug are visible. The dose for a fine scan is less than 3 cGy.
<b>Sample result image:</b>	
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• <i>Tomo</i>-phantom</li><li>• Density and spatial resolution inserts for <i>Tomo</i>-phantom</li><li>• A1SL ion chamber and electrometer</li></ul>

# Theory of *CTrue* Image Quality Verification

The MVCT imaging system creates *CTrue*™ images, as described in the System Overview chapter.

Prior to performing *CTrue* image quality verification, it is recommended to run an air scan and CT Number Calibration. These procedures realign the CT reconstruction to its baseline, accounting for drift in the imaging beam and detector response over time.

Scan the *Tomo*-phantom to test any of the *CTrue* reconstruction settings that are used clinically (**Standard**, **IR General**, and **IR Soft Tissue**). Verify the image quality, resolution, noise, and uniformity of the reconstruction setting.

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◆ CTrue Image Noise and Uniformity . . . . .	249
◆ CTrue Image Dose . . . . .	250

## ◆ Air Scan

The air scan is an imaging procedure performed with no couch or object in the beam. The air scan procedure collects data that is used to account for the detector response to the imaging beam as a function of detector channel and gantry angle.

## ◆ CT Number Calibration

The CT Number Calibration procedure acquires an MVCT scan of the *Tomo*-phantom. The software checks CT numbers in regions of interest within the *CTrue* image that are expected to contain air and the phantom. The software then adjusts the scaling of the CT numbers in the *CTrue* image generation process, so that future scans will yield the expected values for air and phantom. Running this procedure weekly helps to improve the stability of *CTrue* image numbers, as the properties of the imaging beam may drift over time.

*CTrue* image generation includes a post-reconstruction step in which pixel values are linearly scaled and offset according to coefficients stored in the **Linearity Settings** part of the **Edit Machine** tree for the MVCT beam. When you run the CT Number Calibration procedure, the **Calibration Slope** and **Calibration linearity offset** are automatically adjusted to maintain the default

values specified in the **Linearity Settings** part of the **Edit Machine** tree. These values are -1000 HU for air, 25 HU for the Med-Cal *Tomo*-phantom, or near 0 HU for the Sun Nuclear *Tomo*-phantom HE in the reconstructed image. Accuray will configure this setting to match site equipment.



**NOTE:** The **Edit Machine** area contains a system-level **Linearity Settings** section of the parameter tree (which stores the default HU values for air and water), as well as an MVCT beam-level **Linearity Settings** section of the parameter tree (which stores the **Calibration Slope** and **Calibration linearity offset**).



**IMPORTANT:** The CT number calibration scales the range of CT numbers according to measurements of only two materials (air and phantom). The CT number calibration does not replace the TG-148 requirements for regular checks of your MVCT density model, if you are calculating dose on MVCT images.



**IMPORTANT:** The CT number calibration does not update your density model. The site physicist should manually update the density model whenever there is a change in the correspondence between CT numbers and density.

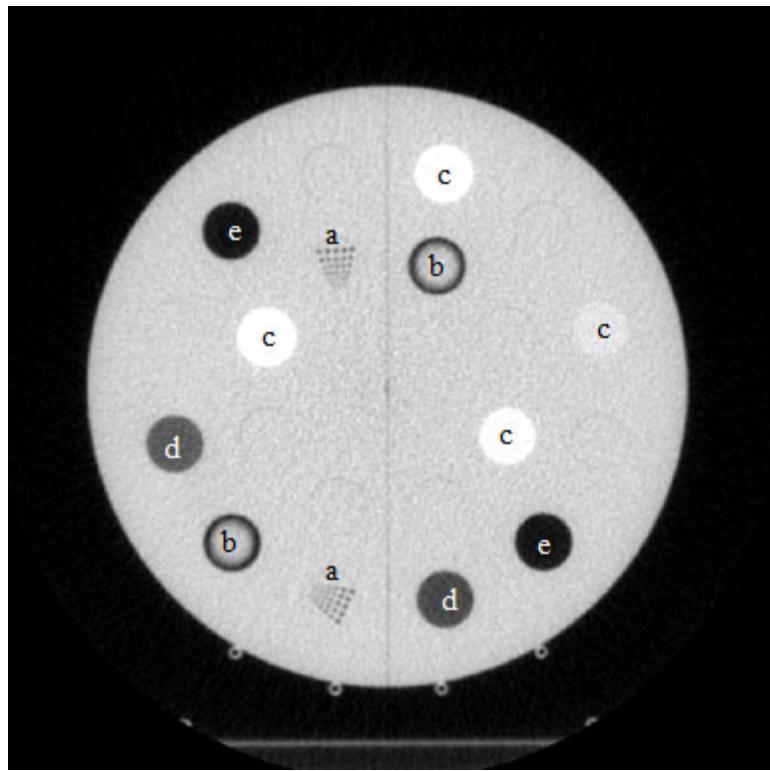
## ◆ Subjective Image Quality Verification

*CTrue* image commissioning should include subjective observation of a scanned image, to ensure that it is free from excessive artifacts. For example:

- Verify there are no rings in the phantom images (usually caused by a bad detector channel).
- Verify there are no streaks (lines) in the phantom images.
- Verify that the phantom does not appear to move back and forth as you page through the transverse image slices.

As a subjective check of contrast resolution, the density plug inserts should be visible in a scan of the *Tomo*-phantom, when you have chosen appropriate window/level settings.

Refer to the following *CTrue* image example. The image includes: (a) two resolution plugs, (b) two vials of water, (c) four bone plugs of different densities, (d) two lung plugs of different densities, (e) two empty cavities, and several plugs of the same material as the phantom.



CT Image of the *Tomo*-phantom

#### ◆ *CTrue* Image Dimensions

The dimensions of a phantom image in the software should be compared against physical measurements to ensure that spatial distances are properly reconstructed. The image viewer on the **Register** tab of the TDC includes ruler and diameter measurement tools.

You should also check that the phantom image orientation is consistent with the physical orientation of the phantom.

If using the *Tomo*-phantom, TG-148 suggests attaching fiducial markers to the *Tomo*-phantom or using the fiducial markers that are embedded in the surface of the cheese phantom, since these will be easier to delineate in the image.

#### ◆ *CTrue* Image Spatial Resolution in the Transverse Plane

The Accuray Incorporated specification for the spatial resolution in the transverse plane is that objects of diameter 1.6 mm, with center-to-center spacing of 3.2 mm, should be distinguishable in the image. The CT resolution plug included in the Standard System QA kit is suitable for this test. The plug should be inserted holes-first into the *Tomo*-phantom, and a

*CTrue* image should be acquired. The third largest row of pin holes should be visible in the image, with each hole distinguishable from neighboring holes.

On each system in manufacturing, Accuray performs a quantitative test of the spatial resolution in the transverse plane. Although not prescribed by TG-148, this test may also be performed by the customer if desired.

The test involves imaging a tungsten wire, 0.53 mm in diameter, oriented along the IEC Y axis, using the **Fine** pitch and **2.0 mm** reconstruction interval. The Point Spread Function is determined in IEC X and IEC Z. The full-width at half-maximum of the Point Spread Function must not exceed 2 mm. This specification is expected to be met for images reconstructed with the **Standard**, **IR General**, and **IR Soft Tissue** reconstruction options.

## ◆ *CTrue* Image Spatial Resolution in the Longitudinal Direction



**NOTE:** This section is for informational purposes. TG-148 does not specify a QA test for the longitudinal image resolution.



**NOTE:** Slice sensitivity profiles are not required for commissioning, as their measurement involves reconstruction of raw MVCT data at slice intervals not available in the treatment system software.

The ability to resolve objects in the longitudinal direction depends on the collimation size, couch motion, and the spacing of the reconstructed slices. Theoretically it would be possible to reconstruct the slices with any desired spacing, given the raw helical data. Each reconstructed slice uses data from an entire rotation (the data is weighted so that the data at the ends of the rotation aren't used as much). The treatment system software provides **Reconstruction Interval** options to reconstruct two or four slices per gantry rotation. With four slices per gantry rotation, there is more redundancy in the data used to reconstruct neighboring slices than with two slices per rotation.

In the factory, slice sensitivity profiles are measured by Accuray Incorporated, using a method described by Polacin 1994. A disk .64 mm thick is scanned, and images are reconstructed at 0.5 mm intervals (using non-commercial software outside of the treatment system). The average pixel values for the high contrast object are measured and plotted as a function of slice position.

The specification for the full-width at half-maximum (FWHM) of the profiles is specified to be 3.9 mm +/- 1.0 mm for **Fine** pitch, 5.3 mm +/- 1.0 mm for **Normal** pitch, and 7.2 mm +/- 1.0 mm for **Coarse** pitch. This specification should be met for the **Standard**, **IR General**, and **IR Soft Tissue** reconstruction options.

## ◆ *CTrue* Image Noise and Uniformity

The *CTrue* image noise is represented by the standard deviation in a region in the *Tomo*-phantom. Uniformity is represented by the consistency of average CT numbers in the center versus the edge of the *Tomo*-phantom. The *CTrue* image noise and uniformity should be evaluated.



**NOTE:** Accuray Incorporated does not perform a numerical test of the image noise and uniformity at ATP, but each system is tested in the factory for uniformity and noise.

The internal specification for uniformity is based on the difference in average CT numbers in a region of interest near the center of the phantom, versus average CT numbers in a region of interest near the edge of the phantom. Accuray's internal specification for uniformity is 25 HU. The internal specification for noise is based on the standard deviation in regions of interest near the edge of the phantom. Accuray's internal specification for noise is 43 HU for the Standard reconstruction option and 21 HU for the IR General and IR Soft Tissue reconstruction options.

TG-148 provides a calculation for image noise that is based on the standard deviation of the HU values in a region of interest and the Contrast Scale (Equations 9 and 10 in TG-148). The Contrast Scale is intended to account for the range of HU values produced by the scanner. If a CT scanner produces HU values according to the standard definition, the HU value of air should be -1000, and the HU value of water should be 0. But for example, if the range of values produced by a particular scanner were narrower, e.g., air at -800 HU and water at 0 HU, a particular value for the standard deviation (e.g., 43 HU) would have a relatively larger impact on the image quality.

For the imaging system, the range will be very stable if you run the CT Number Calibration procedure regularly. As mentioned previously, the CT Number Calibration maintains values in the *CTrue* image of -1000 HU for air and 25 HU for the Med-Cal *Tomo*-phantom or 0 HU for the Sun Nuclear *Tomo*-phantom HE.

Equations 9 and 10 of TG-148 base the contrast scale on the HU values and attenuation coefficients of water and polycarbonate, but any materials could have been used to determine the contrast scale. To simplify the equations and avoid requiring information about polycarbonate, we choose water and air for our two materials. If the system produces values near -1000 HU for air and 0 HU for water, and considering the linear attenuation coefficient of air to be 0, Equation 9 in TG-148 conveniently reduces to approximately:

$$\text{Noise} = \frac{\sigma_{CT}}{10}$$



**NOTE:** Strictly speaking, the definition of HU means that vacuum should be -1000 HU. However, in practice, the attenuation is calculated by comparing the detector signal to an air scan. Thus, if the signal is the same as the air scan, the attenuation is calculated to be zero. So in practice, air has a CT number of -1000 HU.

## ◆ *CTrue* Image Dose

The imaging dose is highest for a scan with the **Fine** acquisition pitch. The patient imaging dose for a **Fine** scan is less than 3 cGy, when measured with a calibrated A1SL placed in one of the central cavities of the *Tomo*-phantom (there is no cavity in the exact center of the phantom, but a cavity 1 cm from the center of the phantom may be used). Accuray Incorporated specifies that the scan should include at least 7 slices in the center of the phantom. TG-148 specifies that the scan should cover the entire phantom.

The beam quality factor for the imaging beam is not the same as for the treatment beam. However, since the goal of this test is only to verify that the dose is less than 3 cGy, it is not necessary to account for the differences. The ion chamber calibration factor, electrometer calibration factor, and temperature/pressure correction should be applied.

Acquisition Pitch	Maximum Imaging Dose
Fine	3 cGy
Medium	2 cGy
Coarse	1 cGy



**NOTE:** The treatment planning system does not account for the imaging dose.

## XML Description

**Air Scan** and **CT Number Calibration** are tasks accessible from the home screen of the TDC. Whenever you run these procedures, the detector data is processed automatically. The results from the most recent air scan and the most recent CT number calibration are used for image reconstruction.

For the subjective and numerical image quality verification tests consider using the **MVCT\_Open\_Field\_Rotating.xml**, available from Accuray Customer Support. This .xml contains an image of sufficient length to allow you to scan the entire *Tomo*-phantom.



**NOTE:** Considerations for selecting a patient or procedure to acquire a phantom image from the **Scan** tab:

- The Superior/Inferior extent of the planning image impacts the available scan length for slice selection on the **Scan** tab (you can scan approximately  $\pm 9$  slices beyond the planning image).
- The Y resolution of the patient planning image impacts the image display on the **Register** tab (MVCT image is interpolated to slice positions of planning image).

# Set Up and Deliver the Test

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**IMPORTANT:** Before performing QA tasks, warm up the system as described in “System Startup” (page 76) to help achieve a stable beam output.

## ◆ Air Scan

Instructions for performing the Air Scan may be found in the *Treatment Delivery Manual*.

## ◆ CT Number Calibration



**IMPORTANT:** The *Tomo*-phantom must be used for the CT number calibration, because the results are processed assuming CT numbers appropriate for the *Tomo*-phantom (nominal 25 HU for the Med-Cal *Tomo*-phantom and 0 HU for the Sun Nuclear *Tomo*-phantom HE). Do not use a different phantom.

Instructions for performing the CT number calibration procedure are located in the *Treatment Delivery Manual*.

## ◆ Subjective Image Quality Verification

1. Set up the *Tomo*-phantom on the couch. Position the phantom so that the small ion chamber holes are on the +Y side of the phantom and are aligned vertically (rotation consistent with green bore lasers). Align the phantom center to the green lasers in X, Y, and Z.
2. Insert the variable density plugs and resolution plugs into the *Tomo*-phantom. The resolution pattern of the resolution plugs should be inside the phantom. Leave two open air cavities. Fill additional cavities with the *Tomo*-phantom plugs, which are labeled, "1.0." Fill all the ion chamber

- holes with plugs. If desired, attach additional fiducial markers to the phantom surface, to help you check the image dimensions.
3. If you have a camera, take a photograph of the plug positions for your reference. Or, record the positions and values of the plugs in a diagram.
  4. From the TDC Tools menu, open a machine QA patient such as **ZZZ MVCT Open Field Rotating**.



**NOTE:** Alternatively, you could open the **Acquire Planning Image** task from the **Tools** menu of the TDC, but in this case you will not have access to the **Register** tab, and will need to export your images to other software for viewing.

5. Choose the **Fine** acquisition pitch and the **1 mm** reconstruction interval. Choose the reconstruction setting: **Standard**, **IR General**, or **IR Soft Tissue**.
6. Select about 200 mm of slices, or about 200 images covering the entire phantom.
7. Prepare and deliver a scan.
8. View the image on the **Register** tab of the Machine QA task, or in third party software, to verify that the image is free from artifacts and that the density plug inserts are visible.



**NOTE:** From the Machine QA task or Review Machine QA Registration task, click **Tools > Export Machine QA Scans**, and select the scan that you would like to export. This will save the DICOM data to the local drive of your TDC workstation (C:\accuray\exports\Machine QA scans). Machine QA procedures are purged nightly. Only the most recent several images are retained. You can set the Maximum number of Machine QA Procedures to Keep in the Policies tab of the System Administration task on the Accuray Precision software.

## ◆ *CTrue* Image Dimensions

Use the same phantom image as in the previous section.

1. Measure the physical dimensions of your phantom, or the distances between fiducial markers.
2. Use the ruler tool on the **Register** tab to verify the image dimensions. For instructions on using the ruler tool, refer to the *Treatment Delivery Manual*.
3. Identify an image slice where you can see the ion chamber pegs, and verify in the image that the line of ion chamber pegs is parallel to the green lasers.
4. Identify an image slice where you can see the density plugs. Compare density plug positions against the positions recorded in “Subjective Image

Quality Verification” (page 246), Step 3, to confirm that the image was reconstructed in the proper orientation.

## ◆ *CTrue* Image Spatial Resolution in the Transverse Plane

Use the same phantom image as in the previous section.

1. Identify the best image slice for viewing the CT resolution plug and set the window/level for optimal viewing.



**NOTE:** From the Machine QA task or Review Machine QA Registration task, click **Tools > Export Machine QA Scans**, and select the scan that you would like to export. This will save the DICOM data to the local drive of your TDC workstation (C:\accuray\exports\Machine QA scans). Machine QA procedures are purged nightly. Only the most recent several images are retained. You can set the Maximum number of Machine QA Procedures to Keep in the Policies tab of the System Administration task on the Accuray Precision software.

2. Verify that you can distinguish the third row of holes in the resolution plug.

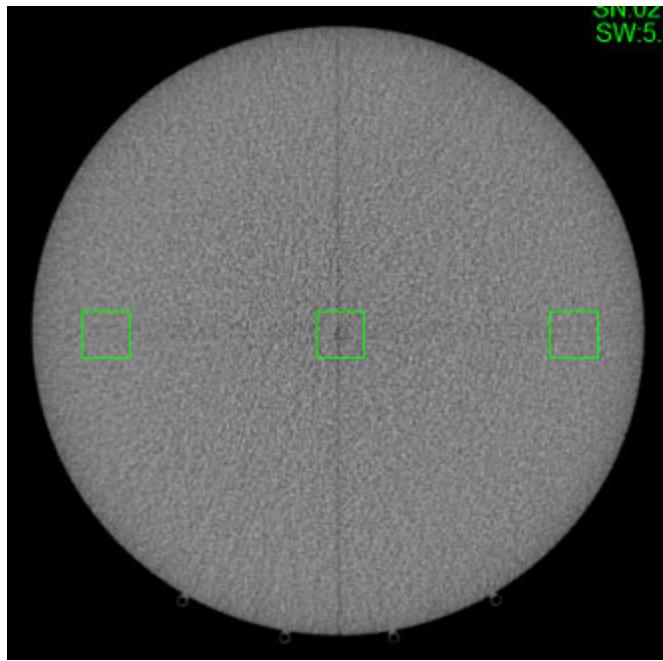
## ◆ *CTrue* Image Noise and Uniformity

Use the same phantom image as in the previous section.

1. Since the system does not include tools for evaluating the standard deviation or average CT numbers of a region of interest in a *CTrue* image, you will need to send the *CTrue* images to third party software for numerical evaluation.
2. Use the tool of your choice to select slices of the phantom image that do not contain density plugs. Evaluate the average and standard deviation of CT numbers in regions of interest near the center and edge of the *Tomo*-phantom, as shown in the following figure.



**TIP:** Section VI.B.4 of TG-148 mentions examples of free third party tools to find the average and standard deviation of CT numbers in regions of a DICOM image.



Example of regions of interest drawn in third party software near the center and edge of the *Tomo*-phantom for image noise and uniformity evaluation.

## ◆ *CTrue* Image Dose

1. Place the *Tomo*-phantom on the couch, with the ion chamber holes in the vertical orientation and facing away from the gantry. Align the center of the phantom with the stationary overhead green laser. Adjust for couch sag to ensure the center of the *Tomo*-phantom is at isocenter height when at the machine isocenter inside the bore.
2. Remove a dowel 10 mm from the center of the *Tomo*-phantom, and insert an A1SL ion chamber.
3. Prepare the electrometer to measure integrated dose.
4. Select a patient on the TDC.
5. Set the acquisition pitch to **Fine** and select enough slices to cover the entire phantom.



**NOTE:** The scan acquisition process is the same for all scans with a fine pitch, so it does not matter which reconstruction algorithm is used for this test.

6. Start the electrometer and run the scan.
7. Calculate the dose from the charge using the standard method.

## What to Do if the Test Fails

If images fail to meet Accuray Incorporated specifications, the service representative will need to address the problem by adjusting the MVCT beam and/or the MVCT image reconstruction parameters in the software.

Solutions may range from simply flagging a bad channel not to be used for reconstruction (to resolve a ring artifact), to measuring a new MVCT spectral calibration (the file that accounts for beam hardening in the image reconstruction).

If the FSE makes adjustments, the site physicist should follow up by repeating the tests in this section to ensure that they pass, starting with the **Airscan** and **CT Number Calibration**. If you use MVCT images for dose calculation (e.g., for treatment planning or adaptive calculations), you may need to create a new MVCT density model.



## Monitor Unit Display Calibration

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# Overview of Monitor Unit Display Calibration

<b>TG-148 reference:</b>	Monitor chamber signal scaling during ATP (section V.A.1) and Monitor chamber constancy (section V.B.2.d)
<b>Purpose:</b>	Calibrate the <b>Cumulative (mu)</b> display on the TDC for Dose1 and Dose2 in a meaningful way (typically 1 cGy/MU at 850 mm SAD, 50 mm x 400 mm field, 15 mm depth in <i>Virtual Water</i> ).
<b>Method:</b>	Use an ion chamber to measure the dose for a 60 s procedure, 50 mm x 400 mm field, 850 mm SAD, at 15 mm depth in <i>Virtual Water</i> , and set the calibration factors accordingly.
<b>Accuracy specification:</b>	When an IMRT plan has been successfully delivered: <ul style="list-style-type: none"><li>• Cumulative (mu) values for Dose1 and Dose2 are within 2% of each other.</li><li>• The Expected (mu) and Cumulative (mu) display values on the OS are within 2% of each other.</li></ul>
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• A1SL ion chamber</li><li>• Electrometer</li><li>• <i>Virtual Water</i>: one (1) block of 50 mm x 150 mm x 550 mm, and one (1) block of 5 mm x 150 mm x 550 mm</li></ul>

# Theory of Monitor Unit Display Calibration

In this section, the monitor unit display will be calibrated. The conversion factors from raw counts to displayed monitor units will be set, and the conversion factor from planned treatment time to monitor units will be set. The calibration controls the display but does not affect the machine performance, since TDC and interlocks are based on the raw counts.



**IMPORTANT:** The monitor unit display should be calibrated at a time when the system performance is known to be within specifications.

The display is typically calibrated to 1 cGy/MU at 850 mm SAD (source to ion chamber distance) for a 50 mm x 400 mm field size, at 15 mm depth in *Virtual Water*.

The general workflow is:

1. Measure the output under your preferred calibration conditions, and record the cumulative Dose 1 and Dose 2 values displayed.



**TIP:** If you find it easier to set up the *Virtual Water* at 850 mm SSD, you may do so, then multiply the result by  $(86.5/85)^2$  to perform the inverse square correction to 850 mm SAD.

2. Scale the **MU per chamber count** parameters for Dose1 and Dose2 to achieve a display of 1 cGy/MU.
3. Set the **Expected MU (MU/min)** parameter to match the dose that you measured in cGy during the 60 s procedure.
4. Run the procedure again to ensure that the TDC displays for Dose1 and Dose2 agree, and that the cumulative counts displayed match your ion chamber dose measurement.
5. Run a treatment plan. The cumulative and expected counts for the plan should agree.

This section primarily focuses on calibration of the treatment beam display. The system does not calculate the imaging dose or predict the expected MUs for the scan beam. If desired, the scan beam MU display calibration may be verified using the same workflow as described above, except that the scan beam does not use an **Expected MU (MU/min)** parameter.

# XML Description

Example of MU Display Calibration	
<b>Where to get the XML:</b>	Accuray Incorporated does not supply the .xml file for the MU display calibration. Follow the instructions in the chapter “Appendix C” (page 525) to create your procedure.
<b>Patient Name:</b>	ZZZ MU display calibration
<b>Procedure Description:</b>	60s all open, 5x40, SetuptoReady0
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	J42 (nominal 5 cm field width)
<b>MLC:</b>	All open
<b>Beam-on time:</b>	60s with leaves open



**IMPORTANT:** For machine QA procedures, the cumulative MU display starts counting from the beginning of the procedure. Do not include a 10 s warmup in the MU display calibration procedure.

# Set Up and Deliver the Test

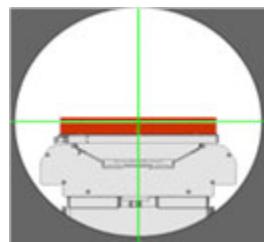
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**IMPORTANT:** Before performing QA tasks, warm up the system and run an air scan as described in “System Startup” (page 76) to help achieve a stable beam.

## ◆ Measure the Dose Rate

1. Connect a calibrated A1SL ion chamber to the electrometer, then set up the electrometer to measure integrated dose at +300 V (see “Set up the Tomo-Electrometer” (page 88)).
2. At the green lasers outside the bore, set up the *Virtual Water* stack, with the long edge parallel to the X axis. The chamber should be at 15 mm depth, with a few cm of backscatter beneath the chamber. The chamber collection volume should be centered on the green lasers in X and Y. The surface of the *Virtual Water* should be at 850 mm SSD.
3. Bring the couch exactly 700 mm into the bore, and correct for couch sag using the **Step Move** function, to ensure that the surface of the *Virtual Water* is at 850 mm SSD.
4. If you will be performing the measurement at 850 mm SAD, use the **Step Move** function to raise the couch by 15 mm (see the following image for reference). If the couch **Setup to Ready** distance in your .xml file is zero, do not bring the couch out of the bore.



Chamber at 15 mm depth, 850 mm SAD

5. Run the procedure and record the integrated charge.
6. Also record the displayed **Cumulative (mu)** values for Monitor Chambers 1 and 2.

7. Calculate the ion chamber dose as discussed in “Dosimetry for the Treatment System” (page 97).
8. Repeat as many times as desired to achieve a stable measurement.

## ◆ Adjust the Machine Parameters



**WARNING:** Do not modify any parameters except for the **MU per chamber count** and **Expected MU (MU/min)**. The **MU per chamber count** and **Expected MU (MU/min)** affect the display but do not affect the machine performance. Changing other parameters may result in system damage, the inability to run beam, or a discrepancy between planned and delivered patient dose. Contact Accuray Customer Support if you need help modifying parameters.

This section presents the workflow for adjusting machine parameters. An example calculation is provided in the next section.

1. From the TDC, click the **Tools** menu and select **Edit Machine**.
2. Navigate to the folder **Beams/Beam type: Treatment/Controls**.
3. Enter the dose in cGy from step 7 of the previous section (round to the nearest integer value) in the **Expected MU (MU/min)** field. The modified field will be displayed in yellow.



**NOTE:** The **Expected MU (MU/min)** parameter is used by the system to determine the expected monitor units from the calculated beam-on time for a plan.



**NOTE:** If you update the **Expected MU (MU/min)** parameter:

- Future plans that you create will use the new value to calculate expected monitor units in the Plan Report (accessible from the Precision Planning System) and Delivery Report (accessible from the TDC).
- For plans that have already been made, the expected monitor units in the Plan Report will not be updated, and the expected monitor units in the Delivery Report will be updated only for those fractions that have not yet been treated.

4. Determine the correction factors for the cumulative MU display:

*Dose1 Factor = (Measured Dose)/(Cumulative (mu) displayed on TDC for Monitor Chamber 1)*

*Dose2 Factor = (Measured Dose)/( Cumulative (mu) displayed on TDC for Monitor Chamber 2)*

where the measured dose was determined in Step 7 of the previous section, and cumulative MU display was determined in Step 6 of the previous section.

5. Multiply the **MU per chamber count** values by their respective factors determined in Step 4, and enter these new values in the **MU per chamber count** fields. The modified field will be displayed in yellow.
6. Click **Save**, enter your password when prompted, and click **OK**.

## ◆ Example of Monitor Unit Parameter Calculation

This section provides an example of an adjustment to the monitor unit display parameters. You will need to enter machine-specific values into your system.

Example parameters:

- Prior to calibration, the MU1 and MU2 cumulative values for a 60 second procedure are 866 and 876, respectively.
- When measuring the dose rate using an A1SL ion chamber at 15 mm depth in *Virtual Water* and an 850 mm SAD setup, a measurement of 880.6 cGy is obtained.
- Current values for monitor chambers 1 and 2 in the **MU per chamber count** fields are 1.6834E-6 and 2.2547E-6, respectively.

To calibrate the monitor unit display:

1. Enter 881 in the **Expected MU (MU/min)** field.
2. Enter the new coefficients into the field for **MU per chamber count**:

$$\text{For monitor chamber 1: } \frac{881}{866} \times 1.6834 \times 10^{-6} = 1.7126 \times 10^{-6}$$

$$\text{For monitor chamber 2: } \frac{881}{876} \times 2.2547 \times 10^{-6} = 2.2676 \times 10^{-6}$$

3. Save the machine data.

The machine data is now updated to reflect the correct factors needed for the MU counts to display the same value that was measured. The planning system will multiply the number of minutes for each treatment by 881, to calculate the expected monitor units for each treatment.

## ◆ Verify the MU Display Calibration

1. Repeat the procedure in “Measure the Dose Rate” (page 261). Verify that the **Cumulative (mu)** displays for Monitor Chambers 1 and 2 match each other within 2%.
2. Run a fraction of a **TomoPhant** plan, e.g., Plan 3. It does not matter if there is a phantom on the couch. Verify that the **Cumulative (mu)** displays for Monitor Chambers 1 and 2 match the **Expected (mu)** within 2%.
3. If you were unsuccessful in performing the calibration, contact Accuray Customer Support for guidance.

## What to Do if the Test Fails

During initial system calibration, an adjustment to the monitor unit display calibration will be necessary.

In the future, if a discrepancy arises, the cause of the discrepancy should be investigated:

- A discrepancy between Dose1 and Dose2 counts may be caused by a deviation in the beam energy. The beam energy affects the transverse profile shape, because the Bremsstrahlung from the target becomes more forward-directed with increasing energy. Since the Dose1 chamber is larger than the Dose2 chamber, the ratio between Dose1 and Dose2 is a very rough consistency check of the energy of the beam.
- A discrepancy between cumulative and expected counts may be caused by a change in the dose rate of the system.
- A discrepancy may also indicate that one or both of the independent ion chambers is no longer functioning properly.

The site physicist should verify the beam output and energy using a calibrated ion chamber. The site physicist may also need to contact Accuray Customer Support for assistance in checking the health of the monitor chambers. If the beam output and energy are found to be within specification and the monitor chambers are in good working order, it may be necessary to re-calibrate the display.





## Establish Baseline References

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## Overview of Baseline References

<b>TG-148 reference:</b>	Output-static consistency (section V.B.2.d), Beam quality consistency with baseline (V.B.2.a), and Transverse profile consistency with baseline (V.B.2.b)
<b>Purpose:</b>	Create baseline references that can be used for daily and monthly QA of the static output, PDD, and transverse profile. Create references for all <i>TQA</i> tests.
<b>Method:</b>	Static dose and beam quality should be measured using an ion chamber in <i>Virtual Water</i> , and also in any other device that will be used for daily QA. <i>TQA</i> references are created by running the respective modules when the machine is known to be in a commissioned state.
<b>Accuracy specification:</b>	Typical ranges for treatment beam output and PDD measurements in <i>Virtual Water</i> for twinned machines (85 cm SSD, 5 cm x 40 cm field, all leaves open): <ul style="list-style-type: none"><li>• Static output at 1.5 cm depth: <math>850 \pm 30</math> cGy/min for the standard dose rate configuration, or 1025 cGy/min (with a few percent machine-to-machine variation) for the high dose rate configuration</li><li>• PDD at 85 cm SSD in Med-Cal Virtual Water: 10/1.5 ratio: 0.592 to 0.617; 20/1.5 ratio: 0.311 to 0.323</li><li>• PDD at 85 cm SSD in Sun Nuclear Solid Water: 10/1.5 ratio: 0.593 to 0.618; 20/1.5 ratio: 0.315 to 0.327</li></ul>
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• Set of <i>Virtual Water</i> blocks (15 cm x 55 cm x variable thickness).</li><li>• Ion chamber and electrometer</li><li>• See the <i>TQA Manual</i> for materials for each <i>TQA</i> module</li></ul>

# Theory of Baseline References

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## ◆ Static Output and Beam Quality

TG-148 specifies that beam profiles should be measured annually in a water tank, and the helical IMRT dose output should be verified monthly against values calculated by the Treatment Planning System. For monthly beam profile measurements and daily/monthly static output measurements, a consistency check is sufficient.

Machine-specific baseline values for the consistency checks should be established when the machine is confirmed to be in a well-commissioned state (alignment, profiles, and water tank data match the reference data associated with the beam model to within specification).

References should be established for an ion chamber in *Virtual Water*, as well as for any other equipment that the site intends to use for daily QA.

## ◆ TQA References

When the machine is confirmed to be in a well-commissioned state, *TQA* references should be established for all *TQA* modules that are included with the site's purchase and that are applicable to the site configuration (some *TQA* modules use dynamic jaws).

The following modules require a site-specific reference measurement:

- Basic Dosimetry
- Daily QA
- Step Wedge Static
- Step Wedge Helical
- Jaw Sweep - Dynamic Jaws

Accuray Incorporated provides reference files for the following modules:

- Field Width
- Field Width - Dynamic Jaws
- Water Tank

The following *TQA* modules do not require a reference file:

- LINAC Longitudinal Alignment
- LINAC Transverse Alignment
- Airscan

The *TQA Manual* includes instructions for setting *TQA* references. The Accuray Incorporated representative who performs your ATP will assist you in initially setting up the references.



**TIP:** *TQA* has database backup/restore functionality, storing backups to the D volume, located on the gateway server at the hospital. If an additional backup is desired, download and save your reference *TQA* files and other important files to a secure location.

# XML for Static Output and Beam Quality Baseline



**NOTE:** Because the daily/monthly static output and energy QA is a consistency check, the exact parameters for the procedure are at the site physicist's discretion. For example, some physicists may prefer to open only leaves 25 through 40, to achieve a 50 mm x 100 mm field (with the nominal 50 mm field width).

## Example of static output and energy check

<b>Where to get the .xml:</b>	The <b>Static Output and Energy.xml</b> may be requested from Accuray Customer Support.
<b>Patient Name:</b>	ZZZ Static Output and Energy
<b>Procedure Description:</b>	J42 - TX Beam - AllLeavesOpen - SetuptoReady 0cm - 70sec J42 - MVCT Beam - AllLeavesOpen - SetuptoReady 0cm - 70sec
<b>Couch movement in IEC Y when Ready is pressed:</b>	None
<b>Couch translation during the procedure:</b>	None
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	J42 (nominal 5 cm field width)
<b>MLC:</b>	All open to achieve a 5 cm x 40 cm field
<b>Beam-on time:</b>	10 s warmup with leaves closed, then 60s with leaves open

# Set Up and Measure the Static Output and Beam Quality Baseline

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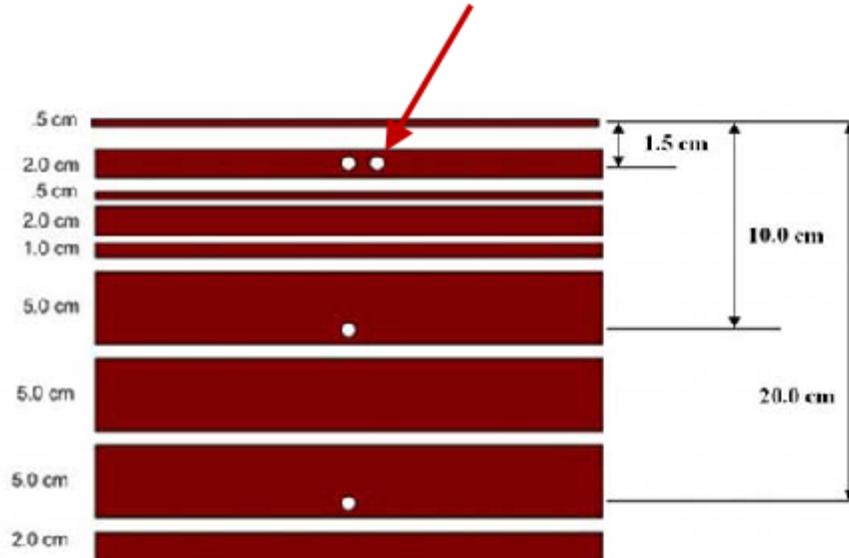
**IMPORTANT:** Before performing QA tasks, warm up the system as described in “System Startup” (page 76) to help achieve a stable beam.



**NOTE:** The static output and energy baseline must be measured for the treatment beam. If desired, you could optionally measure them for the MVCT beam as well.

## ◆ Set Up the Equipment

1. Stack the *Virtual Waterblocks* on the table such that the center of the ion chamber holes are at depths of 15 mm, 100 mm, and 200 mm from the top surface of the stack.
2. Adjust the table height so that the top surface of the stack is at 850 mm SSD.
3. Center the stack on the green lasers in Y, and align the column of ion chamber measurement holes with the green lasers in X (the second reference hole will be slightly offset from the green lasers).



*Virtual Water Stack*

Use the *Virtual Water* stack for measuring the static output and energy baseline. The blocks are illustrated with empty space between them to help you see them better, but there will be no empty spaces in the actual setup, and the dimensions in the figure do not include the empty space. The 20 mm block contains two ion chamber holes. This design allows for one chamber to stay in place as a reference chamber in the position indicated by the red arrow, while the other chamber is positioned in sequence at each depth for the beam quality check.

4. Bring the couch 700 mm into the bore, and adjust for couch sag, so that the bore green laser skims the top surface of the block. Do not bring the couch out of the bore, if the Setup to Ready distance for your .xml is 0.
5. Record the temperature and absolute pressure.
6. Connect two A1SL ion chambers to the *Tomo-Electrometer*. Set the bias to +300 V, and prepare the electrometer to measure integrated charge. For detailed instructions, see “Set up the Tomo-Electrometer” (page 88).

## ◆ Measure the Static Output

1. Place an ion chamber in the hole at 15 mm depth that is aligned with the green lasers. Plug the adjacent hole.
2. Prepare the procedure and start the electrometer integrating.
3. Run the procedure and record the charge.
4. Repeat steps 2-3 to ensure a stable measurement.

## ◆ Measure the Beam Quality

1. Place a reference A1SL chamber in the position indicated by the arrow in the virtual water stack diagram under “Set Up the Equipment” (page 272). This chamber will not move between measurements, and will be used to verify output stability.
2. Place the measurement chamber in the hole at 15 mm depth.
3. Run the procedure and record the charge for the measurement chamber and the reference chamber. Repeat to ensure a stable measurement.
4. Move the measurement chamber to the hole at 100 mm depth, while keeping the reference chamber in place at 15 mm depth. Plug the measurement hole at 15 mm depth. Perform the measurement as in Step 3.
5. Move the measurement chamber to the hole at 200 mm depth, while keeping the reference chamber in place at 15 mm depth. Plug any unused holes. Perform the measurement as in Step 3.



**NOTE:** Alternatively, if you have multiple chambers, you could take beam quality measurements at two or three depths simultaneously, without using a reference chamber (plug the reference chamber hole). The chambers at shallower depths may impact the measurement at deeper depths. This can be acceptable for a consistency check as long as you record your setup and make all future measurements in the same way.

## Analyze the Result

1. Calculate the dose for each charge measurement you collected.
2. If necessary, normalize the beam quality measurements to account for any run-to-run variation in the reference charge measurement.
3. Calculate the beam quality ratios for the 10/1.5 and the 20/1.5.
4. If you used the same measurement conditions as indicated in “Overview of Baseline References” (page 268), compare your results against the typical ranges provided.



**IMPORTANT:** Do not adjust the beam output or energy based on the typical range of dose and beam quality ratios listed in “Overview of Baseline References” (page 268). The beam output and energy should have been set to match the beam model during machine commissioning. If your result falls outside the typical range, check your .xml procedure file and your measurement setup.

5. Save the measurement data, setup notes, and calculations with your QA records, as a reference for future static output and beam quality constancy checks.





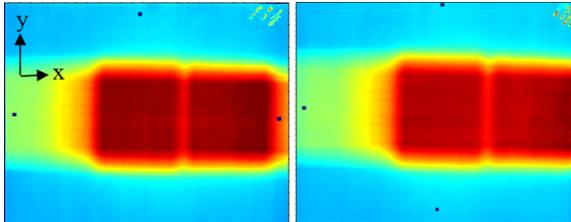
## Completion Procedure Test

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# Overview of Completion Procedure Test

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- ◆ Alternate Methods for Performing this Test ..... 279
- ◆ Plan Description ..... 279

TG-148 reference:	Interrupted Procedure (section V.B.4.a)
Purpose:	Verify that an interrupted and completed delivery gives the same dose distribution as an uninterrupted procedure.
Method:	Verify that an interrupted and completed delivery gives the same dose distribution as an uninterrupted procedure.
Accuracy specification:	<ul style="list-style-type: none"><li>• The sum of the absolute doses measured by an ion chamber for the interrupted and completed procedure is within 3% of the dose for the uninterrupted procedure.</li><li>• When comparing the central 80% of the plateau region, the interrupted and completed film is within 3% of the uninterrupted film, and the offset is less than 3 mm.</li><li>• TG-148 additionally specifies that the overall length (FWHM) of the dose distribution for the interrupted and completed procedure should be within 1 mm of the FWHM for the uninterrupted procedure.</li></ul>
Sample result images:	 <p>Images shown are for a two-target plan.</p>
Equipment needed:	<ul style="list-style-type: none"><li>• Tomo-phantom</li><li>• Film scanner, computer, Analysis software</li><li>• Ion chamber and electrometer</li><li>• 2 EDR or EBT films per modality tested (recommended minimum size 20 cm x 25 cm)</li></ul>

## ◆ Theory of Completion Procedure Test

Completion procedures (make up procedures) are discussed in “Manage Treatment Interruptions” (page 79). Because completion procedures may be delivered to patients, it is important to test the workflow to ensure that the same cumulative dose distribution is achieved for an interrupted and completed procedure as for an uninterrupted procedure.

## ◆ Alternate Methods for Performing this Test

The spatial resolution of an array device may not be sufficient for this test.

## ◆ Plan Description

You will need an optimized plan for this test. Completion procedures may be delivered for patient treatment plans, phantom plans, and patient QA plans. Completion procedures are not available for Machine QA plans.

For example, use a plan from the *TomoHelical*-Phantom patient, introduced in “Absolute Dose Calibration” (page 211).

At Acceptance Testing, Accuray Incorporated performs this test for one *TomoHelical* plan and one *TomoDirect*-Phantom plan.

TG-148 suggests to run this test with a different field width each month. If you have the *TomoDirect* feature and the dynamic jaws feature, you could include these types of plans in your monthly test rotation as well.

# Set Up and Deliver the Test

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## ◆ Set Up

1. At the TDC, select your treatment plan.
  - If you want to acquire a setup verification image, prepare a scan.
  - If you do not want to take an image, prepare a treatment.



**NOTE:** The precise position of the phantom for this test (e.g., couch sag correction) is not critical. However, the setup position must be consistent for the uninterrupted versus interrupted and completed films.

2. Set up the phantom to the lasers as indicated in the plan. Rotate the phantom so that a film may be inserted in the coronal plane.
3. If you prepared a scan, perform the scan, register to the planning image, and accept registration offsets. Then prepare a treatment and press **Setup** to apply the shifts to the couch.
4. Remove the top half of the phantom, and insert a film in the coronal plane. Tape the film in place.
5. Mark the green lasers on the film, about 1 cm from each film edge. Also, make an orientation mark in the +X, + Y corner of the film. Label the film as "uninterrupted."



**TIP:** If you are using EBT film, find a way to label the film that does not add extra marks on the film itself, which may affect the analysis. For example, store the film in a paper folder labeled "uninterrupted."

6. Replace the top half of the phantom, being very careful not to disturb your setup.
7. Remove the dowel just below the film plane, and insert an ion chamber. Connect the ion chamber to the electrometer and set up the electrometer to measure integrated charge.
8. Use tape to mark the Y position of the overhead green laser on the couch, for reference.

## ◆ Deliver the Test

1. Press **Ready** to send the couch into the bore. Deliver the full treatment to the phantom and record the dose.
2. Remove the “uninterrupted” film from the treatment room, and label the new film as “interrupted and completed.”
3. Repeat the setup for the interrupted procedure, being careful to maintain the same phantom setup position.
4. Begin to deliver another treatment fraction. Approximately halfway through the delivery, press the yellow **Stop** button to interrupt the procedure.
5. Stop the electrometer, record the dose for the interrupted procedure, and start the electrometer again. Leave the film in place.
6. Turn the key to **Program** and resolve the interruption at the TDC.
7. Select the completion procedure from the fraction list, and click **Load Fraction**.
8. Click the **Prepare Treatment** button.
9. Before pressing **Ready** on the Positioning Control Panel, press **Setup** to bring the couch back out of the bore to the registered setup position. Check that the couch is aligned to the mark you made in Step 8 of “Set Up and Deliver the Test” (page 280).
10. Deliver the completion procedure and record the dose.
11. Process (if necessary) and digitize the two films.

# Analyze the Result

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## ◆ Dose Comparison

Compare the dose for the uninterrupted treatment to the sum of the doses for the interrupted and completed treatments, to ensure that they agree within 3%. If desired, you may use the **Dose Measurement** page of the Accuray Incorporated provided completion procedure spreadsheet.

## ◆ Profile Comparison Using the Accuray Provided Spreadsheet

1. In your film analysis software, plot a profile through the green laser marks along the Y direction of each film. The origin of the profile should be at the intersection of green lasers, so that the two profiles can be compared.



**TIP:** The “Appendix B” (page 511) appendix includes instructions for obtaining the profiles in the RITg148+ software.



**TIP:** To reduce the impact of inherent film noise on the profiles, it may be helpful to apply an image filter (e.g., median 3x3 filter). Apply the same filter for both films in the analysis.



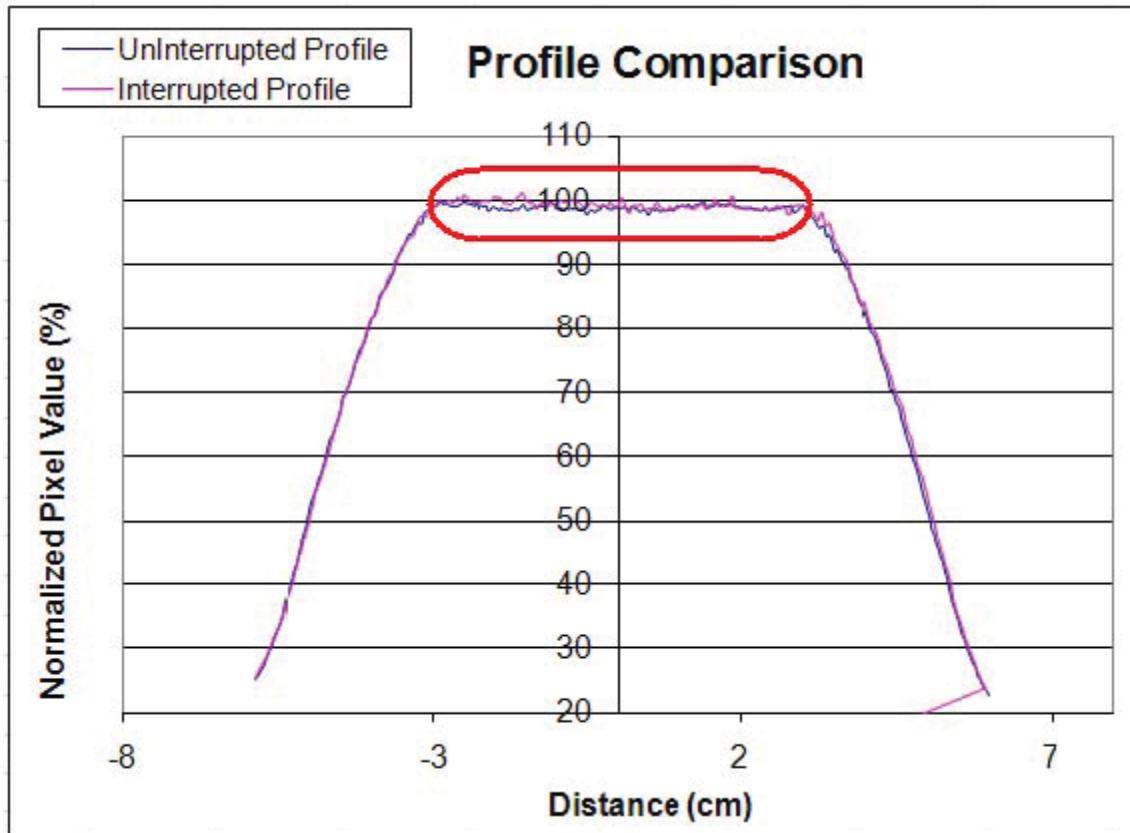
**NOTE:** When Accuray Incorporated performs this test during initial acceptance testing, a film calibration file is not applied to the films. You may choose to apply a film calibration file for film dosimetry.

2. Save the profile for each film as a **.csv** file (comma separated variable file). This file should include a column representing the positions relative to the green laser intersection in cm, and a column representing the film values.
3. Open the **Film Data** page of the spreadsheet. Fill out the SN, date, and file names in the yellow boxes.
4. Open the **.csv** profile data in Excel™ (comma delimited file). Select and copy the uninterrupted profile positions and values.
5. Select and copy the uninterrupted profile positions and values.



**NOTE:** A locked component of the Accuray Incorporated spreadsheet prevents analysis across the entire range of data, if the analysis region is too long. To view the central region of the data plot, select and copy rows and position values containing a limited amount of background data. This can be determined by the values in the file or by the plot of the profile from the RIT interface. It often works well to start at a position value of about -50 mm. Try to avoid including the rows representing the pin pricks.

6. Paste the uninterrupted profile data into the appropriate rows of columns A and B of the completion procedure spreadsheet. (**Paste Special > Values Only**).
7. Select, copy, and paste the interrupted and completed profile data into the appropriate rows of columns E and F of the completion procedure spreadsheet. Again, do not include any pin pricks.
8. On the **Profile Comparison** page of the completion procedure spreadsheet, the two profiles will be plotted together. Enter values in the green boxes to shift the interrupted and completed film to match the uninterrupted film. Ensure that your shift value is in the range of  $0 \pm 0.3$  mm.
9. Compare the plots to ensure that they agree within  $\pm 3\%$  in the central 80% of the plateau region. To do this, adjust the scale value for the interrupted and completed profile in the spreadsheet to verify that for each point in the central 80% of the plateau region, there is a scale value in the range of 0.97 to 1.03 that results in a match between the two profiles.



#### Profile Comparison

In the image, the profile comparison with plateau region is circled. Approximately the central 80% of the plateau is used for analysis. The small jag in the Interrupted profile near 50 mm is probably due to a pin prick.

10. The spreadsheet provided by Accuray Incorporated does not list the FWHM of the profiles, but you may perform a visual evaluation to ensure that they agree within 1 mm.

## What to Do if the Test Fails

The most common causes of failure are:

- The user did not appropriately position the couch for the completion procedure.
- The digitized film was noisy (due to inherent film noise or processor artifacts). It may help to run the test with a fresh box of film, or apply a median 3x3 filter to the films prior to performing the analysis.

If the test still fails, contact Accuray Customer Support for assistance.





## Synchronicity Tests

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# Introduction

Synchronicity tests are intended to verify that the couch, gantry, and leaves maintain their expected relationships for procedure delivery. These tests, shown in the following table, are also described in TG-148 Section V.B.3.

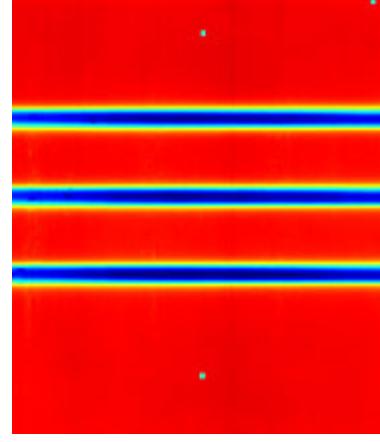
At the time that TG-148 was written, the TomoDirect™ feature was new. Thus, TG-148 does not address QA for treatment delivery with a static gantry and moving couch. Accuray Incorporated recommends extending the TG-148 recommendations to include a static star shot film, ensuring that the leaves open at the expected gantry angles for a static procedure.

Synchronicity Test Name	Test Purpose
Couch translation	Couch translation and MLC leaf opening are synchronized.
Static star shot	The leaves open at the expected angles for a static procedure.
Helical star shot	The leaves open at the expected angles for a helical procedure.
Couch speed uniformity	The couch velocity is constant throughout the procedure.

# Couch Translation

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## ◆ Overview of Couch Translation Test

<b>TG-148 reference:</b>	Couch translation per gantry rotation (section V.B.3.c)
<b>Purpose:</b>	Verify that the leaves open at the expected couch positions.
<b>Method:</b>	Place a film on the couch in the coronal plane. Translate the couch across the beam at 0.5 mm/s, and open the leaves at specified intervals. Check distances between exposures on the film.
<b>Accuray specification:</b>	Accuray does not have a specification for this film test, but TG-148 specifies that exposure centers on the film should be separated by $50 \text{ mm} \pm 1 \text{ mm}$ , for the procedure parameters listed in “XML Description” (page 290).
<b>Sample result image:</b>	

**Equipment needed:**

- Two 2-cm blocks of *Virtual Water* (55 cm x 15 cm x 2 cm)
- Two 1-cm blocks of *Virtual Water* (55 cm x 15 cm x 2 cm)
- 1 EDR or EBT film (recommended minimum size: 20 cm x 25 cm)
- Pin for marking the EDR film, or medium-point permanent marker for EBT film
- Masking tape
- Film scanner, computer, analysis software (e.g., RITg148+)

## ◆ Theory of Couch Translation Test

This test evaluates the correspondence between couch position and MLC delivery. The couch travels 10 mm per gantry rotation. At the 2nd, 7th, and 12th of 13 rotations, all leaves are open for  $\frac{1}{2}$ -gantry rotation. The exposures on a film in the coronal plane are expected to be separated by 50 mm along the Y axis.

TG-148 refers to this test as "couch translation per gantry rotation" because the linac pulses and leaf movement are triggered by the gantry position, while the couch speed and position are controlled independently of the gantry position.

## ◆ XML Description

### Couch Translation

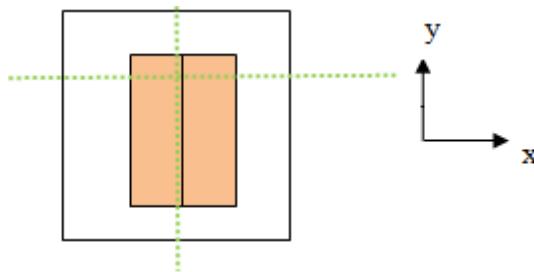
<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" XML package. See "XML Files for Film Alignment Tests" (page 120).
<b>Patient Name:</b>	ZZZ TG148 Film Alignment Tests-MultiFragment, or ZZZ GAF TG148 Film Alignment Tests-MultiFragment
<b>Procedure Description:</b>	Couch translation
<b>Couch movement in IEC Y when Ready is pressed:</b>	700 mm
<b>Couch translation during the procedure:</b>	0.5 mm/s

## Couch Translation

<b>Gantry:</b>	20 s/rotation; 13 rotations of the gantry
<b>Jaws:</b>	J07 (nominal 1 cm field width)
<b>MLC:</b>	All leaves open for 180° of the 2nd, 7th, and 12th rotations of the gantry.
<b>Beam-on time:</b>	260 s

### ◆ Set Up and Deliver the Test

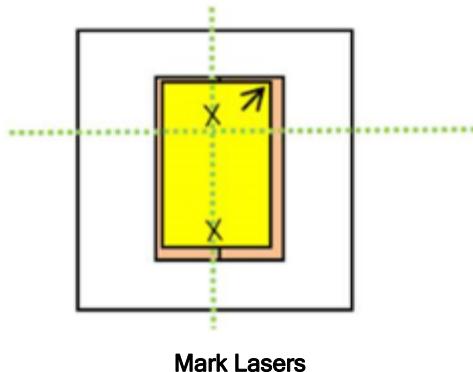
1. This procedure will deliver an exposure pattern that is about 150 mm long. Place two 20-mm *Virtual Water* blocks on the couch next to each other, to create a platform of uniform 20-mm backscatter for the film. This will prevent lines on the film where the *Virtual Water* ends. The surface of the *Virtual Water* blocks should be at isocenter height. The superior edge of the *Virtual Water* blocks should be about 50 mm superior to virtual isocenter, to allow room for marking the film superior to the exposure region.



Two *Virtual Water* blocks side-by-side on the couch. The superior edge of the *Virtual Water* blocks is about 5 cm superior to the green overhead laser.

2. Move the couch 700 mm into the bore and account for couch sag. Then, bring the couch back out of the bore.
3. Tape a film on the *Virtual Water* block in a Portrait orientation. Ensure that the film is long enough to accommodate the length of the exposure pattern (more than 150 mm).
4. Place a mark (dot with a permanent marker) in the +IEC X, +IEC Y corner of the film. This mark needs to have a more positive IEC Y position than any laser marks that you make on the film.

If desired, mark the IEC Y laser line on the film with dots, in the positions indicated by the "x" in the following image. Make one mark superior to the green lasers, and one mark more than 170 mm inferior to the green lasers, so that the laser marks do not obscure the exposures on the film.



Two *Virtual Water* blocks side-by-side on the couch, with a film in portrait orientation on top. The couch will move 700 mm into the bore when **Ready** is pressed, and as the couch continues to move into the bore during the delivery, the exposure pattern will be delivered in the film area between the two Xs. (Arrows and Xs are shown in the diagram, but it is better just to make a small dot at these positions.)

5. Cover the entire film with uniform 10 mm buildup (use two 10-mm blocks side-by-side).
6. Run the procedure.

## ◆ Analyze the Result

The couch translation film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.



**IMPORTANT:** Prior to accepting the RIT results, check the **Aligned Image** to ensure that the exposures are in the horizontal orientation, and the red and yellow **Top Crop** lines separate the exposures from the alignment mark at the top of the film (adjust the **Top Crop Percentage** if needed).



**NOTE:** The sign of the result for this test is not important. So, it is not critical that the software orients the film so that the alignment mark is in the upper right corner.



**IMPORTANT:** Prior to accepting the RIT results, check the **Analyzed Image** to ensure that it properly identified the exposure centers.



**NOTE:** If laser marks are present, RIT draws the analysis profile through the two laser marks (even if the laser marks are not perpendicular to the exposures). If laser marks are absent, RIT draws the analysis profile through the center of the region of interest and perpendicular to the exposures.

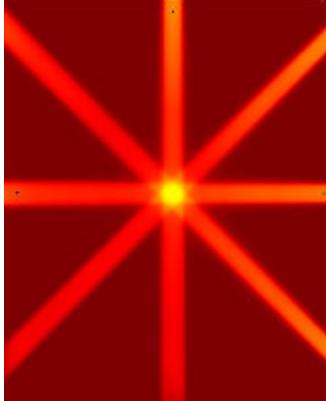
## ◆ What to Do if the Test Fails

Contact Accuray Customer Support for troubleshooting assistance.

# Static Star Shot

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## ◆ Overview of Static Star Shot Test

<b>TG-148 reference:</b>	TG-148 does not include QA for static gantry angle treatments. This test is analogous to the helical gantry angle test recommended by TG-148 (section V.B.3.a), except that it uses static gantry angles with no couch motion.
<b>Purpose:</b>	Verify that the static gantry positioning is consistent with the room lasers.
<b>Method:</b>	Place a film at isocenter in the transverse plane, and mark the bore lasers on the film. Open the central two leaves at four different beam angles. Compare exposure positions to laser marks.
<b>Accuracy specification:</b>	Accuray Incorporated does not have a specification for this test. If the room lasers are well-aligned and the film is marked carefully, the zero-degree beam typically matches the IEC Z laser axis within 1° or less, and the other beam angles have their expected relationship to the zero-degree beam, within a fraction of a degree.
<b>Sample result image:</b>	

**Equipment needed:**

- Two 5-cm blocks of *Virtual Water* (55 cm x 15 cm x 5 cm)
- 1 EDR or EBT film (recommended minimum size: 20 cm x 25 cm)
- Pin for marking EDR film, or medium-point permanent marker for EBT film
- Masking tape
- Couch indexing bar
- Film scanner, computer, analysis software (e.g., RITg148+) or protractor

## ◆ Theory of Static Star Shot Test

The static star shot test can be used to verify that static delivery angles are consistent with the room lasers, and to verify the beam entrance direction.

Like the helical star shot test discussed in the next section, the static star shot should be performed on a quarterly basis. It should also be performed by the customer if a service representative recalibrates the gantry positioning system.



**NOTE:** Unlike a typical star shot film in radiation therapy, the primary purpose of this test is to check the angles of the beams, not to check for beam/gantry isocenter coincidence where all the beams converge. The MLC center/gantry isocenter alignment is verified with a different film, as discussed in “MLC Center of Rotation (COR)” (page 176).

## ◆ XML Description

### Static Star Shot

<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" XML package. See "XML Files for Film Alignment Tests" (page 120).
<b>Patient Name:</b>	ZZZ TG148 Film Alignment Tests-MultiFragment, or ZZZ GAF TG148 Film Alignment Tests-MultiFragment
<b>Procedure Description:</b>	<i>Static star shot</i>
<b>Couch movement in IEC Y when Ready is pressed:</b>	None

## Static Star Shot

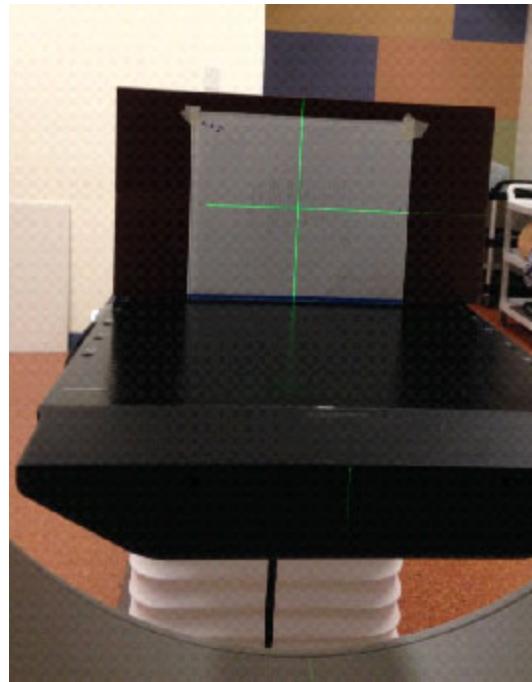
Couch translation during the procedure:	None
Gantry:	0°, 45°, 90°, and 135°
Jaws:	J20 (nominal 2.5 cm field width)
MLC:	Leaves 32 and 33 open simultaneously
Beam-on time:	20 seconds at each gantry angle



**NOTE:** Previous iterations of this procedure opened leaves 32 and 33 alternately to achieve a dark line down the middle of each beam, caused by the leaf penumbra. While the dark lines down the middle of each beam were convenient for visual analysis, analysis in the RITg148+ software is more effective without the dark line down the middle of the each beam.

### ◆ Set Up and Deliver the Test

1. Verify that green bore laser is properly aligned.
2. For this procedure, you will place the film in the transverse plane at isocenter. Stack two *Virtual Water* blocks on their long end to support the film as in the following image.



**Setup for static star shot procedure**

3. Tape the film to the +Y side of the blocks so that you can see the green bore laser on the film when looking from the back side.



**TIP:** To facilitate analysis in the RITg148+ software:

- Consider using a couch indexing bar inferior to the *Virtual Water* blocks.
  - Place the film in portrait or landscape orientation, not at an angle.
  - Ensure that the entire film surface is supported by the *Virtual Water* blocks, to avoid a line of attenuation change across the film.
  - Center the film on isocenter in the X/Z plane. Depending on the programmed gantry angles, you may wish to offset the film slightly to avoid a beam that passes directly through one of the four corners of the film. (RITg148+ reserves the four corners of the film as potential locations to search for your alignment mark; if the beam is going through any corner, it can confuse the automatic alignment.)
4. With the film at the green lasers 700 mm outside the bore, lean around the back side of the setup to mark the +IEC X, +IEC Z corner and the four green lasers.



**TIP:** Effective marking technique:

- Make small dots with a regular point permanent marker about 1 cm from the film edges.
- Do not lean on the table while marking the film, as this will change the table deflection.
- Remember that the +IEC X, +IEC Z corner of the film is in the upper left corner, when viewed from the back side.

5. Send the film exactly 700 mm into the bore. Use **Step Move** to correct for couch sag, so that the laser marks on the film match the lasers when the film is in the bore. (Alternatively, you could have marked the film while it was in the bore, but it is difficult to reach the film inside the bore for accurate marking.)
6. Run the procedure. The procedure delivers all four beam angles in sequence.



**TIP:** Using EBT film with a patient camera looking through the back end of the bore, you can watch the exposure as it appears on the film.

## ◆ Analyze the Result

The static star shot film can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.

RITg148+ analysis requires four beam angles for the static star shot procedure (but three beam angles for the helical star shot procedure).

RITg148+ reports the beam angles relative to the two pin pricks that define the IEC Z line. The IEC X pricks are required as a matter of convention. The software checks that the IEC X laser line is perpendicular to the IEC Z laser line, but the IEC X laser line is not otherwise included in the analysis.



**IMPORTANT:** Prior to accepting the RIT results, check the **Analyzed Image** to ensure that the software properly identified the beams.

## ◆ What to Do if the Test Fails

### RITg148+ Software is Unable to Analyze the Film

1. Ensure that you followed the setup instructions in this test and in the RIT manual. For example, ensure that:
  - Four beam angles were delivered.

- The film was supported against a uniform amount of *Virtual Water*, so there is no attenuation line across the film.
  - Leaves 32 and 33 were opened simultaneously (see note in “XML Description” (page 295)).
  - The intersection of the beams (isocenter) is approximately in the center of the film.
  - There should be no marks on the film, except as described in the test. Do not trace the exposures with a pen or write on the film.
2. The RITg148+ modules include several adjustable analysis parameters that may need to be customized to your film. These are discussed in the RITg148+ user guide, and in a troubleshooting appendix to the RITg148+ user guide.

## Film Can Be Analyzed but the Beam-Entrance Direction is Incorrect

If the analysis reports an unexpected beam entrance direction (i.e., beam angle is reported 180° different from expected):

1. Ensure that the film was oriented properly for the analysis (film was not flipped over when scanned, and the orientation mark is in the upper right corner).
2. Ensure that you marked the +X, +Z corner of the film in the room (if you are looking from the back side, this is the upper LEFT corner of the film).
3. Ensure that the film was supported against a uniform amount of *Virtual Water*, so there is no attenuation line across the film to confuse the analysis. If there is an attenuation line across the film, you will need to start over with a new film.
4. Observe the beam divergence on the film to confirm the beam entrance direction.



**NOTE:** RITg148+ identifies the beam entrance direction by the beam intensity (exit side is expected to be more faint). By eye, it is easier to observe the beam divergence on the film.

5. Double-check that you know the expected beam angles. Run the procedure and note the gantry angle reported on the TDC (**Position** field of **Auxiliary Machine Data**).
6. If you still suspect a 180° calibration error, ask the service representative to open the gantry covers. Load a procedure with a known gantry position (**Prepare Calibration** and acknowledge messages, but there is no need to turn the beam on), and observe the LINAC position in the room to see if it is approximately correct.



**WARNING:** Avoid contact with the treatment system gantry when the covers are removed. Risk of serious injury or death exists due to exposed electrical components and potentially rotating parts. Do not operate the machine when the covers are removed unless specifically trained to do so. Do not touch an operating MLC. Pinch points exist that may cause serious injury. Do not touch any lead parts or leaking fluids on the machine without proper personal protective equipment.

7. If the problem is not yet resolved, the service representative may need to recalibrate the gantry positioning system. Contact Accuray Customer Support if you would like to discuss this process. When the service representative is finished, repeat the static and helical star shot films to ensure that they pass.



**NOTE:** The LINAC should be at the top of the gantry, pointing down at the floor, for a 0° gantry position. The gantry rotates clockwise when viewed from the couch side. So, at 90°, the LINAC should be located on the +IEC X side of the bore and pointed in the -IEC X direction.



**WARNING:** Suspected gantry mis-calibration should be investigated immediately and reported to your service representative. Treatments may result in injury or death if the gantry positioning system is mis-calibrated.

## Film Can Be Analyzed but the Numerical Results are Failing



**TIP:** The action tolerance for this test should depend on how well the room lasers are aligned and how carefully you marked the film.

If the analysis appears to have adequately identified the beams, but the numerical results are failing:

1. Review the delivery instructions to ensure that you have accurately set up and marked the film.
2. Double check that you know the expected beam angles. Run the procedure and note the gantry angle reported on the TDC (**Position** field of **Auxiliary Machine Data**).
3. Use a protractor to confirm the beam angles on the actual film.
4. Use a level to confirm the rotation of the bore lasers about the Z axis.
5. If the numerical results are failing by several degrees, ask the service representative to open the gantry covers. Load a procedure with a known gantry position (**Prepare Calibration** and acknowledge messages but no need to turn the beam on), and observe the LINAC position in the room to see if it is approximately correct.



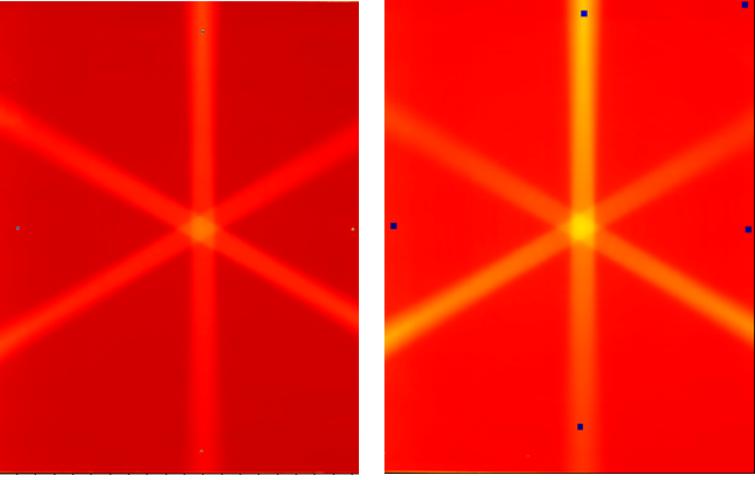
**WARNING:** If the gantry covers are opened by the service representative, stay clear of the gantry. See detailed warning in previous section.

6. If you still suspect an angle calibration error exceeding the action tolerance, the service representative may need to recalibrate the gantry positioning system. Contact Accuray Customer Support if you would like to discuss this process. When the service representative is finished, repeat the static and helical star shot films to ensure that they pass. See notes and warnings in previous section.

# Helical Star Shot Test

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## ◆ Overview of Helical Star Shot Test

<b>TG-148 reference:</b>	Gantry angle consistency (section V.B.3.a)
<b>Purpose:</b>	Verify that the leaves open at the expected gantry angles for a helical procedure.
<b>Method:</b>	Place two films in the transverse plane, several cm apart in Y, and mark the bore lasers. Run a procedure with a rotating gantry and moving couch. Open the central two leaves each time the gantry reaches 0°, 120°, or 240°. Check the beam angles on the film.
<b>Accuray specification:</b>	Accuray Incorporated does not have a specification for this test. TG-148 requires that the angles are correct and consistent within 1°.
<b>Sample result image:</b>	

**Equipment needed:**

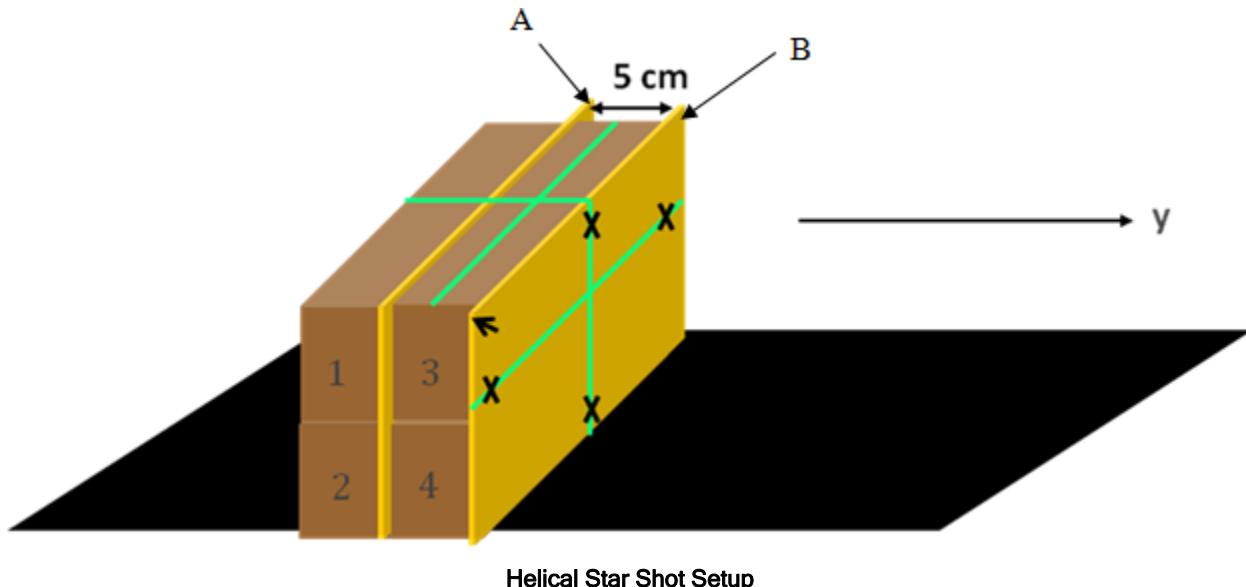
- Four (4) 5-cm blocks of *Virtual Water* (55 cm x 15 cm x 5 cm)
- Two (2) EDR or EBT films (recommended minimum size: 20 cm x 25 cm)
- Pin for marking the EDR film, or medium-point permanent marker for EBT film
- Masking tape
- Couch indexing bar
- Film scanner, computer, analysis software (e.g., RITg148+)



**TIP:** If four 50-mm blocks are not available, tape some of the thinner blocks together to make a 50-mm stack (e.g., two 20-mm blocks plus one 10-mm block), or find another material that can support the films in the correct position in the transverse plane.

## ◆ Theory of Helical Star Shot Test

This test requires two films in the transverse plane, separated by 50 mm in the IEC Y direction (see the following image for reference). The couch moves 650 mm into the bore when **Ready** is pressed, so that the front film (B in the following image) starts at the inferior edge of the 50-mm field, and enters the beam as the helical procedure begins.



To facilitate marking the film, the front film (B) is supported on only one side by *Virtual Water* blocks, and the back film (A) is sandwiched between the *Virtual Water* blocks.

The procedure involves 40 rotations of the gantry. For the first 20 rotations, the front film is in the beam. For the last 20 rotations, the back film is in the beam. Every time the gantry reaches an angle of 0°, 120°, or 240°, the central two leaves open.

If the gantry positions of open leaves are appropriately consistent with each rotation, the cumulative effect of all the rotations is a helical star shot pattern on the films. The exposed angles can be compared against the laser positions to check that they were delivered at 0°, 120°, and 240°. The exposed angles should be the same for the front film and the back film.

There is inherent uncertainty in the measurements due to the blurring of the beam angles. For helical treatments, there are 51 projections per rotation (7.06° per projection), but for this test, the number of projections per rotation was increased to 72 (5° per projection) to reduce the blurring effect. Even so, it is very difficult to measure the beam angles on the helical star shot film with a protractor and achieve a precision better than 3°.

The absolute result of the 0° angle depends on the accuracy of the room lasers, and the marking of the film, as well as the actual delivery.

## ◆ XML Description

The film exposure for this test is very low, since each film is in the beam plane for only half of the procedure, and the two central leaves are only open about 4% of the time (3 of 72 projections per gantry rotation). The original TG-148 procedure was designed for Kodak® X-Omat V film. The procedure recommended by Accuray Incorporated has been adapted for EDR or EBT film as follows:

- The field size has been increased from 25 mm to 50 mm, to allow each film to be in the beam plane for more rotations of the gantry.
- The distance between films has been decreased from 60 mm to 50 mm.
- It is recommended to run the 800 s procedure twice to achieve a sufficient exposure.

### Helical Star Shot

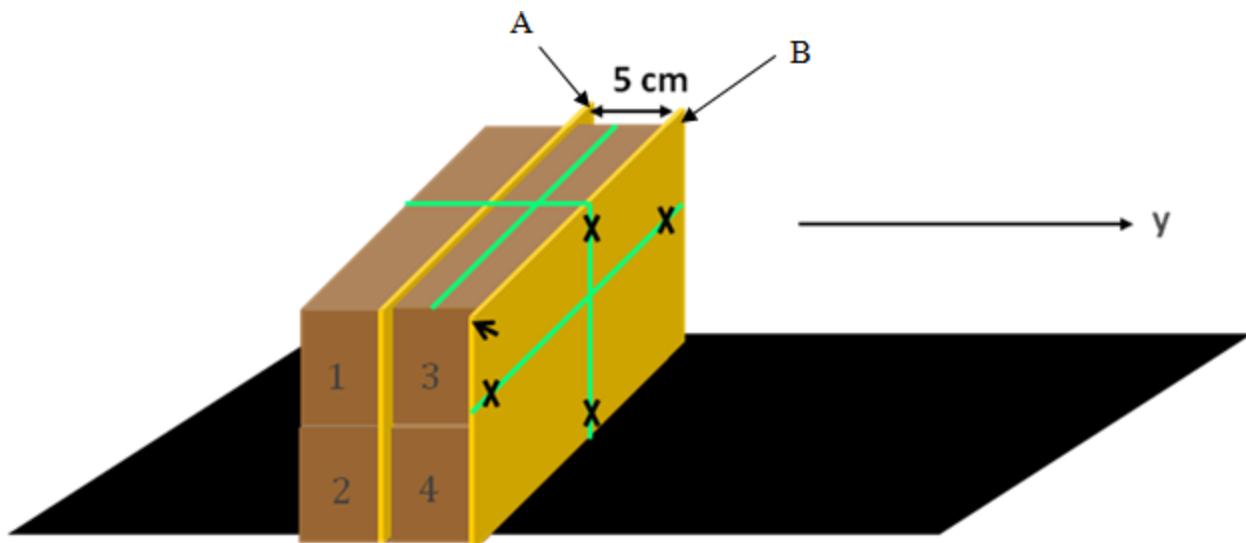
<b>Where to get the .xml:</b>	This procedure is part of the "TG148 Film Alignment Tests-MultiFragment" or "GAF_TG148 Film Alignment Tests-MultiFragment" .xml file package. See "XML Files for Film Alignment Tests" (page 120).
<b>Patient Name:</b>	ZZZ TG148 Film Alignment Tests-MultiFragment, or ZZZ GAF TG148 Film Alignment Tests-MultiFragment
<b>Procedure Description:</b>	Helical star shot

## Helical Star Shot

Couch movement in IEC Y when Ready is pressed:	650 mm
Couch translation during the procedure:	0.125 mm/s
Gantry:	20 s/rotation for 40 rotations
Jaws:	J42 (nominal 50-mm field width)
MLC:	Use 5-degree projection angles. Leaves 32 and 33 open simultaneously whenever the gantry reaches projection angles centered on 0°, 120°, and 240°.
Beam-on time:	800 s (but should deliver the procedure twice for EDR or EBT film)

### ◆ Set Up and Deliver the Test

The films are supported by four 50-mm *Virtual Water* blocks (numbered 1-4). If four 50-mm *Virtual Waterblocks* are not available, tape some thinner blocks together to make a 50-mm stack, or replace blocks 1 and 2 with some other material that can support the film in the transverse plane. If an attenuating material is used for support, it is important that the films be supported by a uniform amount of attenuating material across the entire film, to prevent an attenuation transition line from appearing on the film.



1. Verify that the green bore laser is properly aligned.
2. You may wish to place an indexing bar inferior to your setup, for stability.

3. Place blocks 1 and 2 (or other supporting material) on the couch.
4. Tape the back film to the +IEC Y surface of blocks 1 and 2, so that you can see the green bore laser when looking from the back side.



**TIP:** To help facilitate analysis in the RITg148+ software:

- Place the film in portrait or landscape orientation, not at an angle.
  - Ensure that the entire film surface is supported by the *Virtual Water* blocks, to avoid a line of attenuation change across the film.
  - Center the film on isocenter in the X/Z plane.
5. With the Y position of the back film at the green overhead lasers outside the bore, lean around the back side of the setup to mark the +IEC X, +IEC Z corner and the four green lasers. Mark dots at the positions shown in the setup diagram.



**TIP:** For effective marking:

- Make small dots with a regular-point permanent marker about 10 mm from the film edges.
  - Do not lean on the table while marking the film, as this will change the table deflection.
  - Remember that the +IEC X, +IEC Z corner of the film is in the upper left corner, when viewed from the back side.
6. Without disturbing the back film, place blocks 3 and 4 in front of the back film as shown in the setup diagram.
  7. Tape the front film to the +IEC Y surface of blocks 3 and 4. See step 4 for tips.
  8. Lean around the back of the setup to mark the +IEC X, +IEC Z corner and the four green lasers on the front film, as in Step 5.
  9. Send the setup 700 mm into the bore. Correct for couch sag, so that the marks on the front film are aligned to the bore lasers.



Helical Star Shot Procedure Setup Example (front film is visible, but the back film is sandwiched between the *Virtual Waterblocks*)



**NOTE:** As shown in the diagram and example, the front film is only supported on one side, and the back film is supported on both sides. This allows access to the front film for marking. We cannot see the back film anymore, but we assume that since both films were marked outside the bore at virtual isocenter, if we adjust for couch sag by looking at the front film, the back film will also be aligned with the bore lasers.

10. Bring the couch out of the bore until the overhead transverse laser is halfway in between the two films.
11. Run the procedure twice, without disturbing the setup between procedures.

## ◆ Analyze the Result

The helical star shot films can be analyzed using the RITg148+ software. See the RITg148+ manual for instructions.

RITg148+ analysis requires three beam angles for the helical star shot procedure (but four beam angles for the static star shot procedure).

RITg148+ lists the beam angles relative to the two pin pricks that define the IEC Z line. The IEC X pricks are required as a matter of convention. The software checks that the IEC X laser line is perpendicular to the IEC Z laser line, but the IEC X laser line is not otherwise included in the analysis.



**IMPORTANT:** Prior to accepting the RIT results, check the *Analyzed Image* to ensure that the software properly identified the beams.

## ◆ What to Do if the Test Fails

### RITg148+ Software is Unable to Analyze the Films

1. Ensure that you followed the setup instructions in this test and in the RIT manual. For example, ensure that:
  - Each film was supported against a uniform amount of *Virtual Water*, so there is no attenuation line across the film.
  - The intersection of the beams (isocenter) is approximately in the center of the film.
  - There should be no marks on the films, except as described in the test setup. Do not trace the exposures with a pen or write on the films.
  - If using EDR or EBT film, ensure that the exposure was run twice so that it is sufficiently dark.
2. The RITg148+ modules include several adjustable analysis parameters that may need to be customized to your films. These are discussed in the RITg148+ user guide, and in a troubleshooting appendix to the RITg148+ user guide.

### Films Can Be Analyzed but the Beam Entrance Direction is Incorrect

1. Ensure that the film was oriented properly for the analysis (film is not flipped over and the orientation mark is in the upper right corner).
2. Ensure that you marked the +X, +Z corner of the films in the room (if you are looking from the back side, this is the upper *left* corner of the film).
3. Ensure that the film was supported against a uniform amount of *Virtual Water*, so there is no attenuation line across the film to confuse the analysis. If there is an attenuation line across the film, you will need to start over with a new film.
4. Observe the beam divergence on the film to confirm the beam entrance direction.



**NOTE:** RITg148+ identifies the beam entrance direction by the beam intensity (exit side is expected to be more faint).

5. Acquire a *CTrue* image of an asymmetrical object, and confirm that it is reconstructed in the proper orientation.
6. If you still suspect a gantry alignment error, the service representative may need to re-calibrate the gantry positioning systems. (Contact Accuray Customer Support if you would like to discuss this.) When the service representative is finished, repeat the static and helical star shot films to ensure that they pass.

## Films Can Be Analyzed but the Numerical Results are Failing



**TIP:** The action tolerance for this test should account for the uncertainties in the delivery discussed in test theory. .

If the analysis appears to have adequately identified the beams, but the numerical results are failing:

1. Review the results to determine both the absolute error in the beam that is expected to be 0 degrees, and the relative differences in the three beam angles (expected to be 120° apart).
2. Review the delivery instructions to ensure that you have accurately set up and marked the film.
3. Use a level to confirm the rotation of the bore lasers about the Y axis.
4. If the numerical error is several degrees or more, use a protractor to confirm the beam angles on the actual film.



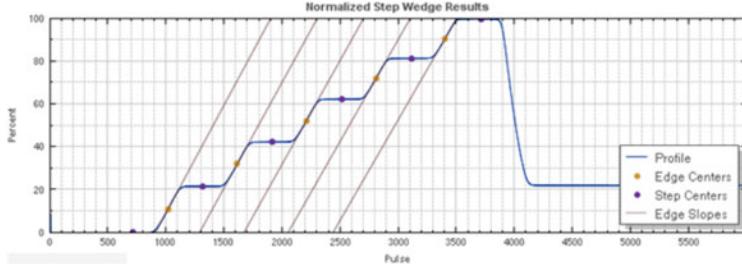
**NOTE:** The precision of a protractor measurement is limited by the inherent blurring of the helical delivery.

5. Acquire a *CTrue* image of an asymmetrical object, and confirm that it is reconstructed within ±0.5° of the expected orientation.
6. If you still suspect a problem with the gantry angle positioning, the service representative may need to re-calibrate the gantry positioning systems. (Contact Accuray Customer Support if you would like to discuss this.) When the service representative is finished, repeat the static and helical star shot films to ensure that they pass.

# Couch Speed Uniformity

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## ◆ Overview of Couch Speed Uniformity Test

<b>TG-148 reference:</b>	Couch speed uniformity (section V.B.3.b)
<b>Purpose:</b>	Verify that the couch speed is smooth and constant throughout the procedure.
<b>Method:</b>	TG-148 recommends using a film. Accuray Incorporated recommends using the <b>TQA Step Wedge Static</b> module to translate a step wedge across the beam, and evaluate the transitions between the steps in the detector data.
<b>Accuray specification:</b>	TG-148 specification is based on film and cannot be directly interpreted in terms of couch speed. Accuray Incorporated has no specification for this test.
<b>Sample result image:</b>	 A line graph titled "Normalized Step Wedge Results". The y-axis is labeled "Percent" and ranges from 0 to 100. The x-axis is labeled "Pulse" and ranges from 0 to 5500. The graph shows a blue line representing the "Profile" which rises in steps, reaching approximately 100% at pulse 3500. Four points on the profile are marked: a yellow dot at pulse ~1000 (labeled "Edge Centers"), a purple dot at pulse ~1800 (labeled "Step Centers"), another yellow dot at pulse ~2800, and another purple dot at pulse ~3200. A legend on the right identifies the lines: "Profile" (blue), "Edge Centers" (yellow dots), "Step Centers" (purple dots), and "Edge Slopes" (grey lines).
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• TQA Advanced Package</li><li>• TQA step wedge</li></ul>

## ◆ Theory of Couch Speed Uniformity Test

TG-148 recommends verifying that the couch velocity remains constant and smooth throughout the procedure. TG-148 recommends irradiating a film in the coronal plane, with gantry 0° and constant couch speed, then verifying the smoothness of a profile through the film along the Y axis. TG-148 states that the profile should vary by less than 2%.

The smoothness of the TG-148 profile provides inconclusive information about couch performance. The test is sensitive to dose variations during delivery, and to film non-uniformities. The dose at any point on the film is the convolution of the field width and the couch motion.

As a relative constancy check of the couch speed, Accuray Incorporated recommends using the **TQA Step Wedge Static Module**. This module translates an aluminum step wedge across the beam, and uses the onboard detector data to identify the transitions in the steps. The results are compared against a reference file that was created when the machine was commissioned, and the **speed difference** is reported as a percentage of the reference speed. For more information, see the *TQA Manual*.

## ◆ XML Description

TQA Step Wedge Static Test	
<b>Where to get the .xml:</b>	This .xml file can be downloaded from the <i>TQA Step Wedge Static</i> module of the <i>TQA</i> software.
<b>Patient Name:</b>	zzzzz TQA Step Wedge Static
<b>Procedure Description:</b>	Topo 1.5mm per sec 200 sec J7mm 39cm setupToReady
<b>Couch movement in IEC Y when Ready is pressed:</b>	390 mm
<b>Couch translation during the procedure:</b>	0.15 mm/s
<b>Gantry:</b>	Static at 0°
<b>Jaws:</b>	J07 (nominal 1 cm field width)
<b>MLC:</b>	All open
<b>Beam-on time:</b>	200 s

## ◆ Set Up and Deliver the Test

See the *TQA Manual* for instructions.

- ◆ **Analyze the Result**

Open the **TQA Step Wedge Static** report and check the **Speed Difference** parameter.

- ◆ **What to Do if the Test Fails**

Contact Accuray Customer Support for assistance.



## Verify Integrity of Data Import to TPS

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## Overview of Data Import Test

<b>TG-148 reference:</b>	CT data and structure set import to the TPS (section VII.B.1)
<b>Other names for this test:</b>	Image data import; geometric validation tests
<b>Purpose:</b>	Verify that CT images and contours imported into the system retain the correct dimensions, voxel sizes, orientation, gray scale values, and associated text info.
<b>Method:</b>	Import a sample CT image and contour set using the same workflow that will be used for patient treatment planning. Compare the images and contours before/after import. Also compare the image dimensions against the physical dimensions of the phantom.
<b>Accuray specification:</b>	Accuray Incorporated does not have a specification for this test, since it involves third party equipment. TG-148 specifies that all data must be transferred correctly, and the dimensions of the imported object should match the physical dimensions within 1 kVCT voxel.
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• Phantom</li><li>• kVCT scanner and contouring software (if applicable) that will be used for patients</li></ul>

## Theory of Data Import Test

Correct CT and structure import is required for correct treatment planning.  
See Section VII.B.1 of TG-148 for more information.

The data import test should use the same equipment and workflow that will  
be used for your patients.

## Set Up and Deliver the Test

1. Choose a phantom that includes some features that are not homogeneous in density nor symmetrical in shape (e.g., one half of the *Tomo*-phantom with various density plugs inserted).
2. Measure the physical dimensions of the phantom.
3. Take a kVCT image of the phantom using the same scanner that will be used for patient treatments.
4. Measure and record the phantom dimensions, orientation (both physical orientation and text label of orientation), CT values, and voxel size from the kVCT image.
5. If you will be using third party software for image contouring, use your patient contouring software to draw some structures of known size on the phantom.
6. Import the phantom image set and accompanying structures to the Accuray *Precision* System.
7. Within the Accuray *Precision* System, verify the parameters mentioned in steps 2, 4, and 5.

## What to Do if the Test Fails

To the extent that the cause of failure is from the Accuray system, Accuray Customer Support is available to assist you.





## Required Tasks for Planning and QA

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# Enter a Density Model

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## ◆ Overview of Density Model Creation



**NOTE:** Before you can begin creating treatment plans, you will need to enter a density model. These steps should be completed as soon as you have access to the *Tomo-phantom*.

The treatment planning system needs to know the density distribution of the patient in order to accurately predict the dose distribution in the patient. A density model relates Hounsfield Units from your CT scanner to mass density ( $\text{g}/\text{cm}^3$ ). The site physicist is responsible for creating the density model.

CT numbers vary from one scanner to another. When creating a treatment plan, select the density model that was measured for the same scanner used to acquire the patient image. If your department receives planning images from multiple CT scanners, you will need a separate density model for each scanner, to accurately calculate dose. CT numbers from a given scanner may also depend on the scan acquisition parameters (e.g., scan field of view, tube potential (kVp), and choice of reconstruction filters). Different density models may be necessary to account for these differences.

An accurate density model is necessary to achieve an accurate dose calculation. If the HU values change due to scanner calibration or drift over time, a new density model will be needed. The density model is used in the treatment planning workflow as follows:

1. A planning CT image is acquired.
2. The density model is applied to the CT image data to convert HU to mass density ( $\text{g}/\text{cm}^3$ ).
3. A plan is created and dose is calculated on the mass density image.

Phantom-based patient QA is unlikely to detect a problem with your patient density model. QA plan calculations use the density model selected for the phantom image, not the density model selected for the patient image, so QA plan results may pass even if an inappropriate density model was selected for the patient plan.



**WARNING:** An incorrect density model can lead to incorrect dose calculations, and patient injury or death.

- Select the density model appropriate for the scanner and scan acquisition parameters used to acquire the planning image.
- After applying a density model, always review the density image for reasonable values.
- The selection of an appropriate density model should be confirmed during physics chart checks.
- Phantom-based patient QA results may not help to determine if the correct density model was selected for patient planning.
- The density model should be checked (and updated if necessary) whenever the scanner is calibrated, or when a change in the CT numbers is suspected.
- Additional instructions are included in the following sections.

In addition to the above, observe the following if you are calculating dose on MVCT images:

- The imaging beam properties are not as precisely maintained as the treatment beam, and may drift over time. The MVCT density model should be checked and updated regularly, according to the schedule recommended by TG 148.
- The MVCT density model should be checked after any adjustments are made to the beam or image reconstruction properties by the service representative.
- The **\_CT number calibration** helps to stabilize the MVCT numbers, but is not a substitute for verification of your density model on the schedule recommended by TG 148. See “CTrue Image Quality Verification” (page 243).



**NOTE:** It is only necessary to enter a density model for your system if you will calculate dose on MVCT images (e.g., when MVCT images are used for treatment planning, or when calculating dose using the *PreciseART* software).



**WARNING:** The density model determines the CT number to density conversion for all voxels in the planning CT image, including the patient, couch, air, etc. Never use the density model to manipulate the density of some aspect of the image. A non-standard density model may result in incorrect density values in other parts of the image, such as the patient, air, or couch. This could cause patient injury or death.



**IMPORTANT:** If your patient density model contains values that deviate significantly from the standard HU definition, the density of the couch image will be impacted.

## ◆ Physics of Density Representation

### Dose Calculation

The appendix “Algorithms for Optimization and Dose Calculation” (page 434) describes the *Accuray Precision* dose calculation algorithm. One step in the dose calculation process requires scaling paths traversed by primary photons to radiological depth ( $\text{g}/\text{cm}^2$ ), so that the mass attenuation values can be determined from a FAT (Fluence Attenuation Table) that provides mass-attenuation values as a function of radiological depth ( $\text{g}/\text{cm}^2$ ) traversed by primary photons. The mass density values of each voxel in the CT image must be accurately known to facilitate scaling to radiological depth and determining the TERMA.

### Definition of Electron Density

Electron density  $\rho_e$  [ $\text{electrons}/\text{cm}^3$ ] may be defined as the product of mass density  $\rho_m$  [ $\text{g}/\text{cm}^3$ ] and the number of electrons/gram:

$$\rho_e = \rho_m N_A \frac{Z}{A}$$

where  $N_A$  is Avagadro's number,  $Z$  is the atomic number, and  $A$  is the atomic weight. For example, see Kahn 1994.

The Compton interaction cross section is the dominant interaction at megavoltage energies and is proportional to electron density.

### Relative Electron Densities and Mass Densities of Human Tissue

*Relative electron density* is the electron density of the material normalized to the electron density of water.

The relative electron densities of all soft tissues within the human body are numerically within 1% of their mass densities (i.e.,  $Z/A$  is relatively constant and similar to water for soft tissues within the human body). The relative electron density of bone is not as numerically close to its mass density, because of a lower  $Z/A$ .



**NOTE:** Electron density and relative electron density are introduced here for the purpose of physics discussion, but the density model relates HU to mass density [ $\text{g}/\text{cm}^3$ ], not relative electron density. The *Accuray Precision Treatment Planning System* allows the entry of relative electron density values in the density model for the purpose of *CyberKnife* planning. Relative electron density values are not used by the Treatment Planning System for other plan modalities.

## ◆ Guidelines for Density Model Entry

The treatment planning system incorporates mass-attenuation coefficients into the dose calculator. The mass density column of the density model is used by the system for all calculations related to the system. The relative electron density column of the density model is not used for planning.

The Accuray *Tomo*-phantom may be scanned for the density model creation. The density plugs that fit into the phantom are manufactured by Gammex, Inc., and are labeled with mass densities ranging from 0.3 to 1.8  $\text{g}/\text{cm}^3$ . Accuray Incorporated recommends using the plugs labeled: "true water" (this plug fits inside the *Tomo*-phantom and is filled with water), "cortical bone," "inner bone," "CB2 30%," "CB2 50%," "LN 300 lung," and "LN 450 lung." The mass densities displayed on the plugs are the actual mass densities that should be used in the density model. We have found the Gammex "bone" plugs to be a good representation of real bone, both for electron density and mass density.

Gammex sells additional "soft tissue" plastic plugs with densities near water: "breast," "brain," "CT solid water," "liver," and "adipose." These plugs have mass densities and Z/A ratios that deviate from the actual values in soft tissue by several percent. These plugs should not be used in the density model creation process. Instead, use real water to map the density model for the soft-tissue data points, which provides accurate input for the system dose calculations.

Inhomogeneity corrections are performed by converting the CT information into density values using a user entered conversion table. This table allows the user to enter both mass and electron density calibration curves. In order to calculate dose to a patient with the superposition algorithm, the density model selected must contain a mass density calibration curve.

The density model linearly interpolates between the mass density points you enter in the table. If your density model does not include a point at -1024 HU, the model will assign a value of 0  $\text{g}/\text{cm}^3$  at -1024 HU. Air should be measured to obtain a density model point near -1000 HU and 0.001  $\text{g}/\text{cm}^3$ . If no density model point for air is defined, the -1000 HU value will be linearly interpolated between -1024 HU and the closest density model point (often near water), which can result in air being mapped to a density approximately 2.4% of the density of water, or 24 times the actual density of air.

When you enter values for a density model, the system also allows the user the ability to select which extension method to use for HU values higher than those entered by the user. The options are **Flat** or **Extrapolate**. The **Flat** option extends the density model with a horizontal line, i.e., all points with HU values exceeding the maximum point entered are assigned the same density as the maximum point entered in the table. **Extrapolate** extends the model by creating points on the straight line generated by the two user-entered points with the highest HU values. The maximum density value that will be created by this method is  $22.6 \text{ g/cm}^3$ . Values calculated via the **Extrapolate** option that exceed this limit will be replaced with a value of  $22.6 \text{ g/cm}^3$ .



**IMPORTANT:** An on-screen message will appear when you save a plan, if the density model does not cover the full range of HU values in the planning image. If this warning appears, check to determine if the density extension is appropriate.

Use the following steps to locate high-density points in your image and verify that the mass density is acceptable.

1. Examine your density model in the Accuray Precision™ Treatment Planning System software and record the HU value of the highest HU point listed in your model.
2. Display the (A = couch) HU image of your planning CT image in the Accuray Precision software (click on the upper left corner of the image to set the display).
3. Click the Window-Level icon from the menu of icons on the right side of the screen. Then, click in the right corner of the image to type in the values for the window/level.  
The window/level scales the display so that HU values below ( $L - W/2$ ) are black, and values above ( $L + W/2$ ) are white. Set the window  $W$  to 2 (a very small value). Set the level  $L$  to the maximum HU point in your density model. With these settings, points in the planning image with HU above the max of your model range will be white spots, and the rest of the image will be black.
4. Click in the upper-left corner of the display to view the (A = mass ( $\text{g/cm}^3$ )) image.
5. Search through the image slices for white spots.
6. Select the Pointer icon from the menu on the right side of the screen. Click on the white spots, and check for appropriate density values in these locations.

If you prefer to scan a higher-density object and include it in your density model, you may do so.



**IMPORTANT:** The density model accepts density values in the range 0 to 22.6 g/cm<sup>3</sup> and -1024 to 31743 HU. Some CT scanners however limit the CT numbers to a value lower than 31743 HU (for example, 3071 HU). If you measure a high-density object and the resulting CT number is at the maximum of your scanner's CT number range, that value should not be used.



**IMPORTANT:** Observe the following guidelines for accurate density model entry:

- Mass density should be entered in the density model to calculate attenuation [g/cm<sup>3</sup>].
- Do not use any plugs that have a CT number between -100 and +100 HU. Real water should be measured to obtain a density model point near 0 HU and 1.0 g/cm<sup>3</sup>.
- If you do not have a “true water” plug, another container that fits snugly into the *Tomo*-phantom may be used. Alternatively, a jug of water could be scanned, but it should be of a size similar to the *Tomo*-phantom or a transverse cross-section of a human patient.
- Air should be measured to obtain a density model point near -1000 HU and 0.001 g/cm<sup>3</sup>. (It is recommended to determine the CT numbers of air outside the phantom. There may be a difference in CT numbers of air outside the phantom versus inside the phantom.)

## ◆ Create the Density Model

In this section, you will acquire a CT image on the scanner(s) that supply images to be used for treatment planning.

1. Place the *Tomo*-phantom on the CT couch, and center it on the lasers. The long axis of the plugs should be parallel to the direction of couch travel.
2. Insert the density plugs in the phantom ("true water," "cortical bone," "inner bone," "CB2 30%," "CB2 50%," "LN 300 lung," and "LN 450 lung"). Fill unused cavities with *Virtual Water* plugs.



**NOTE:** If desired, you may also insert the CT resolution plugs, and leave a couple of unfilled air cavities. These will not be used to create points in the density model.



**IMPORTANT:** The density plugs should be inserted in the *Tomo*-phantom for the scan. On both KVCT and MVCT scanners, the CT numbers will be adversely affected if you scan the density plugs by themselves without inserting them in the *Tomo*-phantom. The density plugs by themselves are not of a size that is relevant for treatments.

3. Take a photo of the plug positions, or note them in a diagram.
4. Scan the phantom using the same scan acquisition parameters that you would use for a patient.
5. Determine the average CT numbers in circular uniform regions of interest inside each plug, and in the air outside the phantom.



**TIP:** Your CT scanner software may have tools to measure average CT numbers in regions of interest. The software does not include tools to measure average CT numbers in regions of interest. See TG 148 Section VI.B.4 for suggestions of third-party software that can be used for the analysis.

6. Follow the instructions in the *Treatment Planning Manual* to enter the density model data into the software. Assign a density of  $1.0 \text{ g/cm}^3$  to the water point, and  $0.001 \text{ g/cm}^3$  to the air point. Do not include any additional points in the range of  $0 \pm 100 \text{ HU}$ .



**NOTE:** Do not create a point for the material of the *Tomo*-phantom itself, but only for the appropriate plugs and for air.



**NOTE:** To access the density model for editing, click the **Planning Settings** task from the planning system home screen. You can also view the density model from the **Settings** tab when creating a plan, but you cannot edit the density model from the **Settings** tab.



**NOTE:** Density models are stored in *iDMS* and accessed from all connected workstations. When a plan is created, it generates a copy of the density model that is separate from the server version. When you update your density model, understand the following:

- If a plan has not yet been delivered, you can keep the plan version of the density model and continue with treatment, or you can choose the server version of the model and update the optimization of your plan.
- If you had previously performed plan optimization, you will lose the results when you update the plan with the revised density model.

# Prepare a Scan of the Phantom for Patient QA

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## ◆ Scan the Phantom



**NOTE:** Before you can begin performing patient QA, you will need a CT image of the phantom that you will use for patient QA. These steps should be completed as soon as you have access to the *Tomo-phantom*.

Scan the phantom(s) on your planning CT scanner:

- Set up the phantom in the orientation that will be used for QA.
- If desired, place fiducial markers on the phantom.
- For accurate dosimetry, do not insert ion chambers in the phantom.



**NOTE:** Ion chambers are calibrated to measure dose to water. If you inserted ion chambers in the phantom, scanned the phantom, and then performed dose calculations on the image, the dose calculator would calculate dose to the chamber cavity and the dose calculation would be inconsistent with the expected ion chamber measurement.

- Use a flat couch top to avoid rotations.
- Scan the entire phantom, extending the scan length 20 mm from the superior and inferior phantom edge. Use the most common slice thickness that you will use for patient simulation CTs.
- Ensure that the entire phantom is visible and that the top of the CT couch is included.

## ◆ Create the Corresponding Density Model

For each phantom image, an appropriate corresponding density model needs to be acquired. The image used to determine the density model should be acquired on the same scanner, close in time (so that scanner characteristics are consistent), and using the same scanner settings.





## Commissioning for Upgrades and New Features

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# Introduction

This chapter outlines commissioning responsibilities for the site physicist, following a major upgrade.



**NOTE:** Please contact your Accuray sales representative with any questions about eligibility, schedule, and cost of software and hardware upgrades.

TG-148 recommends that after a software upgrade, a phantom based end-to-end test should be performed, as discussed in “Annual QA” (page 371).

Additional tests will depend on the components and subsystems affected by the upgrade, and the discretion of the site physicist. For software upgrades and major feature additions, the Accuray training department may provide feature-specific information including:

- New feature training
- Upgrade preparation instructions
- Post-upgrade QA recommendations

Typical upgrade preparation instructions may include:

- Finishing any treatment plans in progress through plan authorization.
- Backing up items on the local workstations affected by the upgrade.
- Running pre-upgrade QA tasks that Accuray may request, to facilitate proper tuning of the system after the upgrade.
- Following any instructions to ensure that Machine QA procedures may be run after the upgrade.

Contact *Accuray* Support if you have questions about the items listed above. If you are adding *TomoDirect* or the *TomoEDGE* dynamic jaws feature, see “QA Tests for Special Modalities” (page 373) for feature-specific QA requirements; these tests are the responsibility of the site physicist.



**IMPORTANT:** Ensure that the Accuray Training department has current contact information for individuals at your facility who should receive upgrade training information from Accuray. Ensure that you share any information received by Accuray Training with the relevant personnel at your site.



**IMPORTANT:** Accuray does not determine when a machine is ready to treat patients. This is the decision of the site physicist.

## Twining to a New Beam Model



**NOTE:** This section applies to a major beam model update. If only the leaf data and/or JFOF's in the beam model are updated, a smaller set of commissioning tasks is required, as discussed in "Post-Service Considerations" (page 376).

Some types of feature upgrades may require Accuray Incorporated to "twin" the machine to a new beam model. See "Beam Model" (page 412) for more information about the beam model.

To ensure accurate patient treatments, the machine performance must be consistent with the beam model. If the beam model data is substantially altered, it will be necessary to re-commission the machine as described in "Commissioning Overview" (page 95) to match the new beam model data provided by Accuray. The following tests should be performed:

- Alignment tests
- Beam profile measurements against the new reference data provided by Accuray Incorporated.
- Absolute LINAC dose calibration
- *CTrue* image quality verification
- MU display calibration
- Establish baseline references (Accuray Incorporated will provide references for the TQA Water Tank, Field Width, and Field Width - Dynamic Jaws modules)
- MVCT density model verification, if calculating dose on *CTrue* images

Additional commissioning tests may be performed at the site's discretion.

A beam model update will invalidate all patient plans currently under treatment. In order to resume patient treatment, the plans must either be re-planned, or transferred to the new beam model. For information on Self Transfer, see "Self Transfer" (page 388) and "Plan Transfer Algorithm" (page 467).



**TIP:** If re-planning, the plan can be saved with a new name to efficiently create new plans that can be optimized using the latest beam model.



**IMPORTANT:** Accuray Incorporated recommends creating new patient specific QA plans and performing patient specific QA following a transfer.





## Chapter 4

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### QA Recommendations and Tasks

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# Quality Assurance Recommendations and Tests

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## ◆ Introduction

This chapter summarizes the quality assurance aspects discussed in the previous chapters and arranges them in accordance with their recommended frequencies.



**IMPORTANT:** Before performing QA tasks, warm up the system and run an air scan as described in “System Startup” (page 76) to help achieve a stable beam and optimal image quality.

This chapter covers the following topics:

- Daily QA
- Monthly QA
- Quarterly QA
- Annual QA
- Post Service QA
- QA Tests for Special Modalities
- Post-Upgrade Tests

## ◆ QA Program and Documentation

As traditionally practiced, QA tests are used to document and ensure the ongoing correct performance of any medical radiation device and also to identify non-compliance with defined performance criteria as soon as it might be manifested. This practice also applies to treatment planning and treatment delivery of the Accuray System.

System QA provides benefits such as the following:

- Reliability: Easier to maintain the system in optimal condition over the life of the equipment.
- Uptime: Reduces the time to troubleshoot and repair problems.
- Safety: Ensures accurate prescription delivery to the target.
- Risk reduction: Documentation satisfies regulatory and professional standards of practice.

To minimize the risk inherent to the use of medical radiation, each treatment system site must develop and implement a robust QA program of measuring and maintaining system performance. Each site must maintain detailed documentation of the QA program.

The treatment system owner is responsible for ensuring that the system is used in accordance with applicable regulations governing the operation of medical radiation linear accelerator (LINAC) systems.

The system quality assurance instructions given in this guide are intended to be performed by a fully qualified radiation oncology physicist. Typically, a qualified Medical Physicist performs all QA of the treatment system, the LINAC, and the Treatment Planning System.

This guide does not include planned maintenance and service procedures that are regularly performed by Accuray Incorporated service representatives. Accuray Customer Support representatives will provide a written record of all work completed to maintain optimal compliance with the Accuray Incorporated calibration specifications. If you determine that the system requires service, always contact the Accuray Customer Support.



**TIP:** Accuray recommends that the Medical Physicist presents the results of daily, monthly, quarterly, annual, and post-service testing with the Quarterly and Annual Radiation Safety Reports so that the results are available for administrative oversight.



**TIP:** If you would like to conduct an independent dose accuracy verification test, you may perform a treatment delivery using the phantoms provided by the Radiological Physics Center (RPC) at the MD Anderson Cancer Center.



**NOTE:** To support your comprehensive QA program, Accuray Customer Support Representatives may request your QA records to determine the current performance status of your system.



**IMPORTANT:** If any test result is outside the tolerance range recommended by Accuray, or outside the tolerance range indicated in the published regulations and recommendations, the site physicist should:

- Investigate the problem and identify any system parameters that may require adjustment.
- Assess the impact of the out-of-tolerance result on scheduled patient treatments, and determine whether or not patient treatments may continue before the adjustment is made.
- In most cases, ask the service representative to perform the adjustment.
- After the adjustment is made, repeat the test to ensure it is within tolerance.

- Test any related parameters that may have been impacted by the adjustment, to ensure they are within tolerance.

Contact Accuray Customer Support with any questions. Accuray can provide information about the machine, but does not advise whether clinical treatments may continue.

## ◆ Quality Assurance Tests and Schedules

### Applicable AAPM Protocols

TG-148 is the AAPM Task Group report specifically for quality assurance of helical products. Most clinics choose to adopt the TG-148 recommendations for routine quality assurance procedures.

Section I of TG-148 introduces the helical tomotherapy protocol in the context of other related protocols, and explains their relevance to quality assurance:

- TG-40: Comprehensive quality assurance for radiation oncology
- TG-45: Code of practice for radiotherapy accelerators
- TG-142: Quality assurance of medical accelerators

### Relevance of Accuray Recommendations to the Applicable Protocols

This chapter makes recommendations for QA tests and frequencies that are similar to the TG-148 protocol. This chapter also includes recommendations for the *TomoDirect* and *TomoEDGE* dynamic jaws features, which are not discussed in the TG-148 protocol.

Standard safety tests should also be performed per TG-142 and local regulations, but they are not included in this chapter. The section “Standard Safety Checks” (page 77) references system-specific instructions for checking the interlocks, indicators, and stop buttons.

The QA tests recommended in this chapter are considered to be the essential minimum. Conventional, additional, or equivalent tests may also be performed as necessary. An example of this would be patient-specific dosimetry verification.

# Daily QA

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## ◆ Overview of Daily QA Tests

<b>TG-148 reference:</b>	See Table II of TG-148.
<b>Purpose:</b>	Verify that the red lasers in their "home" position overlap the green lasers, that the lasers properly identify the image isocenter, that the image registration process can be used to successfully position a phantom, and that the static or rotational output is consistent with baseline values.
<b>Method:</b>	<ol style="list-style-type: none"><li>1. Create a QA plan on a phantom (first time only). In the plan, set up the phantom to the green lasers, but intentionally offset the red lasers from the planned setup position by different known distances in X, Y, and Z.</li><li>2. Check red/green laser overlap when machine is first turned on.</li><li>3. Set up the phantom to the red lasers with an intentional, known setup offset. Scan the phantom on the treatment system and check the image quality.</li><li>4. Register the phantom and verify the shifts.</li><li>5. Prepare a treatment, apply the shifts to the couch using <b>Setup</b>, and verify red laser and couch movement.</li><li>6. If a daily rotational QA output test is used, the phantom is now in the proper position for treatment. Or, set up the <i>Virtual Water</i> stack for a static output check.</li></ol>

<b>Accuracy specification:</b>	<ol style="list-style-type: none"> <li>1. Red and green lasers overlap within 1.5-1 mm (non SRS/SBRT-SRS/SBRT).</li> <li>2. Image quality is visually acceptable.</li> <li>3. Registration results are consistent with expected values within 1 mm.</li> <li>4. After using <b>Setup</b> to align the phantom, the phantom is within 2-1 mm of the expected position (non SRS/SBRT-SRS/SBRT).</li> <li>5. Output is within <math>\pm 3\%</math> of baseline.</li> </ol>
<b>Equipment needed:</b>	<ul style="list-style-type: none"> <li>• Phantom (<i>Tomo</i>-phantom or other phantom for image alignment and rotational output test; <i>Virtual Waterstack</i> or other phantom for static output test)</li> <li>• Dose measurement equipment (ion chamber and electrometer, or other device)</li> </ul>

In addition to the above:

- Standard safety tests should be performed according to TG-142 and local regulations. “Standard Safety Checks” (page 77) includes instructions for checking the interlocks, indicators, and stop buttons.
- If you are calculating dose on MVCT images, the CT Number Calibration should be run on a weekly basis. See “CTrue Image Quality Verification” (page 243).
- Sites with the *TomoEDGE* dynamic jaws feature may run the *TQA Daily QA* module each day to check the performance of the MLC and jaws. See the *TQA Manual*.
- All sites that do not have dynamic jaws should run the *TQA Daily QA* or Basic Dosimetry procedure on a weekly basis. This test provides valuable information that a service representative can use to monitor beam health.



**NOTE:** TG-148 recommends alternating between static and rotational output checks on a daily/weekly basis. You can perform a daily static and a weekly rotational check, or a daily rotational and a weekly static check.



**NOTE:** TG-148 does not require a daily beam quality energy check. However, it would be convenient and useful to also check the beam quality each time you perform a static output check. See “Set Up and Measure the Static Output and Beam Quality Baseline” (page 272) for instructions.

## ◆ Theory of Daily QA Tests

The sample QA workflow in this chapter is based on the "Example of Daily Test Procedures" from Appendix D of TG-148, which includes tests of image/laser coordinate coincidence, image registration/alignment, and rotational output.

You will need to create a plan on the *Precision* System for the phantom of your choice. The same plan will be used each day for your morning QA. In the suggested workflow, plan the phantom to be centered on the green lasers. On the **Plan Settings** tab, shift the red lasers with respect to the green lasers by known arbitrary amounts in X, Y, and Z.



**TIP:** When you create a patient treatment plan or phantom plan, the number of delivery fractions is set in the plan, and you cannot deliver additional fractions. To avoid running out of daily QA fractions (resulting in an eventual need to copy the plan or make a new plan), set up your daily QA as a patient QA plan (i.e., re-calculate the patient delivery on a phantom image). The number of fractions is not limited for patient QA plans.

The daily workflow will then be:

1. Set up the phantom in the known incorrect position (shifted with respect to the planned position). Center the phantom on the red lasers, even though the plan indicated that the phantom should be centered on the green lasers.



**NOTE:** For patient treatments, the green lasers are typically not used and may be turned off. For patient treatments, patient fiducials are aligned to red lasers to set the patient up in the planned position. But for the daily QA, the green lasers are used to indicate the planned setup position, and the red lasers are used to indicate a shifted (incorrect) position. This approach is taken to verify the system's ability to detect a setup offset.

2. Take an MVCT image of the phantom on the treatment system to verify image quality and perform image registration.
3. Compare your registration results against the known introduced shifts.

Because the phantom is initially set up to the red lasers, there is no straightforward way to correct for couch sag prior to acquiring the CT image. Thus, the registration result in Z is expected to include the couch sag. The expected registration results  $R_x$ ,  $R_y$ , and  $R_z$  are:

- $R_x = -P_x$
- $R_y = -P_y$
- $R_z = -P_z + |S|$

where  $P_x$ ,  $P_y$ , and  $P_z$  are the red laser shifts in the original treatment plan, and  $S$  is the couch sag in Z from the setup position outside the bore to the beam plane.

4. Prepare a treatment, and apply the registration results to the couch.
5. Observe that the phantom is in the planned setup position. If you followed the suggested workflow for use of the red and green lasers:
  - The phantom should now be centered on the green lasers.
  - The green and red lasers should now overlap in X and Y.
  - The **current laser position** on the **Positioning Control Panel** should be 0.0 (within the tolerance range) in X and Y.
  - The **current laser position** on the **Positioning Control Panel** in Z indicates the amount of couch sag.
6. If you wish to confirm the couch sag correction, send the phantom 700 mm in the bore, and walk behind the gantry to check that the phantom is centered on the green lasers in Z.



**NOTE:** If you place the phantom in the same longitudinal region of the couch every day, and if there are no other heavy items on the couch, the couch sag is expected to be consistent from day to day. Thus, the couch position Z value on the **Positioning Control Panel** should be consistent from day to day.

7. The phantom is now in the appropriate position for a daily rotational output check using the same treatment plan. The expected dose may be obtained from the *Precision System*.

Or, you may set up a different phantom for the static output check, and compare against your baseline value.

## ◆ Alternate Methods for Performing this Test

TG-148 lists the system parameters that should be checked on a daily basis. However, TG-148 allows the site to choose the daily methods and equipment.

This chapter outlines a QA process using the *Tomo*-phantom and other basic equipment discussed in the Equipment section of the Commissioning chapter.

Some sites prefer to use a diode device for the static constancy measurement, or to use the *TQA* step wedge phantom (with optional ion chamber insertion) instead of the *Tomo*-phantom.



**NOTE:** The Dose1 monitor chamber reading is used to adjust the system output via the Dose Control System. The daily output check will be more robust if you include a measurement with a device that is independent of the treatment system.



**NOTE:** The *TQA* Daily QA procedure does not check all the parameters recommended by TG-148 for daily QA (for example, it does not check image quality and image registration), but it is an efficient way to check the constancy of a large array of system parameters.

## ◆ Daily QA Plan Creation

### Plan for Image Quality, Image Registration, and Rotational Output Tests

Accuray does not provide the patient QA plan for your daily QA. You will need to create your own plan to meet the requirements for image/laser coordinate coincidence, image registration/alignment, and rotational output consistency.

Before you create your daily QA plan, you will need:

- A patient treatment plan (calculated on a patient image, or calculated on a phantom image that was imported as if it were a patient image).
- A DICOM image set of your phantom of choice.



**IMPORTANT:** For accurate dosimetry in the *Tomo*-phantom, plug all the ion chamber holes with *Virtual Water* sticks, and do not insert the ion chamber for the scan.

- A deliverable phantom template plan calculated on your phantom image. This will make your phantom image available for calculating the patient QA.

Create the daily QA (patient QA) plan as described in “Patient QA Plans” (page 390). Center the phantom image on the green lasers. Offset the red lasers from the green lasers by different known distances in X, Y, and Z (e.g., 10 mm in X, 20 mm in Y, and 30 mm in Z).



**NOTE:** Here, we are using the red lasers to mark a known shifted (incorrect) position. This is not a clinically typical use of the red lasers.



**IMPORTANT:** Consider re-optimizing your rotational output test plan if the beam model gets updated or the MLC gets replaced. This will ensure that the dose calculation uses the current beam model and MLC data.

## Plan for Static Output Test

For the static output constancy check, use the Machine QA plan and reference data that was created at commissioning. See “Establish Baseline References” (page 267).

### ◆ Set Up and Deliver the Test



**IMPORTANT:** Before performing QA tasks, warm up the system as indicated in “System Startup” (page 76) to help achieve a stable output and optimal image quality.



**NOTE:** In addition to the steps listed in this section, you will also need to run your standard safety tests as mentioned in “Overview of Daily QA Tests” (page 337), and possibly run the *TQA Daily QA* module or *TQA Basic Dosimetry* module.

### Red Laser Initialization

Follow the instructions under the heading “Verify that the red lasers coincide with the green lasers in the ‘home’ position” from “Set Up and Deliver the Test” (page 126).

### Set up the Phantom with a Known, Intentional Offset and Acquire a Scan

1. On the TDC, select the **Patient QA** task, open the plan you created in “Daily QA Plan Creation” (page 341) and prepare a scan. At a minimum, select enough slices to include both the green and red lasers in Y.
2. After the red lasers have moved to the plan position, set up the phantom to the red lasers and acquire a scan.



**TIP:** Ensure that the couch is not too far out of the bore in Y, or you may not be able to perform the necessary adjustments in the following steps.



**TIP:** It may help to insert an ion chamber in the *Tomo* Phantom for the daily MVCT scan, so you can see the ion chamber in the *CTrue* image (even though there was no ion chamber in the planning image).

## Check the Image Quality

Look at the image slices on the **Register** tab to subjectively evaluate the image quality. Take note of image artifacts or excessive noise.

## Register the Phantom and Verify the Shifts

1. Perform image registration on the **Register** tab.

The expected registration results  $R_x$ ,  $R_y$ , and  $R_z$  are:

- $R_x = -P_x$
- $R_y = -P_y$
- $R_z = -P_z + |S|$

where  $P_x$ ,  $P_y$ , and  $P_z$  are the red laser shifts in the original treatment plan, and  $S$  is the couch sag in Z from the setup position outside the bore to the beam plane.



**TIP:** If your phantom does not have much variation in shape or density in X, Y, and Z, manual registration will be necessary. The automatic registration is unlikely to give an appropriate result in a symmetrical phantom.



**TIP:** For manual registration of the *Tomo*-phantom, use the outer boundary of the phantom in the transverse view to determine the X and Z shifts (the checkbox tool will be helpful). Use the inserted ion chamber or fiducial markers for the registration in Y.

2. Accept the registration results.

## Prepare a Treatment and Apply the Shifts

1. Proceed to the **Treat** tab and prepare a fraction for treatment.
2. **Apply** the registration results.
3. Go into the treatment room and press **Setup** on the **Positioning Control Panel** to apply the shifts to the couch.
4. Verify that the phantom is now centered on the green lasers.
5. Verify that the green and red lasers overlap in X and Y.
6. Verify that the **current laser position** on the **Positioning Control Panel** is within tolerance of 0.0 in X and Y. Verify that the **current laser position** indicates a reasonable amount of couch sag in Z.
7. Verify that the couch position Z value on the **Positioning Control Panel** is consistent with the typical value.

## Check the Rotational Output Consistency

If you wish to perform a dose check of the rotational output for the same treatment plan, your phantom is now in the setup position. Insert a chamber in the desired position and compare the dose against the planned value.

## Check the Static Output Consistency

If you wish to perform a static output check, follow the steps in “Set Up and Measure the Static Output and Beam Quality Baseline” (page 272), and compare your measurement against the baseline established at commissioning.

### ◆ What to Do if the Test Fails

If a daily QA test fails, the qualified radiation oncology physicist will need to make a clinical evaluation of the potential impact of the failing parameter on scheduled treatments, and determine the appropriate time frame for the corrective action.

## Red/Green Laser Overlap

First, make sure the red lasers are in their "home" position ("current laser position" on **Positioning Control Panel** is 0.0 in X, Y, and Z). If the red lasers are not in their "home" position, they are not expected to overlap the green lasers.

If the red lasers are not overlapping the green lasers when the red lasers are in their "home" position, the red lasers and/or the green lasers have moved, and you will need to investigate further.

Some possible causes of a change in laser alignment may include: intentional adjustment, building walls settling (new building, nearby construction, or earthquake), laser housing bumped during service or room cleaning, or mechanical laser issue.

If you have marked the laser positions on the walls or floor, this may help you to identify the change. However, lasers should not be adjusted based on marks on the walls or floor.

“Stationary Laser Alignment” (page 141) outlines tests to verify the position of the green stationary lasers.



**IMPORTANT:** If you make laser adjustments, complete all of the steps in the prescribed order to address the inter-dependency of various aspects of the laser alignment.

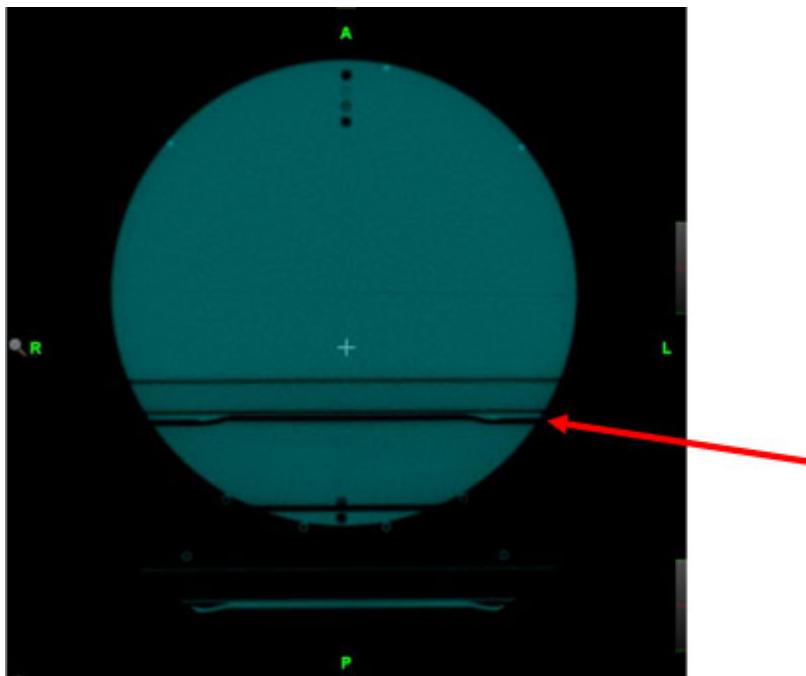
After the green laser alignment has been confirmed to be correct, the red lasers should be adjusted to overlap the green lasers, as described in “Moveable Laser Alignment Tests” (page 163). Contact Accuray Customer Support if you need assistance.

## Image Quality

If the image quality is unacceptable, it may help to take another air scan, then scan the phantom again and see if the image quality has improved. If the couch was left in the bore during the most recent air scan, you may see a shadow of the couch subtracted from your phantom image, as shown in the following figure. The sample shows the *Tomo*-phantom image with couch subtracted from the phantom, due to an incorrectly acquired airscan.

Make sure that the bore is clear of objects. A screwdriver or other object sitting on the bore covers can impact the beam attenuation for both images and treatments.

See “What to Do if the Test Fails” (page 185) for additional troubleshooting suggestions.



Tomo Phantom image with shadow of couch

## Image Registration and Adjustments

If the shifts on the **Register** tab do not match the expected values, or the couch does not move to the expected position when **Setup** is pressed:

- Check your phantom setup.
- Check the image registration.
- Check that you have selected the correct plan.
- Prepare a scan or treatment for a plan for which the red lasers move from their home position, and use a ruler to verify the distance and direction of the laser shifts against the **current laser position** values on the **Positioning Control Panel**. If the red/green lasers overlap properly

at initialization, but the laser movement is not correct, contact Accuray Customer Support for assistance.

- Verify the green laser alignment according to the steps in “Stationary Laser Alignment” (page 141). If you adjust the green lasers, the red lasers will need to be adjusted to overlap the green lasers according to the instructions in “Moveable Laser Alignment Tests” (page 163). Contact Accuray Customer Support if you need assistance.



**IMPORTANT:** If you make laser adjustments, complete all of the steps in the prescribed order to address the inter-dependency of various aspects of the laser alignment.

If you identify a problem with the laser movement, couch movement, or image position, contact Accuray Customer Support for assistance.

## Rotational Output Consistency

If daily rotational output measurements indicate a discrepancy between planned and calculated dose, you may need to contact Accuray Customer Support to adjust the output rate of your machine. Verify that the daily rotational output test was performed correctly. Check to see if measurements consistently indicate that the output is too high or too low, and investigate other potential contributing factors. Contact Accuray Customer Support if you have questions.

### Verify that the test was performed correctly

- Ensure that you are using the correct plan.
- Confirm *Tomo*-phantom setup with an MVCT image.
- Confirm that ion chambers were placed in the intended holes in the *Tomo*-phantom, unused holes were plugged with *Virtual Water* sticks, and chambers and electrometer channels were not mixed up.
- Ensure that measurement equipment is functioning properly.

### Perform additional dose checks

A high or low output result may be confirmed by additional tests or a survey of recent results for:

- Daily static output consistency measured by an external device
- Patient QAs
- *Tomo*-phantom IMRT dose calibration measurements

The above tests are generally expected to consistently indicate that the output is high or low. If these tests do not give a consistent result, look for other contributing factors as described in the next section. Contributing factors can cause the results to depend on the test plans, which can differ in MLC usage, the selected field size, or the depth of measurement.

If the discrepancy among test results persists after addressing other contributing factors, the *Tomo*-phantom IMRT dose calibration results should take precedence for determining necessary output adjustments. See “Absolute Dose Calibration” (page 211) for more information.

### Consider possible contributing factors

A discrepancy between planned and calculated dose may be caused by other contributing factors, including but not limited to:

- Energy
- System alignment
- Longitudinal profiles
- MLC performance
- Monitor chamber performance and calibration

Consider running a beam planarity film and a subset of the monthly QA tests to get a general idea of the beam status, prior to making a decision to adjust the beam output. If any of the above parameters are found to be out of tolerance, these should be corrected first with help from Accuray Customer Support, and then you can check the output again.

If your machine was recently serviced, you may wish to contact Accuray Customer Support to discuss the potential impact of recent service on your dose measurements. Some kinds of machine service (e.g., MLC replacement) impact the beam model data and should prompt the site physicist to transfer or re-optimize the daily QA plan.

## Static Output Consistency

Static output consistency results should not be used directly to determine machine adjustments. See “Theory of Absolute Dose Calibration” (page 213).

However, static output consistency results can help identify possible problems that require further investigation. Static open-field consistency results are less sensitive than IMRT plans to other contributing factors, such as MLC performance.

See the previous sub-section for suggestions for further investigation.

# Monthly QA

Table III of TG-148 lists 21 recommended monthly QA tests, which are divided into three sub-groups: “Beam Parameters,” “Alignment and Misc.,” and “MVCT.” Instructions for most of these tests may be found in the Commissioning chapter, while the remaining instructions are provided in this chapter.

Accuray has expanded the TG-148 recommendations to accommodate the *TomoDirect* and *TomoEDGE* dynamic jaws features. In addition, standard safety tests should be performed.

In this chapter, the order of the tests has been arranged to minimize dependencies on subsequent tests, in the event that a machine adjustment is needed. If it is necessary to ask a service representative to perform a machine adjustment, the possible impact on tests already completed should be considered. For example, an adjustment to the beam energy will also affect the beam profiles and the rotational output measurement.

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- ◆ Beam Parameters .... 349
- ◆ Additional Test for Dynamic Jaws. .... 353

## ◆ Alignment and Misc.

The following table lists the alignment parameters and other miscellaneous parameters required by TG-148, and interpretation of tolerances by Accuray Incorporated. These tests are covered in the respective sections of the Commissioning chapter. For the monthly completion procedure check, it is recommended to use a different field width each month on a rotating schedule.

Parameter	Tolerance	Equipment Needed
Interrupted Procedure	Film profile for interrupted and completed procedure consistent with film profile of uninterrupted procedure within 3%	<i>Tomo</i> Phantom, film, ion chamber, and electrometer
Red laser movement	1 mm	Ruler
Treatment Couch	<ul style="list-style-type: none"><li>• Digital readout consistent with actual movement within 1 mm</li><li>• Couch is level within 0.5°</li><li>• The couch travel diverges &lt; 1 mm in X over 200 mm displacement in Y</li><li>• The couch does not sag more than 2 mm over 700 mm travel in Y.</li></ul>	Ruler and level

## ◆ Beam Parameters

The following table lists the monthly beam parameter checks required by TG-148, and interpretation of tolerances by Accuray Incorporated. The tests are discussed on the following pages.

Parameter	Tolerance	Equipment
Rotational output variation	Variation $\leq \pm 2\%$ of average output	TQA Essentials
Transverse profile	TG-148 spec: $\leq 1\%$ average difference in field core. Accuray specification: Gamma $< 1$ (for gamma criteria of 2% and 1 mm).	TQA Essentials
Beam quality	PDD <sub>10</sub> or TMR <sup>20</sup> <sub>10</sub> within $\pm 1\%$ of baseline	<ul style="list-style-type: none"> <li>Set of <i>Virtual Water</i> blocks (15 cm x 55 cm x variable thickness), ion chamber and electrometer</li> <li>Or, <i>TQA Advanced</i> package</li> </ul>
Longitudinal profiles (each slice width)	Measured longitudinal profiles at 15 mm depth: <ul style="list-style-type: none"> <li>Symmetric profiles: FWHM is within 1% of the reference FWHM. Gamma <math>&lt; 1</math> over a range of three times the field width (gamma criteria: 2% dose difference and 1% of the field width for the distance to agreement (DTA))</li> <li>Asymmetric profiles for systems with dynamic jaws: gamma <math>&lt; 1</math> over a range of three times the field width (gamma criteria: 3% dose difference and 0.5 mm DTA)</li> </ul>	<ul style="list-style-type: none"> <li>Ion chamber</li> <li>Electrometer</li> <li>Software to plot the measured data (TEMS)</li> <li><i>TQA Advanced</i>, or computer with Microsoft Excel</li> <li><i>Virtual Waterblocks</i>, allowing for measurement at a depth of 15 mm.</li> </ul>
Rotational output	Ion chamber measurement within $\pm 2\%$ of calculated dose from planning system	<ul style="list-style-type: none"> <li><i>Tomo Phantom</i></li> <li>Ion chamber</li> <li>Electrometer</li> </ul>
Static output	Ion chamber measurement within $\pm 2\%$ of baseline	<ul style="list-style-type: none"> <li>Set of <i>Virtual Water</i> blocks (15 cm x 55 cm x variable thickness)</li> <li>Ion chamber</li> <li>Electrometer</li> </ul>

Parameter	Tolerance	Equipment
Monitor chamber constancy	Cumulative Dose1 and Dose2 displays on TDC agree within 2%	N/A

## Rotational Output Variation and Transverse Profile

TG-148 was published in 2010. At the time of writing of TG-148, and prior to the introduction of the Dose Control System, most tomotherapy-based machines exhibited output variation with gantry rotation. The Dose Control System helps to stabilize the output with gantry rotation. See “Dose Control System” (page 54) for more information.

Transverse profiles are verified annually in a water tank for all field widths. On a monthly basis, a consistency check of at least one field size is required.

The rotational output variation and transverse profile consistency can be easily checked using the **TQA Basic Dosimetry** module, as discussed in “Rotational Variation Procedure” (page 354).

## Beam Quality

Beam quality (PDDs) are verified annually in a water tank for all field widths. On a monthly basis, a consistency check is sufficient.

The consistency check may be performed with an ion chamber in *Virtual Water* and compared against the baseline reference determined in “Establish Baseline References” (page 267). Alternatively, the TQA™ Advanced package includes a Step Wedge module for checking energy consistency.

TG-148 recommends a monthly PDD check at a minimum. If you perform the daily/weekly static output check with an ion chamber in *Virtual Water*, it would be convenient to use the same setup to check the PDD ratio more frequently.

For the measurements in *Virtual Water*, follow the steps in “Set Up and Measure the Static Output and Beam Quality Baseline” (page 272). TG-148 specifies that the  $PDD_{10}$  or  $TMR^{20}_{10}$  should be consistent within 1% of the baseline.



**TIP:** Measurements at deeper depths are more sensitive to energy changes, so it is useful to include the measurement at 20 cm depth.

For the *TQA Step Wedge Static* test, follow the instructions in the *TQA Manual*. Check the Energy Difference result on the Results tab of the *TQA* report. The mathematical definition of the Energy Difference is given in the *TQA Manual*.

If the test fails, verify the setup, and verify that the correct XML file is being used.



**NOTE:** The 10 cm and 20 cm depths are referenced from the center of the chamber to the surface of the *Virtual Water*.

If it is determined that the energy needs to be adjusted, contact Accuray Customer Support to request an energy adjustment. When the service representative is finished with the adjustment, measure the energy again to ensure it is within tolerance. An adjustment in energy can impact the system output, transverse profiles, and longitudinal profiles, so these should be re-tested after an energy adjustment.

## Longitudinal Profiles

On an annual basis, longitudinal profiles are measured in a water tank. On a monthly basis, all longitudinal field widths should be verified in *Virtual Water*. If the longitudinal field size does not match the beam model used by the Planning System, the overlap from one rotation to the next, and thus the patient dose, will be incorrect.

## Static and Rotational Output

A calibrated ion chamber should be used for the static and rotational monthly output QA, and TG-148 specifies that a different ion chamber serial number or other measurement device should be used for the daily/weekly QA.

The static output measurement is a consistency check in *Virtual Water* against the baseline established at commissioning. For daily/weekly QA, the static output should match the baseline reference within  $\pm 3\%$ . For monthly QA, the tolerance is tighter at  $\pm 2\%$ .

The rotational output measurement is a comparison between measured ion chamber data and the dose calculated by the planning system. The TG-148 recommended tolerance is  $\pm 2\%$ . TG-148 does not specify which plan(s) should be used for the monthly rotational output test. If daily/weekly rotational output QA is performed in the *Tomo*-phantom, the same procedure could be used for monthly QA. A more thorough option would be to check a few dose points on all of the *Tomo*-phantom plans in the *Tomo*-phantom (including the *TomoHelical* and *TomoDirect* plans for all field widths, both fixed and dynamic jaws where applicable). See “Absolute Dose Calibration” (page 211) for more information. The Accuray Incorporated tolerance for each point dose measurement in the *Tomo*-phantom plans is consistent with the TG-148 tolerance for annual dosimetric verification, at  $\pm 0.06$  Gy (i.e.,  $\pm 3\%$  of 2 Gy) and  $\pm 3$  mm.

If the results are not within tolerance, see troubleshooting suggestions under What to Do if the Test Fails.

## MVCT

The following table lists the MVCT tests required by TG-148, and the Accuray Incorporated interpretations of the tolerances. These tests are covered in the respective sections of the Commissioning chapter.

Parameter	Tolerance	Reference	Equipment Needed
MVCT Image Quality	<ul style="list-style-type: none"><li>Distance between fiducial marks in <i>CTrue</i> image should match actual distances within 2 mm (or 1 mm if the system is used for SRS/SBRT)</li><li>Noise, uniformity, and contrast consistent with baseline. If CTrue images are used for dose calculation, HU values should be consistent in the center and edge of phantom within 25 HU.</li><li>The third row of holes in the resolution plug should be visible.</li></ul>	“CTrue Image Quality Verification” (page 243)	<ul style="list-style-type: none"><li><i>Tomo</i>-phantom</li><li>Resolution plug</li></ul>
MVCT density model	If <i>CTrue</i> images are used for dose calculation, check the HU values for lung, bone, and water, to ensure they are within 50 HU (for lung and bone) or 30 HU (for water) of the current MVCT density model.	“Enter a Density Model” (page 320)	<ul style="list-style-type: none"><li><i>Tomo</i>-phantom</li><li>Density plug inserts for <i>Tomo</i>-phantom</li></ul>



**IMPORTANT:** The MVCT density model must be kept up to date if you are calculating dose on MVCT images. The PreciseART™ adaptive feature calculates dose on MVCT images.

### ◆ Additional Test for Dynamic Jaws

In addition to the tests recommended by TG-148, you may wish to perform QA of the jaw motion on a routine basis. This can be done using the TQA Jaw Sweep - Dynamic Jaws module.

# Rotational Variation Procedure

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## ◆ Overview of Rotational Variation Procedure

<b>TG-148 reference:</b>	Rotation output variation (section V.B.2.d) and Monthly transverse profile (section V.B.2.b)
<b>Other names for this test:</b>	Basic Dosimetry
<b>Purpose:</b>	Verify that the output is stable with gantry rotation. Verify that the transverse profile shape is consistent with the baseline measurement.
<b>Method:</b>	Run the <i>TQA</i> Basic Dosimetry module.
<b>Accuracy specification:</b>	<ul style="list-style-type: none"><li>• Variation <math>\leq \pm 2\%</math> of average output</li><li>• TG-148 transverse profile specification: <math>\leq 1\%</math> average difference in field core.</li><li>• Accuray transverse profile specification: Gamma &lt; 1 (for gamma criteria of 2% and 1 mm).</li></ul>
<b>Sample result image:</b>	<p>The figure consists of two vertically stacked line graphs. The top graph is titled 'Normalized Output' and plots 'Percent' (y-axis, 97 to 103) against 'Pulse' (x-axis, 0 to 6000). It shows a sharp initial peak at pulse 0 (reaching ~102%) followed by a stable baseline around 100% with minor noise. A legend indicates 'Measured' (blue line) and 'Reference' (green line). The bottom graph is titled 'Exit Detector Ratio' and plots 'Percent' (y-axis, 95.5 to 100.5) against 'Channel' (x-axis, 0 to 550). It shows a stable ratio near 100% across all channels, with a slight dip around channel 250. A legend indicates 'Ratio' (blue line) and 'Normalized Ratio' (orange line).</p>

## ◆ Theory of Rotational Variation Procedure

### Rotational Output Variation

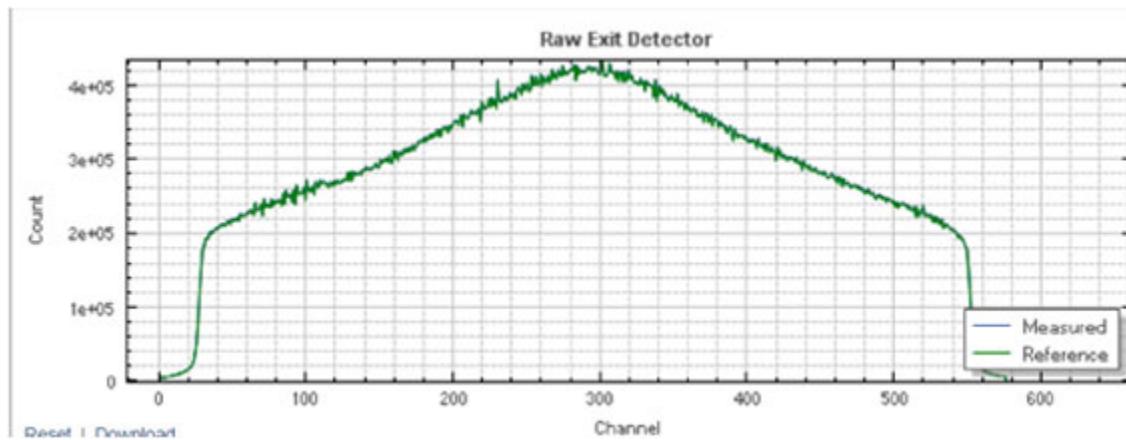
TG-148 specifies that the amplitude of variation with gantry rotation should not exceed  $\pm 2\%$ . This is most easily accomplished by plotting the on-board Dose1 monitor chamber data in the *TQA Basic Dosimetry* module. With the couch not in the bore, all leaves are open and the beam is run for 200 seconds while the gantry rotates.

### Transverse Profile

Transverse profiles are verified annually in a water tank for all field widths. On a monthly basis, a consistency check of at least one field size is required.

The easiest way to perform a consistency check of the transverse profile is to use the on-board detectors, and compare against a machine-specific reference established by the site physicist at the time of commissioning. This can be accomplished using the *TQA Basic Dosimetry* module.

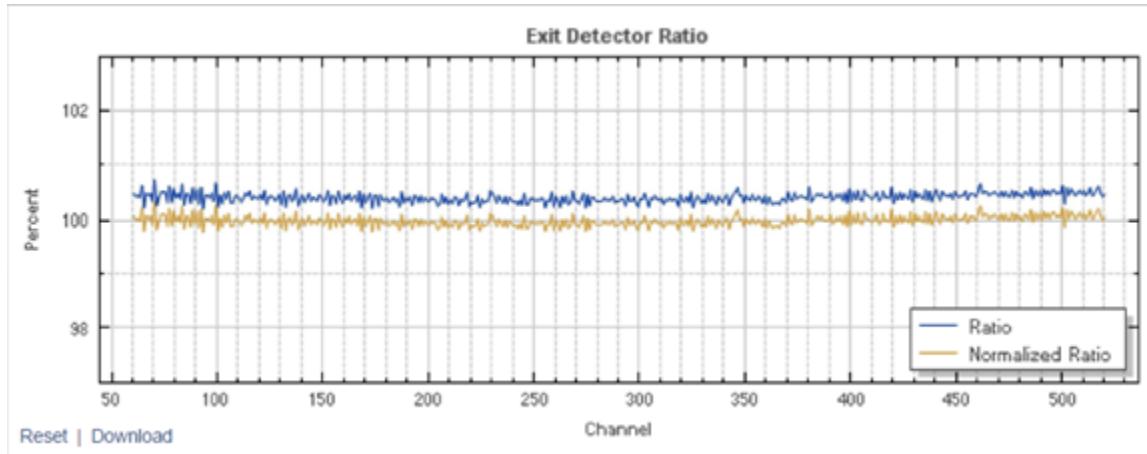
The graph below is an example of a **Raw Exit Detector** from a *TQA* report for the Basic Dosimetry module. The **Raw Exit Detector** graph plots the measured and reference detector signals as a function of detector channel.



The graph below shows an example of the **Exit Detector Ratio** in the TQA Basic Dosimetry report. The exit detector ratio is the ratio of the current transverse profile to the reference profile for each channel, multiplied by 100. This relative comparison can be used to detect changes in energy of

the beam from the time the machine was commissioned. A flat line (exit detector ratio = 100% for all channels) would indicate perfect agreement with the reference transverse profile.

The **normalized ratio** is the exit detector ratio minus the average ratio, plus 100. The normalized ratio represents the ratio offset to account for any net signal differences between the current data and the reference data, in order to focus on differences in the shape of the curve.



Higher-energy bremmstrahlung radiation tends to be more forward-directed. As a result, a more sharply peaked transverse profile corresponds to a higher energy beam. When the ratio between the measured and reference profiles is plotted, a "Λ" shape indicates that the current detector profile is more sharply peaked than the reference, implying that the current energy is higher than the reference. Conversely, a "V" shape indicates that the current detector profile is less sharply peaked than the reference, implying that the current energy is lower than the reference. In this way, the shape of the transverse profile can serve as a secondary indicator of the beam energy.

However, Jeraj (2004) demonstrated that changes in the transverse profile may also be attributed to changes in the scatter properties of the beam.



**IMPORTANT:** If changes are detected in the shape of the transverse profile, the site physicist should follow up with PDD measurements to confirm the energy by a more direct method.

The signal at the most central detector channels and the edge channels is sensitive to system alignment. If the detector or LINAC is replaced, or if the position is slightly changed during service, the ratio between the measured and reference detector profiles may exhibit spikes at the central channels

and the edge channels. These spikes can usually be ignored when evaluating the **normalized ratio**. If desired, a new reference could be collected after the next annual QA to remove the spikes.

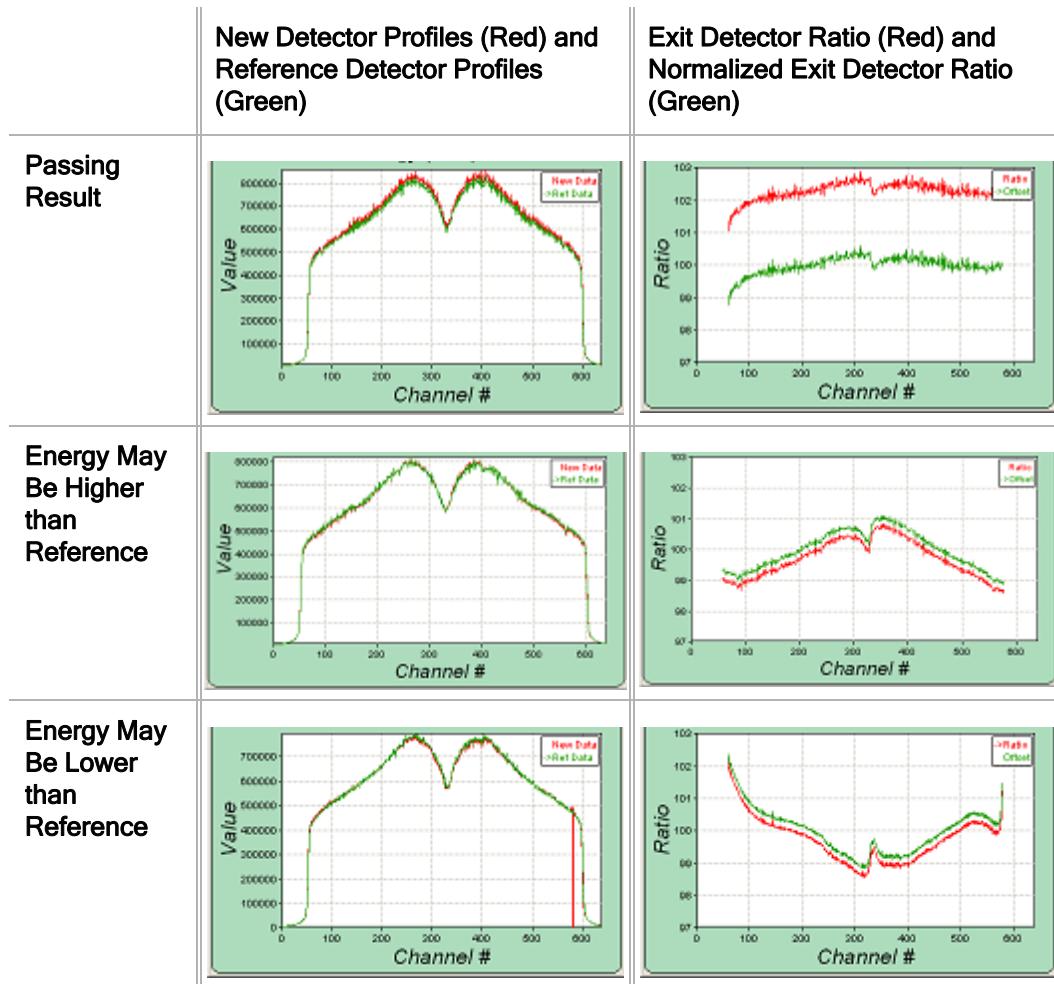
To illustrate how the transverse profile results may be interpreted, examples of rotational variation results are given below. These results were collected using service representative software that plots graphs similar to the raw exit detector and exit detector ratio examples provided above.



**NOTE:** The figure below shows internal service representative software that displays plots very similar to *TQA*. Data was collected on an older style detector that exhibits a low detection efficiency region in the central channels; this dip will not be present on the new detectors.

1. The first row shows an acceptable normalized exit detector ratio. In this example, a signal level difference between the current data and the reference data may be observed; the signal level difference is usually not a concern.
2. In the second row, a "Λ" shaped normalized exit detector ratio can be observed. The result is near the  $\pm 1\%$  specification of TG-148. Additional PDD tests should be performed because the energy may be higher than the reference.
3. In the third row, a "v" shaped normalized exit detector ratio can be observed. Additional PDD tests should be performed because the energy may be lower than the reference.

It can also be observed in the third row that a single channel (around channel number 580) is not responding properly. The service representative should flag any bad channels not to be used for image reconstruction in the software.



## ◆ Alternate Methods for Performing this Test

### Other Procedures using On-Board Chamber and Detector Data

A similar test using the on-board monitor chambers and detectors, called the J48 rotational variation procedure (also known as "rotvar"), is used by Accuray service personnel for tuning the beam output and energy.

Rotational variation results are compared against a machine-specific reference that was measured by Accuray during initial specification testing.

The *TQA Daily QA* module can also be used to perform this test. Graphs of the **Output Ratio** and **Exit Detector Ratio** are included in the *TQA* report.

## Rotational Output Variation with Ion Chamber

As an alternative to using the monitor chambers to measure the rotational output variation, the output variation with gantry rotation may be measured using an ion chamber at isocenter. For example, the A17 chamber, when connected to Channel 8 of the *Tomo-Electrometer* (the high range channel), is suitable for this test. The couch must be out of the bore to avoid couch attenuation dependence on gantry angle, so this test will require a special setup to support the inferior end of the chamber.

When rotational variation is measured with the on-board monitor chambers, it is not sensitive to jaw position. When rotational variation is measured with an ion chamber, the result is sensitive to variation in jaw position with gantry rotation. (The *TQA Airscan* module and Daily QA module checks jaw stability with gantry rotation using the on-board CT detectors).

## Transverse Profile

Besides the on-board detectors, an array device of suitable size could be used for a monthly consistency check of the transverse profile. The result should be compared against a reference measured with the same device when the machine was known to be in a well-commissioned state.

### ◆ XML Description

Test Name: <i>TQA Basic Dosimetry Module</i>	
Where to get the XML	This XML can be downloaded using the <i>TQA Basic Dosimetry</i> module.
Patient Name	zzzzz TQA Basic Dosimetry (RotVar J7mm)
Procedure Description	Tx Beam J7mm 10 twenty sec rot
Couch movement in IEC Y when Ready is pressed	None
Couch translation during the procedure	None
Gantry	20 s/rotation
Jaws	J07 (nominal 1 cm field width)
MLC	All open
Beam-on time	200 s

## ◆ Set Up and Deliver the Test

Run the *TQA Basic Dosimetry* procedure with the couch out of the bore.  
See instructions in the *TQA User Manual*.

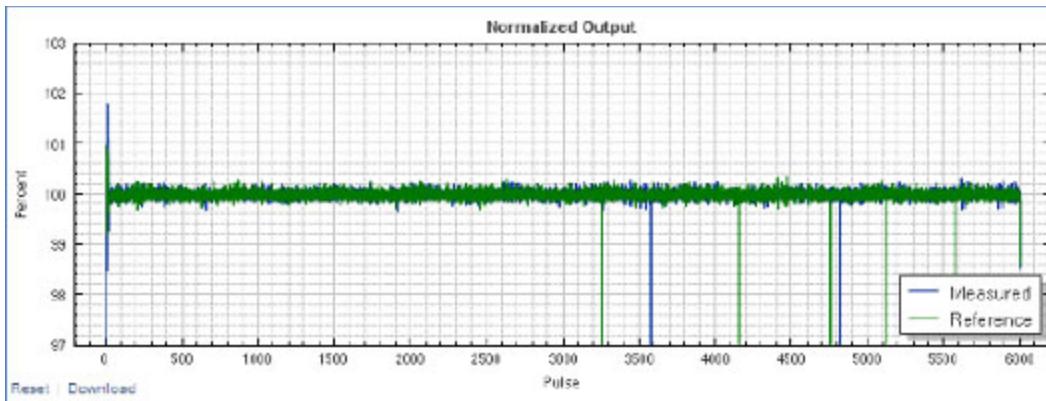
## ◆ Analyze the Result

Open the *TQA* report and click on the **Graphs** tab.

### Rotational Output Variation

The **Normalized Output** graph shows the raw Dose1 signal normalized so that its average value is 100%, as a function of LINAC pulse. (For the treatment beam, there are 300 LINAC pulses per second. For a 200 second procedure, there are 60,000 LINAC pulses. A data compression factor of 10 is applied, so that 6,000 pulses are plotted in 200 seconds.)

Observe the **Normalized Output** graph to ensure that the output remains in the range of 98% to 102%. It is normal to see a few dropped pulses. Since all treatment procedures include a 10-second warmup (300 pulses in the graph), noise at the beginning of the procedure does not affect patient treatments.



### Transverse Profile

To check if the transverse profile meets the TG-148 specification, ensure that the **Normalized Ratio** in the **Exit Detector Ratio** plot is in the 99% to 101% range.

The TQA report also includes a **Gamma Index** plot, with criteria of 2% and 1 mm. To check if the transverse profile meets the Accuray gamma specification, ensure that gamma is less than 1 for all channels.

## ◆ What to Do if the Test Fails

### Rotational Output Variation

If the rotational output variation amplitude exceeds 2%, or if the dose drift or number of dropped pulses is excessive, contact Accuray Customer Support to tune the beamline.

### Transverse Profile

#### Signal Level

Detector signal drift by a few percent of the reference is usually not a concern, if measurements with an external ion chamber indicate that the machine output is within tolerance. If the detector signal drift seems excessive, or if the drift is accompanied by a degradation of image quality, inform your service representative. The detector gas pressure may need to be checked.

#### Profile Shape

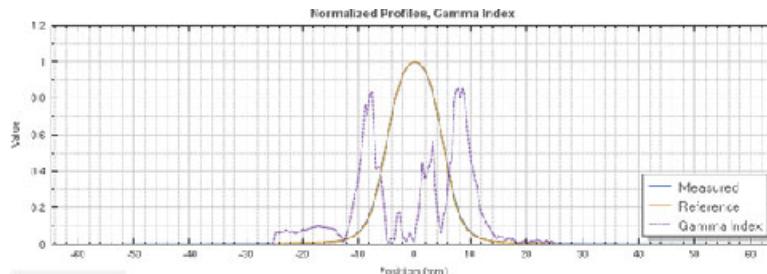
If the **Normalized Ratio** in the **Exit Detector Ratio** plot is out of tolerance, this usually indicates a change in energy from the reference data. Use PDD measurements to check the beam quality.

If the transverse profiles are failing but the PDDs are within tolerance, it could be that the **TQA Basic Dosimetry** reference is not representative of the desired beam state. You could measure the transverse profiles in a water tank, and consider making a new **Basic Dosimetry** reference when the next annual QA is confirmed to be passing.

# Longitudinal Profiles in Virtual Water

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## ◆ Overview of Longitudinal Profiles Test

<b>TG-148 reference:</b>	Monthly longitudinal profiles (V.B.2.c)
<b>Other names for this test:</b>	Topographic profiles
<b>Purpose:</b>	Verify that longitudinal profiles for each slice width are consistent with the reference data.
<b>Method:</b>	With a static gantry, use the couch to carry an ion chamber across the beam and plot the resulting data.
<b>Accuracy specification:</b>	Measured longitudinal profiles at 15 mm depth: <ul style="list-style-type: none"><li>• Symmetric profiles: FWHM is within 1% of the reference FWHM. Gamma &lt; 1 over a range of three times the field width (gamma criteria: 2% dose difference and 1% of the field width for the distance to agreement (DTA))</li><li>• Asymmetric profiles for systems with dynamic jaws: gamma &lt; 1 over a range of three times the field width (gamma criteria: 3% dose difference and 0.5 mm DTA)</li></ul>
<b>Sample result image:</b>	 A line graph titled "Normalized Profiles, Gamma Index". The y-axis is labeled "Normalized Profile" and ranges from 0 to 1.2. The x-axis is labeled "Position (mm)" and ranges from -60 to 60, with major ticks every 10 units. Three curves are plotted: a blue line for "Measured", an orange line for "Reference", and a purple line for "Gamma index". The reference curve is a symmetric bell shape centered at 0, reaching a maximum value of approximately 1.0. The measured curve is slightly asymmetric, peaking at approximately 0.95 near -10 mm and 1.0 near 10 mm. The gamma index curve shows small peaks at the ends of the main profile, indicating the range of the distance to agreement (DTA).
<b>Equipment needed:</b>	<ul style="list-style-type: none"><li>• Ion chamber, electrometer, and software to plot the measured data</li><li>• <i>TQA Advanced</i>, or computer with Microsoft Excel</li></ul>

## ◆ Theory of Longitudinal Profiles Test

Most systems with fixed jaws have three available field widths that need to be commissioned and tested on a regular basis. Systems with dynamic jaws have a total of ten available field widths that need to be commissioned and tested. *TQA Advanced* includes a **Field Width - Dynamic Jaws** module which can conveniently collect all ten field widths in one procedure run.



**NOTE:** The *TQA Field Width - Dynamic Jaws* module procedure is only suitable for data collection in Med-Cal *Virtual Water* or Sun Nuclear *Solid Water*, not in a water tank. Because of the weight of the water tank, water tank profiles should be collected with a static couch and moving scan arm as discussed in “Measuring Beam Profiles” (page 187). This will help prevent variation in the amount of couch sag during data collection.

The procedure involves running a 0° beam at the specified field width, with an ion chamber in *Virtual Water* on the couch. The surface of the *Virtual Water* is at 850 mm SSD, and the chamber is at 15 mm depth.

To reduce chamber stem irradiation, only the central 40 leaves are open, projecting to a transverse field width of approximately 250 mm. The couch translates at 1 mm/s, effectively scanning the chamber across the beam while data is collected using the electrometer and plotted using the measurement software. The resulting plots can be compared against the reference data in *TQA* or in *Microsoft Excel*. The reference data is provided by Accuray and is specific to your beam model.



**NOTE:** Profiles measured in plastic water may be slightly different than profiles measured in a water tank, due to differences in the collection medium, scatter properties, and performance of the scan arm. Accuray uses the same reference data for profiles in *Virtual Water*, *Solid Water*, and in the water tank.

## ◆ Alternate Methods for Performing this Test

Array devices (typical diode or chamber spacing  $\geq$  5 mm) generally do not have sufficient resolution to measure longitudinal profiles with sub-millimeter tolerances.

It is difficult to obtain field size measurements with film. The FWHM size of the field is sensitive to the film calibration, and it is difficult to compare against the reference measured with an ion chamber.

## ◆ XML Description

### Longitudinal Profiles in Virtual Water - Static Field Widths Only

<b>Where to get the XML</b>	The <b>zzzzz_TQA_Top.Profile_10_25_50mm.xml</b> file can be downloaded from the <b>Field Width</b> module of the <b>TQA</b> software.  Even if you do not plan to analyze the static field widths in <b>TQA</b> , you can use the <b>TQA</b> XML. Contact Accuray Customer Support for the XML if you do not have access to <b>TQA</b> .
<b>Patient Name</b>	<b>zzzzz TQA Field Width Module (Topo)</b>
<b>Procedure Description</b>	FW50mm (J42mm) 600 mm setupToReady 200 seconds FW25mm (J20mm) 600 mm setupToReady 200 seconds FW10mm (J7mm) 600 mm setupToReady 200 seconds
<b>Couch movement in IEC Y when Ready is pressed</b>	600 mm
<b>Couch translation during the procedure</b>	1 mm/s for a total distance of 200 mm
<b>Gantry</b>	Fixed at 0°
<b>Jaws</b>	Fixed at J42 (nominal 50 mm), J20 (nominal 25 mm), or J07 (nominal 10 mm)
<b>MLC</b>	Leaves 13-52 (central 40 leaves) open
<b>Beam-on time</b>	200 s

### Longitudinal Profiles in Virtual Water - Dynamic Jaws

<b>Where to get the XML</b>	The XML file can be downloaded from the <b>Field Width</b> module of the <b>TQA</b> software.
<b>Patient Name</b>	<b>zzzzz TQA Field Width Dynamic Jaws</b>
<b>Procedure Description</b>	80sec Topographic Scans
<b>Couch movement in IEC Y when Ready is pressed</b>	660 mm

### Longitudinal Profiles in Virtual Water - Dynamic Jaws

Couch translation during the procedure	9 consecutive passes of the couch across the beam at 1 mm/s, each a total distance of 80 mm. The couch retracts to the initial beam-on position between each fragment.
Gantry	Fixed at 0°
Jaws	<ol style="list-style-type: none"> <li>1. Fixed at J42 (nominal 50 mm)</li> <li>2. Fixed at J20 (nominal 25 mm)</li> <li>3. Fixed at J14</li> <li>4. Fixed at J07 (nominal 10 mm)</li> <li>5. Asymmetric J20 on the -IEC Y side (<b>backJawIECMm</b> = -1 mm; <b>frontJawIECMm</b> = -21 mm)</li> <li>6. Asymmetric J20 on the +IEC Y side (<b>backJawIECMm</b> = 21 mm; <b>frontJawIECMm</b> = 1 mm)</li> <li>7. Asymmetric J14 on the -IEC Y side (<b>backJawIECMm</b> = -7 mm; <b>frontJawIECMm</b> = -21 mm)</li> <li>8. Asymmetric J14 on the +IEC Y side (<b>backJawIECMm</b> = 21 mm; <b>frontJawIECMm</b> = 7 mm)</li> <li>9. In one pass of the couch across the beam: Asymmetric J07 on the -IEC Y side (<b>backJawIECMm</b> = -14 mm; <b>frontJawIECMm</b> = -21 mm), followed by asymmetric J07 on the +IEC Y side (<b>backJawIECMm</b> = 21 mm; <b>frontJawIECMm</b> = 14 mm)</li> </ol>
MLC	Leaves 13-52 (central 40 leaves) open
Beam-on time	$(9 \text{ fragments}) * (80 \text{ seconds}) / \text{fragment} = 720 \text{ seconds total beam-on time}$

## ◆ Set Up and Deliver the Test

If you have *Advanced TQA*, follow the instructions for the Field Width or Field Width-Dynamic Jaws modules in the *TQA User Manual*.

If you do not have *Advanced TQA* you can still use the setup and delivery instructions for the Field Width module in the *TQA User Manual* but you will need to use an alternate method for the analysis. See “Analyze without TQA Software” (page 367).



**NOTE:** You will not be able to analyze test results in *TQA* if you do not have *Advanced TQA*.

## ◆ Analyze the Result

### Analyze with *TQA* Software

The *TQA Field Width* or *Field Width - Dynamic Jaws* modules can be used to analyze longitudinal profile results, as described below.

1. Ensure that the field width reference data appropriate for your beam model is loaded into the *TQA* software. The reference data may be requested from Accuray Customer Support.
2. On the **Results** page of the *TQA* report, verify that each **Field Width Percent Difference** for the symmetric field widths does not exceed  $\pm 1\%$ .



**NOTE:** Accuray Incorporated does not specify a percent difference tolerance for the asymmetric field widths. For more information, see “Explanation of Accuray Incorporated Tolerances” (page 189).

3. On the **Results** page of the *TQA* report, verify that the **Gamma Index** is less than 1 for all symmetric and asymmetric field widths.

If the **Gamma Index** is failing for any profile, check the corresponding plot on the **Graphs** tab to see where the failure occurred. Failures due to dropped pulses can be addressed by running the procedure again. If the gamma failure occurs in the tail region of a profile, disregard the failure if measured or reference data does not exist at the location of the failure.

4. For the non-dynamic module, you can compare the measured and reference field widths (projected to isocenter) on the **Misc** tab.



**NOTE:** On the **Misc** tab for the *TQA* static field width module, *TQA* multiplies the measured and reference FWHM values by 86.5/85, to project each of them to isocenter.

## Analyze without *TQA* Software

1. In the TEMS software, normalize the profile to 100% by clicking **Analyze > Normalize Data**.
2. Since TEMS does not receive data directly from the machine, tell TEMS how fast the couch was moving by clicking **Analyze > Couch Velocity**, and set the value to 1 mm/s to match the XML procedure.
3. In the upper right corner of the screen, select the **Translation Position** scale for the horizontal axis of your plot.
4. To determine the FWHM of the profile, click **Analyze > Full Width % Max**, and set the value to 50%. You can read the result from the output line for the appropriate channel at the bottom of the screen.
5. Compare the measured FWHM to the reference FWHM to ensure they agree within  $\pm 1\%$ .

Ensure consistency between the conditions for the measured and reference data:

- Longitudinal profiles are always measured at 850 mm SSD and 15 mm depth.
- Reference profiles were measured and plotted at 850 mm SSD and 15 mm depth.
- TEMS reports the FWHM of the measured profile (does not project to isocenter).

Contact Accuray Support to determine the reference FWHM for your beam model - be sure to clarify whether the values are quoted under the measurement conditions or after projecting to isocenter.

6. If desired, you may also save your measured profile data in **.csv** format and compare it against the Treatment Commissioning (TCOM) water tank data in *Microsoft Excel*. See “Analyze the Result” (page 360).

## ◆ What to Do if the Test Fails

Here are some possible reasons for failing longitudinal profiles, and recommended actions:

- Incorrect SSD or chamber depth. Be sure to take a *CTrue* image to confirm your setup (850 mm SSD, 15 mm depth in *Virtual Water*).
- LINAC alignment with MLC or jaws is too close to the edge of the respective tolerances. This can especially be an issue for systems with dynamic jaws. You may wish to check your recent QA records for these tests, or repeat them according to the instructions in the Commissioning chapter.

- Beam is not aligned with the plane of gantry rotation (you may wish to run the beam planarity film as described in “Beam Planarity” (page 136)).
- Incorrect energy. Ensure that you measured the beam quality (PDDs) first, as described in “Beam Quality” (page 350).
- The system requires a jaw width or spot size adjustment. (The spot size impacts the shape of the field.) Contact Accuray Customer Support to request that a service representative perform the adjustment. Then repeat all the longitudinal profile measurements to ensure that they pass. If the spot size is adjusted, you should also repeat the beam quality and transverse profile verification. If the jaw width is adjusted, you should also verify the system output.



**NOTE:** Field width and spot size adjustments will affect the machine delivery of all field widths. There are no adjustable parameters that only impact one field width. The service representative will adjust the field width and spot size to achieve a passing result for all commissioned field widths. Individual field widths may vary differently within their tolerances.

# Quarterly QA

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- ◆ Relevance of Synchronicity Tests to TQA Modules ..... 369

## ◆ Overview

The quarterly QA tests prescribed by TG-148 are outlined in the following table. Table IV of TG-148 lists recommended quarterly QA tests, which are divided into two sub-groups: Synchronicity and MVCT. TG-148 quarterly QA includes a check of the MVCT dose (introduced in “CTrue Image Quality Verification” (page 243)), and several tests of the synchronicity of the treatment system (introduced in “Synchronicity Tests” (page 287)).

Test Section	Test Name	Test Purpose
“CTrue Image Quality Verification” (page 243)	MVCT dose	Dose for a fine scan does not exceed 3 cGy
“Synchronicity Tests” (page 287)	Couch translation	Couch translation and MLC leaf opening are synchronized.
“Static Star Shot” (page 294)	Static star shot	The leaves open at the expected angles for a static procedure.
“Helical Star Shot Test” (page 302)	Helical star shot	The leaves open at the expected angles for a helical procedure.
“Couch Speed Uniformity” (page 310)	Couch speed uniformity	The couch velocity is constant throughout the procedure.

## ◆ Relevance of Synchronicity Tests to *TQA* Modules

The **TQA Step Wedge Helical** module has relevance to the helical star shot film test, although the **TQA** module monitors different aspects of the synchronicity of helical delivery than does the helical star shot film. In the **Step Wedge Helical** module, the aluminum step wedge on the couch is translated through the beam while the gantry rotates. The on-board detector data is automatically analyzed by **TQA**. The report includes parameters to monitor the constancy of couch/gantry synchronicity, gantry speed, and MLC leaf open/close timing. All parameters are relative constancy checks, compared to a reference created when the machine was commissioned. For theory details and delivery instructions, see the **TQA** Manual.

The **TQA Step Wedge Static** module is similar to the helical version, but with a static gantry at 0°. Accuray recommends to use the **TQA Step Wedge Static** module to verify the couch speed uniformity constancy.

The **TQA Step Wedge Static** module also has some relevance to the static star shot film test. If the gantry angle for this test deviated significantly from 0°, it might impact the results for the **TQA Step Wedge Static** module. However, the static star shot film is a very important tool to check the gantry calibration, and the film test should not be neglected.



**IMPORTANT:** The static star shot film is the most critical of the quarterly synchronicity tests. Perform the static star shot film test on a quarterly basis, and after any service of the gantry positioning system. Accuray service representatives do not perform the static star shot film.

# Annual QA

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## ◆ Overview

The tests for annual QA as prescribed in Table V of TG-148 are very similar to the initial commissioning tests covered in “Commissioning” (page 93).

The order of the tests listed in the Commissioning chapter should be maintained to help reduce the dependency of later tests on earlier tests:

1. All of the beamline, laser, and couch alignment tests in the commissioning workflow should be performed annually, except for the subset of couch alignment tests that are performed monthly.
2. PDDs, longitudinal profiles, and transverse profiles should be measured annually in a water tank.
3. *Tomo*-phantom plans should be measured annually for all field widths, with the 3% and 3 mm criteria for all plans.
4. TG-148 recommends an annual TG-51 “calibration” of the treatment system, which includes a static measurement in a water tank (for which there is no reference value, so it is not used to calibrate the treatment system), and a rotational measurement in the *Tomo*-phantom which can be compared against the value generated by the *Precision Treatment Planning System* (this measurement is very similar to the *Tomo*-phantom dose calibration plan with the 5 cm field width).
5. The import of CT images and structures into the treatment system should be verified as discussed in “Verify Integrity of Data Import to TPS” (page 313).
6. TG-148 also recommends an annual end-to-end test of the entire patient workflow in a phantom to check the imaging and treatment coordinate coincidence. See “Phantom Based End-to-End Test” (page 372).
7. TG-148 recommends using an external service for independent dose verification via TLDs on an annual basis. See TG-148 Section V.B.5.c.

## ◆ TG-51 Dose Calibration

As discussed in the Commissioning Overview section, the TG-51 protocol is not directly applicable to the treatment system. Appendix A of TG-148 is a step-by-step worksheet with the appropriate modifications for measuring static and rotational output.

The static output should be determined for a 5 cm x 10 cm field size in a water tank. You will need to create your own XML file for this procedure, similar to the XML procedure described in “XML for Static Output and Beam Quality Baseline” (page 271). The Accuray *Precision* System does not calculate the expected output for a procedure with a static couch and static MLC. After you follow the steps in TG-148 Appendix A to measure the dose per minute for a static field at 10 cm depth and at  $d_{max}$ , there is no expectation value against which you can compare your measurement. Thus, the static measurement will not be used to adjust the machine or determine how well it is calibrated. TG-148 acknowledges that the use of this static output measurement is limited, but considers the exercise worthwhile for determining a basic beam parameter and for satisfying state regulations.

The rotational output should be determined in the *Tomo*-phantom, in a plan similar to the *TomoHelical*-phantom plan with the 5 cm field width. TG-148 specifies that the ion chamber measurement, when converted to dose according to the formalism described in TG-148 Appendix A, should agree with the planned dose to within  $\pm 1\%$ . See TG-148 Section V.B.5.b for details.

## ◆ Phantom Based End-to-End Test

This test verifies the geometry of the end-to-end process of patient treatment. See Section VI.B.1.b of TG-148.

The test may be performed in the *Tomo*-phantom or an array device, and the steps should include:

1. Scan the phantom, e.g., on your CT simulator.
2. Plan the phantom on the *Precision* Treatment Planning System.
3. Set up the phantom on the treatment couch.
4. Acquire a *CTrue* setup verification image.
5. Register the *CTrue* image to the planning image.
6. Apply registration results.
7. Treat the phantom, while measuring the dose distribution with film or an array device.
8. Compare the measured versus planned dose distributions, with special attention to the position of the dose distribution.

The tolerance for the treatment and imaging coordinate coincidence is 2 mm if the system is not used for SRS or SBRT, or 1 mm if the system is used for SRS or SBRT.

# QA Tests for Special Modalities

This chapter outlines ongoing QA expectations for the *TomoDirect* and *TomoEDGE* treatment modalities.

The TG-148 protocol was written while *TomoDirect* was still new, and *TomoEDGE* had not yet been released. Thus, TG-148 does not address QA of the *TomoDirect* and *TomoEDGE* treatment modalities. Accuray has extended the recommendations of TG-148 to test the unique features of the *TomoDirect* and *TomoEDGE* modalities.

Throughout this user guide, *TomoDirect* and *TomoEDGE* modality information is included along with *TomoHelical* modality information. *TomoDirect* and *TomoEDGE* information is included in the chapters on Commissioning, Quality Assurance Recommendations, and Beam Model and Algorithms. Some of the key concepts are also mentioned here for completeness.

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- ◆ TomoEDGE . . . . . 374

## ◆ *TomoDirect*

The *TomoDirect* feature is introduced in System Overview chapter, with further discussion in “Physics Considerations for TomoDirect Treatments” (page 103).

## Annual IMRT Dose Verification

The section “Absolute Dose Calibration” (page 211) includes instructions for IMRT dose verification of *TomoDirect* plans using the *TomoDirect*-phantom patient provided by Accuray. Absolute dose calibration of the machine should be based on the helical plans only, but the *TomoDirect*-phantom measurements should be within their tolerance of  $\pm 3\%$  and  $\pm 3$  mm of the calculated dose.

## Quarterly Static Star Shot

See “Static Star Shot” (page 294) for instructions for performing the static star shot film test. Accuray Incorporated recommends that a site Physicist performs this test quarterly and after any service event that includes the recalibration of the gantry positioning system.

## Monthly Completion Procedure Film

The “Monthly QA” (page 348) section includes instructions for comparing a treatment delivery for a plan delivered completely in one fraction, versus an interrupted and completed film. The test can be extended to include a *TomoDirect* plan, as well as a helical plan.

## Patient QA

Patient-specific QA should be performed for all *TomoDirect* plans.

It is recommended to perform patient QA compositely for all the beam angles in your *TomoDirect* plan. However, if you wish to QA individual beam angles, a **Save Dose Per Angle** option is available.

It is possible for fluence in the beam expansion (flash) region to become large, yet have little effect on the patient dose. Therefore, your patient QA measurement should include both the target and any beam expansion region beyond the target.

### ◆ *TomoEDGE*

Instructions for routine QA of the dynamic jaws are included in “Quality Assurance Recommendations and Tests” (page 334):

- Annual water tank data collection and monthly longitudinal profile verification should include the additional field widths in the dynamic jaws beam model.



**NOTE:** For monthly QA in Virtual Water, the **TQA Field Width - Dynamic Jaws** module facilitates collection of all the monthly longitudinal profiles in one procedure.

- IMRT dose calibration includes plans for both fixed jaws and dynamic jaws.



**NOTE:** As explained in “Absolute Dose Calibration” (page 211), there are five *TomoHelical* plans and five *TomoDirect* plans.

- For automatic verification of the performance of the dynamic jaws, run the **TQA Daily QA** module each day, and run the **Jaw Sweep - Dynamic Jaws TQA** module each month.



**NOTE:** The **TQA Daily QA** module does not include all of the TG-148 recommended tests for daily QA, but it is a quick way to get a large number of metrics on the performance of your system.

# Post-Service QA

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## ◆ Introduction

This chapter outlines post-service QA responsibilities for the site physicist. For certain types of parts replacements that are likely to affect the system alignment, a service representative runs a limited set of post-service tests prescribed by Accuray. These tests are intended to restore the alignment of the system to Accuray specifications. Where applicable, a service representative may also perform basic tuning of the beamline using a rotational variation procedure. As discussed in “Monthly QA” (page 348), the rotational variation procedure may be used to adjust the system output and energy for consistency with the site specific reference for monitor chamber count rates and CT detector profile shape.



**IMPORTANT:** The site physicist should not rely on the results of the service representative for post-service QA. The service representative is not a qualified radiation oncology physicist. The service representative may check the consistency of monitor chamber counts against the site specific reference, but the service representative does not perform absolute dose verification with an ion chamber against the values in the treatment planning system. After the machine is serviced, the site physicist should independently run all applicable post-service physics tests.

The service representative will inform the site physicist when service work is completed. When the service representative has completed their service and testing, the site physicist must perform tests to determine if the machine is in an appropriately commissioned state for delivering patient treatments. The site physicist may request that the service representative make adjustments as indicated by the results of the physics QA. The site physicist would then need to verify the adjustment with additional checks.



**IMPORTANT:** Accuray Incorporated does not determine when a machine is ready to treat patients. This is the decision of the site physicist.

This chapter focuses primarily on system repairs. Accuray typically provides specific QA recommendations if there is a major system upgrade. Post-service QA tasks are at the discretion of the site physicist. Table VI of TG-148 provides a minimal set of recommendations in the event of replacement of the magnetron/SSM, LINAC/target, jaw hardware, or MLC.

The site physicist should talk with the service representative and/or Accuray Customer Support to determine which aspects of the system may have been impacted by the service, then perform QA of those aspects. The next section provides some questions to help guide your conversation with the service representative.

## ◆ Post-Service Considerations

The following list of questions is not exhaustive, but will help to determine some relevant QA tests for the most common service events. The relevant tests should be performed for all applicable questions for which the answer is “yes”; most services will include more than one category.

The following is a minimal set of recommendations. Additional tests may be required according to the specific service performed and the discretion of the site physicist.

### Were the jaws, MLC, or LINAC moved?

Movement of the LINAC, MLC, or jaws includes replacement of these components, or temporarily removing them to access other components. For example, the MLC must be temporarily removed to access the jaws for service.

The site physicist should perform the following tests of the system alignment:

- “MLC Tongue and Groove (MLC TG)” (page 122)
- Jaw Shift Test for a system without dynamic jaws (“Jaw Shift” (page 127)), or **TQA Jaw Sweep - Dynamic Jaws** module for a system with dynamic jaws
- “Beam Planarity” (page 136)
- “Field Center vs. Jaw Setting” (page 181) (if the jaw hardware was serviced)
- “MLC Center of Rotation (COR)” (page 176) (if the MLC was moved or replaced)
- “Longitudinal Profiles in Virtual Water” (page 362)

Some results are inter-dependent (especially the beam planarity and longitudinal profiles), so all results should be confirmed to be passing after the final adjustment is made.



**IMPORTANT:** If you use the Delivery Analysis software, run the Delivery Analysis calibration plans after a LINAC replacement.



**NOTE:** A slight change in the beam alignment, even if the system alignment is within tolerance before and after the service, may result in spikes in the plot of exit detector ratios, as discussed in “Transverse Profile” (page 355). This generally does not indicate a problem with the system.

## Were any changes made that could impact the beam dose, energy, or spot size?

If a service representative tuned the beamline, or if components involved in producing or collimating the beam (e.g., LINAC, magnetron, jaws) were replaced, the site physicist should perform the following:

- Monthly Beam Parameter verification, as outlined in “Beam Parameters” (page 349) table.
- Re-run one or more patient QA plans to ensure that they still pass.
- The imaging and treatment beams have separate tuning parameters. A LINAC or magnetron replacement would impact both the imaging and treatment beams. If the imaging beam may have been affected (due to tuning of the imaging beam or a parts replacement), the site physicist should additionally perform MVCT imaging dose verification, as discussed in “CTrue Image Quality Verification” (page 243). Also verify the MVCT density model, if you are calculating dose on *CTrue* images.



**TIP:** If the CT Number Calibration is unsuccessful because of a large change in CT numbers, contact Accuray Customer Support for assistance. After a service event, it might be necessary for the service representative to adjust the CT number scaling parameters manually.

## Were the dose monitor chambers or Detector Acquisition System replaced?

After replacing the monitor chambers or Detector Acquisition System, the service representative will need to re-calibrate the dose control system and set the dose interlocks.

Afterwards, you should:

- Perform monthly QA of the static output, rotational output, and beam quality as discussed in “Beam Parameters” (page 349).
- Re-run a few patient QAs to ensure they still pass.
- Calibrate the monitor unit display as discussed in “Monitor Unit Display Calibration” (page 257).
- Update *TQA* references for modules that involve constancy checks of monitor chamber data (**Basic Dosimetry**, **Daily QA**, **Step Wedge Static**, and **Step Wedge Helical** modules). New references should be created at a time when the system is verified to be in a well-commissioned state.

## Was the on-board MVCT detector moved or replaced?

Perform *CTrue* image QA as outlined in “*CTrue* Image Quality Verification” (page 243). Verify the density model if you are calculating dose on *CTrue* images. Verify the MVCT density model if you are calculating dose on *CTrue* images.

You may also need to update *TQA* references for modules that involve constancy checks of detector data (**Basic Dosimetry**, **Daily QA**, **Step Wedge Static**, and **Step Wedge Helical** modules), if the modules are failing after the detector replacement. New references should be created at a time when the system is verified to be in a well-commissioned state.



**NOTE:** A slight change in the detector position, even if the system is still within tolerance, may result in spikes in the exit detector ratio plots, as discussed in “Transverse Profile” (page 355). This generally does not indicate a problem with the system.



**IMPORTANT:** If you use the Delivery Analysis software, run the Delivery Analysis calibration plans after a detector replacement.

## Was there a change to the MVCT reconstruction?

For minor changes, such as flagging a bad channel not to be used for reconstruction, it may be sufficient to simply review a *CTrue* image and ensure that it is acceptable.

For more substantial changes, perform *CTrue* image quality verification, as discussed in “*CTrue* Image Quality Verification” (page 243). Also, verify the MVCT density model, if you are calculating dose on *CTrue* images.

## Was the couch alignment adjusted?

Perform couch alignment verification per “Couch Alignment Tests” (page 166). The results of the couch alignment tests are sensitive to the accurate positioning of the green lasers.

## Was the gantry positioning system re-calibrated?

Run the static star shot test (“Static Star Shot” (page 294)) to ensure that the static gantry angles are correct. If desired, you may perform additional quarterly QA tests to verify system synchronicity.

## Were the lasers adjusted?

Perform the appropriate subset of tests in “Couch Alignment Tests” (page 166). Adjustments to a single laser parameter may need to be accompanied by adjustments to other related parameters.

## Was the machine data changed on the Treatment Delivery Console?

The answer to this question will be “Yes” for most major parts replacements. Ensure that you understand the reason for the change and the impact on the system.



**WARNING:** With the exception of the monitor unit display calibration parameters (see “Monitor Unit Display Calibration” (page 257)), machine data adjustments should only be performed by a qualified Accuray Service Representative.

- Improper adjustments can have harmful consequences on machine performance and hardware.
- Improper adjustments can result in a discrepancy between planned and delivered dose that can cause patient injury or death.
- Adjustments may render the machine unable to run treatment procedures until a service representative recalibrates the DCS.



**IMPORTANT:** The physicist should communicate with the service representative to understand any machine data changes that were made, and perform appropriate QA.

### Machine Revision Number and Beam Revision Number

The system keeps track of all changes in the **Edit Machine Area** by incrementing a counter called the **machine revision number**. In addition, the system keeps track of the subset of machine data changes that impact plan calculations by incrementing another counter called the **beam revision number**. The **treatment beam revision number** associated with a particular plan is displayed in most plan lists within the Accuray Precision™ Treatment Planning System. The current values of the **beam revision number** and **machine revision number** can be determined from the System Report (generated from iDMS Report Administration).

All changes in the **Edit Machine** area cause the machine revision number to be incremented, except for Air Scan and machine name. A subset of these changes also cause the beam revision number to be incremented.

#### 1. Changes that do not affect the beam revision number.

This category includes adjustments intended to be made by a qualified FSE to keep the system performing consistently with the beam model. While some of these changes impact beam delivery, they do not affect planning calculations. Examples of service activities in this category include:

- Tuning the beamline
- Adjusting the output or energy
- Re-calibrating the dose control servo

- Adjusting the dose interlock settings
  - Re-calibrating the monitor unit display
  - Re-calibrating the gantry positioning system
  - Adjusting the jaw encoder values to correct for a failing beam planarity test result, or to make longitudinal field widths consistent with reference data.
  - Updating the MVCT reconstruction properties, or updating the list of bad detector channels that will not be used for image reconstruction
2. Changes that increment the beam revision number.

Examples of service activities in this category include:

- Changing the couch lateral offset to reflect the installed couch position
- Changing any of the beam model parameters: EFiOT, cone, penumbras, Fluence Attenuation Table, scatter kernel, jaw to field, jaw field specifications, leaf edges, leaf filters, leaf latency, Leaf Fluence Output Factors, center of rotation, and Jaw Fluence Output Factors

### Beam Change Dialog

On the Treatment Delivery Console, a **Beam Change Dialog** box will appear if the machine revision number has changed and the changes have not yet been reviewed by a physicist. This dialog box lists the parameters that were changed, with their old and new values. The **Beam Change Dialog** includes all changes in the **Edit Machine** area and must be acknowledged before you can proceed with treating the patient. Check the **Reviewed** box on each tab, click **Accept**, and enter your credentials. The **Beam Change Dialog** box can be temporarily dismissed with a therapist password each time you open a patient, but only a physics user ID and password will permanently dismiss the dialog.



**TIP:** After a physicist accepts the **Beam Change Dialog** box, the list of old and new values will no longer be available on the TDC. It is recommended to print the changes for your record, prior to dismissing the dialog. The System Report (iDMS™ Data Management System > **Report Administration** > **System Report**) records the dates when changes were made, but does not list the parameters that were changed.

Some parameters in the **Beam Change Dialog** box point to other file locations, or contain lists of numbers. The site physicist does not have tools to directly verify all the values of the updated data in the software, which are maintained by the FSE.

The **Beam Change Dialog** box sorts machine revision changes into two categories and places them on separate tabs labeled **Machine changes** and **Beam changes**. The **Machine changes** tab includes all **Edit Machine** changes except those in the **Beams** folder in the **Edit Machine** area. The

**Beam changes** tab contains changes in the **Beams** folder in the **Edit Machine** area. A subset of **Machine changes** and a subset of **Beam changes** will also trigger a beam revision change.

After accepting the **Beam Change Dialog** box message:

- If the **Machine Revision** number was changed but the Beam Revision Number was not changed, the TDC allows you to proceed with treating the patient.
- If the **Beam Revision Number** was changed, you will need to transfer the plan or mark equivalent before you can treat the patient.



**IMPORTANT:** If you use the *Delivery Analysis* software, run the *Delivery Analysis* calibration plans after a beam data change.



**TIP:** After verifying machine data changes, a physicist can proactively access the **Beam Change Dialog** from the TDC Tools menu (**Review Beam Changes**), and acknowledge the **Beam Change Dialog** with a physics password so that the message does not appear for future patient treatments.



**IMPORTANT:** If the beam data has been updated, re-calculate the *Tomo-phantom* plans before running them again (e.g., for annual QA). See “Absolute Dose Calibration” (page 211) and “When to Re-Plan the Tomo-Phantom Set” (page 221).



**NOTE:** Running the CT Number calibration procedure increments the machine revision and forces you to review the Beam Change Dialog when opening patients. The site physicist could proactively review and approve the beam change dialog after running a CT Number calibration. To access the Beam Change Dialog open a patient or go to Tools > Review Beam Changes.

### Impact of Incrementing the Beam Revision Number

After the **treatment beam revision number** is incremented, plans calculated before the machine data change are no longer deliverable. If you want to enable a plan that was calculated before the change to be delivered on the machine after the change, you must use the **Plan Transfer** task on the *Accuray Precision* System to authorize the same plan for delivery on the current system (**Mark as Equivalent** workflow), or put the plan through **Self Transfer** to generate a similar plan that accounts for the machine data changes. Delivery instructions for plans created prior to the beam revision are not updated to account for the new beam data unless you perform **Self Transfer**.

If a plan was not yet approved when the **treatment beam revision number** was updated, you will have the option to finish creating the plan on the current **beam revision number** (in this case the plan will not be deliverable until you run **Self Transfer** or **Mark as Equivalent**), or you can update the plan data to use the new **beam revision number** (this will cancel the plan optimization and dose calculation).

### Beam Revisions and Patient QA Plans

When you select a patient QA plan on the TDC, if the beam revision of the patient QA plan does not match the current beam revision, a message will appear to alert the user that the beam calculation data has changed since the patient QA plan and associated treatment plan were created. Running the original patient QA plan may be useful after an MLC replacement to measure the impact of latency changes on dose delivery, and to determine whether the plan may be marked equivalent. However, if the beam revision of the patient QA plan does not match the current beam revision of the patient plan, the patient QA plan should no longer be used. For example, if the patient plan is transferred, the old patient QA plan should no longer be used.



**IMPORTANT:** The Treatment Delivery Console permits inconsistent patient QA plans to be delivered. The site physicist is responsible for keeping track of system changes and determining if it is appropriate to use an old patient QA plan.



**IMPORTANT:** Following a beam revision, new plans will be calculated on the new beam data. Patient QA plans should be used to verify the delivered dose distribution for each new plan.



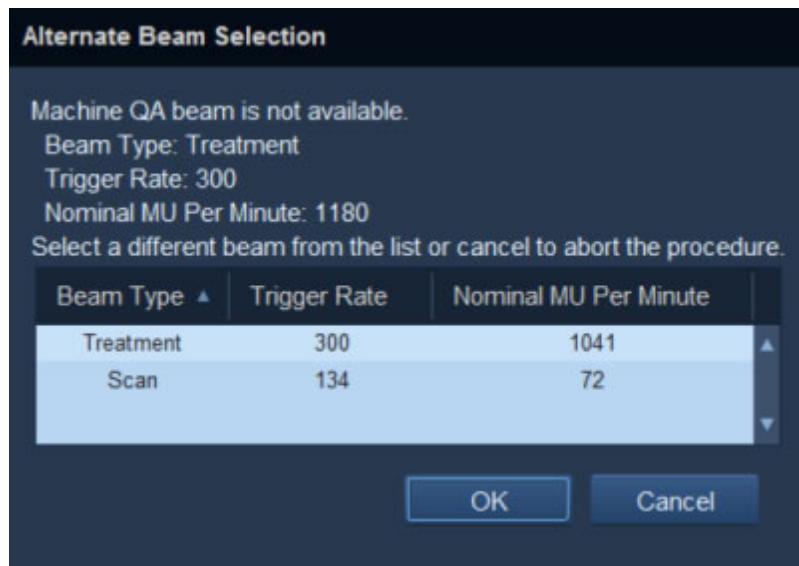
**IMPORTANT:** Repeat patient QA measurements to evaluate the dosimetric impact of the machine performance changes on plans created prior to the beam revision. Do not mark the plan as equivalent unless the dosimetric impact is acceptably small.



**NOTE:** After performing a **Machine Transfer** or **Self Transfer**, the associated patient QA plan(s) are not transferred along with the patient plan. Thus, you will need to create a new patient QA for the new transferred plan.

### Alternate Beam Selection Dialog

Machine QA procedures do not involve dose calculations. Thus, they may be run after a change in the machine and beam revision numbers. If the **Beam Type**, **Trigger Rate**, or **Nominal MU per Minute** has changed in the **Edit Machine** area, every time you open a machine QA procedure, the **Alternate Beam Selection** dialog box appears, allowing you to select the appropriate current beam to continue using the procedure.



This dialog appears when loading a machine QA procedure that was created for a beam that does not exist. For instance, the user may have entered the pulse rate incorrectly, or the beam may have since been decommissioned.



**WARNING:** If the **Alternate Beam Selection** dialog box appears, the reason for the change should be investigated. The **Beam Type**, **Trigger Rate**, and **Nominal MU per Minute** should not be changed on a clinical machine. Changing these values may result in damage to the machine. Changing beams used for patients may also result in incorrect dose to patients.



**CAUTION:** If the **Alternate Beam Selection** dialog box appears and you have determined that it is OK to proceed, be sure to choose the correct beam type to avoid invalid QA. For example, do not choose **Scan** for QA of the treatment beam.

## Was the MLC planning data updated?



Leaf latency, leaf fluence output factors, leaf filters, and MLC center of rotation are typically updated in the software by a service representative after a service that involves replacement of the MLC or movement of the LINAC or MLC.

**NOTE:** An MLC valve replacement may or may not require the MLC to be temporarily removed. It depends on the position of the valve that needs to be replaced.

Patients planned after the MLC data change will be verified by performing patient QA measurements. Special consideration is needed for patients who were planned on the old MLC data but will be treated on the new MLC.

The MLC supplemental form (“MLC Supplemental Form” (page 384)) provides an indication of the estimated change in delivered fluence for a plan created and approved with the previous MLC but delivered with the replacement MLC, based on latency differences. This form is useful for estimating the magnitude of the change, but is not a substitute for measurements.

The most thorough way to evaluate the dosimetric impact for patients planned on the old MLC data and delivered on the new MLC is by measurements. Re-run patient QAs on the new MLC, and/or re-run the pre-treatment QA for the Delivery Analysis software (purchasable option).

## **Were the Jaw Fluence Output Factors updated?**

Jaw Fluence Output Factors are rarely updated, but may be updated at the time of a major feature upgrade, or by request of the site physicist. See “Absolute Dose Calibration” (page 211), “Request JFOF Adjustment” (page 241), and “Beam Model” (page 412).

## **Were any of the DoseCom Twinnable parameters updated?**

If the beam model update includes changes to parameters in addition to the MLC data and Jaw Fluence Output Factors (i.e., if the beam model update includes the DoseCom Twinnable parameters discussed in “Beam Model” (page 412)), it will be necessary to re-commission the machine. An update to the DoseCom Twinnable parameters is very rare, but may occur at the time of installation of major new features. Individual cases should be discussed with Accuray Physics Support.

### **◆ MLC Supplemental Form**



**IMPORTANT:** The MLC Supplemental Form is not a substitute for patient QA checks and/or other quality assurance established by the site physicist.

Plan calculations include delivery instructions that account for the MLC-specific latency, LFOF, and leaf filter data in the beam model. The MLC properties in the beam model are discussed in “Beam Model” (page 412).

In the event of an MLC replacement, latency and leaf filters for the new MLC are measured and installed by a service representative for use in subsequent treatment planning. However, the old plans are not automatically updated for the new MLC properties. When plans with delivery instructions intended for the old MLC are marked as equivalent and delivered on the new MLC, there is a potential for dose discrepancies. Latency differences between the new and old MLC are usually the dominant contributor to dose discrepancies.

Sometimes, two MLCs have very similar latency values, and sometimes they are very different. The site physicist's decision of how to handle plans under treatment in the event of an MLC change should account for the amount of difference between the specific old and new MLCs. To assist the site physicist in characterizing the similarity or differences between two MLCs, the Accuray service representative provides the customer with an MLC Supplemental Form after the MLC replacement is completed.

The table in the MLC Supplemental Form provides an indication of the estimated change in delivered fluence for a plan created and approved with the previous MLC but delivered with the replacement MLC (i.e., if **Mark as Equivalent** is used). This is estimated from a comparison of the latency responses of the respective MLCs and tabulated as a function of modulation factor and gantry period or maximum leaf open times per projection. This result does not substitute patient QA checks and/or any other quality assurance established by the site physicist.

For *TomoHelical* plans, the maximum leaf open time may be determined from the leaf open time histogram.

For *TomoDirect* plans, the gantry period is not relevant. Determine the *pitch [cm/projection]* and *couch speed [cm/s]* for each beam from the Plan Report. The projection time in milliseconds for a *TomoDirect* plan may be determined as: *projection time = 1000 \* pitch/couch speed*. For projection times greater than 230 ms, the maximum leaf open time is approximately equal to the projection time. For projection times equal to 230 ms, the maximum leaf open time may be smaller than the projection time. The table includes a limited range of maximum leaf open times. Estimated errors are higher for smaller maximum leaf open times.

Refer to the example MLC Supplemental Form below. Estimated fluence differences may range from less than 1% for two MLCs that are very similar, to more than 10% for two MLCs that are very different. The fluence differences tend to be more severe when the maximum leaf open time or gantry period is small and the modulation factor is large.

JAM Update T-PSC-HB0021, Rev D																	
Estimated Fluence Difference																	
Actual Modulation Factor		1	1.2	1.4	1.6	1.8	2	2.2	2.4	2.6	2.8	3	3.2	3.4	3.6	3.8	4
Gantry Period (seconds)	Max Leaf Open Time (ms)																
13	255	-0.21%	-0.36%	-0.50%	-0.65%	-0.80%	-0.94%	-1.09%	-1.24%	-1.38%	-1.53%	-1.67%	-1.82%	-1.97%	-2.11%	-2.26%	-2.41%
14	275	-0.32%	-0.43%	-0.53%	-0.64%	-0.75%	-0.85%	-0.96%	-1.06%	-1.17%	-1.28%	-1.38%	-1.49%	-1.59%	-1.70%	-1.81%	-1.91%
15	294	-0.46%	-0.53%	-0.60%	-0.67%	-0.74%	-0.81%	-0.89%	-0.96%	-1.03%	-1.10%	-1.17%	-1.24%	-1.31%	-1.38%	-1.45%	-1.52%
16	314	-0.49%	-0.54%	-0.60%	-0.65%	-0.70%	-0.76%	-0.81%	-0.87%	-0.92%	-0.98%	-1.03%	-1.09%	-1.14%	-1.20%	-1.25%	-1.30%
17	333	-0.46%	-0.51%	-0.55%	-0.60%	-0.65%	-0.69%	-0.74%	-0.78%	-0.83%	-0.88%	-0.92%	-0.97%	-1.01%	-1.06%	-1.11%	-1.15%
18	353	-0.44%	-0.48%	-0.52%	-0.56%	-0.60%	-0.64%	-0.67%	-0.71%	-0.75%	-0.79%	-0.83%	-0.87%	-0.90%	-0.94%	-0.98%	-1.02%
19	373	-0.43%	-0.46%	-0.49%	-0.52%	-0.56%	-0.59%	-0.62%	-0.65%	-0.68%	-0.71%	-0.74%	-0.78%	-0.81%	-0.84%	-0.87%	-0.90%
20	392	-0.42%	-0.44%	-0.47%	-0.49%	-0.52%	-0.54%	-0.57%	-0.60%	-0.62%	-0.65%	-0.67%	-0.70%	-0.72%	-0.75%	-0.77%	-0.80%
21	412	-0.40%	-0.43%	-0.45%	-0.48%	-0.50%	-0.53%	-0.55%	-0.58%	-0.60%	-0.63%	-0.65%	-0.68%	-0.70%	-0.73%	-0.75%	-0.78%
22	433	-0.38%	-0.41%	-0.43%	-0.46%	-0.49%	-0.52%	-0.55%	-0.58%	-0.60%	-0.63%	-0.66%	-0.69%	-0.72%	-0.75%	-0.77%	-0.80%
23	453	-0.35%	-0.39%	-0.42%	-0.45%	-0.48%	-0.51%	-0.54%	-0.57%	-0.60%	-0.63%	-0.67%	-0.70%	-0.73%	-0.76%	-0.79%	-0.82%
24	473	-0.33%	-0.36%	-0.40%	-0.43%	-0.46%	-0.50%	-0.53%	-0.56%	-0.60%	-0.63%	-0.67%	-0.70%	-0.73%	-0.77%	-0.80%	-0.84%
25	490	-0.30%	-0.34%	-0.37%	-0.41%	-0.45%	-0.48%	-0.52%	-0.56%	-0.59%	-0.63%	-0.66%	-0.70%	-0.74%	-0.77%	-0.81%	-0.85%
30	588	-0.27%	-0.30%	-0.34%	-0.37%	-0.41%	-0.44%	-0.47%	-0.51%	-0.54%	-0.57%	-0.61%	-0.64%	-0.68%	-0.71%	-0.74%	-0.78%
35	686	-0.25%	-0.28%	-0.31%	-0.33%	-0.36%	-0.39%	-0.42%	-0.45%	-0.48%	-0.51%	-0.54%	-0.57%	-0.60%	-0.63%	-0.66%	-0.69%
40	784	-0.23%	-0.25%	-0.28%	-0.31%	-0.33%	-0.36%	-0.38%	-0.41%	-0.43%	-0.46%	-0.49%	-0.51%	-0.54%	-0.56%	-0.59%	-0.61%
50	980	-0.18%	-0.20%	-0.22%	-0.24%	-0.25%	-0.27%	-0.29%	-0.30%	-0.32%	-0.34%	-0.35%	-0.37%	-0.39%	-0.40%	-0.42%	-0.44%
60	1176	-0.17%	-0.18%	-0.20%	-0.21%	-0.22%	-0.24%	-0.25%	-0.26%	-0.28%	-0.29%	-0.31%	-0.32%	-0.33%	-0.35%	-0.36%	-0.37%

12-second gantry period table																	
Actual Modulation Factor		1	1.2	1.4	1.6	1.8	2	2.2	2.4	2.6	2.8	3	3.2	3.4	3.6	3.8	4
Max Leaf Open Time (ms)																	
235		-0.13%	-0.33%	-0.52%	-0.72%	-0.91%	-1.10%	-1.30%	-1.49%	-1.68%	-1.88%	-2.07%	-2.27%	-2.46%	-2.65%	-2.85%	-3.04%
200		-0.30%	-0.53%	-0.76%	-0.99%	-1.21%	-1.44%	-1.67%	-1.90%	-2.13%	-2.35%	-2.58%	-2.81%	-3.04%	-3.26%	-3.49%	-3.72%
150		-0.58%	-0.99%	-1.29%	-1.59%	-1.90%	-2.20%	-2.51%	-2.81%	-3.11%	-3.42%	-3.72%	-4.02%	-4.33%	-4.63%	-4.94%	-5.24%
100		-1.44%	-1.90%	-2.35%	-2.81%	-3.26%	-3.72%	-4.18%	-4.63%	-5.09%	-5.54%	-6.00%	-6.45%	-6.91%	-7.36%	-7.82%	-8.28%

N.B.: 235 ms projection time = 12 s gantry period

### Example of MLC Supplemental Form



**NOTE:** The numbers in the above figure are for illustration only. Actual differences between any two MLCs may be greater or smaller than this example.

## How the Dose Differences in the MLC Supplemental Form are Estimated

Consider two MLCs, MLC #1 and MLC #2.

If we program a leaf to open for an amount of time equal to  $x$ , using MLC #1, we would deliver a Leaf Open Time (LOT) of:

$$(1) \text{LOT} = m_1x + b_1$$

Ideally, the slope  $m_1$  would be 1, and the intercept  $b_1$  would be 0, but in practice, the slope and offset differ from one MLC to another. Through empirical analysis, it was determined that setting the slope to 1 and measuring the offsets for each MLC resulted in the most reliable delivery characteristics. These offsets are measured by a service representative and used to adjust delivery instructions.

The error in leaf open times between two MLCs characterized by offsets ( $b_1, b_2$ ) is:

$$(2) \text{LOT Error} = b_2 - b_1$$

In terms of % error, Equation (2) is divided by the planned leaf open time,  $x$ , and becomes:

$$(3) \% \text{Error} = 100\% * (b_2 - b_1) / x$$

The results of the previous analysis can be expanded to the case of an entire sinogram where we have a sequence of programmed leaf open times:

(4):

$$\%Error = 100\% * \frac{\sum_i^N (b_2 - b_1)}{\sum_i^N x_i}$$

This reduces to:

$$\%Error = 100\% * \frac{(b_2 - b_1) \sum_i^N}{\sum_i^N x_i}$$

$$\%Error = 100\% * \frac{(b_2 - b_1) N}{\sum_i^N x_i}$$

$$\bar{x} = \frac{\sum_i^N x_i}{N}$$

$$\%Error = 100\% * \frac{(b_2 - b_1)}{\bar{x}}$$

The modulation factor MF is defined as the ratio of the maximum to average leaf open time for the used leaves, so the average leaf open time is:

$$x_{average} = x_{max}/MF$$

and we have:

$$(6) \%Error = 100\% * (b_2 - b_1) * MF / x_{max}$$

For a helical plan,  $x_{max}$  may be determined from the leaf open times histogram. For a *TomoDirect* plan,  $x_{max}$  may vary from beam to beam.

The projection time in milliseconds for a helical plan is:

$$(7) \text{ Helical projection time} = 1000 * GP / 51,$$

where  $GP$  is the gantry period in seconds.

The projection time in milliseconds for a *TomoDirect* beam angle is:

$$(8) \text{ TomoDirect projection time} = 1000 * \text{pitch/couch speed}.$$

For projection times greater than 230 ms,  $x_{max}$  is approximately equal to the projection time. For plans or beams with projection times equal to 230 ms, the  $x_{max}$  may be smaller than the projection time.

Assuming that the total percent error in the leaf open times is equal to the total dose error, Equation (6) provides a rough estimate of the dose differences between two MLCs as a function of modulation factor and gantry period.

Equation (6) is only an estimate to help the site physicist identify plans that may be more susceptible to MLC latency differences. Actual dosimetric differences depend on the specific MLC sinograms.

## ◆ Self Transfer

The **Plan Transfer** task on the *Precision Treatment Planning System* includes workflows for **Machine Transfer** and **Self Transfer**. **Machine Transfer** allows the transfer of patient treatment plans between treatment systems on the same database. **Self Transfer** is used to account for changes in machine data on the same machine.

If a patient was planned on one machine, but subsequently the machine data was modified in a way that could impact the delivery, the **Self Transfer** workflow could be used to generate a similar plan that takes into account the new machine properties. The original plan is discontinued.

The Plan Transfer algorithm is described in “Plan Transfer Algorithm” (page 467). Workflow instructions are located in the *iDMS Manual*.

The **Plan Transfer** tools do not include a dose comparison of the original plan calculated with the new versus old **beam data**. However, if you perform **Machine Transfer** or **Self Transfer** to generate a similar plan that accounts for the machine data changes, a review tool is available to compare the dose calculation from the original plan to the dose calculation of the transferred plan. After reviewing the transferred plan, you can approve it for delivery or suspend the plan if it is not acceptable.



**IMPORTANT:** Plan Transfer modifies the treatment delivery instructions to account for differences in field width, output, and MLC properties. Differences in beam model profiles are taken into account during the End-of-Planning (EOP) dose calculation, but they are not used to modify the delivery instructions. Thus, the calculated dose distribution of the transferred plan should be examined by the clinician to ensure that it is satisfactory.



**IMPORTANT:** Accuray Incorporated recommends performing patient specific QA following a transfer.



## Chapter 5

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### Patient QA Plans

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# About Patient QA Plans

This chapter provides instructions on how to create patient QA plans. This section includes the following information about patient QA plans.

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## ◆ Patient QA Plans

A Patient QA plan applies the delivery instructions (couch, jaws, gantry, and MLC) from the patient treatment plan to a phantom, for dose calculation and delivery to the phantom. In a Patient QA Plan, the delivery instructions of the patient plan are applied to the phantom calculation. The Patient QA plan is then delivered to the phantom to verify that the calculated phantom dose is consistent with the measured dose.

The patient QA workflow is detailed in the following steps.

1. Create a treatment plan on the patient image. Save the plan as Deliverable or Deliverable and Authorized.
2. Acquire and import a CT scan of the phantom in the desired configuration. Do this only once for each phantom.
3. Create a QA template plan on the phantom. Do this only once for each phantom.
4. Create a patient QA plan with delivery instructions from the patient treatment plan, applied to the phantom image in the QA template plan. Optionally, export DICOM dose.
5. Run the patient QA plan to irradiate the device.
6. Analyze the results.

## ◆ About the MITA Requirement

The Medical Imaging Technology Alliance (MITA) recommends an additional approval step by the physicist for the QA. This requirement may be enabled or disabled from the Policies tab of the System Administration task on the *Accuray Precision™* Treatment Planning System. After changing this setting, it is necessary to restart the TDC software.

If you have enabled the MITA requirement physicist approval is required to make the treatment plan available for delivery to the patient. The *Accuray Precision™* Treatment Planning System software does not check that a patient QA plan was created or that the patient QA results passed, it only checks that the physicist marked the plan as approved.

To assign the approval for a particular plan, go to the **Plan Administration** task on Precision System and choose your deliverable plan. Click on the **Transferred Plans** tab, then click the **Physicist Approval** icon.



**IMPORTANT:** When the MITA setting is enabled, patient plans for which the plan QA is not yet approved will not be visible from the TDC. If you cannot find your patients on the TDC, check the MITA setting for the system, and check the plan QA approval for each patient.

After performing plan QA approval, you can see the approval in the **Plan Report**. If you change your mind and want to un-approve the plan QA prior to treatment, open the plan and re-save it.

## ◆ When to Perform Patient Plan QA

Patient QA should be performed for all patient plans and all treatment modalities. Accuray Incorporated recommends performing Patient QA for 3DCRT and forward planning as well as IMRT plans because the MLC leaves move for all types of plans during treatment delivery.

Patient QA should also be performed in the event of plan transfer to another machine or self-transfer to take into account beam model changes.



**IMPORTANT:** If **MITA Policies** are enabled in the iDMS™ Data Management System, a Physicist must approve plan QA before the plan can be delivered. Unapproved patient plans will not appear in the patient list.



**WARNING:** For patient quality assurance procedures, Accuray Incorporated recommends that absolute dose measurement devices, such as a calibrated ion chamber, be used in addition to devices that sample the relative distribution in a plane, such as film. Failure to evaluate both the absolute dose and the dose distribution may result in patient mistreatment.

# Creating a QA Template Plan

A QA Template plan is required before a Patient QA plan can be created. The QA template plan includes a phantom CT image (primary image) that will be used to create the Patient QA plan. A single QA Template plan can be used to create Patient QA plans for multiple patients.

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Detailed instructions for selecting and creating plans can be found in the *iDMS Manual*.

## ◆ QA Template Plan

The patient QA plan creation workflow requires a QA template plan, also known as a phantom plan or phantom template plan.

A QA template plan is a treatment plan that is optimized and calculated on a phantom. The QA template plan specifies the phantom image, VOIs, density model, density override, couch position and red laser positions for the patient QA plan.



**IMPORTANT:** Inaccurate QA results may occur if you do not select a density model that is appropriate for the phantom image volume when the phantom image volume is imported into the data server. Refer to the *iDMS Manual* for additional information.

The same QA template plan can be used to create patient QA plans for multiple patients. The patient QA plan gets its delivery parameters from the patient treatment plan. Thus, some aspects of the QA template plan are irrelevant to the patient QA plan, including: TomoHelical/TomoDirect choice, IMRT/3DCRT choice, field width, pitch, modulation factor, prescription, constraints, etc.

However, the software requires that the QA template plan be saved as deliverable before it is available for creation of patient QA plans. Because of this you will need to specify some (any) prescription and plan parameters for the QA template plan and run a final dose calculation on the QA template plan.

## Data Included in the QA Template Plan

The following parameters will be applied to the patient plan and should be chosen appropriately.

- Phantom Image: Choose an image of the phantom that will be used for patient QA measurements. When the image is imported, it must be designated as "phantom" type. See "Scan the QA Phantom" (page 402) for more information.

- VOI: Create at least one VOI. If you create VOIs for your ion chamber volumes, the dose statistics for these VOIs will be available in the patient QA plan.
- Density model: Select a density model appropriate for the phantom image.



**IMPORTANT:** Inaccurate QA results may occur if you do not select a density model that is appropriate for the phantom image. Refer to the *iDMS Manual* for additional information.



**NOTE:** A patient QA plan cannot be saved as a deliverable if it was based on sample density model data.

- Density overrides: Use density override as needed to ensure appropriate density values for the calculation.
- Couch height: Replace the couch appropriately.



**IMPORTANT:** Because the patient QA plan derives the vertical couch position from the QA template plan you must replace the couch correctly. You can replace the couch again for the patient QA plan if desired, but it is not always necessary.

- Red Laser Position: Set red laser positions appropriately for the phantom image.



**NOTE:** In the QA template plan, the red lasers are initially aligned to the phantom. In the patient QA plan the red lasers are similarly aligned to the phantom; however, you can move them if necessary.

Since the quality of the optimization and calculation on the QA template plan is irrelevant, it is convenient to calculate the QA template plan with helical 3DCRT mode, using a very low resolution calculation grid.



**NOTE:** The patient QA plan derives the lateral couch offset of the lower and upper pallets from the patient treatment plan, not from the QA template plan. This is achieved by selecting "move couch with patient" if you introduce a lateral shift to the patient during planning.

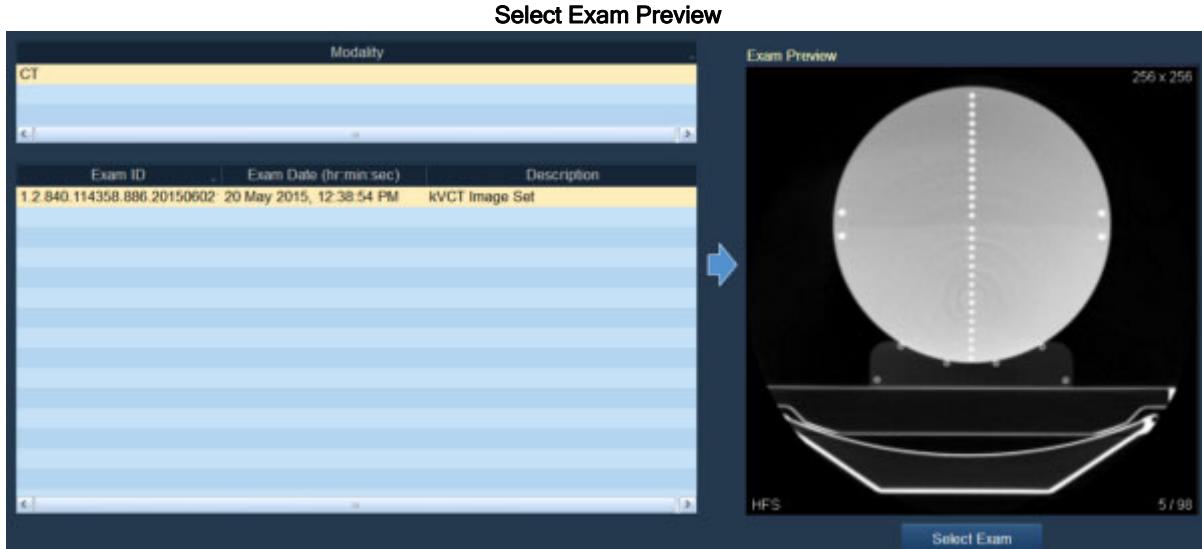
## ◆ Select a Phantom Image and Create VOIs

Complete the following instructions to select a phantom as the primary CT image for the QA Template and create VOIs.

1. Click the **New Plan** icon in the **Patients and Plans** section of the Precision System home page.
2. From the list of patients on the **New Plan** page, click the phantom that will be used to create the QA Template plan. The phantom you select must be listed as a **Phantom** in the **Type** column.
3. Under **Select Type**, click the **Standard** icon.
4. Click **Next >>** to display the **Select Exams** screen.
5. Under **Modality**, click the CT image that will be used to create the QA Template Plan.
6. The image you selected is shown in the **Exam Preview** area of the screen.
7. To include the phantom image in the QA plan, click **Select Exam**.
8. Under **Selected Exams**, the CT image you have chosen is listed. Make sure that the **Pri.** check box is selected for the primary CT.
9. Click **Next >>**. The **Select Optional Plan Template** screen is shown. Click **Ignore Template** to display the **Contour > Manual > Tools** screen.
10. Use the contour tools to create at least one VOI for the phantom. For example, contour an ion chamber collection volume.



**NOTE:** For accurate dosimetry, the ion chamber should not be included in the phantom image unless a density override is used.



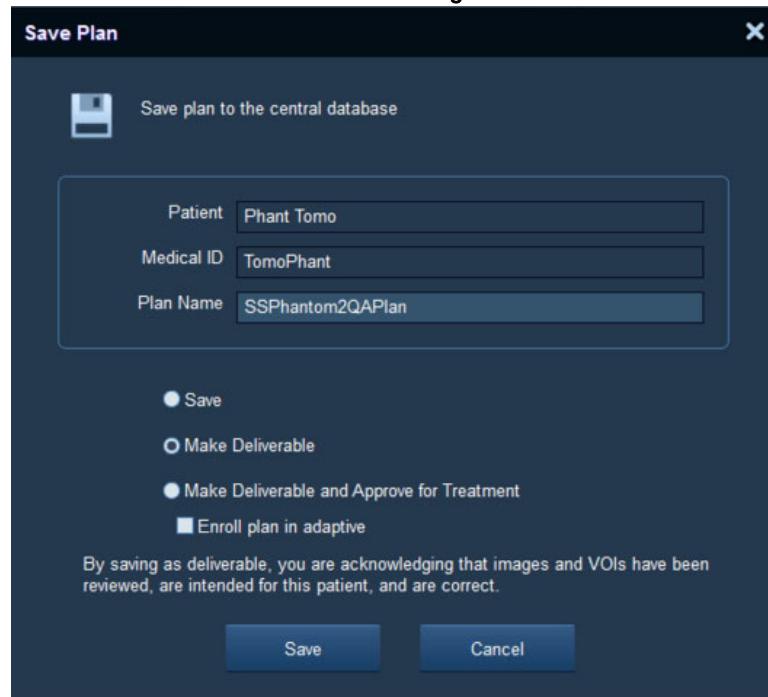
## ◆ Set Up and Save the QA Template

The workflow for patient QA plan creation requires a QA template plan that is saved as **Deliverable**. You can save time by using **3DCRT** mode (no optimization) and the very low calculation grid. The optimization and dose calculation results of the QA template plan do not affect the patient QA plan.

1. Select **Setup > Machine > Tools** and enter the following Machine Parameters:
  - **Appropriate Density Model**
  - **Treatment Machine**
  - **Delivery Mode** (choose Helical to save time)
  - **Plan Mode** (choose 3DCRT to save time)
  - **Jaw Mode**
2. Accurately replace the couch in the phantom CT image.
3. Click **Accept** when finished.
4. Click **Setup > Patient > Tools** to adjust the position of the phantom image and set the red lasers appropriately.
5. Click **Accept Red Lasers** when finished.
6. Click **Plan > Tools** to define plan parameters for the QA Template.
7. Optimize the plan and perform **Final Dose** calculations.
8. Click **Evaluate** to review the plan.
9. Click **Save Plan**.

**10. Save the QA Template as Make Deliverable.**

**Save Plan Dialog Box**



# Creating a New Patient QA Plan

To create a Patient QA plan, select a patient and a QA Template plan. The workflow includes registering the phantom image with the patient image, calculating the Patient QA plan and saving it as **Make Deliverable**.

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Detailed instructions for selecting and creating plans can be found in the *Treatment Planning Manual*.

## ◆ Select Plans and Register Images

Complete the following instructions to select a patient plan, a QA Template plan and then register the phantom image with the patient image.



**NOTE:** The primary CT image set included in the QA Template plan is used as a secondary image set for the Patient QA plan to allow registration of the phantom image with the patient image.

In the Patient QA creation workflow (where image A is the phantom and image B is the patient) the orientation label (HFS, FFS...) will correspond to phantom image A. If the phantom image and patient image have different orientations, the orientation label in the Patient QA workflow will not match the patient.

## Select a Patient Plan and QA Template

When you create a patient QA plan, the auto-registration tools provide options for aligning the patient with the phantom. You can align VOI centers, isocenters, or CT image centers.

You can also manually adjust the phantom position to place the measurement device(s) in the desired location. On the Register tab for patient QA plan creation, you will move the patient image together with the machine isocenter, relative to the fixed phantom image. For the actual delivery the machine isocenter and beam positions are fixed. By moving the patient on the Register tab of the *Accuray Precision™ Treatment Planning System* software you are designating the phantom setup position.



**IMPORTANT:** Measurements of the dose distribution should include the target as well as the beam edge, and any beam expansion (flash) region for TomoDirect™ plans.



**IMPORTANT:** Point dose measurements should be made in a low-gradient region of the delivery. The volume averaging of the chamber may cause poor agreement in a high-gradient region.

Complete the following instructions to select a patient plan, a QA template plan, and register the phantom image with the patient image.

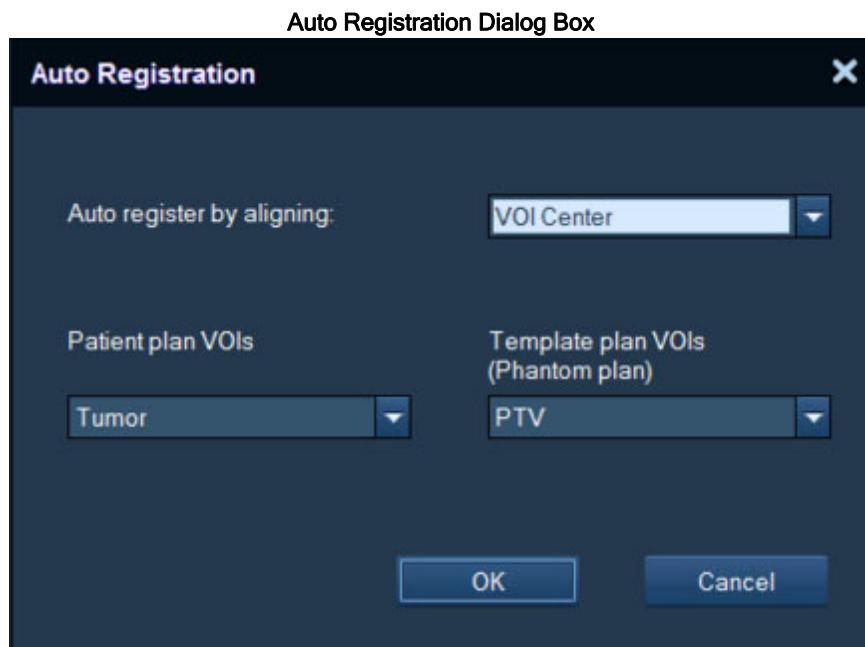
1. Click the **New Plan** icon in the **Patients and Plans** section of the *Accuray Precision™ Treatment Planning System* home page.
2. On the **New Plan** screen, click the patient that will be used to create the QA plan.
3. Under **Select Type**, click the **QA** icon.
4. Click **Next** to display the **Select a patient plan for a new QA plan** screen.
5. Click a patient plan. The patient plan you select must be listed as **Deliverable** in the **Status** column.
6. Click **Next >>** to display the **Select a template plan for a new QA plan** screen.
7. Click the phantom record for the new QA plan. The record you select must list **Phantom** for the **Type** column.
8. Under **Select Plan**, select a QA Template plan.
9. Click **Finish**.
  - The system loads the data from the patient plan and the QA template plan.
  - The **Setup > Register** screen appears with the **Auto Registration** dialog box displayed.
10. Use one of the following options to auto register the phantom image with the planning image (Refer to the *Accuray Precision™ Treatment Planning System Manual* for detailed instructions to register images.).
  - **Align VOI Center:** Select a VOI from the phantom image and align with the VOI Center of the patient image.
  - **Align Isocenters:** Align the isocenter from the phantom image with isocenter of the patient image.
  - Align the **CT Image Center** of the phantom image with the patient image.
11. Click **OK** to auto register the images. If needed, perform manual adjustments or repeat the auto registration process.
12. On the **Register** screen, click **Confirm** when finished.



**NOTE:** To assist with alignment, phantom isodoses are calculated and displayed with low resolution. For example, if the original planning image contains  $2^n \times s \times 2^n$  voxels in (IEC X, IEC Y, and IEC Z), low resolution is  $2^{(n-2)} \times s \times 2^{(n-2)}$  voxels. Patient isodoses and patient VOIs are not available within the patient QA plan creation workflow. The phantom isodoses do not update instantaneously as you move the phantom around. Click **Confirm** to update the phantom isodose calculation and to update the couch replacement.



**NOTE:** If you align isocenters or CT image centers, you must also introduce a non-zero manual offset to enable the Confirm button.



## Set Up and Save the Patient QA Plan

If you do not want to keep the values that were transferred over from the QA template plan, the patient QA plan creation workflow provides an additional opportunity to modify the density model and set the red laser positions. You can also replace the couch again but it is not required.

1. Click **Setup > Phantom**.
2. Verify the red laser positions and adjust them if necessary.
3. Click **Accept Red Lasers**.
4. If the phantom is positioned far from isocenter in the IEC Y direction, the red lasers may not be able to reach the position of the phantom. In this case, set the red lasers to the phantom in IEC X and IEC Z. Set the red lasers to

overlap the green lasers in IEC Y and measure the IEC Y distance from the phantom to the lasers that will need to be implemented during the setup.

5. Click **Evaluate > Review**.
6. From the **Final Dose Resolution** drop-down menu, select **High**.
7. Click **Get Final Dose**.
8. Click **Save Plan** and save the Patient QA plan as **Make Deliverable**.



**WARNING:** Always check the calculated phantom dose for the patient QA against the prescribed patient dose. If the phantom and the patient have a similar size and composition, the calculated phantom dose for patient QA should be similar to the patient's prescribed dose. If these values are significantly different there may be an error in the patient density model or density override. An error in the patient density representation could lead to incorrect dose calculations and patient injury or death, even if the patient QA measurement matches the patient QA calculation.

## Load an Existing Patient QA Plan

Load an existing Patient QA plan to review it and adjust its parameters, if needed.

1. Click the **Load Plan** icon from the **Patients and Plans** section of the Precision System home page.
2. Click a patient name from the list on the panel.
3. The plans associated with the selected patient will be displayed.
4. Select a QA plan from the **Select Plan** list. QA plans are identified with **QA** in the **Type** column.
5. Click the **Load Plan** button to load the selected data.
6. Review the Patient QA plan and make any necessary changes.
7. Click **Save Plan** and the Patient QA plan as **Make Deliverable**.

# Perform a Patient QA Workflow

- ◆ Scan the QA Phantom and Perform Registration..... 401
- ◆ Deliver the Patient QA Procedure..... 403

## ◆ Scan the QA Phantom and Perform Registration

Scan the QA phantom to create a *CTrue* image for image registration. Register the *CTrue* image with the phantom image volume. Registration adjustments are then applied.

### Set Up the QA Phantom



**TIP:** If you use a phantom that is homogenous in the longitudinal direction select scan slices that include a feature to help verify the longitudinal position of the phantom, such as an ion chamber, fiducials, or the superior or inferior phantom edge.

1. Make sure the mode switch on the **Status Console** is set to **Program**.
2. On the **Scan** tab, click the **Prepare Scan** button. The red lasers move automatically based on the QA plan.



**CAUTION:** If the same phantom is not used for QA planning and a QA procedure, analysis results can be affected. Always use the same phantom that was used for QA planning to perform a *CTrue* image scan and QA procedure.



**TIP:** If you introduced a lateral shift to the patient when creating the patient plan, and if **Move couch with patient** was selected, the lateral couch position of the patient plan carries over to the patient QA plan. For accurate dosimetry use a delivery setup that replicates the lateral couch position of the patient QA plan and the patient treatment plan.

3. On the couch, position the same phantom that was used to set up the QA plan. Make sure the phantom is in the same orientation as defined by the QA plan.
4. Continue to “Align the Phantom with the Lasers” (page 402).



**CAUTION:** If the QA phantom is not correctly positioned, analysis results can be affected. Make sure the QA phantom is in the same orientation that was used during QA planning and that you position the QA phantom based on the saved laser positions from the QA plan.

## Align the Phantom with the Lasers

1. Align the phantom with the red lasers. Use the manual couch controls to position the phantom.



**IMPORTANT:** The position of the phantom must match the position that was used for patient QA calculation.



**NOTE:** If the position of the phantom is greater than 20 cm from the virtual isocenter in IEC Y, the red lasers cannot reach the phantom position. Set the phantom to the green lasers in IEC Y, then use the Step Move function to shift the phantom to match the position that was used for patient QA calculation.

2. Press **Ready** on the **Positioning Control Panel**.
3. Press **Yes** to move the couch to the ready position. Press **Cancel** if you want to re-position phantom.
4. Continue to “Scan the QA Phantom” (page 402).

## Scan the QA Phantom

1. Exit and secure the entrance to the treatment room.
2. At the **Status Console**, do the following:
  - Turn the mode switch to **Image**.
  - Press the **Start** button when the **Ready** light turns on.
3. After the *CTrue* image scan is finished, turn the mode switch on the **Status Console** to **Program**.
4. Continue to “Perform *CTrue* Image Registration” (page 402).

## Perform *CTrue* Image Registration



**CAUTION:** Couch sag can affect the position of the phantom and analysis results. Always perform *CTrue* image registration to position the phantom before a QA procedure is delivered.

Perform manual or automatic image registration and reposition the QA phantom based on the registration results. See the *Treatment Delivery Manual* for instructions to apply registration adjustments. When finished, continue to “Deliver the Patient QA Procedure” (page 403) to position the film or point dosimetry devices, and deliver the QA procedure.

## ◆ Deliver the Patient QA Procedure

### Position a Film

**IMPORTANT:** Apply registration shifts before marking the film.



1. In the treatment room, ensure that registration shifts have been applied and that the phantom has not moved out of the planned set up position.
2. Without changing the phantom position, insert the film in the plane that was used to calculate dose.
3. On the film or the jacket, mark the orientation of the film and the green lasers. If the green lasers are not on the film, mark features of the phantom that will be easy to identify. Avoid making marks in the area you want to analyze.
4. Verify that the phantom is positioned correctly. If necessary, return it to its planned setup position. If the phantom is moved, laser marks may no longer correspond to the actual laser positions.

### Position Point Dosimetry Devices

Due to sensitivity to positioning as well as the volume averaging effect, TG-148 recommends that ion chambers should be placed in regions of low dose gradient.

1. In the treatment room, verify that the phantom has not moved out of the planned set up position.
2. Make sure you position each point dosimetry device so that it corresponds to the desired location on the calculated dose volume for QA planning.
3. Verify that the phantom is positioned correctly. If necessary, return it to its planned setup position.

### Deliver the Procedure



**WARNING:** A patient QA procedure is used to compare the planned dose against the actual dose for a fraction. To avoid serious injury to a patient, do not deliver a patient QA procedure to a patient.

1. For instructions to deliver a procedure, see the *Treatment Delivery Manual*.

# Perform a Static Couch Patient QA Workflow

**Static Couch Patient QA** procedures can be created on the TDC from any scheduled patient fraction. The procedure is delivered to the detector array without the couch in the gantry bore so there is no couch attenuation. The collected detector data can then be compared against the fraction's planned dose using third-party analysis software.

Accuray Incorporated recommends performing QA of treatment plans with the same delivery instructions that are used for treatment (including a moving couch). However, a static couch procedure may be required for QA with some third-party devices.



**NOTE:** The Delivery Analysis Option involves measurements with a moving couch, not a static couch.



**WARNING:** For delivery quality assurance procedures, Accuray Incorporated recommends that absolute dose measurement devices, such as a calibrated ion chamber, be used in addition to devices that sample the relative distribution in a plane, such as film. Failure to evaluate both the absolute dose and the dose distribution may result in patient mistreatment.

1. Go to the dashboard, and click **Static Couch Patient QA**.
2. Select a patient from the **Patients** list, and then select a plan and fraction. The **Treat** tab opens.
3. Select a procedure from the **Procedures** list.
4. Click **Prepare Treatment**. An **Informational** dialog box is displayed.
5. Verify that there is no patient or object in the beam path, and click **OK**.



**CAUTION:** No patient or object can be in the beam path during this procedure.

6. Enter the treatment room, and press **Ready** on the **Positioning Control Panel**.
7. Exit the treatment room, and secure the entrance.
8. Press the **Setup** on the **Positioning Control Panel** to remove the couch from the bore of the gantry.
9. At the **Status Console**:
  - Turn the mode switch to **Treat**.
  - When the **Ready** light turns ON, press the **Start** button.

10. Turn the mode switch on the **Status Console** to **Program** when the “Procedure Finished” message displays.

# Analysis of Patient QA Results

This section provides information for analyzing dose results that have been collected from Patient QA plans, using third-party software. It also provides information for recording analysis results using the *Accuray Precision™ Treatment Planning System* software.

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◆ Export DICOM Dose .....	407
◆ Use of Film and Ion Chambers .....	407
◆ Use of Array Devices .....	407
◆ Record Analysis Results .....	408

## ◆ Independent Dose Calculations

The purpose of an independent dose calculation is to verify that the dose distribution calculated on the patient planning image is approximately correct, given the beam model and delivery parameters including gantry motion, couch motion, jaw motion, and MLC sinogram. The independent dose calculation does not verify the performance of the treatment system.

By definition, second check software needs to be developed and tested independently from Accuray Incorporated. Before using second check software, ensure that it can accommodate the beam model installed on your system, and the treatment modalities that you will use (e.g., *TomoHelical*, *TomoDirect*, *TomoEDGE*).

## ◆ Density Representation



**WARNING:** An inappropriate density representation in the patient image can cause patient injury or death. However, a passing patient QA result in the phantom does not confirm that the patient density distribution is correct.

During chart checks, the site physicist should confirm that the calculated patient QA dose in the phantom is similar to the calculated plan dose in the patient, to the extent that the phantom and patient are similar in size and composition. If the calculated doses in the phantom and patient are very different, check the density representation in the patient and/or phantom images.

For example, suppose that the air in the patient image has an incorrect density value of  $1.0 \text{ g/cm}^3$ . A very high fluence will be calculated in the plan to deliver the prescription dose to the target. If the phantom density representation is correct the patient QA can still pass. However, the patient will be mis-treated.

## ◆ Export DICOM Dose

The following steps explain how to export the DICOM and Planar doses and how to download the RT plan.

1. Open the patient QA plan.
2. On the right side of the screen, click the **Export DICOM Data** icon. The Export DICOM Data window opens. This window lets you select the items to export. Examples would be: the phantom image in the same position as the original DICOM image file, volumes of interest, and RT dose.



**NOTE:** If the Reference Image is set to New Couch Image, the image will contain the phantom with the Accuray couch. This is the image on which dose was calculated.

You can also export Planar doses. The Planar dose location is determined by the location of the slice viewers when the **Export DICOM Data** icon is selected.

You can also download the RT Plan via **Plan Administration**.

1. Navigate to the **QA Plans** tab.
2. Click to expand **Generate QA Plans**. This will add the RT Plan to the QA Plan DICOM Series list.

See the iDMS™ Data Management System Manual for more information.

## ◆ Use of Film and Ion Chambers

To determine the calculated dose at the positions of your ion chambers, you can use the Dose Statistics table (if you created VOIs in your phantom template plan at the positions of your ion chambers) or use the Dose Points tool to determine the calculated dose at any point in the patient QA plan.

For film analysis, export DICOM dose as described in the previous section. Use third party software to compare the measured film to the calculated dose plane.

## ◆ Use of Array Devices

An array device can be used to avoid the need for film and ion chambers for routine patient QA. If an array device is used, choose a device with a uniform response to radiation, for all beam angles. Also, note the following:

- It is not possible to attach an accessory to the linac.
- It is not possible to set all the gantry angles to zero for *TomoDirect* or *TomoHelical* plans.



**IMPORTANT:** Accuray Incorporated acknowledges the benefit of third-party QA devices, but does not provide training or troubleshooting for them. Contact the device manufacturer for assistance.

## ◆ Record Analysis Results

After analyzing results of the plan QA procedure, you can record analysis results using the **Plan Administration** application of the *Accuray Precision™ Treatment Planning System* software. You can also add notes and attach files to the analysis record.

For information on recording analysis results, see the *iDMS Manual*.

1. Click the **Plan Administration** icon on the *Precision* home page.
2. Select the patient and the patient treatment plan.
3. Highlight the associated QA plan and click the **Manage Selected QA Plan** icon.
4. In the **QA Plan Fractions** section, highlight the QA Plan.
5. Click the **Add or Update Analysis Record** icon.
6. Enter the result of the analysis (pass/fail).
7. Optionally import a screenshot of the analysis result (saved as a .TIF).

## ◆ What to Do if Patient QA Fails

If the patient QA results fail, the decision of whether or not to treat patients is at the discretion of the site physicist.

Patient QA measurements are a composite test of all the factors that impact patient treatments. Patient QA results may fail if any aspect of the measurement technique or delivery is incorrect.

The following tasks may help to pinpoint the source of the discrepancy. The order in which these tests are performed is at the discretion of the site physicist. Contact Accuray Physics Support if you have questions.

1. Verify the patient QA setup and equipment:
  - a) Verify phantom orientation and setup using an MVCT image. The delivery will be sensitive to couch position if most beams enter near the couch edge (especially for TomoDirect plans).
  - b) Verify that the measurement device (e.g., ion chamber) is in the expected location.

- c) Ensure that the measurement equipment is in good working order and that calibrations for equipment and film are up to date. Try a different chamber and electrometer if possible.
  - d) If your patient QA measurement fails for an array device, try creating a patient QA plan in the Tomo-phantom. If the patient QA passes with film and ion chambers, but fails with the array device, there may be a problem with the array device.
2. Verify the patient QA plan:
    - a) Verify that the chamber is not in a region of high dose gradient.
    - b) Verify that an appropriate density model was applied to the patient QA phantom.
    - c) Check for artifacts in the phantom image that may result in incorrect density.
  3. Examine the leaf-open times histogram to see if the treatment plan includes an excessive number of short leaf open times. If the mean leaf open time is shorter than 100 ms, consider re-planning with a larger number for the pitch.



**NOTE:** When leaf open times are short, any small inherent difference between the programmed and delivered leaf open times may represent a significant fraction of the programmed open time, potentially leading to Patient QA discrepancies, as reported by Westerly 2009.

4. Look for clues in the recent machine history:
  - a) Determine the extent of the problem. How many plans are failing, and for which field sizes? By what percentage are they failing? When did you first notice the failure?
  - b) Examine recent patient QA results, machine QA results, and service events to identify any issues that might be connected to the failing QA result.
5. Verify the machine performance:
  - a) Perform monthly QA checks of the output, energy, or longitudinal profiles. See “Monthly QA” (page 348).
  - b) Verify that the beam is pointed in the plane of gantry rotation. See “Beam Planarity” (page 136).
  - c) Run the TomoPhant plans. See “Absolute Dose Calibration” (page 211).
6. If the cause of the failing patient QA is still unclear, contact Accuray Physics Support. The results of the tests above will provide valuable information to

help determine the cause of the problem. Additionally, Accuray Physics Support may:

- a) Request plan information for analysis.
- b) Examine the recent machine service history to identify any recent changes or potential problems.
- c) Ask the Service Engineer to verify the MLC performance. (Accuray Support may require some of the tests numbered 1-5 to be completed by the site physicist first.)
- d) Suggest additional tests for the site physicist to perform.



## Chapter 6

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### Beam Model and Algorithms

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# Beam Model

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## ◆ Introduction

The beam model data for the treatment delivery system, which is used by the Accuray *Precision* Treatment Planning System for dose calculations, is accessible from the **Edit Machine** task of the Treatment Delivery Console, in the part of the data tree that describes the treatment beam, in folders called **DoseCom Twinnable** and **DoseCom Non-Twinnable**.

Systems have a “twinned” beam model that includes a combination of standardized (“twinnable”) and machine-specific (“non-twinnable”) parameters, as summarized in the Beam Model Parameters table below.

The beam model for a particular machine depends on the software version of the original installation, and on the LINAC style. Certain product upgrades may require the system to be twinned to a new beam model.

Twinned beam models were created from beam data averaged over ten machines. Each set of data used in the ten-machine average was collected from systems equipped with the appropriate LINAC and acquired using a Standard Imaging A1SL chamber and water tank.

The **Edit Machine** structure holds the actual data for some parameters. For other parameters, the **Edit Machine** structure points to a location on the TDC workstation where the beam model files are stored. Beam model files on the TDC workstation are protected from modification by a password-protected checksum.



**NOTE:** Because the **Edit Machine** data and associated files are not configured in a way that is easy for a person to read, your beam model data is also provided in Excel format by Accuray at the conclusion of acceptance testing; this TCOM spreadsheet may be referenced by the site physicist when evaluating annual QA results.

For information on the machine data parameters in the **Edit Machine** area that are not considered part of the beam model, see “Machine Data” (page 99). For information on how the delivery system handles revisions to the **Edit Machine** data, see “Post-Service QA” (page 375).

Beam Model Parameters		Purpose
DoseCom Twinnable	EFIOT (MeV/(cm <sup>2</sup> s))	Energy Fluence per Ideal Open Time; specifies the energy fluence rate at isocenter in air for a 5 cm x 40 cm field
	Cone	Transverse fluence filters; models the off-axis fluence fall-off due to the absence of a flattening filter
	Penumbras	Longitudinal fluence filters; models the fluence fall-off due the moveable jaws
	Fluence Attenuation Table	Attenuation values versus radiological path length in water ( $\mu_w/p$ ) and cortical bone ( $\mu_b/p$ )
	Parametric Kernel	Coefficients used in the parametric representation of the scatter kernel
	Jaw to Field	Relates jaw numbers to actual field widths at isocenter
	Jaw Field Specifications	List of commissioned field widths
	Leaf edges (mm)	Geometrical projection of leaf edges at isocenter
DoseCom Non-Twinnable	Leaf fluence table	Leaf filters; models the fluence distribution across leaves
	Leaf Latency	Used to adjust programmed leaf open times to achieve the intended effective leaf open times
	Tongue and Groove Penumbra (TAGP)	$TAGP = LFOF - 1$ ; represents the effect of the open/close state of neighboring leaves on the fluence through a particular leaf
	Center of Rotation	A single parameter that represents the alignment of the MLC with respect to isocenter
	Jaw Fluence Output Factor (JFOFs)	Accounts for field width-specific differences in the fluence rate

## ◆ Standardized (DoseCom Twinnable) Parameters

### Energy Fluence per Ideal Open Time

The output rate parameter in the beam model is the Energy Fluence per Ideal Open Time (EFIOT). This parameter specifies the energy fluence rate at isocenter in air for a 5 cm x 40 cm field, in MeV/(cm<sup>2</sup> s). The EFIOT is the maximum fluence output rate of the source. As discussed in the following sections, transverse filters, penumbra filters, leaf filters, and Jaw Fluence Output Factors reduce the fluence relative to the EFIOT.

EFIOT values are specified to achieve agreement between sample dose calculations and measurements. The EFIOT is proportionally higher for the nominal 1000 MU/min beam than for the nominal 850 MU/min beam.

### Cone (Transverse Filters)



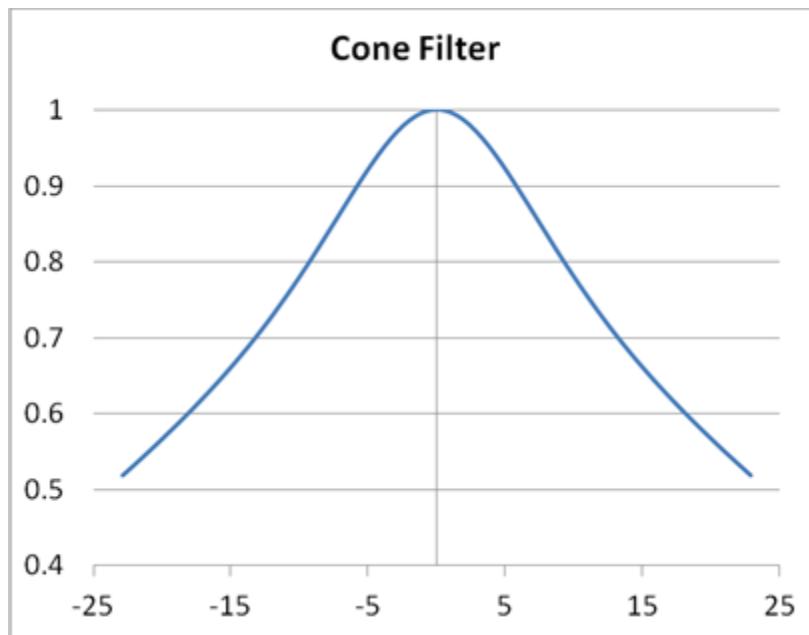
**NOTE:** In the beam model, the parameter that references the transverse filter files is called “cone.” In this context, “cone” is not the name of an accessory that attaches to the linac, but a description of the profile shape. Accessories are not attached to the LINAC.

The transverse profile data in each standardized beam model was determined by averaging transverse profile measurements using an ion chamber in a water tank for ten machines.

The transverse filter models the off-axis fluence fall-off due to the absence of a flattening filter. As the system is flattening filter free, the fluence has a forward-peaked distribution with approximately radial symmetry.

In the beam model, the transverse filter (also referred to as a cone filter) is stored as a one-dimensional (1D) transverse filter that is effectively rotated 180 deg to form a two-dimensional (2D) filter.

Differences with field sizes are very subtle, so there is only one transverse filter (J42). The subtle differences between the field widths have been incorporated into the individual penumbra filters. A sample is shown in the following image. The leaf filters are used to define the edges of the transverse profile (not shown).



Example of a 1D Transverse Fluence Filter

### Penumbra (Longitudinal) Filters

Penumbra filters model the fluence falloff due to the moveable jaws. For a given field setting, a penumbra filter for the front jaw is combined with a penumbra filter for the back jaw. The front and back jaw penumbra filters ( $f_{back}$  and  $f_{front}$ ) are combined using:

$$f_{combined} = f_{back} + f_{front} - 1$$

The resulting combined penumbra filters contain subtle cone effects unique to each front and back jaw combination. Each beam model includes penumbra filters based on ten longitudinal profiles. As shown in the following figure and table, every profile is either the symmetric or asymmetric variety of the J07, J14, J20, or J42 jaw widths:

- The 5 cm, 2.5 cm, and 1 cm field widths are called the “symmetric” and “fixed” field widths. The nominal FWHM values are 5 cm, 2.5 cm, and 1 cm (at 1.5 cm depth in water, projected to isocenter), but the precise values are slightly different for each beam model, since a model is created by averaging measured data over ten machines.
- Six transitional, asymmetric jaw settings provide for accurate interpolation between the many jaw positions required for dynamic delivery. The asymmetric field widths have one outer field edge sharing a boundary with the J42 jaw width.
- The symmetric J14 is a transitional jaw position for dynamic jaws planning, and results in a nominal field width of about 18 mm. It is not a commissioned field width and is not selectable for treatment planning.

The gold standard 10-machine average data was processed to generate individual fluence “filters” (penumbral data for a single field edge) that are independent of scatter and scaled to isocenter.

Ideally, a beam model is built from profiles that are independent of any anomalies or characteristics introduced by detector response. However, any profile measured with a detector is inherently a convolution of the actual beam profile and detector response:

$$\text{Measured Profile} = (\text{Actual Profile}) \otimes (\text{Detector Response})$$

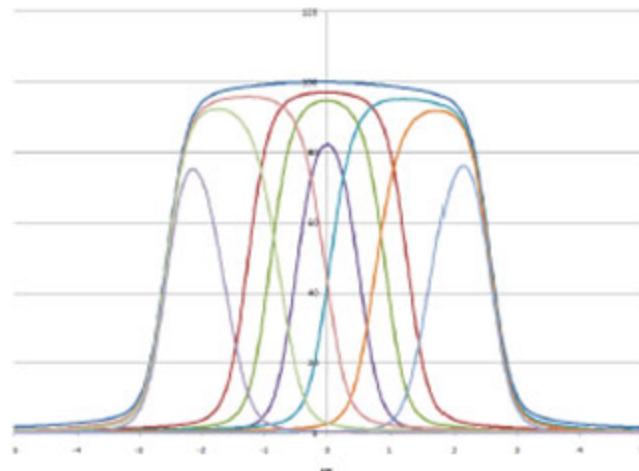
Detector response can have a significant impact on profile measurements in the high gradient regions. Volume averaging occurs during measurements and impacts the shape of measured profiles. To improve the modeling accuracy of longitudinal profiles, the longitudinal profiles used to determine the beam model data were deconvolved from the A1SL response, to make them independent of the A1SL chamber characteristics.



**NOTE:** The transverse profile data did not need to be deconvolved from the detector response, because the high gradient regions of the transverse profile (penumbra region) are modeled by the leaf filters, not the transverse profile data.

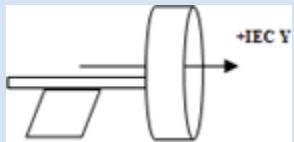


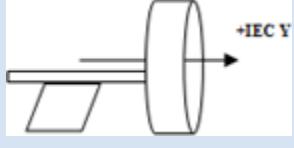
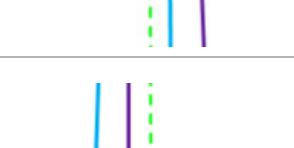
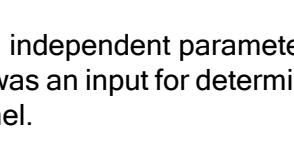
**NOTE:** The PDD data did not need to be deconvolved from the detector response, because the high gradient (build up) region of the PDD data is outside the comparison range. Accuray Incorporated tolerances apply to depths from 10 mm to 200 mm, because a cylindrical ion chamber is not appropriate for measuring the buildup region of a PDD. Reference PDDs are only provided for central-axis (IEC X = 0) measurements.



Sample Jaw Profiles in the Beam Model

The following table contains the jaw profile settings used to determine the fluence filters in the beam model. The beam model includes asymmetric longitudinal fluence filters to accommodate dose calculations for dynamic delivery. The J14 field setting is not commissioned for fixed jaw treatment planning. The green dashed line indicates the center of a symmetric field. The blue line indicates front jaw position. The purple line indicates back jaw position.

Notation (jaw number)	Symmetric/Aymmetric	Nominal field width [cm]	Front Jaw Position [cm]	Back Jaw Position [cm]	Cartoon Representation
J42	sym.	5	-2.1	2.1	 Front jaw             Back jaw

Notation (jaw number)		Symmetric/Asymmetric	Nominal field width [cm]	Front Jaw Position [cm]	Back Jaw Position [cm]	Cartoon Representation
J20	sym.	2.5	-1.0	1.0		
	asym. +IEC Y	2.5	0.1	2.1		
	asym. - IEC Y	2.5	-2.1	-0.1		
J14	sym.	1.8	-0.7	0.7		
	asym. +IEC Y	1.8	0.7	2.1		
	asym. - IEC Y	1.8	-2.1	-0.7		
J07	sym.	1.0	-0.35	0.35		
	asym. +IEC Y	1.0	1.4	2.1		
	asym. - IEC Y	1.0	-2.1	-1.4		

### Energy Spectrum (Implicit in the Beam Model)

The treatment beam energy spectrum is not an independent parameter in the beam model. Rather, the energy spectrum was an input for determining the Fluence Attenuation Table and scatter kernel.

The treatment beam energy spectrum was determined by averaging measured water tank PDD data for 10 good machines, then using internal Accuray software to determine the weightings of the components of the energy spectrum to produce a match with the 10-machine average PDD.

The weightings of the spectral energy components (bins of specified width centered on  $E$  MV) were determined by optimizing the parameters  $\alpha$  and  $\beta$  of a power-exponential formula that is exposed in the PDD\_DATA tabs of the TCOM spreadsheet:

$$Weight = m^2 E^\alpha e^{-\beta E}$$

In the above equation,  $m$  is a normalization factor.

The resulting energy spectrum can be used to calculate a PDD that can be compared against the measured 10-machine average reference data, to determine the quality of the fit. The same beam energy spectrum is used for all twinned beam models to date.

### Fluence Attenuation Table

The pre-computed Fluence Attenuation Table (FAT) gives attenuation values vs. radiological path length in water ( $\mu_w/\rho$ ) and cortical bone ( $\mu_b/\rho$ ). The FAT is the same across all standardized beam models. The FAT accounts for beam hardening by allowing the effective mass attenuation coefficients to vary with radiological depth. For more information, see “Optimization Step 4: Calculating the Dose” (page 455).

### Parametric Scatter Kernel

All beam models use the same scatter kernel. The scatter kernel is polyenergetic; it is made up of a weighted sum of monoenergetic kernels. The monoenergetic kernels were computed using Monte Carlo by Mackie 1988. Beam hardening is neglected in the kernel.

The scatter kernel is based on water. Patient inhomogeneities are scaled in voxel space to water-equivalent distance.

The kernel representation is parametric:  $b_1(1 - e^{-a_1 r}) + b_2(1 - e^{-a_2 r})$ . Defining the kernel as a function with only four parameters ( $a_1$ ,  $b_1$ ,  $a_2$  and  $b_2$ ) significantly decreases computation time.

The kernel indicates how dose spreads around 24 different radially symmetric zenith angles with respect to an incoming photon.

The kernel must be tilted to represent the beam direction. A gantry rotation is divided into 24 sectors (happenstance that this is the same as the number of zenith angles in a kernel). Thus, each sector represents 15 degrees of gantry rotation. The kernel is tilted to match the average direction of the rays within the sector. The same kernel tilt is applied to all rays within a 15-degree sector.

### Jaw to Field

The Jaw to Field table relates the jaw numbers (see “Jaw Numbers” (page 15)) to the actual field widths at isocenter. This table is not used for dose calculations, but is used for labeling field widths on the TPS and in the TDC.

### Jaw Field Specifications

The Jaw Field Specifications is a list of the commissioned field widths. These values can be related to the field sizes at isocenter via the Jaw to Field table.

### Leaf Edges

The DoseCom Twinnable data includes the geometrical projection of the leaf edges at isocenter.

Machine-specific leaf filters are used for dose calculation, but leaf edges common to all systems with the same beam model are used in other places, for example:

- For initial selection of beamlets that pass through the target, in preparation for optimization (see “Optimization Step 1: Calculating the Initial Sinogram” (page 435); the subsequent dose calculations use leaf filters instead of leaf edges).
- For visually rendering *TomoDirect* beams in the TPS.
- For determining if the couch intersects a given *TomoDirect* beam.

## ◆ Machine-Specific (DoseCom non-Twinnable) Parameters

### Leaf Latency

MLC timing and leaf penumbra characteristics are measured individually for each system by a service representative, and entered into the system for use in treatment planning.

The MLC is binary; each leaf is programmed to be fully opened or fully closed. It takes approximately 11 to 17 milliseconds from the time a leaf starts opening or closing until it finishes opening or closing.

The dose calculator assumes leaves to be fully opened or fully closed at any instant. Leaf timing is handled by the planning and delivery systems as follows:

- Very short leaf-open times are not achievable by the MLC. The planning process ensures that the final MLC delivery instructions do not include very short leaf-open times. At the **Get Final Dose** stage, the Planning System discards leaf-open times in the optimized sinogram that are less than or equal to 18 milliseconds, then calculates dose in their absence.
- Very short leaf-closed times are not achievable by the MLC. However, the optimized delivery plan may include very short leaf-closed times. The MLC will not be able to achieve delivery instructions for very short leaf-closed times (e.g., less than approximately 18 milliseconds), so the leaves may remain open for very short intervals where the dose calculator expected them to be closed. This can occur where consecutive projections are assigned leaf-open times that are very close to, but slightly less than, the projection time.
- Leaf open times delivered by the MLC differ slightly from the programmed MLC instructions. When preparing machine delivery

instructions, **latency** data is used to assign programmed leaf open times to achieve the intended effective leaf open times.

The service representative measures machine-specific leaf latency data using the on-board detector. Effective delivered leaf open times are plotted against programmed leaf open times for a variety of projection intervals. At each projection interval, latency data is measured for sample programmed leaf intensities ranging from 0 to 100% of a projection interval.

The resulting leaf latency data consists of an offset in milliseconds applied to all projection times. The same latency data is applied across all leaves. This data is entered by the service representative into the **Edit Machine** data on the TDC, and it is used by the TPS at fractionation to convert the end-of-planning fluence sinogram into machine delivery instructions to ensure that the requested leaf open times result in the desired, planned, leaf open times.

### Tongue and Groove Penumbra

Due to the finite spot size of the beam, it takes more than one open leaf to fully “uncover” the source. The fluence through a leaf thus depends on the opened or closed state of the neighboring leaves. Detector data is used to calculate factors (Leaf Fluence Output Factors, LFOFs) to characterize the output dependence on the opened/closed state of neighboring leaves, for use in dose calculations.

A full set of LFOFs include three lists of numbers: one list of 63 numbers for an open leaf and its lower-numbered neighbor, one list of 63 numbers an open leaf and its higher-numbered neighbor, and one list of 62 numbers for an open leaf and a neighbor on each side. The LFOFs only account for the fluence dependence on the nearest neighbors, because the effect is minimal beyond the nearest neighbors. The three lists of LFOFs are defined as:

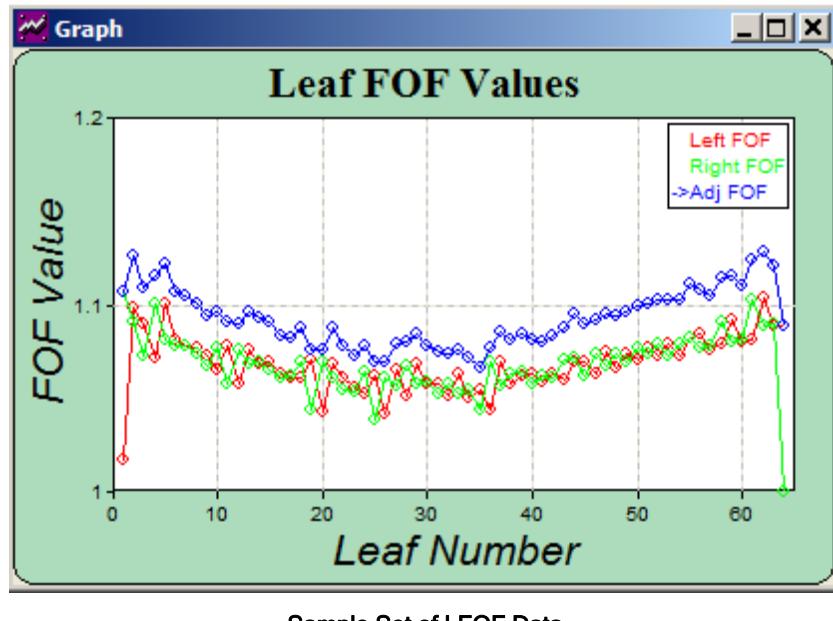
$$LFOF_i |_{\text{lower neighbor}} = \frac{Fluence_{\{i \cup i-1\}}}{Fluence_i + Fluence_{i-1}}$$

$$LFOF_i |_{\text{upper neighbor}} = \frac{Fluence_{\{i \cup i+1\}}}{Fluence_i + Fluence_{i+1}}$$

$$LFOF_i |_{\text{both neighbors}} = \frac{Fluence_{\{i \cup i-1 \cup i+1\}}}{Fluence_{i-1} + Fluence_i + Fluence_{i+1}}$$

The LFOFs compare the signal measured by the on-board detector when the leaf of interest and its neighbor are opened simultaneously versus consecutively (in the equation,  $i$  denotes a specific leaf number). Due to the finite source effect, the output is approximately 4-13% higher when the leaves are opened simultaneously versus consecutively. The LFOF ratios

are higher for the edge leaves than for the central leaves, due to the curvature of the MLC. Leaf FOF values also exhibit tooth-like fine structure that is likely due to the individual MLC characteristics.



Sample Set of LFOF Data

Three sets of numbers called TAGP (Tongue and Groove Penumbra), which are derived from the LFOF data, are recorded in the **Edit Machine** area on the TDC for the commissioned treatment field widths:

$$TAGP = LFOF - 1.$$

#### Leaf Fluence Table (Leaf Filters)

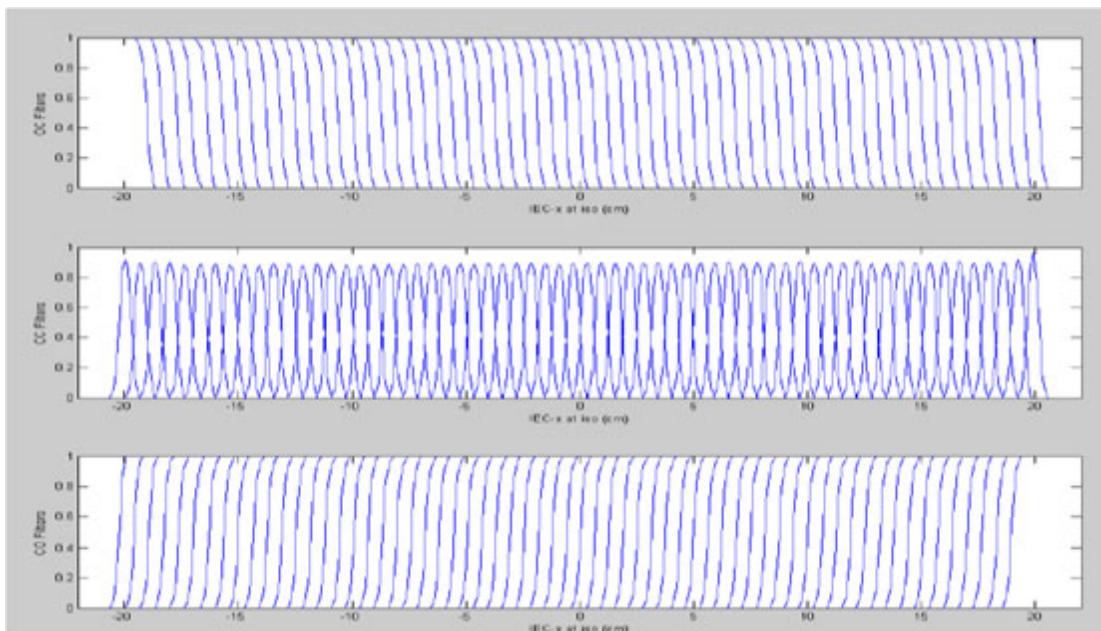
The TPS has the ability to account not only for the average fluence through a leaf, but also for the fluence distribution across a leaf opening, effectively modeling the leaf edges. A leaf filter is a profile in the beam model that describes the fluence distribution across a leaf opening for a given leaf configuration.

For helical procedures, the introduction of measured leaf filters has minimal impact on the accuracy of dose calculations, due to blurring with gantry motion. However, for static gantry procedures (i.e., *TomoDirect* procedures), it is more important to model the fluence shape. A complete set of leaf filters includes 190 filter profiles:

- An  $OC_i$ (open, closed) filter represents the relative fluence profile for the edge function of a series of open leaves followed by a series of closed leaves. Values range from 1 to 0. Since there are 64 leaves, there are 63 OC filters.
- An  $CC_i$ (closed, closed) filter represents the relative fluence profile for a single open leaf  $i$ , with the neighbors closed. When only one leaf is open, the leaf filter looks ‘Gaussian’, and the maximum filter height is less than 1.0 due to the finite source effect. There are 64 CC filters, one for each leaf.

- A  $CO_i$  (closed, open) filter represents the relative fluence profile for the edge function of a series of closed leaves followed by a series of open leaves. Values range from 0 to 1. There are 63 CO filters.

Nomenclature	Leaves < i	Leaf i	Leaves > i
$OC_i$	Open	Open	Closed
$CC_i$	Closed	Open	Closed
$CO_i$	Closed	Open	Open



Example of a Complete Set of 190 MLC Leaf Filter Curves

The sinogram used by Accuray representatives to measure leaf filter data includes patterns for measuring both leaf filters and LFOFs. Leaf filters provide information about the profile shape that cannot be gained from LFOFs, but LFOFs are more accurate for determining the area under a filter (integral fluence). This is because leaf filters are determined by connecting discrete detector data in a piece-wise function, but it is more accurate to integrate the detector data directly (i.e., integrate LFOF data) than to integrate the piece-wise function. Also, leaf filters are derived from data that spans fewer detectors than LFOFs. Thus, LFOFs are always measured along with filters, and the area under the filters is adjusted to achieve consistency with LFOFs by shifting CO and OC filters, and by scaling CC filters.

### Jaw Fluence Output Factors

The fluence rate of the system is field size-dependent. Relative to the 5 cm field, the fluence rate of the 2.5 cm field is typically 99.2%, and the fluence rate of the 1 cm field is typically 89.2%. This information is incorporated into the fluence filters for each jaw setting.

Sometimes these values need to be adjusted slightly during initial specification conformance testing according to the results of IMRT dose calibration measurements for the *Tomo*-phantom patient. The relative Jaw Fluence Output Factors (JFOF's) are used to make this adjustment. By default, all relative JFOF values for the Dynamic Jaws models are 1.000, but may be adjusted up or down during initial system specifications testing.

The field width, or jaw number, is the primary parameter that determines the JFOF. Source occlusion has a secondary effect on the fluence rate. The specification for the LINAC alignment with the jaws is tighter for systems licensed for dynamic jaw delivery ( $\pm 0.2$  mm for systems with the *TomoEDGE* feature, versus  $\pm 0.3$  mm for systems without the *TomoEDGE* feature). With proper beam alignment, differences between JFOF's for symmetric and asymmetric jaw settings are negligibly small, and Accuray currently assigns identical JFOF values for both the symmetric and asymmetric settings of a given field size. The use of the same JFOF's for symmetric and asymmetric fields is further justified when considering that asymmetric jaw settings are only used during the transitional stage at the superior and inferior edges of a target.

#### Center of Rotation

The MLC Center of Rotation can be evaluated using film, as discussed in the Commissioning chapter. A similar result is usually obtained when the MLC Center of Rotation is measured using on-board detector data, as part of the leaf filter measurement procedure that is performed by Accuray. The MLC Center of Rotation parameter in the beam model is a single value that is determined from the leaf filter procedure.

## ◆ Combining the Fluence Parameters

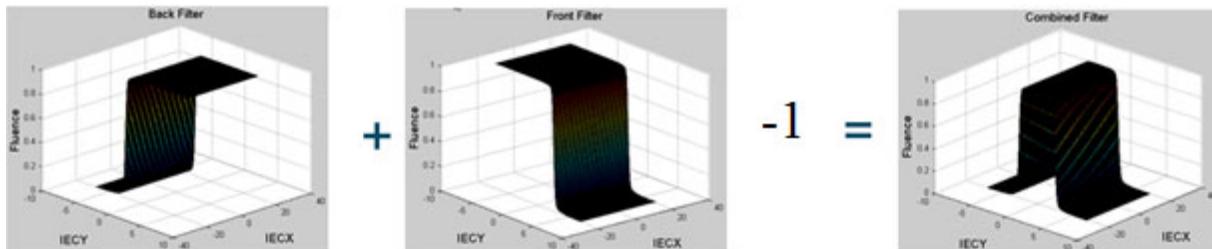
The source output is modeled by the EFiOT. For helical plans, the dose is calculated for three samples at each of the 51 projections per rotation. For *TomoDirect* plans, the dose is calculated for two samples per slice of the planning image or one sample per projection, whichever gives finer sampling. A sample is a distinct source position from which rays are traced, and corresponds to discrete positions of the gantry, couch, and jaws.

During a dose calculation:

1. The corresponding front and back jaw penumbra filters for all transverse (IEC X) positions are combined, creating a single 2D filter array. The filters are combined according to:

$$f_{combined} = f_{back} + f_{front} - 1$$

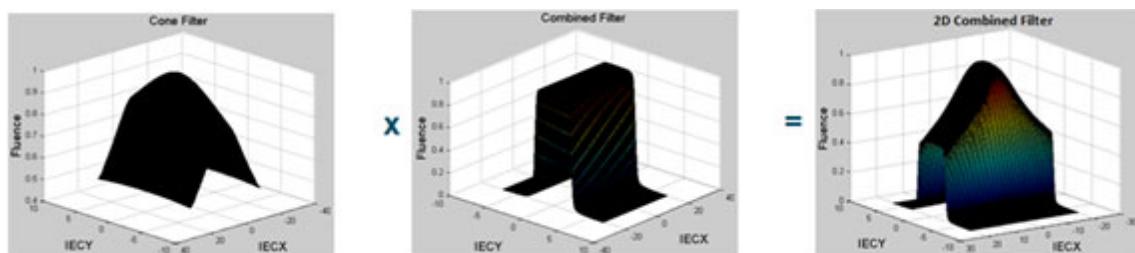
The resulting combined penumbra filters contain subtle cone effects unique to each front and back jaw combination.



**Step 1: Penumbra Filters**

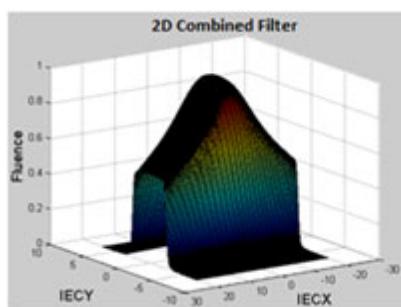
2. The 1D cone filter is used to create a 2D cone filter with the same IEC X and IEC Y dimensions of the combined penumbra filter.

The 2D cone is then multiplied into the combined penumbra filter (from Step 1), creating the 2D fluence filter.



**Step 2: Cone Filters**

3. The EFIOT, relative JFOF, and leaf filters (LFT) are multiplied into the 2D filter created in Step 2, creating the final 2D Fluence used during the dose calculation.



**x EFIOT x Relative JFOF x LFT = Final 2D Fluence.**

**Step 3: Final 2D Fluence**

# Algorithms for Planning Images

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## ◆ Image Import

### Planning Image Resolution

CT images of 256 x 256 or 512 x 512 resolution in the transverse plane may be imported for treatment planning.

See “Longitudinal Resampling” in the *Treatment Planning Manual* for an explanation of how images with non-uniformly spaced slices are resampled to uniformly spaced slices at the time of DICOM import.

See “Full Dose Calculation: Implementation of Convolution-Superposition” (page 456) for information about the dose calculation grid.

### Couch Replacement

Beams may pass through the couch before reaching the patient. The couch in the planning CT image must be replaced with a default image of the treatment couch. The patient density model is applied to the couch image.

A single couch image slice (with no indexing holes) is repeated in the provided planning image.

The **Edit Machine** area contains a parameter to indicate the lateral position of the couch installation (centering of the lower pallet). This feature enables more accurate insertion of the treatment couch image for planning and phantom-based patient QA.

The position of the upper pallet for planning may be further modified by using the “Move Couch with Patient” checkbox, as described in the *Treatment Planning Manual*.

### Hounsfield Unit (HU) to Mass Density Conversion

The selected density model is used to convert the imported planning image to density. The density model gives mass density values as a function of HU values. Density values are determined by linear interpolation between the nearest two density model points that bound the HU value of interest. For HU values that are greater than the highest point of the density model, the density depends on the selected **Extension Method**, which is set to **Flat** or **Extrapolate**.

The density override feature allows the user to assign density values to a selected VOI, as discussed in the *Treatment Planning Manual*. Separate copies of the image are maintained to contain the image values (HU) and mass density ( $\text{g}/\text{cm}^3$ ). Density replacement is applied to the mass density image only.



**NOTE:** The density replacement is implemented by converting the user-entered density replacement value to the nearest integer HU value via the density model, then converting back to density. This approach may result in slight “rounding” differences between the requested and achieved density replacement values.

The density override table includes a density override priority assignment (not the same as the overlap priority settings for optimization). If two VOIs overlap, the VOI with a density override will be used in the overlapping region. If two VOIs with density overrides overlap, the density values of the VOI with the higher density override priority will be used in the overlapping region.

If a skin VOI exists, the density override tool includes an option to override the density values Outside Skin to  $0\text{g}/\text{cm}^3$ . This option overrides densities outside of all VOIs and above the couch. Outside Skin is prioritized last in the override table.

## ◆ Image Fusion

Secondary datasets in the Precision System can be aligned with the primary dataset using Rigid Fusion and Deformable Fusion algorithms. Deformable Fusion feature is available after completing Rigid Fusion or after checking the **Already Registered** checkbox.

Rigid Fusion can be performed in one of three ways:

1. By interactively manipulating the secondary dataset translational and rotational corrections.
2. By interactively defining correspondence seed point pairs in primary and secondary datasets. (One seed point pair is required for translation registration. Three seed point pairs are required for translational and rotational registration.)
3. By using the automatic intensity based image registration algorithm.

The intensity based rigid registration algorithm can be initialized with manual alignment or seed point inputs to improve convergence. Additionally, the user can specify the registration ROI to define the anatomical region over which the image similarity measure (normalized mutual information) is computed during registration.

The Deformable Fusion feature uses a proprietary nonparametric non-rigid image registration algorithm. It estimates the deformation field subject to smoothness regularization. The user can choose between **Low**, **Medium**, and **High** deformation smoothing settings. **Medium** smoothing is the default and recommended setting. **High** smoothing is more rigid, and may be more appropriate for datasets with limited contrast to noise ratio or low spatial resolution. **Low** smoothing allows more flexibility in the deformation and may be useful for datasets containing large deformations.

After completing deformable registration, a new deformed secondary dataset is created. Only one deformed dataset can be created for each secondary dataset. The deformed dataset must be deleted prior to executing the deformation algorithm with modified parameters.

## ◆ Deformable Registration in Adaptive Planning (CT to CT)

The *PreciseART* feature lets you monitor the patient's course of treatment in order to determine whether re-planning is necessary.

For offline monitoring purposes, the original planned contours must be automatically mapped to the daily *CTrue* images, and the daily dose must be mapped to the planning image.

Because the daily *CTrue* images may span a limited range of slices, and because the *CTrue* image field of view is limited to approximately 39 cm, daily *CTrue* images are embedded in the planning CT image to approximately represent the daily anatomy. This embedding requires that the planning image be aligned to the daily *CTrue* image.

That is, the *CTrue* image is kept fixed, defining the location of the patient at treatment time. The planning kVCT is rigidly registered to the daily MVCT, using the translational shifts that were applied for treatment (X, Y, and Z). Image data from the registered planning image is then used to extend the *CTrue* image to create a full-sized image (known as the merged image) that can be used for dose calculation. The native resolution of the daily MVCT image is maintained, and the kVCT planning image is interpolated to match the MVCT resolution.

Since the couch extends beyond the MVCT field of view, couch replacement is performed. Couch replacement in the merged image depends on the daily vertical couch position on the Positioning Control Panels and the couch height at isocenter parameter from the Edit Machine area of the TDC.



**IMPORTANT:** For accurate couch replacement in the merged image, perform QA of the Couch height at isocenter parameter.

Dose is calculated on the daily merged images using the same dose calculation algorithm as for treatment plans.



**IMPORTANT:** For meaningful Adaptive calculations, the daily MVCT must contain the anatomy of interest. PreciseART calculations cannot account for changes in the anatomy outside the MVCT field of view, or slices that were not scanned. PreciseART calculations assume that the patient anatomy outside the MVCT Field of View is consistent with the planning image. When creating a treatment plan, check that the anatomy of interest is inside the MVCT Field of View (approximately 39 cm diameter). When selecting slices for the daily MVCT, select enough slices to cover the anatomy of interest.

The density values of the merged image are determined as follows:

1. Planning image voxels are mapped to density using the density model selected during planning.
2. MVCT image voxels are mapped to density using the MVCT density model.
3. Images are merged.
4. Dose is calculated on the daily merged images using the same dose calculation algorithm as for treatment plans.



**IMPORTANT:** To avoid confusion do not name other density model bins MVCT. One of the provided density model bins begins with "MVCT" and also includes the name of the machine. This is the density model referenced for the daily MVCT images in Adaptive.



**IMPORTANT:** Keep the MVCT density model up-to-date. MVCT values can drift over time. Adaptive applies the MVCT density model that was present when the fraction was delivered. Changes to the density model cannot be retroactively applied to previous fractions.

The mapping between the planning image and the daily merged image is deformable, to address possible anatomy changes between the planning image and subsequent images. For example, if there is weight loss, some areas of tissue will shrink more than others.

The algorithm for computing this deformation is the same as the one for deformable fusion, with different settings to account for the different image types, and a predetermined smoothing value based on typical image data. Deformable registration should be evaluated to determine the clinical relevance of Adaptive results. It is not possible to edit the deformable registration.

For re-planning purposes, the original planned contours, planned or accumulated dose distribution can be mapped to the new planning CT image. As with offline monitoring, this mapping is deformable, and the same algorithm is used, with settings suitable for registering two kVCT images together.



**NOTE:** You can review the merged image in the PreciseART software, but cannot modify the merged image.

The following assumptions are inherent in Adaptive monitoring:

- The machine delivery is consistent with the plan.
- The patient anatomy outside the MVCT Field of View is consistent with the planning image.
- The patient position during treatment is stable from daily MVCT image acquisition through daily treatment.



**IMPORTANT:** If you re-plan with more fractions than needed (because you forgot to account for already-delivered dose), and deliver these fractions to the patient, it could result in patient injury or death. When creating a new plan, be sure to reduce the prescription to account for fractions already delivered. Discontinue the original plan if you do not intend to use it.

## ◆ VOI Operations

VOI Operations in the Precision System are performed by converting the contour representation of one or more VOIs into a single volumetric representation. Then new contours are extracted from the volumetric representation based upon the desired operation.

All VOI Operations are performed in three steps:

1. Convert a VOI into its volumetric representation. Optionally, this volumetric representation is grown (or shrunk) during the conversion process. Growth can be performed independently along the six patient directions (Anterior, Posterior, Superior, Inferior, Patient Left and Patient Right).
2. Optionally convert a second VOI into its volumetric representation with the same optional growth. The result of these two steps is a single volumetric representation where individual voxels are tagged as belonging either to VOI 1, VOI 2, both or neither.
3. Generate a new set of contours that encompasses all of the voxels in the volumetric representation that meet the criteria defined by the operand and either combine them with or replace the destination VOI.

There are a total of 5 possible VOI Operation operands:

1. Plus - The new set of contours encompass voxels that are tagged as either the first VOI, the second VOI or both.
2. Minus - The new set of contours encompass voxels that are tagged as the first VOI but not the second VOI.

3. Copy - The new set of contours encompass voxels that are tagged as the first VOI.
4. Intersect - The new set of contours encompass only the voxels that are tagged as both the first and second VOI.
5. Resize - The new set of contours encompass voxels that are tagged as the first VOI and the destination VOI is constrained to be the same as the first VOI.

The destination VOI can be affected in two ways by a VOI Operation:

1. Add To - The current destination VOI is combined with the resultant contours produced from the VOI Operation. The combination is done in the same manner as a Plus operation (both sets of contours are converted to their volumetric representation and a final set of contours is extracted).
2. Replace - Any contours that are contained in the destination VOI are deleted and the contours produced by the VOI Operation are copied to become the new destination VOI.

## ◆ VOI Contour to Mask Volume Conversion

The Precision System uses what is termed a “mask volume” to store a volumetric representation of the VOIs contoured by the user during the process of treatment plan creation. This volumetric representation is used by the system for various purposes during the planning process, primary amongst which are the calculation of the DVH graphs and the dose statistics table. The mask volume consists of a series of integer values conceptually arranged into a rectangular prism whose dimensions match the base CT scan and which represent sub-volumes called voxels. The volumetric representation of a VOI indicates which voxels in the mask volume are parts of a VOI.

The mask volume generation algorithm is designed to convert the VOI contours, either drawn by the user or generated by the system via contouring algorithms, into the volumetric representation stored in the mask volume. The algorithm processes the contours on a slice-by-slice basis and therefore is similar in nature to the rasterization algorithms used in 2D computer graphics. The Precision System features an enhanced version of this algorithm which is designed to provide more precise handling of the contours and improved speed. This algorithm uses the following rule to determine whether a voxel should be considered part of a VOI: if the center of a voxel, viewed in the same plane as the contour, falls inside or on the contour, then the voxel is treated as inside the contour.



**WARNING:** If a VOI has contours that extend beyond the boundary of the primary CT image, the density override that the user has defined for this VOI will not be applied to the portion that is outside the boundary of the primary CT image. If this occurs, an invalid dose calculation will result.

## ◆ AutoSegmentation

The AutoSegmentation™ tools on the Precision Planning System can be used to automatically contour skin or structures for male pelvis, head and neck, and brain. Brain *AutoSegmentation* requires a T1-weighted MR image.

### Skin

The skin is automatically contoured using a threshold-based algorithm. There are three user-specifiable parameters: the threshold, the maximum number of contour sets, and the minimum contour size. The threshold value can be increased if the contour captures too much of the image, or decreased if the contour does not capture enough.

The maximum number of contour sets should generally equal the maximum number of contours that are expected on a single slice. For instance, in a head and neck case, the outline of the head (or upper shoulders) has only one contour, so 1 is a good choice. But, for a thorax case, 3 is a good choice so that both arms will be contoured as well. Setting this value as low as possible can reduce spurious contours.

The minimum contour size, measured in voxels, can also be used to prevent spurious contours.

### Brain

The Brain *AutoSegmentation* feature provides automatic segmentation of a number of cranial structures, including cortical parcellations, using an atlas-based segmentation approach. The approach relies on a set of anatomical atlases, consisting of gray level images and corresponding contours. The gray level atlas images are registered to the patient's T1-weighted MR images using a nonrigid registration algorithm, providing a mapping between contours and the patient image.

The nonrigid registration of the patient MR images to the MR atlases is performed in a three-stage process. First, an affine registration between the two images is computed, using a tri-level multi-resolution pyramid. Second, a multi-resolution nonrigid registration is performed, using the affine transformation parameters as an initial transformation. Third, the resulting nonrigid transformation is used to warp the atlas label image, resulting in a mapping between anatomical delineation in the atlas and the patient image.

Because of the inherent variability of cranial anatomy between patients, the system matches the patient image with multiple atlases and subsequently determines an optimal combined segmentation. The most appropriate MR atlases are automatically selected by the system from an atlas database.

To achieve the highest possible segmentation accuracy, it is recommended to use T1-weighted MR scans with imaging sequence parameters similar to the parameters listed in the table below.

Sequence	MP-RAGE
TR (msec)	9.7
TE (msec)	4.0
Flip angle(°)	10
TI (msec)	20
TD (msec)	200

## Head and Neck

As with Brain *AutoSegmentation*, the Head and Neck *AutoSegmentation* algorithm is atlas-based, using the same rigid and nonrigid registration algorithms that are used for the brain. The image to be segmented is matched against a number of segmented atlas images, and the resulting information is combined to create a single segmentation.

The eyes and lenses are segmented using a model-based algorithm. Because the atlas framework is different from the Brain method, the algorithm is not identical, but it uses the same principles.

In other places, the results of the atlas segmentations are modified to satisfy anatomical constraints. Key constraints that the user should be aware of are as follows:

- The parotids cannot overlap the mandible.
- The top slice of the spinal cord must be adjacent to the bottom slice of the brainstem.
- The spinal cord must be contained within the spinal canal.
- The optic nerves cannot overlap the eyeball or the chiasm.
- The lenses must be contained within the eyeballs.

For the head and neck, there is editing functionality that operates in 3 dimensions, extending user edits to neighboring slices in a smooth way. Where possible, the editing algorithm respects the above constraints, except that user-modified contours generally take priority. For convenience, the optic nerves and parotids are treated specially in this regard. If the user bumps a parotid into the mandible, or the optic nerve into the eyeball, those edits are “pushed back out” when the **Update** button is pressed.

## Male Pelvis

Male Pelvis *AutoSegmentation* uses atlas-based segmentations for some of its structures, but it also relies significantly on model-based segmentation. Model-based algorithms have explicit models for the organs of interest. These include the range of shapes that each may assume under

various conditions (for example, bladder empty or full, distension of the rectum). The models also include the expected spatial relationships among the organs (for example, the bladder is superior to the prostate), the typical image intensities associated with the organs and other material (surrounding tissue, fat, urine, fecal matter, and gas) and various visible landmarks in the images.

The models are developed via a process called training. During training, data is extracted from a series of segmentations of the desired anatomy. The data is encapsulated into a shape model that captures the typical shape variations seen in the training data and an associated appearance model that captures the distribution of image intensities typically seen in each region of the shape model.

The *AutoSegmentation* algorithm leverages this model-based information, CT image intensities of the user-supplied image set, and user-defined initialization points (optional) to automatically segment the anatomy. If supplied, the initialization points are used to guide the automatic segmentation process in areas where the image data is ambiguous. This allows the user to guide the automatic segmentation to produce a result that better matches their own judgment of where the VOI's boundary is. After *AutoSegmentation*, the user can adjust the resulting boundary using the editing tools in the Precision System as needed.

The algorithm operates in three dimensions. Once the algorithm has reached a solution, 2D contours are extracted from the 3D objects. These 2D contours are then displayed to the user as overlays on associated image data.

For both the male pelvis and the head and neck, contours that are displayed in the Precision System have been smoothed using first-order interpolation between points in 2D and 3D. However, a voxel representation of the VOI is used when computing dosimetric information. The voxel representation is deduced from the smoothed 2D line segment representation. Users can view the voxel representation by choosing to view VOIs as semi-opaque overlays and zooming in on a VOI.

# Algorithms for Optimization and Dose Calculation

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## ◆ Optimization Steps Overview

The optimization sections of this chapter describe optimization for IMRT inverse planning. 3D Conformal planning is discussed in “3D Conformal (3DCRT) Algorithm” (page 466), and Forward Planning is discussed in “Forward Planning Algorithm for TomoDirect” (page 464).

In planning, optimization is the iterative process of adjusting the fluence delivery pattern (MLC sinogram) to achieve a dose distribution that meets the prescription DVH point, and attempts to satisfy other plan goals indicated by DVH points, importances, and penalties. At each iteration, the dose distribution in the patient is calculated, either by performing a full dose calculation or by using a simple ray-tracing method to predict small changes with respect to the most recent full dose calculation.

The MLC sinogram is the only plan parameter that is optimized by the planning system. The delivery mode (helical or *TomoDirect*), plan mode (IMRT in this case), field width, jaw mode (fixed or dynamic), and pitch must be set by the user before optimization begins. The gantry speed and couch speed are later computed, not optimized, as indicated in “Calculating the Final Dose” (page 462).

Here is the optimization cycle:

1. Calculate the initial sinogram (first iteration only; “Optimization Step 1: Calculating the Initial Sinogram” (page 435)). Then, skip to Step 4.
2. Adjust the beamlet weights of the sinogram according to the fluence update equation (“Optimization Step 2: Updating the Beamlet Weights” (page 448)). Then, proceed to Step 3.
3. Truncate any beamlet weights that exceed the maximum allowed by the modulation factor (“Optimization Step 3: Applying the Modulation Factor” (page 454)). Then, proceed to Step 4.

4. Calculate the dose for the current sinogram (“Optimization Step 4: Calculating the Dose” (page 455)). Then, proceed to Step 5.
5. Scale the dose to meet the primary prescription point (“Optimization Step 5: Scaling the Dose to Meet the Prescription” (page 460)). Then, proceed to Step 6.
6. Update the DVH and isodose display on the *Precision* System (“Optimization Step 6: Displaying the Dose” (page 460)).

If the optimization has not been paused by the user and the designated number of iterations has not been exceeded, proceed to Step 2 for the next iteration.

The final dose calculation steps are discussed in “Calculating the Final Dose” (page 462). When you click **Get Final Dose**, the optimized sinogram is converted into a delivery sinogram to be used by the system.

## ◆ Optimization Step 1: Calculating the Initial Sinogram

### Introduction to Sinograms

A **sinogram** is a two-dimensional data array consisting of rows representing **projections** and 64 columns representing the MLC leaves. Each element in the sinogram represents a **beamlet**. The gray-level of each beamlet indicates the amount of fluence or leaf-open time for a particular leaf at a particular range of gantry and couch positions corresponding to that projection.

#### *Projections*

For optimization of the MLC delivery pattern, the continuous gantry rotation and couch translation are divided into discrete units called **projections**.

For a *TomoHelical*/treatment plan, there are 51 projections per 360-degree gantry rotation. Thus, each projection corresponds to a 7.06-degree arc of continuous gantry rotation. For *TomoDirect* plans, each gantry angle is divided into a number of projections, as determined by the user-defined pitch value.

A projection represents an opportunity for each MLC leaf to open and close up to one time. A leaf may be open for the entire projection, closed for the entire projection, or open for some percentage of the projection. If a leaf is open for less than 100% of the projection time, the leaf is opened when the gantry and couch are located in the central portion of the projection. For example, a beamlet with 50% intensity would open 25% of the way into the gantry and couch travel across the projection, and close 75% of the way into the gantry and couch travel across the projection, to achieve 50% open time centered on the projection.

For a *TomoHelical* treatment plan, the number of projection angles per rotation in the planning system is set at 51 to achieve acceptable delivery resolution without exceeding the memory capacity of the optimizer and dose calculator. An odd number of projections per rotation was used to avoid parallel-opposed projections.

In earlier software versions, the helical dose calculation was discretized to assume that all radiation was delivered from the gantry and couch positions at the center of each projection. This approximation yielded good agreement between treatment plans and delivery measurements, except in the case of small, off-axis targets and small modulation factors (i.e., leaves open for a large fraction of the projection time). The approximation was improved in recent software versions by a technique that is sometimes referred to as *super-sampling*:

- For helical plans, the dose calculation approximates the dose to be delivered from three discrete samples per projection.
- For *TomoDirect* plans, at least two discrete samples per slice of the planning image are generated, rounded up to the nearest odd number of samples per projection.

A "sample" is a distinct source position from which rays are traced, and corresponds to a discrete gantry and couch position.

#### *Beamlets*

A **beamlet** represents the leaf open-time or fluence through a given leaf at a given projection position. Beamlets represent the basic units of optimization.

For a helical treatment plan, there are  $64 * 51 = 3264$  beamlets per gantry rotation. The number of gantry rotations depends on the target length, field size, and pitch.

MLC delivery instructions are stored as double-precision floating point values, resulting in a very large number of discrete intensity "levels" (higher precision than deliverable). The number of possible intensity levels for a single beamlet depends on the LINAC pulse rate and the projection time, where *projection time* = *gantry period*/51, for helical plans.

#### *Sinogram*

The vertical axis of the sinogram may be considered as a discretized representation of time and couch position. For helical treatments, the vertical axis of the sinogram is also a discretized and cyclical representation of gantry position. Stepping through the rows (projections) of the sinogram in time, the leaves are configured as indicated in each row, while the couch, gantry, and jaws (where applicable) move as specified in the plan.

Sinograms get their name from the sinusoidal pattern seen in the beamlet intensity for a helical plan. It is not a perfect sinusoid due to beam divergence and non-uniform target shapes. The following observations apply to the sinogram for a helical plan:

- The amplitude of the sine wave indicates the distance of the target from the central axis. If the target were located precisely at machine

isocenter, only the central leaves would be needed to treat the target, and the sinogram would contain a straight vertical line down the center of the sinogram (sine wave of zero amplitude). For targets not located on the central axis, a range of leaves is employed to treat the target as the gantry rotates.

- The thickness of the sine wave indicates the width of the target in the transverse plane. A larger target requires more open leaves at each projection angle.
- The period of the sine wave corresponds to one rotation of the gantry (51 sinogram rows). While there may be multiple sine waves representing multiple structures in a complex plan, all sine waves will have the same period.
- The length of the sine wave (number of projections) is determined by the length of the target, field width, and pitch.
- A dark sine wave represents a target, and a white sine wave represents an avoidance structure.

In the planned fluence sinogram shown in the plan report, all gray levels are relative to the maximum leaf open time in the sinogram. Thus, there is a black pixel in every sinogram.

## Determining the Number of Projections in the Sinogram

The optimizer requires as input an initial sinogram that identifies those beamlets that are available for optimization. Beamlets are projected through the patient to determine if they intersect a target or blocked structure. This requires basic information about the plan geometry: couch, gantry, and jaw positions at each sinogram projection

The sinogram is initially created with enough projections to cover the entire planning image volume.

For helical plans, the pitch  $P_H$  defines the relationship between couch and gantry positions:

$$[\text{Helical Pitch Equation}] P_H = d / W$$

where  $d$  is the couch travel distance per gantry rotation, and  $W$  is the nominal field width at isocenter (1.0 cm, 2.5 cm, or 5.0 cm).

The number of rotations  $N_R$  in the initial sinogram for a helical plan is:

$$[\text{Number of Rotations Equation}] N_R = \frac{N_S x}{P_H W},$$

where  $N_S$  is the number of slices in the planning image, and  $x$  is the slice spacing of the planning image.

The number of projections  $N_P$  in the initial sinogram for a helical plan is:

$$[\text{Helical Projection Count Equation}] N_P = 51 N_R$$

The helical pitch is unitless. The maximum allowed value is 0.5. The helical pitch may be conceptualized as the “tightness,” or amount of overlap, in the helical delivery pattern. A smaller number for the pitch implies more overlap in the rotations. For a smaller pitch number, more rotations are required to cover the same target length.

For helical plans, the first row of a sinogram initially represents a projection centered on 0 degrees gantry angle. However, the sinogram is later truncated to remove closed-leaf projections from the beginning of the sinogram. Thus, the first row of the sinogram displayed in the plan report does not necessarily represent a projection that is centered on 0 degrees gantry angle. (Later, a closed-leaf warmup of at least 10 seconds is also added to the delivery, but this is handled by the TDC, and the 10-second warmup is not included in the *Precision System* or in the plan reports.)



**TIP:** For a helical plan, as the gantry rotates around an off-axis target, the source-to-target distance varies, impacting the dose rate (inverse square effect), beam size (divergence effect), and fluence rate (transverse profile shape). Together, the overlapping rotations can result in a pattern of ripples in the dose distribution along the longitudinal axis, which are sometimes referred to as the helical thread effect. The ripples are predicted by the TPS dose calculation and are a consequence of the helical delivery pattern. By selecting the pitch value appropriately for the field width, off-axis position of the target, and prescription dose, the thread effect can be minimized. See Table II in Mingli Chen 2011 for recommended pitch values.

For *TomoDirect* plans, the pitch  $P_{TD}$  is defined as the couch travel in cm per sinogram projection. The *TomoDirect* pitch has units of cm/projection. The maximum allowed value is 0.5. When the field size is selected for a *TomoDirect* plan, the *TomoDirect* pitch defaults to one tenth of the field width. A projection represents an opportunity for each leaf to open and close up to one time. Thus, *TomoDirect* pitch may be conceptualized as the resolution of the *TomoDirect* delivery pattern along the longitudinal axis. A smaller number for the pitch implies finer resolution in the delivery pattern.



**IMPORTANT:** If the selected *TomoHelical* or *TomoDirect* pitch is too small, the leaf open times will be very short. This can result in a plan that does not meet the prescription dose (due to thresholding of leaf open times  $\leq 18$  ms), and poor patient QA results (see Westerly 2009 and the Patient QA chapter).

## Determining Dynamic Jaws Motion

The jaw motion for a dynamic jaws plan is not determined through an iterative optimization process. Rather, the jaw positions must be calculated prior to optimization of the MLC sinogram. This section describes how the jaw positions are determined for each sinogram projection.

Jaw positions are an input to the MLC optimization. The jaw positions determine the extent of each beamlet, and thus the intersection of each beamlet with the patient – impacting initial beamlet selection, and optimization and dose calculation at each iteration.

### *Dynamic Jaws Control File*

This section introduces the control files that contain instructions for the motion of the dynamic jaws. A dynamic jaws control file is required for machine QA procedures and treatment procedures with moving jaws. For a

patient treatment plan, the jaw instructions are built into the patient plan. For a machine QA procedure, the files are in text format (*.txt*), and the file name and storage location are referenced in the XML file.

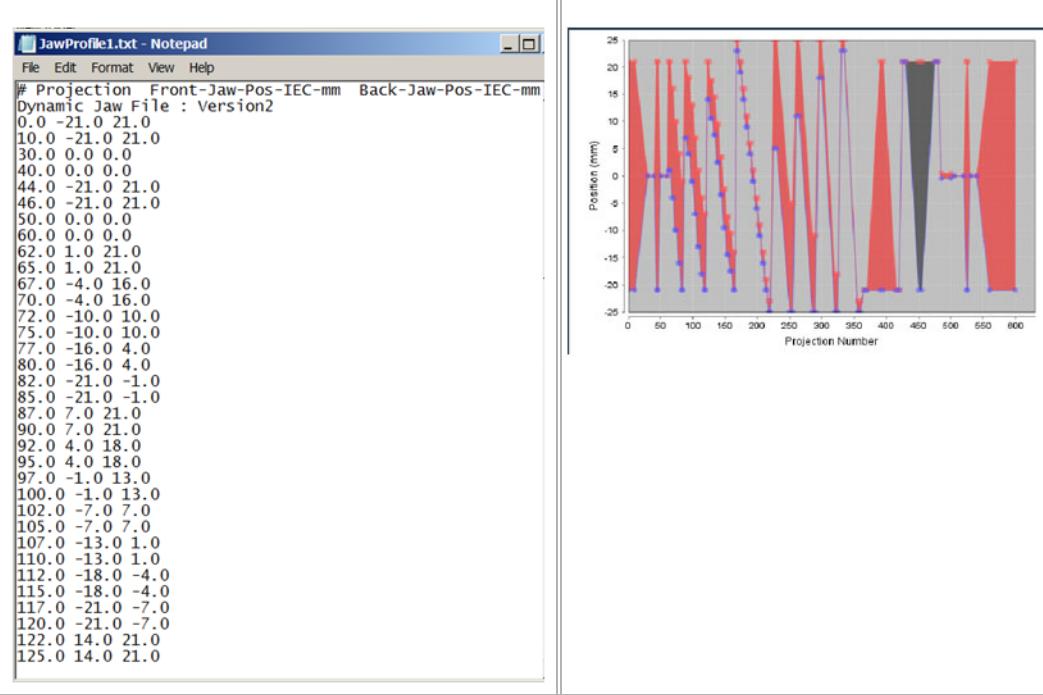
The figure below shows an example of one such file, which is provided by Accuray for use with the TQA™ Dynamic Jaws - Jaw Sweep module (a Machine QA patient). The first column represents the projection number of the MLC sinogram. The second column represents the Front Jaw positions in cm, and the third column represents the Back Jaw positions in cm. Refer to the jaws section of the System Overview chapter for correspondence between jaw positions and nominal field sizes. The control points specify the jaw positions at the start of the MLC sinogram projections listed in the projection column (the first projection is 0). The number of projections per gantry rotation or number of projections per second is specified elsewhere.

If the next control point has different jaw positions than the previous control point, the jaws will move at a constant velocity in order to arrive at the next control point at the start of the indicated projection. The velocity of the jaws will depend on the time and travel distance between control points. The maximum allowed jaw speed is 25 mm/s (projected to isocenter, in jaw numbers).



**NOTE:** To specify the jaw position mid-projection, a decimal value may be used for the projection number (Machine QA procedures only).

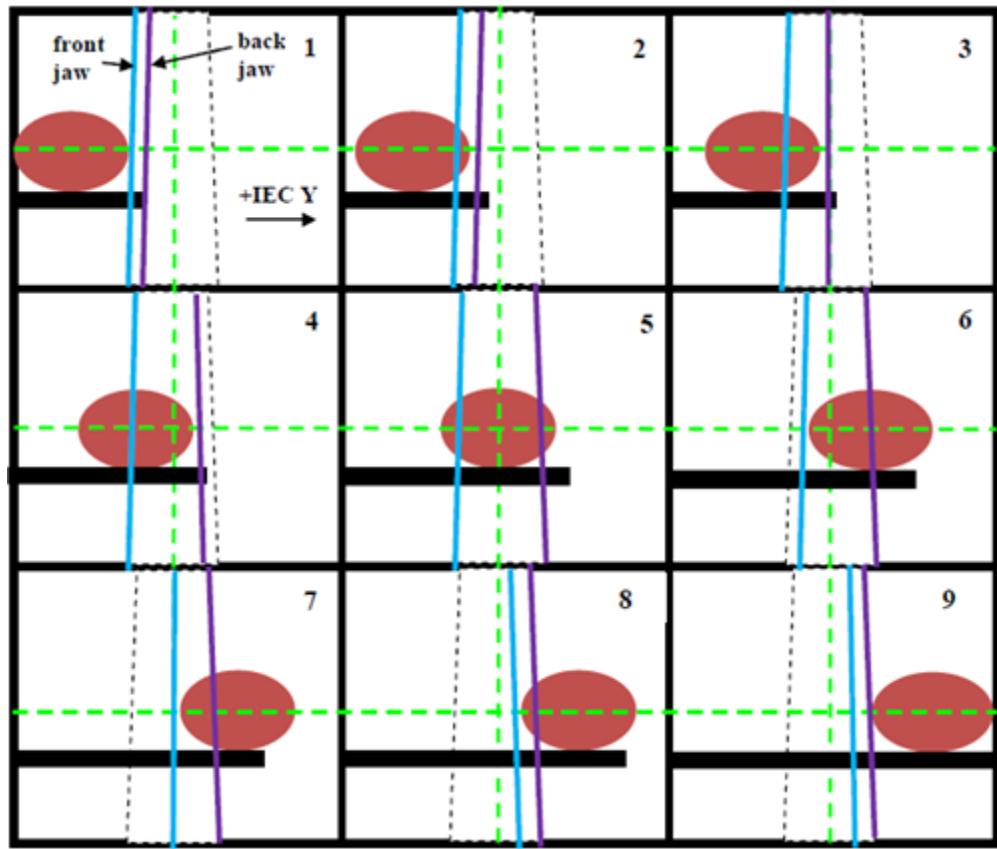
In the example below, the procedure starts with the jaws symmetrically opened to the nominal 5-cm field width. From projections 10 to 30, the jaws slowly transition to a closed position. From projections 30 to 40, the jaws remain closed. From projections 40 to 44, the jaws quickly open to the 5-cm field width. From projections 44 to 46, the jaws remain at the 5-cm field width. From projections 46 to 50, the jaws quickly close. From projections 50 to 60, the jaws remain closed. From projections 60 to 62, the jaws move to an asymmetric width of J20mm centered on a jaw position of 11 mm, where they stay until projection 65. From projections 65 to 67, the jaws move to an asymmetric width of J20mm centered on a jaw position of 6 mm, and so on.



Example of dynamic jaws file: TQA “Dynamic Jaws - Jaw Sweep” module. *Left:* Screenshot of the first several rows in the dynamic jaws text file. *Right:* Dynamic jaws file chooser plot in **Basic Create** tool of the TDC. The position axis is in jaw numbers. Purple control points correspond to the front jaw, and red control points correspond to the back jaw.

### Dynamic Jaws Example

The image below shows a dynamic jaws treatment with the 5-cm field width. The couch travels at a constant velocity in the +IEC Y direction, into the beam. The intersection of the green lines marks the radiation isocenter. The black dashed lines represent the 5-cm field width. The solid blue and purple lines represent the front jaw and back jaw positions, respectively (the back jaw is always located on the +IEC Y side of the front jaw). As the target enters the beam, the back jaw position moves just ahead of the target (beginning with a minimum jaw separation of J07), continuously expanding until the 5-cm field size is reached. The jaws are fully open to the 5-cm field size while the central portion of the target is being treated. As the inferior portion of the target begins to move past the beam, the front jaw position narrows to the minimum jaw separation, following the inferior target edge. Discrete jaw positions are illustrated here, but the jaw motion is continuous during the “sliding window” portion of the delivery.



Images of 5-cm Dynamic Jaw Delivery

### *Single Target*

The table below describes the stages in dynamic jaws motion to treat a single target. In stages I, III, and V the jaws are not moving. In stage II, the back jaw is moving. In stage IV, the front jaw is moving. The front and back jaws do not move at the same time during a single-target plan.

The minimum separation between the front and back jaws is J07. The minimum jaw width was chosen to ensure stability of the beam output and prevent a situation with excessive modulation for very narrow dynamic field sizes, which could make the treatment time too long. During the running start and stop portions of a dynamic jaws treatment, the jaws gradually transition to or from a minimum jaw width of J07.

The table below refers to the maximum jaw positions on the -IEC Y side and +IEC Y side of isocenter. The maximum jaw positions for a given target are determined according to the following criteria:

- The jaw positions are not allowed to extend outside the boundaries of the selected field width. For example, in the image above, the black dashed lines indicate the boundaries of the 5-cm fixed field width; neither jaw is allowed to be positioned outside of the black dashed lines.
- The maximum dynamic jaw positions may not form a field size that exceeds the target length.

<b>Stage</b>	<b>Panel</b>	<b>Front Jaw</b>	<b>Back Jaw</b>
I	1	Fixed at <i>maximum position</i> on the -IEC Y side of isocenter	Fixed with J07 separation from front jaw
II	2, 3, 4	Fixed at <i>maximum position</i> on the -IEC Y side of isocenter	Jaw is opening, traveling 3.5 mm ahead of the superior end of the target (in jaw numbers)
III	5	Fixed at <i>maximum position</i> on the -IEC Y side of isocenter	Fixed at <i>maximum position</i> on the +IEC Y side of isocenter
IV	6, 7, 8	Jaw is closing, following 3.5 mm behind the inferior end of the target (in jaw numbers)	Fixed at <i>maximum position</i> on the +IEC Y side of isocenter
V	9	Fixed with J07 separation from back jaw	Fixed at <i>maximum position</i> on the +IEC Y side of isocenter



**NOTE:** Dynamic jaws planning is not available for the 1-cm field width selection, since the maximum and minimum field widths would be the same.



**NOTE:** For a target with length  $\leq$  1 cm, the jaws will be fixed at the J07 field size throughout the delivery (effectively a fixed jaws delivery).



**NOTE:** If the target is shorter than the selected field width but longer than 1 cm, the maximum jaw positions will be symmetrically reduced to match the target size. The jaws start with the front jaw at its maximum position and the back jaw at the minimum J07 separation (Stage I). Then, the back jaw begins opening to its maximum position (Stage II). Both jaws are open to the maximum position for only an instant (Stage III), then immediately the front jaw begins to close down (Stage IV), reaching the minimum separation (Stage V).



**NOTE:** For a single target plan with a target length  $\leq$  2.5 cm, there is no difference between a J42 dynamic jaws plan and a J20 dynamic jaws plan.

The back jaw travels 3.5 mm ahead of the target (in jaw numbers) until the maximum field width is reached. As the target begins to move out of the beam, the front jaw follows 3.5 mm behind the target until the J07 jaw width is reached.

### Multiple Targets

This section explains the dynamic jaws motion for plans with multiple targets that have some separation along the Y axis. There are three possible scenarios, depending on the separation of the targets along the Y axis:

- Short gap: If targets are separated by less than approximately 1 cm along the Y axis, the jaws need to remain fully open in the gap between the targets. The back jaw opening can be reduced after the first target finishes exiting the beam. Leaves will only be open for beamlets that intersect a target.
- Long gap: If targets are sufficiently separated (by a little more than one field width) along the Y axis, the jaw aperture will reduce all the way to J07 at the superior and inferior ends of each target. Leaves will only be open for beamlets that intersect a target, so some projections in the gap will not have any open leaves.
- Intermediate gap: If targets are separated by more than 1 cm but less than just over one field width along the Y axis, the jaw aperture will narrow as much as possible at the target edges, but will not reach the minimum J07 width in between the targets. Leaves will only be open for projections that intersect a target, but some primary fluence will be sent into the gap, because treatment of the first target will not be finished before the front jaw must swing open to start covering the second target.

The table below describes the jaw motion at each stage of the delivery. The minimum jaw separation at the inferior end of target  $t$  (jaws on the -Y side of the beam) is the same as the minimum jaw separation at the superior end of target  $t+1$  (jaws on the +Y side of the beam).

**Stages in dynamic jaws delivery as the couch moves the target through the beam, in the case of multiple targets ( $t = 1, 2, \dots$ ) separated in distance along the IEC Y axis.**

Stage	Description	Front Jaw	Back Jaw
I	Start of treatment for target $t$	Fixed at <i>maximum position</i> for target $t$ on the -IEC Y side of isocenter	Fixed with J07 separation from front jaw
II	Target $t$ is entering the beam	Fixed at <i>maximum position</i> for target $t$ on the -IEC Y side of isocenter	Jaw is opening, traveling 3.5 mm ahead of the superior end of the target (in jaw numbers)
III	The central portion of target $t$ is being treated	Fixed at <i>maximum position</i> for target $t$ on the -IEC Y side of isocenter	Fixed at <i>maximum position</i> for target $t$ on the +IEC Y side of isocenter

<b>Stage</b>	<b>Description</b>	<b>Front Jaw</b>	<b>Back Jaw</b>
IV	Target $t$ is exiting the beam	Jaw is closing, following 3.5 mm behind the inferior end of the target (in jaw numbers)	Fixed at <i>maximum position</i> for target $t$ on the +IEC Y side of isocenter
V	Target $t$ finishes exiting the beam	Fixed with <i>minimum jaw separation</i> from back jaw (minimum separation depends on the spacing between $t$ and $t+1$ )	Fixed at <i>maximum position</i> for target $t$ on the +IEC Y side of isocenter
VI	In the gap between two targets $t$ and $t+1$	Jaw is opening quickly to <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter.	Fixed at <i>maximum position</i> for target $t$ on the +IEC Y side of isocenter.
VII	In the gap between two targets $t$ and $t+1$	Fixed at <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter	Fixed at <i>maximum position</i> for target $t$ on the +IEC Y side of isocenter.
VIII	In the gap between two targets $t$ and $t+1$	Fixed at <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter	Jaw is closing quickly to <i>minimum separation</i> from front jaw (minimum separation depends on the spacing between $t$ and $t+1$ )
IX	Start of treatment for target $t+1$	Fixed at <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter	Fixed at <i>minimum separation</i> from front jaw (minimum separation depends on the spacing between $t$ and $t+1$ )
X	Target $t+1$ is entering the beam	Fixed at <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter	Jaw is opening, traveling 3.5 mm ahead of the superior end of the target (in jaw numbers)
XI	The central portion of target $t+1$ is being treated	Fixed at <i>maximum position</i> for target $t+1$ on the -IEC Y side of isocenter	Fixed at <i>maximum position</i> for target $t+1$ on the +IEC Y side of isocenter
XII	Target $t+1$ is exiting the beam	Jaw is closing, following 3.5 mm behind the inferior end of the target (in jaw numbers)	Fixed at <i>maximum position</i> for target $t+1$ on the +IEC Y side of isocenter

<b>Stage</b>	<b>Description</b>	<b>Front Jaw</b>	<b>Back Jaw</b>
XIII	Target $t+1$ finishes exiting the beam	Fixed with <i>minimum separation</i> from back jaw (minimum separation is J07 if $t+1$ is the last target; otherwise minimum separation depends on the spacing between $t+1$ and $t+2$ )	Fixed at <i>maximum position</i> for target $t+1$ on the +IEC Y side of isocenter

If there are additional targets to be treated, let  $t = t+1$  and return to step VI.



**NOTE:** In the case of multiple targets spaced closely in the IEC Y direction so that the minimum J07 aperture is not used at the field edges, if a target is shorter than the field width, it is possible for both jaws to move at the same time (e.g., back jaw is opening according to Step X at the same time as front jaw is closing according to stage XII).

#### *Optimization and Get Final Dose with Dynamic Jaws*

The algorithm for optimization of the MLC delivery pattern with dynamic jaws is no different from optimization with fixed jaws.

When **Get Final Dose** is clicked, the actual gantry period in seconds, couch speed in cm/s, and jaw speed in cm/s are determined. The plan is adjusted to ensure that the couch speed, gantry speed, jaw speed, and leaf open times are within tolerance ranges. Although the jaw positions were limited to a conservative range so that the jaw motion was unlikely to require the plan to be slower than a fixed jaw plan of the same field width, if the jaw speed would exceed 25 mm/s, the plan will be slowed down to accommodate the jaw motion.

### Initial Beamlet Selection

Beamlets are considered available for optimization if any part of the beamlet passes through a target, and if no part of the beamlet passes through a blocked structure.

The **Beam Intersection** setting for each used structure is defined on the **Optimization** tab. The options are: **Allowed**, **Never**, and **Exit Only**.

- VOIs for which the **Beam Intersection** is set to **Allowed** are also known as *unblocked* structures. Beamlets may pass through an unblocked structure to treat a target.



**NOTE:** Importances and penalties may be applied to decrease the intensity of beamlets that pass through a structure, regardless of its beam intersection status.

- VOIs for which the **Beam Intersection** is set to **Exit Only** are also known as *directionally blocked* structures. Beamlets may pass through a directionally blocked structure to treat a target if, within the patient volume covered by the beamlet, the distance between the target and the source is shorter than the distance between the target and the directionally blocked structure. The source-to-structure distance is defined as the distance from the source to the closest point belonging to that structure that also is located within the beamlet.

The previous paragraph is often simplified as, “Beamlets may pass through a directionally blocked structure after passing through the target, but beamlets may not pass through a directionally blocked structure before reaching the target (i.e., beamlets may exit through a directionally blocked structure but may not enter through a directionally blocked structure).” This simplification is acceptable, if it is understood that for beam intersection criteria, the beamlet is not considered as a single line path through the patient, but the beamlet covers some volume. Even if a straight line could be drawn from the source through the target without passing through a directionally blocked structure, a beamlet is not allowed if a portion of the beamlet volume would intersect the directionally blocked structure before reaching the target.

- VOIs for which the **Beam Intersection** is set to **Never** are also known as *completely blocked* structures. Beamlets may not pass through completely blocked structures.



**NOTE:** A completely blocked structure will still receive dose due to scatter from beamlets that do not pass directly through the blocked structure. The dose calculation accounts for scatter dose.

Initial beamlet selection algorithms take into account the range of gantry angles and couch positions covered by each projection.

The fluence profile for an open leaf is wider than its 6.25 mm geometrical projection, due to penumbra and finite source effects. When determining if a beamlet passes through a target, the initial beamlet selector uses a transverse beamlet projection for each individual beamlet that is 0.4 leaf widths wider than the geometrical leaf projection on both the  $+X_g$  and  $-X_g$  sides<sup>1</sup> of the MLC. The initial beamlet selector checks this region of the patient to see if the beamlet passes through a target, when deciding whether to make a particular beamlet available for optimization.

The first beamlets available for optimization are when the superior end of the target crosses the inferior edge of the beam FWHM. The last beamlets available for optimization are when the inferior end of the target crosses the superior edge of the beam FWHM.

The target contours are considered to not only exist at the center of each slice, but to persist across the slice.

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1.  $+X_g$  and  $-X_g$  notation: The gantry rotates clockwise, and the  $+X_g$  side of the MLC is the leading side of the MLC as the gantry rotates.

The initial sinogram thus determined is an array of zeros and ones. Beamlets with zero intensity are not available for optimization; those leaves will remain closed, and no dose calculation is required for those beamlets. Beamlets that are available for optimization are referred to as “used” beamlets. In the initial sinogram, all the “used” beamlets will be assigned 100% intensity (i.e., leaves open for 100% of their corresponding projections). The intensity weightings for the “used” beamlets will be adjusted during the optimization process.



**NOTE:** If you want to change settings that impact the plan geometry, it will be necessary to re-compute the initial sinogram. Thus, optimization must be canceled and restarted. If optimization results exist and you try to change settings on the **Setup** tab such as the plan mode, a confirmation message will be displayed, indicating that this change will delete the optimization. Settings on the **Plan** tab that cannot be changed without canceling the optimization (e.g., pitch) are grayed out while optimization results exist.

## Beam Angles Display for *TomoDirect* Plans

The Beam Angles tab on the Accuray Precision™ Treatment Planning System is enabled for *TomoDirect* plans. See the *Treatment Planning Manual* for more information. There are two different beam display modes on the **Beam Angles** tab:

- **Editing Mode (2D):** During beam angle selection, a fast, simplistic rendering is used to draw the beams, based only on the displayed slice (doesn't account for the target width in neighboring slices). The beam display accounts for blocking and checks flash leaves. Dotted lines indicate the beam angles.
- **Plan Mode:** After clicking **Apply**, the Accuray Precision™ Treatment Planning System does a more comprehensive calculation, considering the width of the target in all slices. The system shows where the beam passes through the current slice. After clicking **View Entire Treatment**, the display on each slice shows the beam coverage on all slices.



**IMPORTANT:** When **View Entire Treatment** is not selected, the beam display is approximate and may not adequately show how the beams intersect the patient. Click **View Entire Treatment** to be certain that all beams are shown correctly. You can also examine the dose volumes to determine the dosimetric impact of the beams.

## ◆ Optimization Step 2: Updating the Beamlet Weights

### Planning Constraints

There are three kinds of DVH points:

- Prescription DVH points for targets ( $A\%$  of the target gets  $B$  Gy).
  - For the primary target (the only target listed in the Prescription area on the **Optimization** tab), the entire plan will be scaled so that the DVH curve passes through this prescription point.
  - For both the primary and other targets, the prescription DVH point is the one with the median dose (or greatest dose less than the median if the number of DVH points is even); it is also referred to as the “pivot.” This median dose ( $B$ ) is the prescription dose that will be attempted during optimization. The percentage  $A$  is not used for the pivot DVH point (other than for scaling the plan to meet the primary prescription and for the DVH display), but is used for the min and max DVH points with doses less than and greater than  $B$  respectively.
- Max DVH points for targets or sensitive structures ( $C\%$  of the target should get no more than  $D$  Gy).
- Min DVH points for targets ( $E\%$  of the target should get at least  $F$  Gy).

The following constraints are required for each target:

- One overall importance factor;
- One prescription/pivot DVH point;
- One max dose constraint (none of the target should get more than  $G$  Gy), and associated penalty factor;
- One min dose constraint (100% of the target should get at least  $H$  Gy), and associated penalty factor.

The following constraints may optionally be included for each target:

- Additional max DVH point (i.e., dose greater than the prescription DVH point), which shares a penalty factor with the target’s max dose constraint.
- Additional min DVH point (i.e., dose less than the prescription DVH point), which shares a penalty factor with the target’s min dose constraint.

The following constraints are required for each Region at Risk:

- One overall importance factor;
- One to three max DVH points and associated penalty factors;
- One max dose constraint (none of the target should get more than  $K$  Gy), and associated penalty factor.

Numbers  $A$  through  $K$  are specified by the user.

All max and min DVH points, as well as max and min dose constraints, represent soft constraints -- goals that the optimizer will attempt to approach by adjusting the sinogram through successive iterations. The prescription DVH point is a hard constraint for the plan, and will be applied in optimization Step 5. The modulation factor will be applied in optimization Step 3.

In the fluence update equation described in the next section, the associated penalties are applied to voxels within a structure for which the iteration dose exceeds the max dose constraint or is less than the min dose constraint.

Associated penalties are also applied to voxels within a structure, if the max DVH constraints ( $E\%$  of the target should get no more than  $F\text{Gy}$ ) or min DVH constraints ( $G\%$  of the target should get at least  $H\text{Gy}$ ) are not met. This requires a decision of which voxels within the structure to penalize, since  $(100 - E)\%$  of the voxels are allowed to get more than  $F\text{Gy}$ , and  $(100 - G)\%$  of the voxels are allowed to get less than  $H\text{Gy}$ . As explained in [Olivera 1999], the penalties are applied to the voxels that have the smallest excess above  $F\text{Gy}$  or the smallest shortage below  $H\text{Gy}$ , since these voxels will presumably require the least effort for the optimizer to bring into conformance with the max and min DVH constraints.

## Fluence Update Equation

The optimizer uses an iterative least-squares minimization approach as described in Olivera 1999.

## Optimization

The TomoTherapy® optimizer utilizes an iterative least-squares minimization approach as described in Olivera, Shepard et al. (1998; 1999), and Shepard, Olivera et al. (2000). The objective function is represented by the following equation:

$$O(\bar{\Psi}) = \sum_{t \in T} \left( \frac{\alpha_t}{N_t} \sum_{i \in t} (\beta_{t,i}^{\max} \beta_{t,i}^{\min} + \Phi_t^i) (D_i^p - D_i^d)^2 \right) + \sum_{r \in R} \left( \frac{\alpha_r}{N_r} \sum_{i \in r} (\phi_{r,i}^{\max} + \Phi_r^i) (D_i^p - D_i^d)^2 \right) [1]$$

where:

$O$  is the optimizer's objective function

$\bar{\Psi}$  is the energy fluence vector (with one entry per beamlet),

$T$  is the set of ROIs designated as targets; each ROI is treated as a set of voxels,

$\alpha_x$  is the Importance value for ROI  $x$  as entered on the Planning Station,

$\beta_{x,i}^{\max}$  is structure  $x$ 's maximum dose penalty if voxel  $i$  is greater than  $x$ 's maximum dose. Otherwise  $\beta_{x,i}^{\max}$  equals 1,

$\beta_{x,i}^{\min}$  is structure  $x$ 's minimum dose penalty if voxel  $i$  is less than  $x$ 's minimum dose. Otherwise  $\beta_{x,i}^{\min}$  equals 1,

$N_x$  is the number of voxels in ROI  $x$ ,

$\Phi_i^x = \sum_{dvh \in DVH(x)} \phi_{x,i}^{dvh}$  is the contribution from DVH point constraints for structure  $x$

at voxel  $i$ ;  $dvh$  is an individual DVH point for structure  $x$ ,

$DVH(x)$  is the set of all DVH point constraints for structure  $x$ . If  $x$  is a sensitive structure, the user specified the volume, dose, and penalty for the points. If  $x$  is a Target, the user specified volume and dose for the points and one of the points is a "pivot" point (marked by a dot on the user interface). Target DVH points at a lower dose than the pivot are treated as minimum dose constraints for their specified volume percentages and use the Min Dose (Gy) constraint penalty for their Targets; Target DVH points at a higher dose than the pivot are treated as maximum dose constraints for their specified volume percentages and use the Max Dose (Gy) constraint penalty for their Targets. Note that the pivot DVH point for a Target is not itself a member of  $DVH(x)$ .

$D_i^p$  is the dose prescribed to voxel  $i$  (always 0 for RARs),

$D_i^d$  is the deposited dose in voxel  $i$ ,

$R$  is the set of ROIs designated as regions at risk (RAR); each ROI is treated as a set of voxels,

$\phi_{x,i}^{\max}$  is structure  $x$ 's maximum dose penalty if voxel  $i$  is greater than  $x$ 's maximum dose. Otherwise  $\phi_{x,i}^{\max}$  equals 0,

$\phi_{x,i}^{dvh}$  is structure  $x$ 's DVH point penalty if voxel  $i$  violates  $x$ 's DVH point penalty constraint. Otherwise  $\phi_{x,i}^{dvh}$  equals 0,

The fluence update equation used in TomoTherapy® optimization is found by solving Equation 1 for its extreme value. This leads to the following, which is used to update the fluence value for each leaf in a given projection:

$$\Psi_j^{k+1} = \Psi_j^k \left[ \frac{\sum_{t \in T} \left( \frac{\alpha_t}{N_t} \sum_{i \in t} (\beta_{t,i}^{\max} \beta_{t,i}^{\min} + \Phi_i^t) d_{ij} D_i^p \right) + \sum_{r \in R} \left( \frac{\alpha_r}{N_r} \sum_{i \in r} (\phi_{r,i}^{\max} + \Phi_i^r) d_{ij} D_i^p \right)}{\sum_{t \in T} \left( \frac{\alpha_t}{N_t} \sum_{i \in t} (\beta_{t,i}^{\max} \beta_{t,i}^{\min} + \Phi_i^t) d_{ij} D_i^d \right) + \sum_{r \in R} \left( \frac{\alpha_r}{N_r} \sum_{i \in r} (\phi_{r,i}^{\max} + \Phi_i^r) d_{ij} D_i^d \right)} \right] \quad [2]$$

where:

$\Psi_j^{k+1}$  is the energy fluence for beamlet  $j$  at iteration  $k+1$ ,

$\Psi_j^k$  is the energy fluence for beamlet  $j$  at iteration  $k$ ,

$d_{ij}$  is the dose contribution to voxel  $i$  from beamlet  $j$  per unit of energy fluence,

Since the prescribed (desired) dose for any RAR is zero,  $D_i^p$  in the second term of the numerator of Equation 2 equals 0 and so this whole second term drops out. Equation 2 then simplifies to:

$$\Psi_j^{k+1} = \Psi_j^k \left[ \frac{\sum_{t \in T} \left( \frac{\alpha_t}{N_t} \sum_{i \in t} (\beta_{t,i}^{\max} \beta_{t,i}^{\min} + \Phi_i^t) d_{ij} D_i^P \right)}{\sum_{t \in T} \left( \frac{\alpha_t}{N_t} \sum_{i \in t} (\beta_{t,i}^{\max} \beta_{t,i}^{\min} + \Phi_i^t) d_{ij} D_i^d \right) + \sum_{r \in R} \left( \frac{\alpha_r}{N_r} \sum_{i \in r} (\phi_{r,i}^{\max} + \Phi_i^r) d_{ij} D_i^d \right)} \right] [3]$$

This fluence updating equation is applied after each iteration once  $D_i^d$  has been computed for all voxels at iteration  $k$ .

Equation 3 essentially states that the energy fluence for a given leaf in a given projection is equal to the energy fluence for that leaf from the previous iteration multiplied by an update factor. This update factor is obtained by querying all of the voxels influenced by the leaf and adding contributions for voxels contained in an ROI that has been declared eligible (via the “Use” checkbox) for optimization as specified in the Planning Station. For a target voxel, the summation in the numerator and the first summation term in the denominator are impacted. For an RAR voxel that is above the maximum or outside of the DVH dose objective specified for the plan on the Planning Station, the second summation in the denominator is impacted. Even though this iterative optimization process could be stopped by specifying a threshold for the change in the objective function for a given iteration, the process is stopped in the current implementation by the user specifying a number of iterations or explicitly pressing the Pause or Get Full Dose button on the Planning Station.

## Interpretation of the Fluence Update Equation

The following is a simplified version of the objective function, to illustrate the roles of importances and penalties in planning:

*Objective Function =*

$$\sum_{\text{used structures}} \frac{1}{\# \text{ voxels in structure}} \sum_{\text{voxels}} ((\text{Prescribed Dose} - \text{Iteration Dose})^2 * \text{Importance} * \text{Total Penalty})$$

The summation includes every voxel in the dose calculation grid of a target or Region at Risk for which the “use” box has been selected.

The fluence update equation effectively minimizes the objective function. A result with a smaller value for the objective function is more “desirable” to the optimizer. Any difference between the prescribed and calculated iteration dose increases the value of the objective function and makes the current sinogram less acceptable to the optimizer. For a target, the prescribed dose is indicated by the target constraints. For an avoidance structure, the prescribed dose is considered to be zero.

The square of the difference between the prescribed and calculated iteration dose is magnified by the importance for each target or avoidance structure. The user can enter any range of positive integer values for the importance, relative to other structures. Higher numbers indicate that it is more important for the optimizer to achieve consistency between the prescribed and calculated dose for that particular structure. The objective function is weighted by the number of voxels in the structure, so that a small structure (which has few voxels) is not less important than a large structure.

The square of the difference between the prescribed and calculated dose is also magnified by a penalty, if the current optimization result fails to achieve specific constraints, such as max dose, min dose, or DVH constraints. Like the importance, the penalty can have any range of positive integer values, and its role in the objective function will be determined by its value relative to the importances and penalties for other structures.

Whereas importance values are applied uniformly to all voxels in the structure, penalties only take effect for those voxels that fail to meet a specific constraint. If all constraints are met for a target voxel, the penalty reduces to unity, and the other terms in the objective function remain for that voxel. If all constraints are met for a sensitive structure voxel, the penalty reduces to zero, and the other terms in the objective function drop out for that voxel.



**TIP:** If you want the optimization to continue attempting to reduce the dose to a sensitive structure, you must assign some DVH constraints or max dose that the optimization has not yet achieved. After the optimization achieves the constraints for a sensitive structure, it does not attempt to further reduce the dose in subsequent iterations.

Individual voxels in the VOI mask used for calculation of DVHs and dose statistics may belong to multiple VOIs, where structures overlap. However, the VOI mask used as an input to the optimizer takes into account optimization overlap priority of like structures. In the VOI mask used as an input to the optimizer, each voxel belongs to not more than one target (the target with the highest optimization overlap priority) and not more than one critical structure (the critical structure with the highest optimization overlap priority). For optimization, targets take precedence over avoidance structures.

Each voxel at medium, low, or very low resolution includes 4, 16, or 64 voxels at the native image resolution, respectively. During optimization, these larger voxels are driven to the target dose if they include any smaller voxels at the native image resolution that belong to the VOI mask for a target. This means that optimizing at lower resolutions tends to enlarge your treated volumes.



**TIP:** The grid choice for optimization is at the discretion of the planner. However, High Resolution is always recommended for Final Dose, to achieve the best spatial resolution for the dose information that will be presented for final plan evaluation.

The objective function includes a summation over all voxels at the selected resolution that intersect targets, and also a summation over all voxels at the selected resolution that intersect avoidance structures. The prescription dose for both target and avoidance summation terms in the objective function is determined as follows:

If the voxel includes any smaller voxels at the native image resolution that belong to a target VOI mask, the prescription dose for that entire voxel is set to the target dose (or to the highest target dose, if the voxel intersects more than one target).

If the voxel does not include smaller voxels at the native image resolution that belong to a target VOI mask but does include smaller voxels at the native image resolution that belong to the VOI mask for an avoidance structure, the prescription dose for that voxel is set to zero.

## Optimization of *TomoDirect* Plans

For a *TomoDirect* IMRT plan, the user chooses two to twelve beam angles per target. The optimizer concatenates the sinograms for all the beam angles into one sinogram, and performs optimization on the entire sinogram on a per-beamlet basis, using the same fluence update equation as for helical plans. The optimizer does not allow the user to manually weight the beam angles.

The user can select to open “flash” leaves for a *TomoDirect* plan. Flash leaves extend the open leaves towards lower leaf numbers (negative flash) or higher leaf numbers (positive flash) starting at the lowest or highest open leaf, respectively. Flash leaves are set independently for each beam angle. The *Treatment Planning Manual* introduces the rotational coordinate system and explains how you can check if the system was able to provide the number of flash leaves you requested, having taken into account the width of the MLC and any blocking constraints.

It is not possible to optimize leaf open times in air. Thus, the fluence through each flash leaf is set as the average of the fluence through the second and third outermost leaves, on the same side of the beam, before expansion. The second and third outermost leaves are used because the leaf on the edge of the field, before expansion, may have a hot fluence value if it passes through a patient/air boundary. Fluence in the expanded region is kept constant, by adjusting flash leaf open times for cone (transverse profile) shape. Dose from flash leaves is accounted for during optimization.

### ◆ Optimization Step 3: Applying the Modulation Factor

The **modulation factor** (MF) is a number that the user enters on the **Optimization** tab to limit the range of leaf-open times for non-zero (used) beamlets in the plan:

$$MF = \frac{\text{maximum beamlet open time in sinogram}}{\text{average beamlet open time for used beamlets}}$$

Two types of modulation factors are used in planning. The planning modulation factor is the desired upper limit set by the user. The actual modulation factor is listed on the **Plan** tab or **Evaluate** tab when dose calculations are available.



**NOTE:** On the first page of a *TomoDirect* plan report, an overall modulation factor is listed. This is an average of the modulation factors for the individual beam angles, weighted by the couch travel distances for each beam.

As a result of sinogram adjustments in Optimization Step 2 and 3, it is possible that the modulation factor could exceed the user-defined limit.

In Optimization Step 3, the average beamlet weighting is determined for all the used beamlets in the current sinogram. For *TomoDirect* plans, the max and average open time is computed separately for each beam angle, so each beam angle's MF can be constrained independently. All beamlet weightings that exceed the product of the modulation factor and the average beamlet weighting will be truncated. These beamlet weightings will be set to the product of the modulation factor and the average beamlet weighting.

Truncation of the large beamlet weightings causes a reduction in plan dose. In Optimization Step 5, all the used beamlets in the sinogram will be linearly scaled to ensure that the prescription dose is achieved.

The final actual modulation factor will be different from the planning Modulation Factor. It can be larger than the desired MF, because applying the modulation factor constraint truncates long leaf open times to  $MF * (\text{average open time})$ , which reduces the average leaf open time. It might also be smaller, because fractionation thresholds away small leaf open times (leaves open 18ms or less), which increases the average leaf open time.

## ◆ Optimization Step 4: Calculating the Dose

The full dose calculation algorithm used is Collapsed Cone Convolution Superposition (CCCS) with pre-computed, Monte Carlo-generated scatter kernels. The implementation of CCCS is similar to that described by Quan Chen 2011.

### Dose Calculation Accuracy

The treatment planning system uses a Convolution/Superposition dose calculation algorithm similar to the *TomoTherapy* one described originally in 1989 (Ahnesjo A). A more recent description of the *TomoTherapy* algorithm, as implemented on GPU hardware, was published in 2011 (Chen Q, Chen M, and Lu W).

In homogeneous media, the *TomoTherapy* algorithm is verified to have less than 3% absolute dose error (relative to the prescription dose level) and less than 3mm distance to agreement error in system testing. For heterogeneous material, like that found in real patients, the *TomoTherapy* Convolution/Superposition algorithm was verified against Monte Carlo. Calculations in heterogeneous media showed overall good agreement, with deviations within 3%-2mm; however, deviations of up to 4% were found for the small lung tumors as published in 2009 (Sterpin E, Salvat F, Olivera G, Vynckier S).

The Convolution/Superposition algorithm accuracy decreases when traversing through large metal objects, such as hip prosthesis. The *TomoTherapy* algorithm only expects bone or water-like materials, and high-Z materials have a lower stopping power than the algorithm expects. Dose near but outside a high density structure will be overestimated, due to excess scatter. Dose further away, but in the shadow of the structure, will be underestimated due to excess beam attenuation. Additionally, high density structures are often accompanied by CT artifacts which also make it difficult to calculate dose accurately for beams passing through them. Hence, users should consider disabling beams that pass directly through large metal objects when planning.

## Full Dose Calculation: Implementation of Convolution-Superposition

Dose calculation is a three-step process:

1. Calculate fluence.
2. Calculate TERMA.
3. Account for scatter dose.

These three steps are described in detail below:

1. Calculate Fluence.

The fluence incident on the patient is determined by the data in the beam model and the optimized MLC intensity pattern. At each projection, the incident fluence is calculated in a two-dimensional plane.

For details on how the fluence is determined from the beam model data, see “Combining the Fluence Parameters” (page 423).

2. Calculate TERMA (Total Energy Released per unit Mass).

The TERMA calculation is a four-step process:

- a) The two-dimensional fluence plane is projected into the patient volume from a Beam’s Eye View perspective.
- b) Density is interpolated along fluence rays to determine the radiological path length.

- c) A Fluence Attenuation Table is used to determine mass attenuation coefficients as a function of radiological path length.
- d) TERMA is interpolated onto the patient dose calculation grid.

These steps are described in detail below:

- a) The two-dimensional fluence plane is projected into the patient volume from a Beam's Eye View perspective.

The dose calculator uses Graphics Processing Unit (GPU) technology to do the TERMA raytrace. Rays are traced using a radial “beam’s eye” perspective, as illustrated in Figure 6 of Lu 2010, because it parallelizes well on the GPU. The number of rays and number of samples per ray is determined by the resolution of the dose calculation grid.

- b) Density is interpolated along fluence rays to determine the radiological path length.

The radiological path length [ $\text{g/cm}^2$ ] traversed by primary photons is used for calculating TERMA. Thus, inhomogeneities are taken into account.

- c) A Fluence Attenuation Table is used to determine mass attenuation coefficients as a function of radiological path length.

The pre-computed Fluence Attenuation Table (FAT) gives attenuation values versus radiological path length in water ( $\mu_w/\rho$ ) and cortical bone ( $\mu_b/\rho$ ). Attenuation at other densities is determined as follows.

For voxels of density less than water, use  $\mu_w$ .

For voxels of density **greater than bone**, use  $\mu_b$ .

For voxels of **intermediate density**, interpolate between  $\mu_w$  and  $\mu_b$ .

The FAT accounts for beam hardening by allowing the effective mass attenuation coefficients to vary with radiological depth.

- d) *TERMA is interpolated onto the patient dose calculation grid.*

The imported planning image contains ( $2^n \times s \times 2^n$ ) voxels in (IEC X, IEC Y, and IEC Z), where s is the number of slices, and n is an integer. For example,  $n=9$  for an image of 512 x 512 resolution in the transverse plane.

For optimization and dose calculation:

<b>High Resolution</b>	The dose is calculated on a grid of $(2^n \times s \times 2^n)$ voxels along dimensions (IEC X, IEC Y, IEC Z).
<b>Medium Resolution</b>	The dose is calculated on a grid of $(2^{(n-1)} \times s \times 2^{(n-1)})$ voxels.
<b>Low Resolution</b>	The dose is calculated on a grid of $(2^{(n-2)} \times s \times 2^{(n-2)})$ voxels.
<b>Very Low Resolution</b>	The dose is calculated on a grid of $(2^{(n-3)} \times s \times 2^{(n-3)})$ voxels.

If the imported planning image is not large enough to contain the couch (53 cm wide), additional voxels are added to the dose calculation grid to contain the couch, but the voxel size will not be affected.



**NOTE:** The discrete voxels of the dose grid may be more visible in *TomoDirect* treatments than in *TomoHelical* treatments, due to the lack of blurring with fewer beam angles.

### 3. Account for Scatter Dose.

To account for scatter dose, the TERMA is convolved with the scatter kernel. The scatter kernel was computed using Monte Carlo. The kernel is based on water. Patient inhomogeneities are scaled in voxel space to water-equivalent distance. The kernel is polyenergetic; it is made up of a weighted sum of monoenergetic kernels. Beam hardening is neglected in the kernel.

All beam models use the same scatter kernel. The kernel indicates how dose spreads around 24 different radially symmetric zenith angles with respect to an incoming photon. The kernel representation for each zenith angle is a parametric function with parameters  $a_1$ ,  $a_2$ ,  $b_1$ , and  $b_2$ :  $b_1(1 - e^{-a_1 r}) + b_2(1 - e^{-a_2 r})$ .

The kernel must be tilted to represent the beam direction. A gantry rotation is divided into 24 sectors (happenstance that this is the same as the number of zenith angles in a kernel). Thus, each sector represents 15 degrees of gantry rotation. The kernel is tilted to match the average direction of the rays within the sector. The same kernel tilt is applied to all rays within a 15-degree sector.

## Adaptive Full Dose Correction

The optimizer employs a dose calculation scheme that is referred to as the “Adaptive Full Dose Correction” method. The method implemented in the planning system is an adaptation of the method proposed by Lu 2010.

The adaptive full dose correction method employs two dose calculation algorithms:

- The full dose calculation algorithm is Collapsed Cone Convolution Superposition (CCCS) with pre-computed, Monte Carlo-generated scatter kernels. This algorithm is discussed in the previous sections.
- The approximate dose calculation is a fast and simple ray-tracing technique, which is called the Fluence Convolution Broad Beam (FCBB) method. As described in Lu’s paper, the fluence function is convolved with a dose distribution function with terms representing attenuation, divergence, and lateral spreading.

In the dose calculation before the first iteration, dose is computed using both the full dose calculation method and the fast and approximate method. The full dose calculation result is used to update the DVH and isodose display. For iterations one through nine, the full dose calculation is not performed. Instead, the fast and approximate FCBB calculation is performed, to save time. The approximate FCBB iterations are used to predict the dosimetric difference impact of small sinogram changes with respect to the most recent full dose calculation, assuming that the full dose and approximate dose calculations would respond similarly to small sinogram changes. For the tenth iteration, dose is again computed using both the full dose calculation method and the approximate method.

The dose calculation for iteration  $i$  may be summarized as follows:

1. Calculate the approximate dose,  $FCBB_i$ .
2. If  $i$  is a full dose iteration, calculate and display the full dose,  $CCCS_i$ . Also, determine the *full dose correction* =  $(CCCS_i - FCBB_i)$ , for use in subsequent iterations.

If  $i$  is not a full dose iteration, calculate and display the *corrected approximate dose* =  $(FCBB_i + \text{full dose correction})$ .



**NOTE:** In the Adaptive Full Dose Correction method, the approximate dose  $FCBB_i$  is never displayed on the TPS screen without the *full dose correction*.

The Adaptive Full Dose correction method assumes that the difference between the full dose and approximate dose remains constant across several iterations of the most recent full dose calculation.

## ◆ Optimization Step 5: Scaling the Dose to Meet the Prescription

Here, the hard constraint of the primary prescription DVH point is applied. The primary prescription point is specified by the user as a percentage of the selected target volume, or as the median (50%), max (0%), or min (100%) target dose.

To apply the prescription constraint to the plan, the calculated dose from optimization Step #4 at the prescription point is compared against the prescribed dose. All used (non-zero) beamlet open times for the sinogram are linearly scaled up by a ratio of the prescribed to the calculated dose.

If **High Optimization Resolution** is not selected, nearest-neighbor interpolation is used during optimization to up-sample the calculated dose to the resolution of the planning image, to determine the dose to the primary target and other VOIs. However, trilinear interpolation is used for dose calculation and display (i.e., the results of the trilinear interpolation are visible to the user). An additional scaling factor is calculated and applied to account for differences between the nearest-neighbor and trilinear interpolation, to ensure that the prescription dose is achieved. The scaling factor is very close to 1.0.

## ◆ Optimization Step 6: Displaying the Dose

The system displays all dose iterations on the *Precision System* (both full dose calculations and corrected approximate dose iterations as described in Step 4), to the extent that the *Precision System* has time to display them. The display of some iterations will be skipped if the *Precision System* can't display them quickly enough.

See "Dose-Volume Histogram (DVH)" in the *Treatment Planning Manual* for a discussion of DVH display modes and how overlapping contours are handled.

Dose is calculated on the voxels of the patient dose calculation grid, then upsampled for display on the resolution of the planning image. For dose calculation, trilinear interpolation is used to up-sample the calculated dose to the resolution of the planning image. The isodose lines are then generated using a 3D algorithm called marching cubes, which was introduced by Lorensen and Cline 1987.

The dose overlay can be displayed on the planning image as a color wash with the **Fill** or **Grid** options. When **Grid** is selected, each voxel in the dose grid is colored appropriately. When **Fill** is selected, the *screen* pixels are colored inside the isodose lines (which are generated as described in the previous paragraph), resulting in a smoother appearance.

A VOI mask is used to identify voxels in the planning image that correspond to each VOI, as discussed in "VOI Contour to Mask Volume Conversion" (page 430). In the mask, each voxel in the planning image is considered to

be inside a VOI if the center of the voxel is on or inside the VOI boundary; partial voxels are not considered. The VOI mask has the same resolution as the primary CT image.

If **High** resolution is not selected, trilinear interpolation is used to up-sample the calculated dose to the resolution of the planning image, to determine the dose to each VOI for dose calculation and display.

The DVH for a VOI is formulated using 256 dose buckets. The range of dose values covered by the buckets is from the minimum dose to the VOI to the maximum dose to the VOI.

## TomoDirect DRR display



**TIP:** The **Beam's Eye View** can be used to check the relative orientation of the patient and the treatment beam, and to identify undesirable hot or cold regions in the beam.

A **Beam's Eye View** display is available for *TomoDirect* Treatment Delivery plans or Forward Plans by selecting a layout that includes this display. This tool displays the relative beam entrance fluence from a given *TomoDirect* angle, overlaid on a digitally reconstructed radiograph (DRR). The DRR is a synthetically computed image generated via tracing of X-rays through the patient CT data. The path length is based on the relative CT numbers in the patient CT scan and is sampled at intervals along each ray path. A CT density model is not applied when generating DRRs. The generated image is the projection onto a plane that is perpendicular to the beam axis of the simulated X-ray, a perspective projection in the IEC X projection, and an orthogonal projection in IEC Y (similar to a scout scan). OpenGL raytracing is used to render the entire CT image volume at the full resolution of the display window.

The relative beam fluence map is the entrance fluence of the IMRT or 3DCRT *TomoDirect* beam delivery (with leaf positions determined by the MLC sinogram), mapped to the same plane as the DRR. When the relative beam fluence map is displayed without the DRR, a legend indicates the gray level correspondence to the relative intensity of beam fluence, expressed as a percentage relative to the maximum fluence value among all the beam angles that make up a given *TomoDirect* plan. That is, the gray levels have the same meaning for all the beam angles within a plan.

The aspect ratio of the **Beam's Eye View** is formatted to fit the window and does not reflect the actual treatment aspect ratio.

In plan reports for *TomoDirect* 3DCRT plans, instead of a sinogram, an outline of the beam fluence is displayed over the patient's DRR for each beam angle. This display for the TomoDirect 3DCRT plan report is generated using the same algorithm as the **Beam's Eye View**, except that only the outline of the fluence map is displayed, and not the fluence map itself.

Note that the beam fluence map or outline on the patient DRR includes overlap of the fan beams during delivery. (The amount of overlap along the y-axis depends on the couch speed and collimator width.) The sinogram seen in IMRT mode is simply a table of leaf open times, and does not include overlap. This means that the sinogram display in IMRT mode will typically appear more elongated than the beam fluence map or outline.

## ◆ Calculating the Final Dose

The output of the completed optimization process is a dose computation including all scatter dose, and an optimized sinogram that will theoretically deliver this dose to the patient. However, the planning system does not determine machine delivery instructions until the Final Dose stage.

When the user clicks **Get Final Dose**, End of Planning (EOP) calculations are performed:

- Adjustments to leaf opening and leaf closing times are made for MLC latency.
- Leaf open times  $\leq 18$  ms are discarded.
- For helical plans, the maximum beamlet open time for the latency-corrected sinogram is determined, and is used to assign the gantry period as:

$$\text{gantry period} = \max \text{ leaf open time in sinogram} * 51$$

If the gantry period equation results in a gantry period of less than 11.8 seconds, the gantry period is set to 11.8 seconds. If the gantry period equation results in a gantry period of more than 60 s, the plan is undeliverable and the *Precision System* will issue a warning.

The couch speed for a helical plan is determined as:

$$\text{helical couch speed} = \text{Pitch} * \text{field width/gantry period}$$

- For *TomoDirect* plans, the projection time determines the couch speed for each beam angle (couch speeds may vary with beam angle). The projection time is the greater of the maximum leaf open time in the sinogram for a given beam angle, or 230 ms.

$$\text{TomoDirect couch speed} = \text{pitch} * \text{projection time}$$

- For the plan to be deliverable, the couch speed must be in the range of 0.0125 mm/second to 50 mm/second for treatment plans.



**NOTE:** For *TomoDirect* plans, the **Plan Summary** page of the plan report lists the composite (total) beam-on time and expected monitor units for all the beam angles in one fraction. Subsequent pages include information about the individual beams: MLC sinogram, beam expansion (flash) information, the delivery angle, the targets used for the beam, and the couch speed.

- To avoid overburdening the MLC air supply during delivery, the number of leaf cycles per second must not exceed an assigned value (e.g., 163 leaf cycles per second). If there are too many leaf cycles per second, the plan is slowed down to bring the leaf usage into range.
- For plans with dynamic jaws, the jaw positions for each projection were determined at the time of initial sinogram creation. After determining the projection times, the software checks that the jaw velocity will not exceed the speed limit of 25 mm/s, in jaw numbers. Although the jaw positions were limited to a conservative range so that dynamic jaw motion was unlikely to slow down the plan, if the jaw speed would still exceed 25 mm/s, the plan will be slowed down to accommodate the jaw motion.
- As discussed in Optimization Step #1, the MLC sinogram is truncated to remove closed-leaf projections from the beginning and end of the sinogram.

The optimized sinogram is now converted into a delivery sinogram to be used by the system. A final, full dose calculation is performed on the adjusted sinogram, using the algorithm described in “Full Dose Calculation: Implementation of Convolution-Superposition” (page 456). This final dose calculation appropriately calculates dose for the final optimized MLC sinogram in which the short leaf open times have been discarded, but for which latency corrections to the delivery instructions have not been made.

## ◆ Determining the Warm-up Time

For all treatment plans, leaves are closed for at least the first 10 seconds of beam-on time to allow for output ramp-up. There is a warm-up period for each beam in a *TomoDirect* plan. The warm-up time is the same for interrupted as for completion procedures.

The warm-up time is not included in any of the treatment times displayed on the *Precision* System, or in the plan reports. The warm-up time is added by the TDC.

The **Recommended linac warmup (ms)** is listed in the **Edit Machine** area, and is 6 seconds for imaging procedures, or 10 seconds for treatment procedures that were planned on the *Precision* System. If you create a Machine QA procedure, warm-up time can optionally be included by adding closed-leaf projections to the beginning of the sinogram.

When the TDC downloads a fraction, it makes a copy of the delivery plan and adds warm-up time to each *TomoHelical*/procedure and each individual *TomoDirect* beam in the delivery plan.

Since treatments are delivered in projections, the actual warm-up time is an integer number of projections. To ensure that at least the minimum 10 seconds is applied, the following equation is used:

$$\text{Warm-up time} = \text{ceiling}(10 \text{ s} / \text{s per proj}) * (\text{s per proj})$$



**NOTE:** The "ceiling" operation rounds up to the nearest integer number of projections, so ceiling(10s/s per proj) is the number of projections in the warmup.

Treatment times listed in the TDC software include the warm-up time.

## ◆ Forward Planning Algorithm for *TomoDirect*

*TomoDirect* plans may be created using IMRT, 3DCRT, or Forward Planning algorithms. Forward planning allows the user to create plans without requiring VOIs to be defined. Forward planning is available for *TomoDirect* planning, but not for helical planning.

All forward plans have fixed beam angles, a moving couch, and leaf modulation. Forward plans can have fixed or dynamic jaws.

In forward planning, the user must select the beam angles, set the field extent, and assign the dose distribution. This information is used to produce a fluence map. The delivery plan is calculated from the fluence map.

## User Inputs

### *Setting the Field Extent of a Beam Angle*

The user sets the extents of the treatment field from each angle by defining a rectangle in a BEV (**Beam's Eye View**) window. The left and right extents of the treatment field correspond to MLC leaves, and the top and bottom extents of the treatment field correspond to positions along the IEC Y axis. Since the left/right extents correspond to MLC leaves, these extents can only be moved in whole leaf increments. The extents along the superior/inferior direction can be set to arbitrary positions.

### *Assigning the Dose Distribution*

Within each beam angle, multiple fields can be defined. The extents of each field are inherited from the parent beam angle. Each field has its own fluence map, which is a rectangular array of pixels that covers the full extent of the field. The planning software provides tools that allow the user to define the fluence map by blocking and opening portions of the field.

Initially, the fluence map for a field is considered to have 100% fluence at every pixel.

Fields within a beam angle have user-specifiable weights associated with them. These values define the weighting of each field relative to other fields within the same beam angle. The sum of weights of fields in an angle is always 100. Beam angles also have weights that define the influence of each beam angle relative to other beam angles assigned to the same dose group. The weights of beam angles within a dose group also sums to 100.

The forward planning workflow produces a preview dose volume while the user edits beam and field weights. Once a satisfactory preview dose volume is achieved, end-of-planning and a dose calculation must be performed to produce a final dose volume.

#### *Computing Preview Dose*

Each field within a beam angle will have a dose volume computed for it. The first step in computing this dose volume is to convert the field's fluence map into a sinogram, and the sinogram into a delivery plan. Conversion of the fluence map to a sinogram is discussed in detail below. The resulting delivery plan for the field is used as input to the same CCCS dose calculation that is performed during optimization of an inverse plan. The dose volume for a field is cleared and recomputed when the user makes any change that affects the fluence map for the field. The per-field dose volumes within a beam angle are summed using the per-field weights to produce a dose volume for the beam angle.

Each dose group prescribes a specific dose constraint that is to be fulfilled by the beam angles that belong to the dose group. The per-beam dose volumes are summed using the weights assigned to the beam angles. The per-beam weights are treated differently depending on the type of prescription on the dose group. If the dose group prescribes an absolute dose to a point, the beam angle weights are interpreted to mean that each beam angle in the group should contribute a percentage of dose to the point equal to the beam angle's weight, relative to other beam angles in the group. If the dose group prescribes to a DVH point for a VOI, the beam angle weights are interpreted as simple scale factors relative to the other beam angles in the group.

#### *Computing Final Dose*

Computing final dose for a forward plan consists of the following steps:

1. Create a delivery plan that contains a fragment for each beam angle. (*A fragment* is a sub-division of a treatment procedure with instructions for the gantry, couch, jaws, and leaves.) This involves creating a fluence map for the beam angle by summing the fluence maps of the contained fields taking into account the weights assigned to each field. The resulting fluence map for the beam angle is then converted into a sinogram for the beam angle, which is used to produce the delivery plan fragment.
2. Perform end-of-planning calculations on the delivery plan from the previous step to produce a final delivery plan. This is the same end-of-planning calculation that is used for inverse planning.
3. Compute final dose on the final delivery plan, using the same CCCS algorithm as for inverse planning.

## **Creating a Delivery Plan from a Fluence Map**

#### *Position the Projections*

The first step in creating a delivery plan from a fluence map is to determine the position of the projections. The center of the first projection is placed one half of a field width from the start extent of the beam angle. The spacing between projection centers is equal to the plan pitch that is specified by the user. The number of projections is computed so that the final projection is at least half of a field width beyond the end extent of the beam angle.

#### *Apply Jaw Settings*

Forward plans support both fixed and dynamic jaws. Fixed jaws are applied in basically the same way as they would be for an inverse plan and are not discussed in great detail here.

Dynamic jaws for forward plans are only applied to the extreme inferior and superior extents defined by each beam angle. In other words, dynamic jaws are not applied to portions of a sinogram where all leaves are closed for multiple projections in the middle of the delivery plan.

#### *Convert Fluence Values to a Sinogram*

The fluence map is a rectangular grid of pixels where each pixel can have a value in the range [0.0, 1.0]. A value of 0.0 indicates no fluence at the pixel and a value 1.0 indicates 100% fluence at the pixel. The corners of the fluence map correspond to the corners of the rectangle defined by the extents of the beam angle. In each projection the normalized leaf open time for each leaf is determined by overlaying a grid that represents the MLC leaves onto the pixels of the fluence map. The leaf grid is centered on the projection. The inferior and superior extents of the leaf grid are determined by adding and subtracting half a field width from the center of the projection. The leaf edge data from the beam commissioning is used to determine the left/right extents of each leaf in the leaf grid. The sinogram value for each leaf is determined by computing the average of all of the pixel values within the corresponding leaf's rectangle in the leaf grid. Partially covered pixels are taken into account and weighted accordingly in the average. Also note that the cone filter data is used in an inverse manner to flatten the fluence values. What results is a normalized leaf-open time sinogram. There is nothing about this sinogram that distinguishes it as being from a forward plan. As a result, the sinogram can be translated into leaf open and close events in the delivery plan using the standard algorithm for doing this.

## ◆ 3D Conformal (3DCRT) Algorithm

3DCRT (3D Conformal Radiotherapy) allows the user to plan and treat simple cases that do not require sophisticated *IMRT* optimization. The basic delivery geometry of a 3DCRT plan is identical to the delivery geometry of its IMRT counterpart (*TomoHelical* or *TomoDirect*). While the beam is on, the binary MLC is operating, the gantry rotates for *TomoHelical* plans, and the couch travels along the +IEC Y axis at a constant velocity. However, the MLC delivery instructions are determined differently for a 3DCRT versus IMRT plan.

The 3DCRT plan mode may be selected from the **Setup/Machine** tab. When 3DCRT plan mode is selected, the **Plan** tab has fewer user controls than for an IMRT plan. The user sets the prescription for each target, but there is no opportunity to specify additional constraints, importances, or penalties. Overlap priorities are irrelevant for calculation. The user can set the blocked status for sensitive structures. Rays passing through blocked structures are discarded during the initial sinogram determination.

There is no **Optimize** button, only a **Calculate** button. Clicking **Calculate** initiates a beamlet weight calculation followed by a **Full Dose** calculation.

Beamlet weighting is used in the plan to account for the fact that the system has no flattening filter, and also for the effects of differential beamlet attenuation in the target.

A **Normal Tissue Dose Uniformity** option is available. The **Normal Tissue Dose Uniformity** option requires an “external” contour. This option treats the entire non-target volume like a single **Region at Risk** (except for the ability to block) and uses beamlet weighting to try to make the dose to the target homogeneous. Priority is given to target homogeneity.

**Low** compensation means less flexibility in differing beamlet weights compared to **High** compensation, so **Low** compensation will generally result in shorter delivery time.

The **Full Dose** calculation uses the same Convolution/Superposition algorithm described earlier in this section. DVHs and isodoses are not displayed until calculation is finished.

For 3DCRT mode, sinograms in the plan report are replaced with Digitally Reconstructed Radiographs (DRRs).

## ◆ Plan Transfer Algorithm

### Summary

The **Plan Transfer** task on the *Precision* workstation provides access to three different workflows: **Machine Transfer**, **Self Transfer**, or **Mark as Equivalent**.

If a patient who was planned on one machine needs to be treated on a different machine, this could be addressed by:

- Re-planning the patient on the new machine, or
- Using the **Machine Transfer** workflow to generate a similar plan for delivery on the new machine. The appropriate plan can then be delivered on the original machine or the new machine (there is no change in the original plan).

If a patient was planned on one machine, but subsequently the **Edit Machine** data was modified in a way that could impact the delivery, this could be addressed by:

- **Mark as Equivalent** if no dosimetric impact is expected (there is no change in the original plan, except that it is now labeled with the new treatment machine revision), or
- Re-planning the patient, or
- Using the **Self Transfer** workflow to generate a similar plan that takes into account the new machine properties (the original plan is discontinued).

The planning software treats transferred plans as separate plans, but grouped with their primary plan. The primary plan and all transferred versions of it share a common fraction delivery record.

There are certain specifics that must be met in order for plan transfer to occur:

1. The system shall fail a plan transfer if the destination treatment machine is not compatible with the plan being transferred. (For example, attempting to transfer a *TomoDirect* plan to a machine that does not support *TomoDirect* will fail.)
2. The system shall fail a plan transfer if the destination machine's corresponding field width differs from that of the primary plan's (actual) field width by more than 5%.
3. The system shall fail a plan transfer if the destination machine's center-of-field (COF) position differs from that of the primary plan's COF position by more than 0.01%.
4. The system shall fail a plan transfer if the destination machine's energy-fluence-per-ideal-open-time (EFIOT) value differs from that of the primary plan's EFIOT value by more than 50%.

Plan Transfer does not require one or both of the involved machines to be twinned to the same beam model. The machines simply have to be within the aforementioned specifications.

Machine Transfer and Self Transfer account for differences in field width, output, and multileaf collimator (MLC) properties between the original and new machines. Differences in beam model profiles are taken into account during the End-of-Planning (EOP) dose calculation but are not used to modify the delivery instructions. The Machine Transfer or Self Transfer workflow creates the required information for delivery on the destination machine. The new EOP dose is then calculated to allow the user to review and/or approve the transferred plan, creating an approval record for delivery on the destination machine.



**IMPORTANT:** Perform daily quality assurance procedures to ensure that the output of the source and destination machine are within 10% of one another. Additionally, it is recommended that patient specific QA be performed following a transfer.

## How Machine Transfer and Self Transfer Affect Patient Plans

A transferred patient plan begins with a set of optimized delivery instructions specific to the plan. In order to allow for delivery of the plan on the destination machine, the delivery instructions must be modified to incorporate the destination machine parameters. Differences in field width and pitch, output, and MLC properties are taken into account during the transfer process. Differences in beam model profiles are not used to modify the delivery instructions. They are, however, used as part of the EOP dose calculation performed during the transfer process.

### *Changes in Field Width and Pitch*

If the treatment field settings of the destination machine are different from those in the source machine, the field width with the field settings nearest the source field settings is chosen on the destination machine for the transferred patient plan. The source and destination machine field settings must fall within the aforementioned constraint. If the field settings, and thus field widths, are different, a new treatment pitch must be used to ensure that the same patient coverage is maintained on the destination machine. The pitch is determined such that the product of the pitch and treatment beam width is the same on both the source and destination machines.

There will generally be small differences in the final delivered dose for a transfer that involves different treatment field widths. These differences are primarily due to using different pitch values on the source and destination machines.

### *Accounting for Output Differences*

Since a transferred patient plan is not re-optimized, using a different pitch would affect the delivered dose to the patient if the delivery instructions were not modified. Larger pitches would result in a lower dose while smaller pitches would result in a higher dose. In order to maintain the same delivered dose to the patient and account for changes introduced by the different pitches and machine outputs, projection time and couch speed are adjusted first. MLC leaf open times are then scaled by a scaling factor. The scaling factor is defined as the ratio of the source machine treatment beam width and output to the destination machine treatment beam width and output. The scale factors are calculated to keep the integral fluence out of each leaf the same given the jaw setting and field parameters between the two plans. The formula for the scale factor for transferring from gantry A to gantry B is as follows:

$$\frac{\int F(field_B, projection) dA_{leaf}}{\int F(field_A, projection) dA_{leaf}}$$

Adjusting projection time to account for output differences will affect treatment time. When transferring a patient to a machine with lower output (as defined in the beam model), the treatment plan will generally take longer to deliver on the destination machine. The difference in delivery time may

not be equivalent to the scaling factor as differences in MLC properties will also impact treatment time. Any differences in machine output should still lead to a final delivered dose on the destination machine that is very similar to the delivered dose on the source machine.

#### *Modifying the Sinogram for MLC Properties*

Differences in MLC properties can also impact doses delivered to the patient. Leaf fluence output factors (LFOFs) and leaf latency values are contained within the beam model data associated with each machine. Once the delivery instructions are modified to account for the LFOF and leaf latency differences, thresholding is applied.

- **Leaf Fluence Output Factors:** During the patient transfer process, the software scales the delivery instructions and modifies the leaf open times to account for the LFOFs of the destination machine.
- **Leaf Latency Values:** There are small differences in latency data from one MLC to the next MLC. As a result, the delivery instructions must be modified to take into account the MLC latency values of the destination machine. Unlike the LFOFs, which only impact leaves without open neighboring leaves, leaf latency values apply to all open leaves at all times. Therefore, a 1% increase in a latency value can be expected to result in a compensatory 1% increase in requested leaf open time in the delivery instructions.
- **Leaf Thresholding:** After the delivery instructions have been scaled and the leaf open times have been modified to account for differences in MLC LFOF and latency values, leaf thresholding is applied. Despite the fact that the transferred plan has the same optimization as the original plan, thresholding may result in different leaves being closed in the transferred plan. These differences arise as the scaling and LFOF and leaf latency corrections applied during the transfer result in different requested leaf open times.

#### *Other Transferred Dose Effects*

Differences in beam model profiles can also exist between the source and destination machines. This includes differences in transverse (IEC X), longitudinal (IEC Y), and/or percent depth dose (IEC Z) profiles as well as leaf filters. Beam profile shape and energy information is contained in the beam model files, as well as the source and destination machine archives. Differences in beam model profiles are not used to modify the delivery instructions during the transfer process. They are, however, used during the End-of-Planning dose calculation that is performed during the transfer. The user can review the resulting dose calculation and compare it to the dose calculation from the source machine to determine how differences in beam model profile shapes impact the dose delivered to the patient.

Because the delivery instructions are not modified to account for differences in beam model profile shape, the delivered dose on the destination machine may be slightly different than the delivered dose on the source machine. Dose differences should be reviewed in the Precision System to determine if the differences are acceptable.



**WARNING:** Failure to review the dose calculation during transfer could lead to incorrect dose delivery to the patient.



**NOTE:** Plan Transfer does not account for differences in the **Lateral Offset** of the couch from one machine to another.

## Algorithms for *CTrue* Images

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# About Imaging Algorithms



**NOTE:** Your imaging options may be different based on your implementation.

The imaging system uses two different types of algorithms for image reconstruction: filtered backprojection and iterative reconstruction. While analytical algorithms such as filtered backprojection are based on a single reconstruction, an iterative algorithm uses multiple reconstructions and statistical weighting to reduce the image noise while preserving spatial resolution and image fidelity.

During treatment workflow, select the desired reconstruction on the **Scan** tab of the Treatment Delivery software. The reconstruction cannot be changed after the scan is complete. The reconstruction algorithm determines the image that is saved to the patient record and used for image registration, PreciseART™ adaptive calculations, and DICOM export.

The scan acquisition process (imaging dose, couch speed, gantry speed, and collimation) is the same regardless of the reconstruction selected. The iterative reconstruction options produce higher quality images than filtered back projection, with the same patient dose.

The iteratively reconstructed image solution is forward-projected to determine the corresponding detector data using basic information about the system geometry. This calculated detector data is compared against the measured detector data, and the image solution is adjusted at each iteration to achieve a more likely match to the measured detector data, based on Poisson counting statistics. The iterative reconstruction includes a regularization term that further reduces noise by limiting high spatial frequencies in areas of the image with small local variation of the image values, for example, areas of homogenous tissue away from edges. The iterative imaging options in the Treatment Delivery Console have different settings for each algorithm's regularization and convergence parameters.

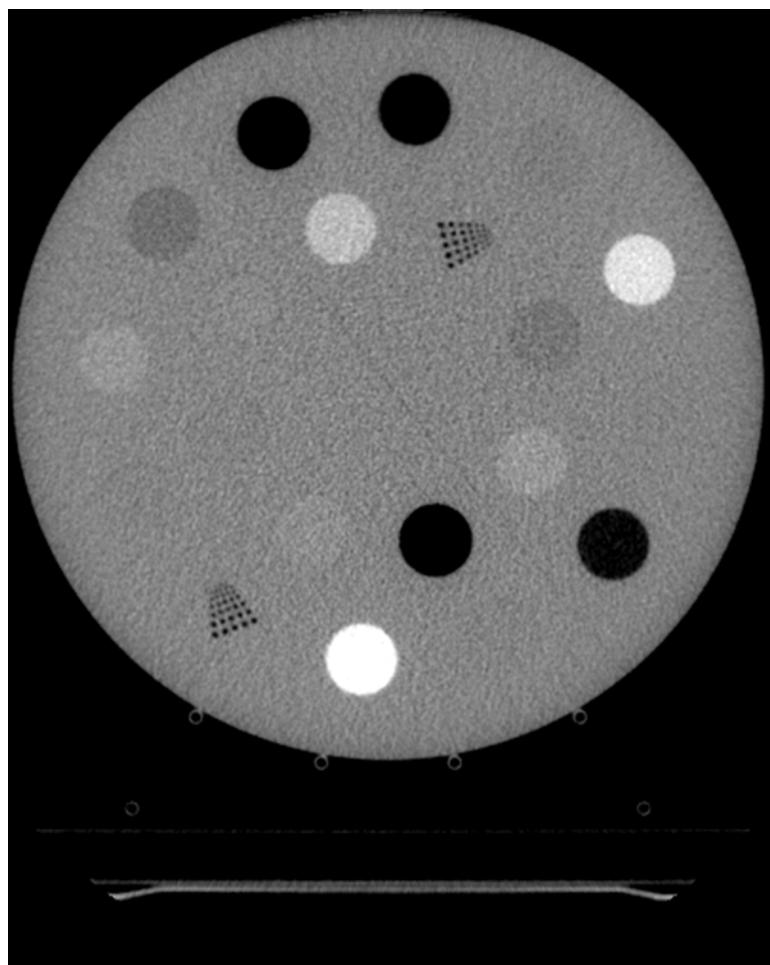


**NOTE:** Beister (2012) has provided a general review of iterative CT reconstruction techniques. Accuray's iterative reconstruction options use a statistical algorithm that most closely matches the Ordered Subset Convex algorithm described by Beister. See "Appendix G" (page 589).

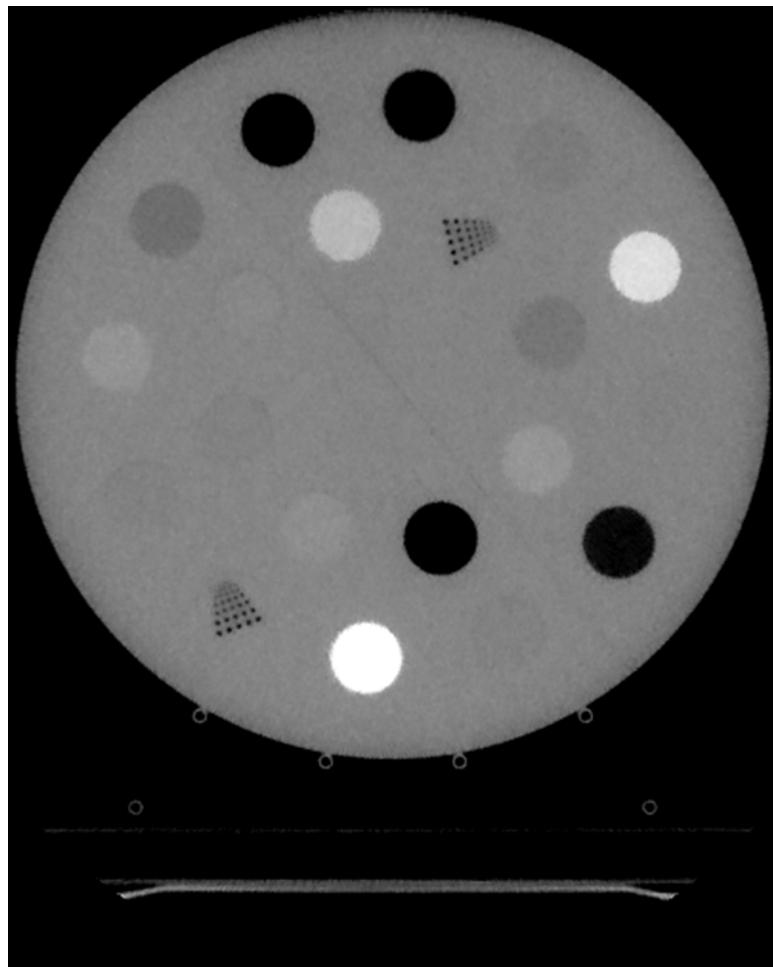
Selection	Algorithm Type	Description
Standard	Filtered Backprojection	The original MVCT images of Radixact™ System.

Selection	Algorithm Type	Description
IR General	Iterative Reconstruction	Image noise is lowered and low contrast visibility is improved relative to the standard MVCT, with similar image texture.
IR Soft Tissue	Iterative Reconstruction	Image noise is lowered and low contrast visibility is improved relative to the standard MVCT, with a smooth image texture.

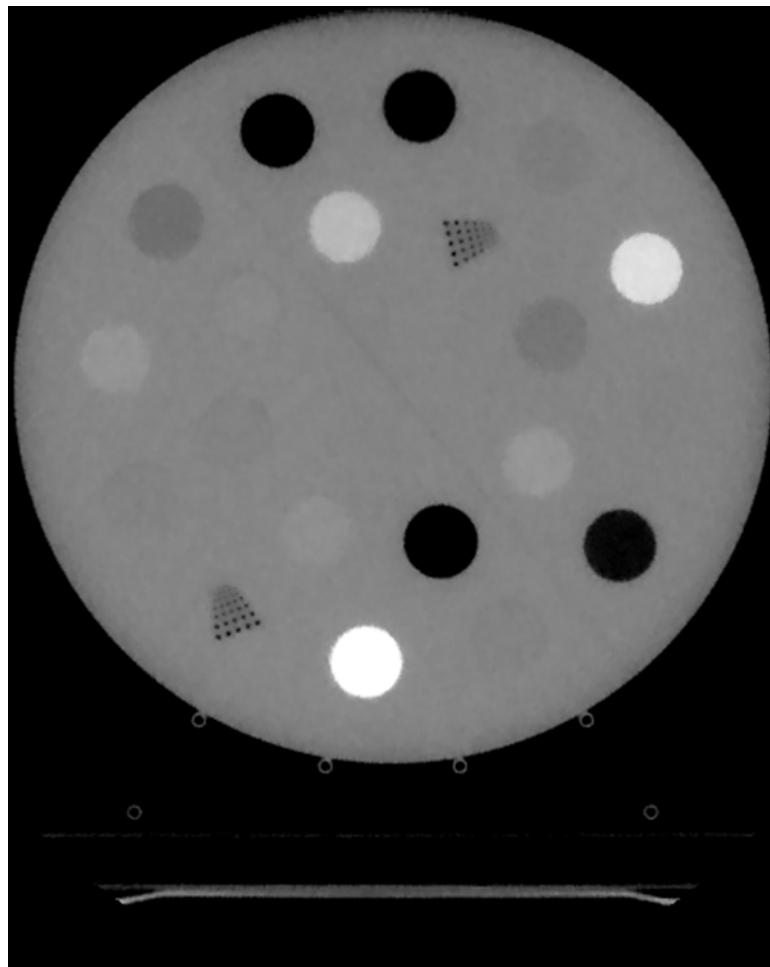
The following images show an example of each reconstruction algorithm using the Med Cal *Tomo*-phantom with various density plugs inserted.



Standard Filtered Backprojection Reconstruction Image



IR General Iterative Reconstruction Image



IR Soft Tissue Iterative Reconstruction Image

## ◆ *CTrue* Image Reconstruction

Reconstruction of MVCT data involves the following steps.

1. Accounting for the signal at the detectors when the beam is off (dark current).
2. Normalizing to the Dose1 monitor chamber to account for output fluctuations.
3. Dividing each channel by the “air scan” signal at each gantry angle. Data from the most recently acquired air scan is used for image reconstruction.
4. Accounting for beam hardening using spectral calibration data. This data is measured and maintained by your service representative.
5. Reconstructing the images from the data using either a filtered back projection algorithm or an iterative reconstruction algorithm.

6. Helical data is interpolated onto discrete slices along the IEC Y axis. Reconstruction is performed on a 512 x 512 pixel matrix. The reconstruction field of view (FOV) is approximately 39 cm.

Two or four images are reconstructed per gantry rotation, resulting in image reconstruction intervals of 2 mm or 1 mm (**Fine**), 4 mm or 2 mm (**Normal**), and 6 mm or 3 mm (**Coarse**).

Each reconstructed slice uses data from an entire rotation (however, the data is weighted so that the data at the ends of the rotation aren't used as much). With four slices per gantry rotation, there is more redundancy in the data used to reconstruct neighboring slices than with two slices per rotation.



**TIP:** Smaller **Reconstruction Intervals** may improve the longitudinal display resolution, with no impact on scan time or patient dose. A more significant improvement in the longitudinal display resolution may be achieved by using a finer **Acquisition Pitch** (but this will increase the scan time and patient dose).



**TIP:** Using the Iterative reconstruction options to reduce noise improves the perceived longitudinal display resolution.



**TIP:** The maximum number of slices allowed for a *CTrue* scan is 300, so use the **Coarse** setting and larger reconstruction interval if you need to cover the maximum possible scan distance.

7. Scaling the CT numbers by the **calibrationSlope** and **calibrationLinearityOffset** in the machine data.
8. Slices displayed on the **Register** tab of the TDC are interpolated to the positions of the planning image.

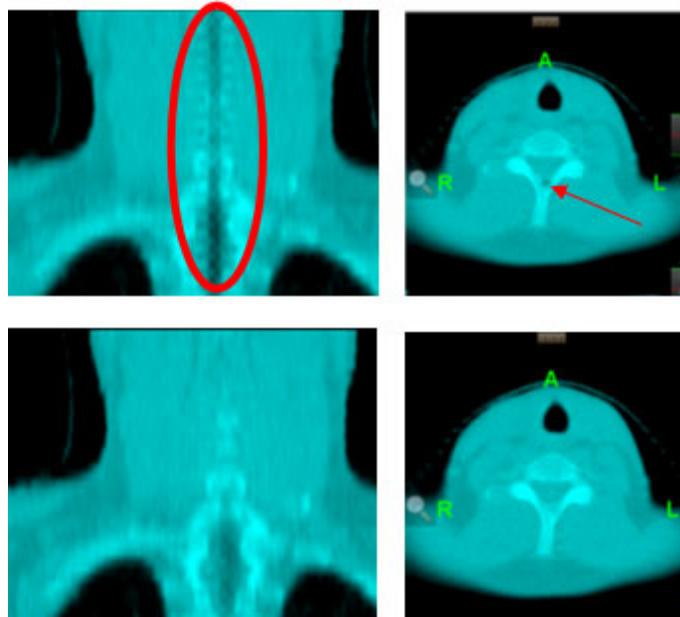


**NOTE:** If the resolution of your planning image is poor (e.g., for a QA procedure), the display resolution on the **Register** tab will be poor.

## ◆ *CTrue* Image Artifact Correction

On the TDC **Register** tab, there is an area called **Scan Image Control** which contains the **CTrue Image Filter** tools: 1) a slider to apply an edge-preserving smooth filter, which is set to **None** by default; and 2) a **Use artifact correction** checkbox. The artifact correction is de-selected (off) by default.

MVCT images acquired on the treatment system have occasionally exhibited an image artifact at isocenter that is commonly referred to as the “button” artifact (smudge at isocenter) when viewed in the transverse plane, or the “zipper” artifact (alternating pattern of dark and light pixels along the IEC Y axis) when viewed in the coronal or sagittal planes.



Coronal and transverse views with artifact correction not used, and a button/zipper artifact is present. Below: Artifact correction used.

The correction option substantially reduces the zipper artifact by scaling down the offending frequency of the image in Fourier space. In addition to the zipper artifact correction, non-alternating (direct current, or DC) artifacts are filtered by comparing the median value of axial columns of pixels with the values of the surrounding pixels. Only the pixels within a 1 cm radius of the image center are filtered. The reconstructed image is stored without the artifact correction, and the image can be viewed with or without the correction applied.

In rare cases, it may be possible for the zipper artifact correction to remove a real anatomical or phantom features near isocenter that is long, uniform, and cylindrical (see sample images below). If your patient or phantom anatomy contains a long, cylindrical feature at isocenter (such as an ion chamber or patient airway), and if you use the artifact correction, you should determine if the artifact correction is obscuring actual patient or phantom features by visually comparing the corrected versus uncorrected images. To see the uncorrected image, look at the *CTrue* image preview on the **Scan** tab (the zipper artifact correction is not applied on the **Scan** tab), or uncheck the artifact correction option on the **Register** tab and click **Apply**. If it is determined that the artifact correction is obscuring a real feature of your patient or phantom, the artifact correction option should be turned off (unchecked) for that patient or phantom image.



**WARNING:** The artifact correction tool may introduce non-physical features into your *CTrue* images. If you use the artifact correction, always compare the images with and without the artifact correction. Turn the artifact correction off if the artifact correction obscures patient features.

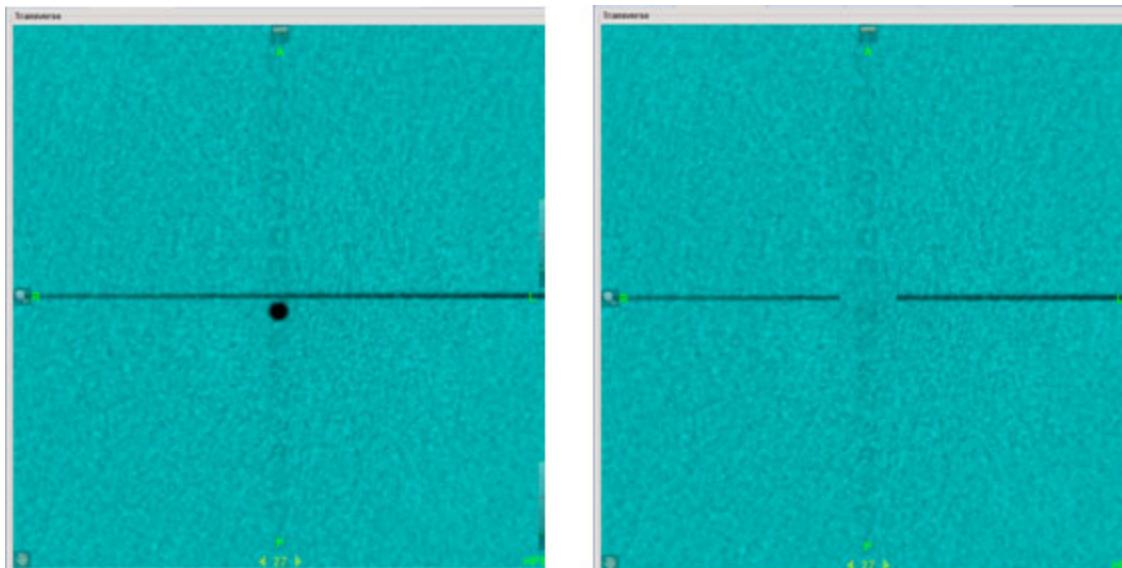
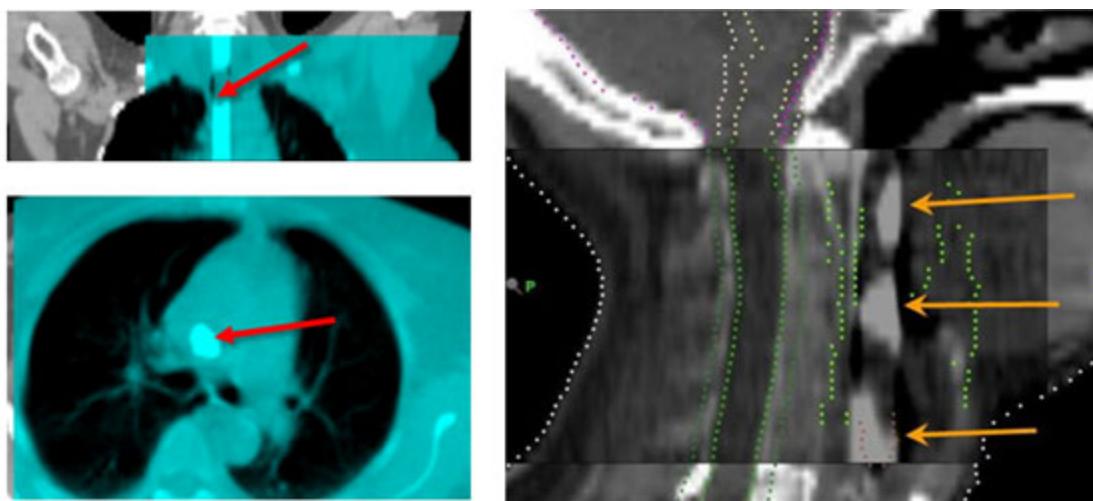


Image of *Tomo*-phantom with plug removed near isocenter. Left: Artifact correction not used. Right: Artifact correction used. In this example, the artifact correction hides a real phantom feature, so it would be better not to use the artifact correction.



Non-physical mass introduced to *CTrue* images in the patient airway. In this case, the artifact correction should be turned off.

## ◆ Automatic Image Registration

The TDC allows you to manually or automatically register a *CT<sub>True</sub>* image to the planning CT image.

Automatic registration is based on a variant of the Mutual Information algorithm, an entropy-based technique which is commonly employed for image registration. The **Full Image** option employs the Mutual Information algorithm. The **Bone** and **Bone and Tissue** options were developed by Accuray and are described in Ruchala 2002. In the **Bone** technique, the image is first thresholded to identify pixels with values characteristic of bone, and then an algorithm very similar to Mutual Information is used to perform registration based only on those qualifying pixels. The **Bone and Tissue** technique is like the **Bone** technique, but with a lower density threshold.

The automatic registration algorithm disregards all pixels below the line of couch replacement in the planning image, so that the automatic registration result is not sensitive to the relative positions of the couch in the planning and MVCT images, but only to the anatomy of the patient on the couch.

Uniform downsampling of the images is offered as a way to increase the speed of the registration computation. **Superfine Resolution** uses 100% of the pixels, **Fine Resolution** downsamplesthe image by a factor of two in the X and Z dimensions, and **Standard Resolution** downsamplesthe image by a factor of four in the X and Z dimensions.

The **Incomplete FOV** box may be checked if the patient extends outside the Field of View, to reduce the effect of edge-of-field artifacts on the automatic registration result, as discussed in Ruchala 2002.

The number of degrees of freedom in the automatic registration can also be selected. The couch position can be adjusted to correct for translations, and the gantry angle can be adjusted to correct for roll offsets. To correct for a pitch or yaw rotation, the therapist would have to physically rotate the patient position on the couch about a prescribed center of rotation. This is an error-prone process that necessitates further setup verification.



**IMPORTANT:** After performing automatic or manual registration, the operator should observe the final registration results in all planes and all slices to make sure that the result is acceptable in all degrees of freedom. If using the **Checker** tool, also check the alignment without the **Checker** tool in all planes and all slices.



**IMPORTANT:** Rigid body registration of images that suffer from inter-fraction anatomical variations does not have a universally right answer. Outlying registration results ( $> 1$  cm error) have been reported for cases of poor initial setup of a test phantom ( $> 3$  cm initial displacement); see Boswell 2006. The human operator should place the highest confidence not in the computer, but in their own subjective evaluation of the registration results based on clinical goals. The human operator must manually tune the automatically registered image and reject any clinically unacceptable results.



**WARNING:** When evaluating image registration results, the **Checker** tool may be used to display alternating groups of pixels (squares) in the Plan and Scan images. When using this option, always place the **Balance** slider on the 100% Scan side. This will ensure that you are comparing pure Plan checker squares with pure Scan checker squares. If the **Balance** slider is used to mix the Plan and Scan images in **Checker** mode, the images may appear to be well-aligned even if they are not. This can result in mis-alignment of the patient and mis-treatment.





## Appendix A

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### Measuring Beam Profiles with the Standard Imaging Water Tank & A1SL Chamber

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# Introduction

This appendix provides step-by-step instructions for measuring beam profiles using the equipment from the Beam Measurement and QA package and the Standard QA package. These packages are available for purchase from Accuray. See “Customer Site QA Equipment” (page 111) for a list of items included in these packages.



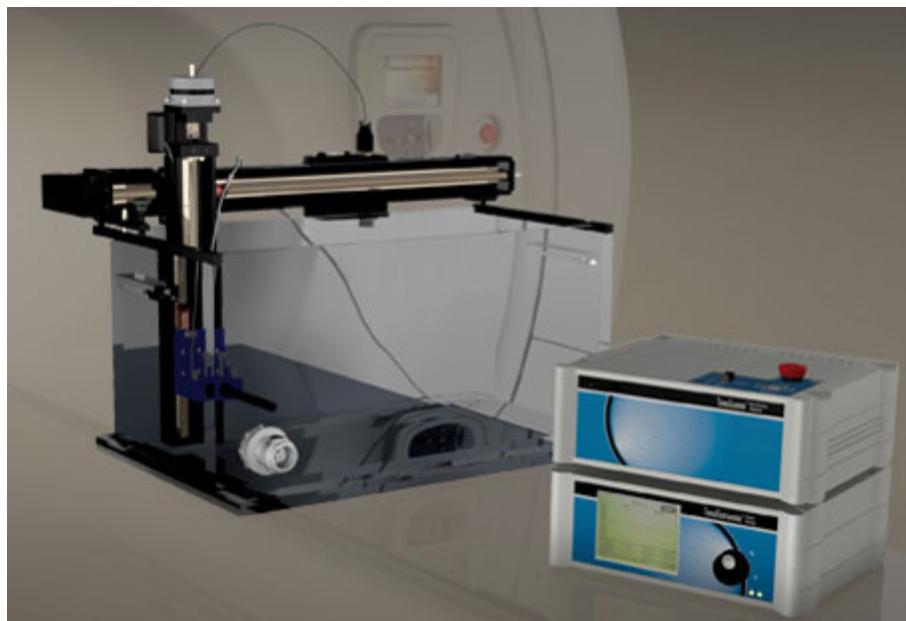
**IMPORTANT:** Accuray provides specific instructions and support for the Standard Imaging water tank only. If you are not using the Standard Imaging equipment and chamber, the instructions in this section may not be appropriate. Refer to the Commissioning chapter for the general workflows, and contact the water tank manufacturer for specific instructions appropriate for your water tank.

# Types of Water Tanks

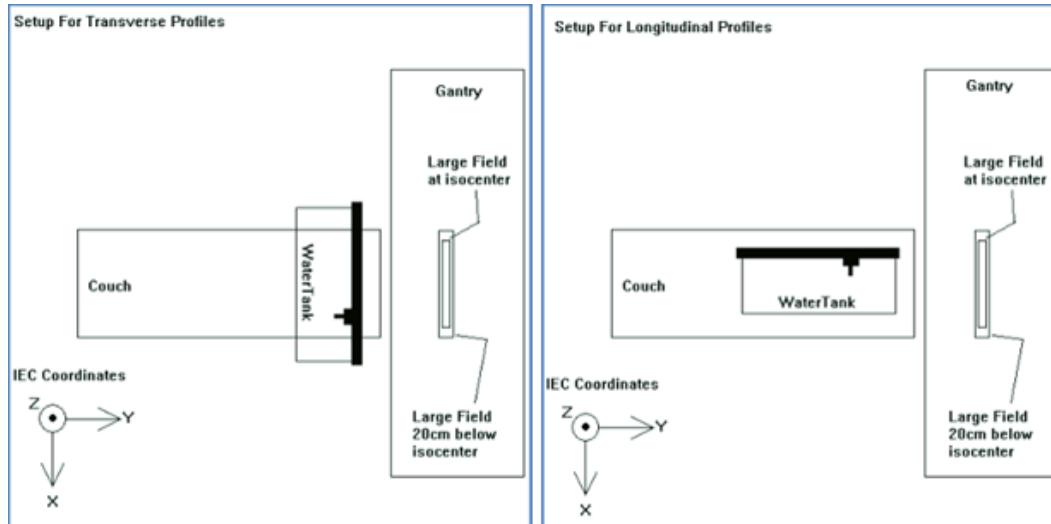
- ◆ Standard Imaging Water Tank ..... 485
- ◆ PTW MP3-T Water Tank ..... 486
- ◆ IBA Blue Phantom Helix ..... 487

## ◆ Standard Imaging Water Tank

The Standard Imaging water tank is the default supplied water tank for the Tomotherapy treatment system. The tank's installation and use guidelines follow standard Accuray protocols and it is used to collect the reference profiles. More information about the water tank protocols can be found in the Dosimetry Analysis Guide.



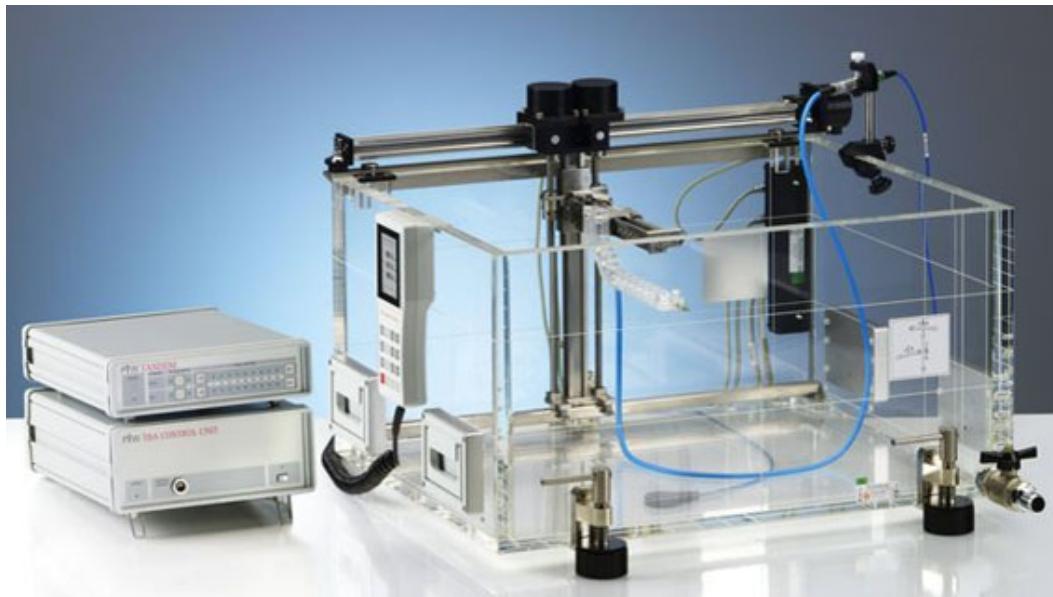
Standard Imaging water tank illustration



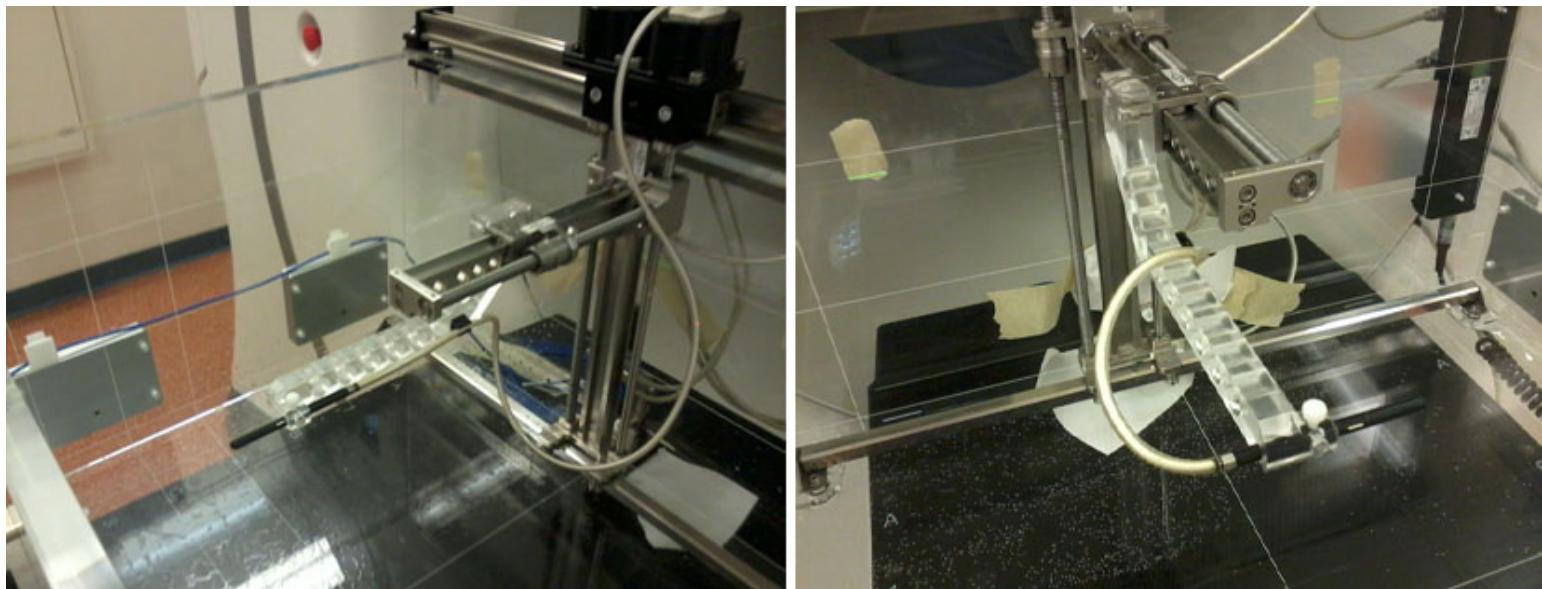
Standard Imaging water tank setup profiles

## ◆ PTW MP3-T Water Tank

The PTW MP3-T water tank is compatible with the treatment system. The ion chamber holder accommodates the A1SL chamber in either orientation. Use the “sideways” orientation to collect longitudinal profiles and PDDs and the “frontways” orientation to collect transverse profiles, then compare directly to the Gold Model data.



PTW MP3-T water tank



PTW MP3-T water tank Transverse and Longitudinal profiles

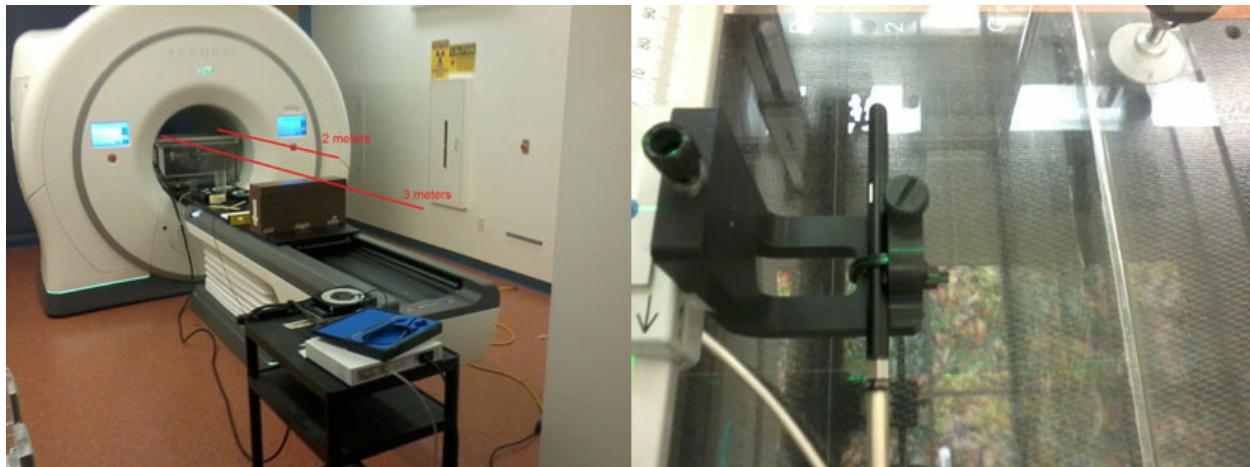
### ◆ IBA Blue Phantom Helix

The IBA Blue Phantom Helix water tank is another type of water tank that is compatible with the treatment system. Ensure that the CCU is as far from the machine as the cable will reach. This can be about 4 meters on the floor behind the foot of the couch so that the couch provides some “shade” from scattered radiation.

Collect transverse profiles with the CC04 in the standard orientation (ion chamber pointed toward foot of couch). Collect longitudinal profiles and PDDs with the A1SL chamber “sideways” (zip-tied to the CC04 holder as shown). Due to their depth correction, compare the PDDs to the provided calculated PDD profiles. If necessary correct the depth axis of the reference PDDs, linearly increasing to 0.9 mm from 0 mm until 80 mm, then constant.



IBA Blue Phantom Helix water tank



IBA Blue Phantom Helix Transverse and Longitudinal profiles

# Initial Tank Setup: Longitudinal Orientation

The initial tank setup instructions from the Commissioning chapter are repeated here, with additional notes specific to the Standard Imaging equipment. The longitudinal tank orientation will be used to collect the symmetric and asymmetric longitudinal profiles, and PDDs.

1. Set the water tank on the couch in the longitudinal orientation at virtual isocenter.



**IMPORTANT:** The *Dosimetry Analysis Guide* contains detailed instructions to set up the tank in the longitudinal orientation, position the A1SL measurement chamber and A17 reference chamber, connect the cables, and fill the tank with water. These instructions are not repeated here. Observe all caution and warning statements in the *Dosimetry Analysis Guide*.



**IMPORTANT:** For a new water tank, first verify that the horizontal and vertical beams of the scan arm are perpendicular to each other. The scan arm has adjustment screws on the back if needed. *Slightly* loosen the screws (if you loosen them too much, the apparatus will fall off), adjust the angle between the beams, and tighten the screws again.

2. Align the yaw rotation of the tank with the green overhead lasers (it may be easier to do this with an empty tank).
3. Fill the tank with water to a depth of about 23 or 24 cm.
4. Place the measurement chamber in the scan arm holder.
5. Place the reference chamber in the appropriate position for the desired test.
6. While you are still in the treatment room, use the scan arm controller to send the chamber around the entire perimeter of the tank. Ensure that:
  - The limit switches prevent the chamber from colliding with the tank walls or compressing the ion chamber cable against the tank walls.
  - The setup does not require your interference to untangle the cable.
  - The measurement chamber cable does not intercept the beam path to the measurement chamber.
  - The reference chamber does not interfere with the beam's path to the measurement chamber, and the measurement chamber does not interfere with the beam's path to the reference chamber.



**CAUTION:** If the measurement chamber cable intercepts the beam path to the chamber, it will cause anomalies in the signal.



**TIP:** To maintain the A1SL cable tension and prevent the cable from doubling over the chamber at shallow depths, thread a large nut through the chamber cable, and tape the nut to the cable so that the nut hangs outside the tank as a counterweight. Ensure that the A1SL chamber has enough slack to descend to the bottom of the tank. If the A1SL chamber does not have enough slack at all positions in tank, this can result in the chamber cable pulling out of the holder, causing damage to the chamber and/or electrometer.

7. With the tank out of the bore at virtual isocenter align the yaw rotation of the tank so that the chamber travels parallel to the overhead sagittal laser.



Alignment Cap



**TIP:** An alignment cap fits over the A1SL chamber. This can be used to identify the approximate center of the collection volume.



**CAUTION:** Be sure to remove the cap before taking measurements, or the results may be affected.



**CAUTION:** To avoid damage to the water tank or gantry covers, check for sufficient clearance as the couch moves into the bore.

8. Move the chamber to the approximate center of the tank in Y. Then, adjust the tank so that the chamber collection volume is centered on the green overhead lasers in X and Y.
9. Send the tank 700 mm into the bore.
10. With the tank in the bore at isocenter adjust the couch height so that the surface of the water corresponds to the green bore lasers (850 mm SSD).
11. Adjust the leveling of the tank or scan arm (pitch) so that the chamber travels parallel to the surface of the water. To determine the needed adjustment, place a small bubble level along the Y axis on the scan arm (or

there may be a bubble level built into the scan arm). You can also use the scan arm controller to move the chamber in Y and ensure that it travels parallel to the surface of the water.



**TIP:** To adjust the pitch of the tank, it may be more effective to verify that the chamber travels parallel to the surface of the water than to rely on the bubble level.



**NOTE:** The water in the tank is always level, due to gravity. With couch sag, the tank itself will not be level since there are no leveling feet under the tank. The leveling screws on the scan arm will need to be adjusted so that the scan arm travels level with gravity.



**IMPORTANT:** The pitch of the tank must be adjusted with the couch in the bore, to account for the effects of couch sag.

12. Adjust the leveling of the tank or scan arm (roll) so that the vertical travel of the chamber is parallel to the Z axis. To determine the needed adjustment, place a small bubble level along the X axis on the scan arm (or there may be a bubble level built into the scan arm).



**NOTE:** Adjusting the leveling screws in one dimension may impact the other dimension. Ensure that parts b) and c) are both passing before moving on.

13. Adjust the depth of the chamber so that it is half-submerged.
14. Re-check the tank setup to ensure that all parameters in Steps 7-9 pass (some parameters are inter-dependent).
15. Send the cylindrical chamber  $0.6 r_{cav}$  deeper into the tank, to account for the effective depth of measurement. To do this in TEMS Follow the instructions in “Plot the Tomo Electrometer Data Using TEMS Software” (page 89) to set up TEMS.
16. In the **Water Tank** section in the lower left corner of the TEMS screen, click **Set Origin** to define the new zero position.
17. Enter a vertical position of +1.2 mm to account for the effective point of measurement for the A1SL chamber. Then click **Move**.



**IMPORTANT:** Ensure that **Relatively** is not selected. **Relatively** should remain de-selected for all measurements in this chapter.

18. Click **Set Origin** again.

19. If desired, bring the couch out of the bore 700 mm and acquire a *CTrue* image to verify the setup (water at 85 cm SSD, chamber at 1.2 mm physical depth). Adjust the setup if needed, then send the couch 700 mm into the bore.

# Alignment Verification: Longitudinal Orientation

The commissioning chapter outlines the workflow for collecting scans to verify the longitudinal alignment of the tank. Instructions for collecting and analyzing the data in TEMS are provided below.

- ◆ Collect Data in TEMS ..... 493
- ◆ Analyze Data in TEMS ..... 493



**IMPORTANT:** Before performing alignment verification scans, perform the initial setup of the tank in the longitudinal orientation, as described in the previous section.

## ◆ Collect Data in TEMS

1. Select **Step Profile** as **Type** and **Longitudinal (SPDD)** as **Orientation**.
2. Manually enter values:
  - **Total Distance (mm): 30**
  - **Step Size (mm): 0.5**
  - **Depths (mm, ~CSV): 15, 200**

A screenshot of the TEMS software interface. On the left, there's a 'Readings' panel with two dropdown menus: 'Type: Step Profile' and 'Orientation: Longitudinal (SPDD)'. Below these are 'Defaults' and 'Run' buttons. To the right is a table titled 'Property' with three rows: 'Total Distance (mm)' set to '30', 'Step Size (mm)' set to '.5', and 'Depths (mm, ~CSV)' set to '15, 200'. The entire 'Readings' panel and the table are highlighted with a red border.

Longitudinal Alignment

3. With the water tank in the bore at the isocenter position, choose the **Machine QA** task and select the **ZZZ Water Tank Longitudinal (Mid40 leaves)** patient on the TDC. Run a **J7mm Mid40Leaves** procedure. After the radiation beam has been on for at least 10 seconds, click **Run** in the TEMS software to measure the profiles.

## ◆ Analyze Data in TEMS

1. When the scans are complete, save the TEMS data for your records as **SN#\_Longitudinal Alignment\_ YYYYMMDD\_raw.csv**.
2. If it is necessary to normalize to the reference channel, **Ctrl-click** to create a pinpoint on the A17 reference channel data. Click **Analyze > Normalize by Channel**.



**NOTE:** The A17 chamber is typically placed in the moat outside the water tank, along the long edge of the tank. The signal at this position is low. In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio, and should not be necessary if the reference chamber data shows that the beam output is stable during the delivery. (Because of the Dose Control Servo, the output of the system is typically stable.)

3. **Ctrl-click** to create a pinpoint anywhere on the A1SL profile data (at either depth).
4. Click **Analyze > Normalize Data** to normalize the profile to its maximum.
5. Click **Analyze > Shift on % Max.** Enter 50% in the pop-up window to center on the FWHM of the profile.
6. Read the results at the bottom of the screen, as shown:

Found the range for channel 2 at depth +15.00 mm set 1 as -15.00/+15.00 mm, with weighted center at -1.76 mm (trans pos).  
With weighted center at -1.76 mm for channel 2 at depth +15.00 mm set 1, the 50.00% max is -7.33/+3.56 mm (centered at -1.83 mm with width of +11.00 mm, trans pos).  
Shifted all channels according to the 50.00% max.  
Found the range for channel 2 at depth +200.00 mm set 1 as -15.00/+15.00 mm, with weighted center at -0.38 mm (trans pos).  
With weighted center at -0.38 mm for channel 2 at depth +200.00 mm set 1, the 50.00% max is -7.33/+6.43 mm (centered at -0.45 mm with width of +13.76 mm, trans pos).  
Shifted all channels according to the 50.00% max.  
center for channel 2 at depth +200.00 mm set 1 as -0.45 mm (trans pos).

Sample channel 2 alignment result showing field centers at -1.83 mm and -0.45 mm.



**IMPORTANT:** If you are measuring more than one channel (e.g., measurement chamber and reference chamber), be sure to identify the output line for the correct channel.

7. If the profiles at different depths differ by more than 2 mm, adjust the leveling of the tank in the room, reset the depth of the chamber, and run the scans again until it passes.  
If the profiles at different depths agree within 2 mm, the rotation of the tank about the X axis (pitch) is acceptable, and you can proceed to step 8.
8. Adjust the home position of the chamber to account for the average Y shift:  
In the **Water Tank** section in the lower left of the TEMS screen, enter 0 in the **Vertical Position** and enter the average of the results for the two profiles in the **Horizontal Position**, then click **Move and Set Origin**.



**Note:** Although you set your chamber Y position to the lasers when it was outside the bore, a small Y adjustment is typically required when the chamber is inside the bore, due to the effect of the couch sag pitch angle on the Y position of the chamber.

# Symmetric Longitudinal Profiles

The commissioning chapter outlines the symmetric longitudinal profile scans.

- ◆ Collect Data in TEMS ..... 495
- ◆ Process Data in TEMS ..... 496



**IMPORTANT:** Verify the scan alignment as discussed in the previous sections, before collecting data.

## ◆ Collect Data in TEMS

1. In the **TEMPS > Readings** menu, set the **Type** to **Quick Scan** and the **Orientation** to **Longitudinal (SPDD)**. Set the **Total Distance**, **Horizontal Velocity**, and **Depths** parameters as shown in the following Longitudinal Profile Settings table:

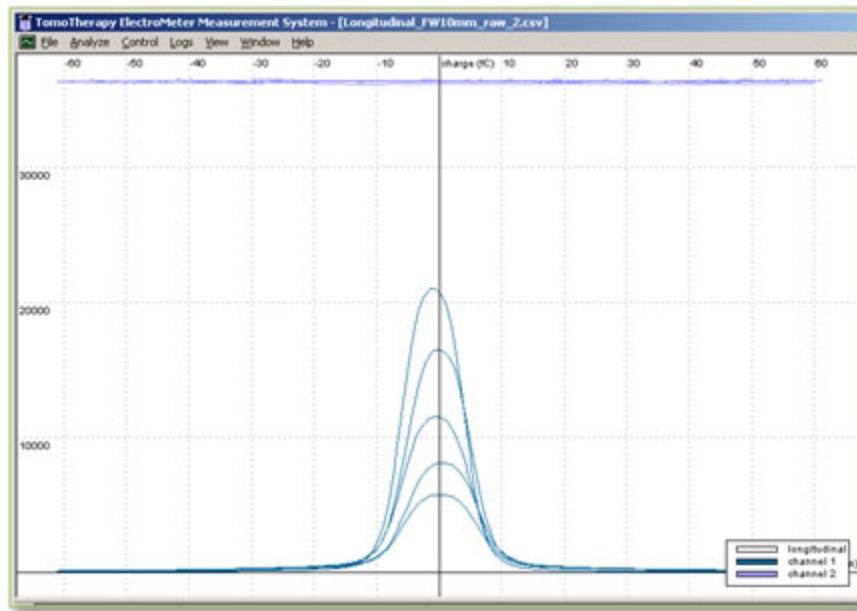
Field Width (mm)	Total Scan Distance (mm)	Scan Speed (mm/s)	Scan Depths (mm)
FW10 (J07)	100	1	15,50,100,150,200
FW18 (J14)	150	2	15,50,100,150,200
FW25 (J20)	150	2	15,50,100,150,200
FW50 (J42)	200	2	15,50,100,150,200

2. With the water tank in the bore at the isocenter position, select the **ZZZ Water Tank Longitudinal (Mid40 leaves)** from the **Machine QA** task on the TDC. Select a procedure of the desired field width. After the radiation beam has been on for at least 10 seconds, click **Run** in the TEMS software to measure the profiles.
3. When the TEMS display indicates the profile has completed, save the data as **SN#\_Longitudinal\_FW##\_YYYYMMDD\_raw.csv**.



**TIP:** You may interrupt the procedure with the yellow **Stop** button when you are finished collecting data. Or, keep the beam running and collect the PDD data for the same field width.

4. Repeat Steps 1-3 for all field widths in the Step 1 table.



Raw Longitudinal Profile Data

## ◆ Process Data in TEMS

This section provides instructions for processing the symmetric longitudinal profiles in TEMS. TEMS will allow you to normalize each profile to its maximum, normalize to the reference channel (if necessary), center all the profiles on their FWHM, and determine the FWHM of a profile. When processing is complete, you can compare the profiles to the reference data in Microsoft® Excel™ as explained in the “Analyze the Result” (page 202) section of the Commissioning chapter.

For each symmetric longitudinal profile data set:

1. If necessary, normalize each depth by the reference channel to account for dropped pulses and/or dose drift. To do so, **Ctrl-click** on the reference chamber data. Select **Analyze > Normalize by Channel**.



**IMPORTANT:** In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio, and should not be necessary if the reference chamber data shows that the beam output is stable during the delivery.

2. Normalize each profile by its maximum value: select **Analyze > Normalize Data**.
3. Shift each depth to its full-width 50% field center for consistency: **Ctrl-Click** a point on the primary data. Select **Analyze > Shift on % Max** and enter **50%** in the pop-up window.



**NOTE:** When profiles are collected in **Quick Scan** mode, TEMS assumes that the scan arm travels at the specified constant velocity (there is no absolute position feedback in **Quick Scan** mode). However, in **Quick Scan** mode there is a brief initial period of scan arm acceleration for each profile, during which the velocity is less than the specified constant velocity. This results in positional uncertainty (shifts) in the data. The direction of the scan acquisition (from positive to negative values or vice versa) alternates for consecutive depths, causing the measured profiles to be shifted back and forth with consecutive depths. Since we have already verified the longitudinal scan alignment with a **Step Profile** scan, we now assume that these shifts are due to scan arm acceleration, and use TEMS to center each profile on its FWHM. (Alternatively, all scans could be collected in **Step Profile** mode for more precise positioning. Since **Step Profile** is slow, **Step Profile** is usually reserved for checking the alignment, troubleshooting, and measuring the asymmetric profiles.)

4. Save the processed data as  
**SN#\_Longitudinal\_FW##\_YYYYMMDD\_processed.csv.**

# PDD Profiles

This section provides TEMS instructions to collect PDDs for all symmetric field widths, as discussed in the Commissioning chapter. You will measure the PDD at depths of 0 to 19 mm in steps of 1 mm, and 20 to 220 mm in steps of 10 mm. You will also perform a serpentine PDD for the 1 cm field (longitudinal profiles at 2 mm/s scan speed over a distance of 2 cm in Y at each depth).

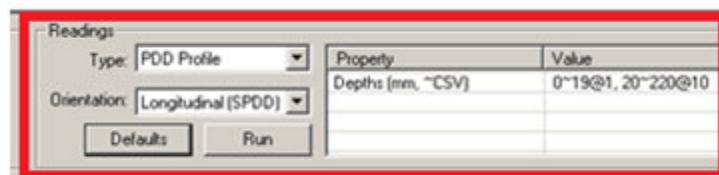
- ◆ Collect Data in TEMS ..... 498
- ◆ Process Data in TEMS ..... 499



**IMPORTANT:** PDD profiles are measured with the same water tank setup used to collect the symmetric longitudinal profiles. If the water tank has been moved since measuring the symmetric longitudinal profiles, repeat “Initial Tank Setup: Longitudinal Orientation” (page 489) and “Alignment Verification: Longitudinal Orientation” (page 493).

## ◆ Collect Data in TEMS

1. In the TEMS Readings menu, select **PDD Profile** from the Type drop-down and **Longitudinal (SPDD)** from the Orientation drop-down. Click **Defaults** to populate the depths the values. Verify that measured depths are 0~19@1, 20~220@10.



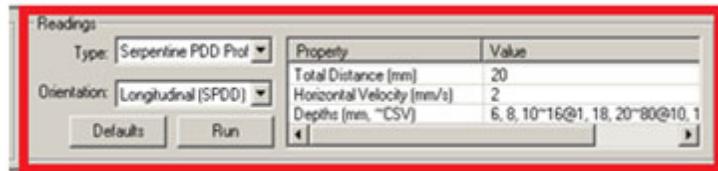
PDD Settings

2. With the water tank in the bore at the isocenter position, select the **ZZZ Water Tank Longitudinal (Mid40 leaves)** patient from the Machine QA task on the TDC. Select a procedure of the desired field width. After the radiation beam has been on for at least 10 seconds, click **Run** in the TEMS software to measure the profiles.



**TIP:** If TEMS stops and a red error line appears in the output area, this often indicates that the scan arm limit switches could not accommodate the range of depths requested. This could be fixed by adjusting the scan settings to remove the 21 and 22 cm depths, or by adding more water to the tank and repeating the setup.

3. When the TEMS display indicates the profile has completed, save the data as **SN#\_PDD\_FW##\_YYYYMMDD\_raw.csv**.
4. Repeat Steps 1-3 for all symmetric field widths.
5. In addition, collect and save a **Serpentine PDD profile** for the Field Width of 10mm using the parameters outlined in this figure:



**Serpentine PDD**

6. In the TEMS Readings menu:
  - Select **Serpentine PDD Profile** from the **Type** drop-down.
  - Select **Longitudinal (SPDD)** from the **Orientation** dropdown.
  - Click **Defaults** to populate the depths. Verify that the depths are 6, 8, 10~16@1, 18, 20~80@10, 150, 100~200@20.
  - Perform steps 2-3 for all the longitudinal profile field widths.

## ◆ Process Data in TEMS

This section contains instructions for processing the PDD profiles in TEMS. TEMS will allow you to normalize each profile to its maximum, and normalize to the reference channel (if necessary). When processing is complete, you can compare the profiles to the reference data in Microsoft Excel as explained in the “Analyze the Result” (page 202) section of the Commissioning chapter.

For each PDD data set:

1. Select **Analyze > Translate PDD**.



**NOTE:** **Translate PDD** identifies all PDD points collected at different depths as members of one data set. (**Translate PDD** does not shift the data as the name might seem to imply.)

2. If it is necessary to normalize each depth to the reference channel, **CTRL-click** a point on the reference chamber data, and select **Analyze > Normalize By Channel**.



**IMPORTANT:** In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio.

3. Select **Analyze > Normalize Data** to normalize by the maximum.
4. Save the processed data as  
**SN#\_PDD\_FW##\_YYYYMMDD\_processed.csv**.

# Asymmetric Longitudinal Profiles (Dynamic Jaws Only)

This section provides TEMS instructions to collect the asymmetric longitudinal (IECY) profiles for systems with the dynamic jaws feature, as discussed in the Commissioning chapter. Asymmetric profiles need only be measured at a depth of 15 mm.

- ◆ Verify Tank Alignment..... 501
- ◆ Collect Data in TEMS ..... 502
- ◆ Process Data in TEMS ..... 502



**TIP:** Symmetric longitudinal (IECY) water tank profiles should be confirmed passing before measuring the Asymmetric Longitudinal Water Tank Profiles.



**IMPORTANT:** Asymmetric longitudinal profiles are measured with the same water tank setup used to collect the symmetric longitudinal and PDD profiles. If the water tank has been moved since measuring the symmetric longitudinal profiles or PDD profiles, repeat “Initial Tank Setup: Longitudinal Orientation” (page 489) to verify setup.

## ◆ Verify Tank Alignment

Prior to measuring the asymmetric longitudinal (IECY) water tank profiles, water tank setup must be re-verified using the longitudinal alignment scan. The asymmetric profiles will be measured only at 15 mm depth. Instead of averaging the shift correction for depths of 15 mm and 200 mm, the correction at 15 mm depth should be applied.

1. Repeat the steps in “Collect Data in TEMS” (page 493) to run the longitudinal alignment verification scan, but use only the 15 mm depth: **Depths (mm,~CSV): 15.**
2. Repeat the steps in “Analyze Data in TEMS” (page 493) and ensure the shift does not exceed  $\pm 0.05$  mm. See the following image for an example of a passing result.

Status  
With weighted center at -0.08 mm for channel 1 at depth +15.00 mm set 1, the 50.00% max is -5.43/+5.40 mm [centered at 0.02 mm with width of +10.82 mm, trans pos].  
Shifted all channels according to the 50.00% max center for channel 1 at depth +15.00 mm set 1 as -0.02 mm [trans pos].  
Found the range for channel 1 at depth +200.00 mm set 1 as -15.00/+15.00 mm, with weighted center +0.01 mm [trans pos].  
With weighted center at +0.01 mm for channel 1 at depth +200.00 mm set 1, the 50.00% max is -6.71/+6.82 mm [centered at +0.05 mm with width of +13.54 mm, trans pos].  
Shifted all channels according to the 50.00% max center for channel 1 at depth +200.00 mm set 1 as -0.05 mm [trans pos].

## Asymmetric Longitudinal Alignment



**IMPORTANT:** Be sure to check the appropriate output line for the measurement chamber and 15 mm depth.

3. If the reported shift is not within  $0 \pm 0.05\text{mm}$ :

- Enter **0** in the **Vertical Position**.
- Enter the reported shift in the **Horizontal Position** box.
- Click the **Move** and **Set Origin** buttons.
- Repeat Steps 1-3 until the result is within  $0 \pm 0.05\text{mm}$ .



**IMPORTANT:** If at any time during the measurement of the asymmetric longitudinal (IECY) profiles it is noticed that the couch position has changed (in IECY or IECZ directions), repeat steps to confirm that the reported field center location at depth 15 mm is within  $\pm 0.05\text{mm}$ . If the field center is outside of  $\pm 0.05\text{mm}$ , adjust the tank home position and repeat any impacted asymmetric profiles.

## ◆ Collect Data in TEMS



**NOTE:** Due to the characteristic shifting of data that occurs when using the **Quick Scan** functionality, **Step Profile** must be used to measure asymmetric longitudinal (IECY) water tank profiles. This maintains absolute position information, useful for comparison with calculated dose profiles in the TCOM spreadsheet.

1. In the TEMS Readings menu, set the **Type** to **Step**, **Total Distance** to 100 mm, **Step Size** to 1.0 mm, and **Depth** to 15 mm.
2. Open the **ZZZ Water Tank Longitudinal (Mid40 leaves)** patient from the **Machine QA** task on the TDC. Select a procedure of the desired field width. After the radiation beam has been on for at least 10 seconds, click **Run** in the TEMS software to measure the profiles.
3. When the TEMS display indicates the profile has completed, save the data as **SN#\_Longitudinal\_FW##\_+/-IECY\_YYYYMMDD\_raw.csv**.
4. Repeat for all asymmetric field widths.

## ◆ Process Data in TEMS

This section contains instructions for processing the asymmetric longitudinal profiles in TEMS. TEMS will allow you to normalize each profile to its maximum and normalize to the reference channel (if necessary). When processing is complete, you can compare the profiles to the

reference data in *Microsoft Excel* as explained in the “Analyze the Result” (page 202) section of the Commissioning chapter.

For each asymmetric longitudinal profile data set:

1. If necessary, normalize each depth by the reference channel to account for dropped pulses and/or dose drift. To do so, **Ctrl-click** on the reference chamber data. Select **Analyze > Normalize By Channel**.



**IMPORTANT:** In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio.

2. To normalize each profile by its maximum value, select **Analyze > Normalize Data**.
3. Do NOT shift asymmetric profiles on their FWHM. Save the processed data as **SN#\_Longitudinal\_FW##\_+/-IECY\_YYYYMMDD\_processed.csv**.

## Initial Tank Setup: Transverse Orientation



**IMPORTANT:** Before changing the water tank setup, confirm that all Longitudinal and PDD profiles are passing.

Follow the steps in “Initial Tank Setup: Transverse Orientation” (page 199) to align the tank in the transverse orientation. Many of the notes specific to the Standard Imaging equipment in “Initial Tank Setup: Longitudinal Orientation” (page 489) also apply to the transverse orientation.



**CAUTION:** When rotating the tank, avoid pushing on the walls of the tank, as this may cause the tank to break. Push on the base of the tank, near the moat. Also, avoid stretching the cables as you are rotating the tank.

# Alignment Verification: Transverse Orientation

This section provides TEMS instructions for collecting and analyzing the profiles used to verify the rotational alignment of the tank, as discussed in the Commissioning chapter.

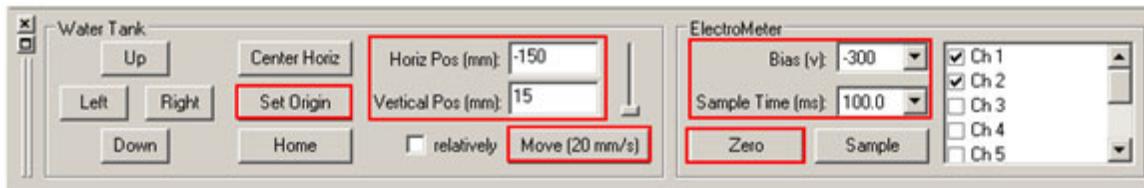
- ◆ Collect Data in TEMS ..... 505
- ◆ Process Data in TEMS ..... 506



**IMPORTANT:** Before performing alignment verification scans, perform the initial setup in the transverse orientation, as described in the previous section.

## ◆ Collect Data in TEMS

1. Ensure that you have completed the steps in the previous section to set the origin of the chamber and account for the effective depth of measurement.
2. In the **Water Tank** section of TEMS, enter the **Horiz Pos** and **Vertical Pos** according to the following table. Then click **Move**. Start with Scan #1.



Chamber Positions

Scan #	Horiz Pos (mm)	Vertical Pos (mm)
1	-150	15
2	150	15
3	0	200

3. Ensure that the **Sample Time** is set to 100 ms and the **Bias** is at -300 V.
4. Open the **ZZZ Water Tank Transverse Setup Topo** patient from the **Machine QA** task of the TDC, and prepare a procedure.
5. If the water tank is currently at isocenter in the bore, perform a -50 mm **Step Move** in Y to bring the couch out of the bore.

6. Press Ready on the Positioning Control Panel.



**Note:** Each **WaterTankTransverseSetup.xml** procedure sends the couch 30 mm into the bore (setup to ready distance). During beam-on, the couch travels in the Y direction to collect a longitudinal profile over 40 mm distance (scanning a range of [-20 mm, 20 mm] in Y with respect to isocenter). When the procedure is finished, the couch returns to the position just before **Ready** was pressed.

7. Before radiation begins, click **Sample** in the TEMS software.
8. When the procedure is complete, click **Sample** to stop sampling.
9. Save the result.
10. Repeat steps 2-9 for scans 2 and 3.

◆ **Process Data in TEMS**

1. In TEMS, click **Analyze > Couch Velocity**, and set it to 1.0.



**NOTE:** TEMS does not have a direct connection to the system and needs to be informed of the couch speed. The couch speed in the XML is 1.0 mm/s.

2. Click **Analyze > Normalize Data** to normalize the maximum of the profile to 100%.



**IMPORTANT:** Do not normalize by channel, because the reference chamber moves across the beam during the procedure.

3. Click and drag a box around the radiation-on corner of the profile to zoom in. Then, **CTRL-click** to select a point on the radiation-on corner of the profile. **Double-click** to zoom out.

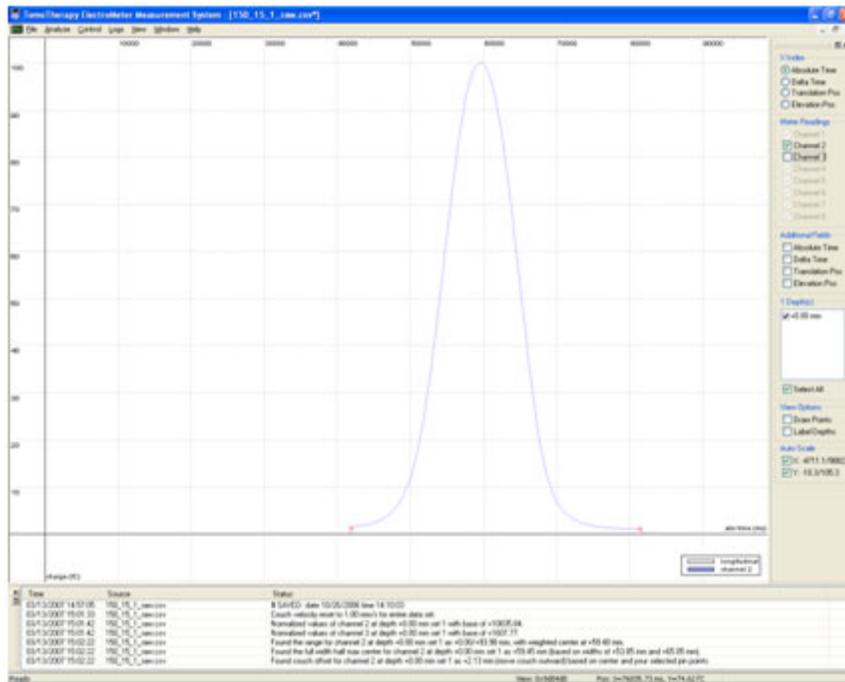


**NOTE:** Since you started the profile measurement before turning the beam on, the beam-on and beam-off corners can be identified in the profiles by the sudden increase in the chamber signal. See the red points at the lower left and lower right edges of the data plot.

4. Repeat Step 3 for the radiation-off corner of the profile.



**TIP:** The location of your beam-on and beam-off points impacts the analysis. Try to choose similar points for the beam-on and beam-off corners.



#### Beam on/off

5. Click **Analyze > Find Couch Offset**. TEMS will check the centering of the profile with respect to the beam-on period indicated by your control points, and report the couch offset in the output window at the bottom of the screen.



**IMPORTANT:** Be sure to identify the output line for the measurement channel, not the reference channel.

6. Repeat Steps 1-5 for scans 2 and 3.
7. Refer to the decision tree in “Alignment Verification: Transverse Orientation” (page 200).  
If the individual profiles differ from their average by more than 1 mm, adjust the leveling of the tank in the room (pitch or yaw), reset the depth of the chamber, and run the scans again until it passes.

If the individual profiles agree within 1 mm of their average, the rotation of the tank about the X and Z axes (pitch and yaw) is acceptable. Adjust the Y position of the couch to correct for the average center position in your 3 scans.

8. Bring the couch 50 mm into the bore (to isocenter).

# Transverse Profiles

The Commissioning chapter outlines the requirements for transverse profile scans. This section contains instructions for collecting and processing the data in TEMS.

- ◆ Collect Data with TEMS ..... 508
- ◆ Process Data with TEMS ..... 509



**IMPORTANT:** Verify the scan alignment according to the instructions in the previous sections, before collecting data.



**IMPORTANT:** If you have not already done so, move the couch **50 mm** into the bore, to isocenter.

## ◆ Collect Data with TEMS

1. Enter the parameters in the TEMS Readings menu as shown:

A screenshot of the TEMS Readings menu. The 'Type' dropdown is set to 'Quick Scan'. The 'Orientation' dropdown is set to 'Lateral (NPDD)'. Below these are two buttons: 'Defaults' and 'Run'. To the right is a table with three rows:

Property	Value
Total Distance (mm)	510
Horizontal Velocity (mm/s)	6

At the bottom of the table, it says 'Depths (mm, ~CSV) 15, 50~200@50'.

Transverse Collection

2. Open the **ZZZ Water Tank Transverse (All Open)** patient from the Machine QA task on the TDC.
3. Select and run the **J42mm All Open** procedure.
4. After the radiation has been on for about 10 seconds, click **Run** in TEMS.



**TIP:** If a red error line appears in the output area of the TEMS and software stops while collecting transverse profiles, this often indicates that the scan arm limit switches could not accommodate the range of widths requested. This could be resolved by adjusting the position of the limit switches (making sure that the scan arm does not collide with the water tank walls) or by slightly shortening the requested scan length (e.g., reduce the **Total Distance** field from 510 to 500 mm in TEMS).

5. When the TEMS display indicates the profile has completed, save the data as **SN#\_Transverse\_FW##mm\_YYYYMMDD\_raw.csv**.

6. Repeat Steps 1 - 5 for the other symmetric field widths.

## ◆ Process Data with TEMS

In TEMS, process the measured data:

1. If necessary, normalize each depth by the reference channel to account for dropped pulses and/or dose drift. To do so, **CTRL-click** on the reference chamber data. Select **Analyze > Normalize By Channel**.



**IMPORTANT:** In some cases, normalizing the measurement to the reference chamber degrades the signal to noise ratio.

2. To normalize by the max, select **Analyze > Normalize Data**.
3. Shift each depth to its full-width 75% field center for consistency. **CTRL-click** on the measured data, then select **Analyze > Shift on % Max** and enter **75%** in the pop-up window.



**NOTE:** See note on scan arm acceleration in “Symmetric Longitudinal Profiles” (page 495). For the transverse profiles, the 75% max is used instead of the 50% max. (The 50% max is near the corners of the profile and is a more difficult place to get a stable field width measurement.)

4. Save the processed data as:  
**SN#\_Transverse\_FW##mm\_YYYYMMDD\_processed.csv**.

When processing is complete, you can compare the profiles to the reference data in *Microsoft Excel*/as explained in the “Analyze the Result” (page 202) section of the Commissioning chapter.





## Appendix B

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### Film Analysis

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## Introduction

Many clinics prefer to eliminate the expense and upkeep of film and film processors. A number of alternatives to film are on the market for patient-specific QA. While an array device can be a viable option for patient-specific QA, the resolution of an array device (typically several millimeters) is not sufficient for TG-148 alignment tests that have sub-millimeter tolerances. Your clinic should account for the need to perform alignment tests using film as part of the routine QA of your treatment system.

## Film Specifications

The most common films used in radiotherapy are Kodak® EDR2 film, and GAFchromic EBT film:

- Kodak EDR2 film requires a wet film processor and darkroom, but some clinics prefer EDR2 film because it is less sensitive to handling and scanning than EBT film, and produces a more uniform result.
- EBT film does not require a wet film processor, and is self-developing when exposed to radiation. EBT film takes several hours to stabilize and is sensitive to scanning orientation.

Medium-sized film (approximately 20 cm x 25 cm) is sufficient for most alignment tests. Large-sized film (approximately 32 cm x 43 cm) is recommended for the overhead laser test.



**IMPORTANT:** Typically, the beam-on time has to be doubled to achieve the same exposure on the EBT film as compared to EDR2.



**IMPORTANT:** Refer to the film manufacturer product specification for proper handling instructions for EBT film.

## Scanner Specifications

Regardless of whether EDR2 film or EBT film is used, it will be necessary to have a medical quality film digitizer (scanner) to convert your film into a digital file for analysis and storage.

Vidar is the only company that makes scanners designed for medical applications. Scanners designed for home use do not have the quality needed for medical testing. Ashland, the seller of EBT film, suggests using an Epson® flatbed scanner such as the 10000XL; however, the *Epson* is not designed for medical applications.

# Overview of RIT Analysis Software

RITg148+ software is a product of Radiological Imaging Technology (RIT). For instructions on using RITg148+, please refer to the RIT manual.

The RITg148+ software can be used to perform the following tasks:

- Scan a film with the Vidar DosimetryPRO® Advantage Digitizer® and save it in a RIT proprietary format.



**NOTE:** With RITg148+ and RIT Complete V6.6 and later, you can also save in .tif format.

- Open a .tif file.
- Analyze all the TG 148 alignment films: y-jaw divergence and gantry rotation plane alignment, overhead laser, MLC lateral offset and twist, treatment beam field centering, static and helical star shots, and couch translation/gantry rotation.
- Draw profiles through a film.
- Additional tasks as advertised by RIT.

The RITg148+ software does not perform patient QA analysis; however, the RIT Complete software has tools for analysis of patient QA films.

If you purchase a RITg148+ license, you will also need to provide your own:

- Film.
- Medical quality scanner.
- Software to drive your scanner and create a .tif file, if needed for patient QA film analysis.



**NOTE:** RITg148+ only drives Vidar scanners. If using a version of RIT older than V6.6, RIT can drive the Vidar to scan a film, but can only save the film in a proprietary format. An upgrade to RIT V6.6 would be needed to enable saving the film in .tif format. Contact RIT to purchase an upgrade to V6.6, or to request an automatic upgrade if enrolled in RIT's Product Maintenance Program.

- Computer to run your RITg148+ license. Accuray does not include the computer. For minimum system requirements, see <http://radimage.com/support/minimum-requirements-for-rit-software/>.

# Tips for Exposing, Marking, and Scanning Films

Most of the RIT analysis modules are highly automated. In many cases, the modules can locate the exposures and pin pricks on the film without user intervention. The automation works best if the films are exposed according to RIT instructions. However, there are some tools available for manual clean-up if necessary.

Tips for exposing the films:

- Use rectangular sheets of film, not oddly shaped or small fragments of film. Some tests require a few cm of clean background around the exposure for accurate analysis.
- Pay attention to the film exposure orientation required for the particular test. In particular, the couch travel, static star shot, and helical star shot films must be exposed in landscape or portrait orientation.

Tips for marking the films prior to scanning:

- Avoid writing on or marking the film except as required for the RIT analysis. (If you want to record information on the hard copy of the film, you could write on the EDR film jacket, or write on the film after scanning it.)
- If you must write on the film before scanning it, you will probably need to use tools within the RIT software to crop or erase the writing prior to analysis. To make it easier to erase the writing, confine the writing to an area far away from the exposures and don't write or mark to the very edge of the film.
- If using EDR2 film, make modest-sized pin pricks shortly before developing the films. If the pin pricks are exposed to too much light prior to development, the pin pricks can grow too large.
- If using EBT film, mark the laser positions with small dots on the film using a regular permanent marker. Do not use a red permanent marker if your scanner has red-channel subtraction. Do not use a fine-point Sharpie (if the marks are too small, RIT will have trouble finding them, especially if a smoothing filter is applied to the film to reduce image noise).
- It is recommended to place the laser marks about 1 cm from the edge of the film.
- Do not make laser marks in the exposure region. (The star shot films are an exception, where it is OK to make marks about 1 cm away from the film edge that may be in the exposure region.)

Tips for scanning the films:

- If using EBT film, follow the film manufacturer's instructions.
- Scan the film in straight, to avoid a bright edge at the boundary of the film that can impede the analysis. (If necessary, you can use the RIT software to crop out bright film edges.)

- For the film alignment tests, do not associate a dose calibration file. You may wish to follow the instructions in the user guide to perform a scanner spatial calibration, to more precisely define the pixel size. You can then apply the spatial calibration to future scans.

# Create a Film Dose Calibration File

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## ◆ Expose the Film



**NOTE:** This section provides one possible method of using the treatment system to irradiate films for the purpose of creating a film dose calibration table.



**NOTE:** For film alignment modules in the RITg148+ software, it is not recommended to apply a film dose calibration file.

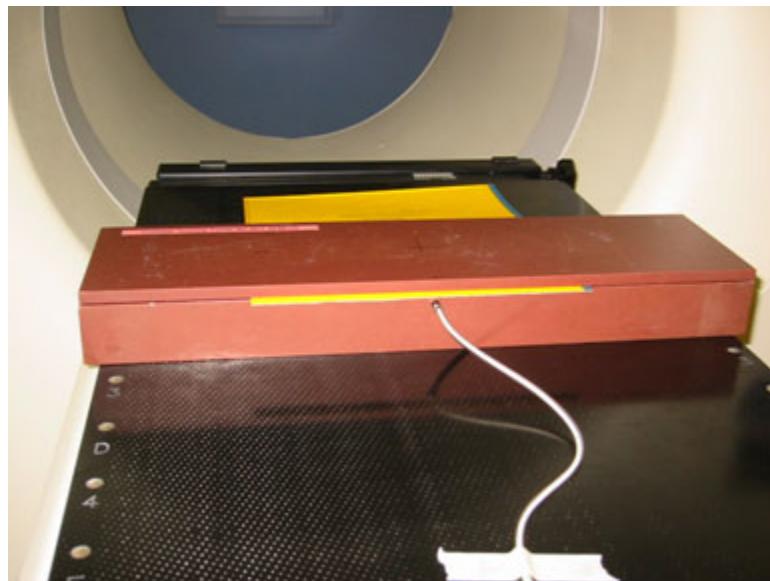


**IMPORTANT:** For film dosimetry, the film calibration file should be uniquely measured for each film box, processor chemical change (if applicable) and film digitizer.



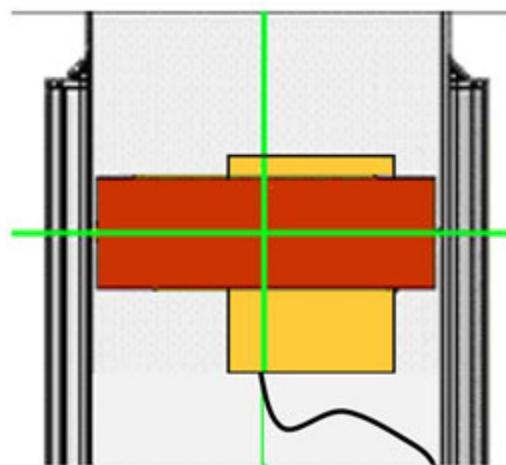
**IMPORTANT:** The film calibration file should extend beyond the full range of dose values that are expected to be measured.

1. Install an appropriate film calibration procedure file on the TDC (e.g., use the **Film\_Cal.xml** or **GAF\_Film\_Cal.xml** file, which are available from Accuray Customer Support.)
2. Use a 5 cm Virtual Water™ slab, an A1SL ion chamber, a film, and a 1 cm Virtual Water slab to reproduce the setup shown in the Film Cal Photo below.



Film Cal Photo

3. The film is at 1 cm depth, and the ion chamber at 2 cm depth, with a few cm of material for backscatter below the ion chamber.
4. Adjust the couch height so the bore laser skims the top surface of the *Virtual Water* stack (85 cm SSD).
5. Position the *Virtual Water* so the ion chamber is centered on the green overhead lasers in IEC X and IEC Y, and so the desired portion of the film is centered on the green lasers. As shown in the Film Cal Diagram image below. The film may be offset to allow multiple exposures on one film, but the ion chamber needs to be centered on the overhead lasers in IEC X and IEC Y for each exposure. Depending on the film calibration file used, the size of each exposure on the film will be approximately 5 cm x 10 cm (EDR version) or 5 cm x 5 cm (GAF version).



Film Cal Diagram

6. Ensure the ion chamber is taped in place so that it will not slip out of the *Virtual Water*. Use a cable to connect the ion chamber in the treatment room to the electrometer outside the treatment room, and prepare the electrometer to measure integrated charge.
7. Use the step move function on the **Positioning Control Panel** to move the table top 70 cm into the bore so the *Virtual Water* is under the LINAC.
8. With the *Virtual Water* stack in the bore, adjust the couch height to account for couch sag. The bore laser should skim the top surface of the *Virtual Water* stack (85 cm SSD).
9. If the XML indicates that the couch will move into the bore when **Ready** is pressed, bring the couch back out of the bore to virtual isocenter (-70 cm in Y). (In the procedures provided by Accuray Incorporated, the **Film\_Cal.xml** does not move the couch into the bore when ready is pressed, but the **GAF\_Film\_Cal.xml** moves the couch 70 cm into the bore when "Ready" is pressed.)
10. Record temperature, pressure, ion chamber calibration factor, and electrometer calibration factor.
11. On the TDC, open the film calibration procedure from the **Machine QA** task, and proceed to the **Run** tab.
12. Select one of the listed procedures that is noted 5 sec.
13. Click **Prepare Calibration**.
14. Start the electrometer integrating.
15. Run the procedure.
16. Record the absolute value of the charge on the electrometer, temperature, pressure, and calibration factors for the ion chamber and electrometer and calculate the dose delivered to the ion chamber.
17. Using the PDD data collected with the water tank for the 5 cm field width, determine the dose ratio D10mm/D20mm (this factor is typically  $\sim 1.03$  but may vary depending on the beam model) and multiply this by the dose measured by the ion chamber to determine the dose delivered to the film.
18. Repeat steps 11-13 for the procedures with other times listed, moving the film each time to irradiate a different part (or replacing it with a new film to avoid crowding the exposures).
19. Develop the film(s), if the film is not the self-developing kind.

## ◆ Create Film Calibration Table

1. Place the developed film in the Vidar scanner.
2. Launch your scanner software and digitize the film.

3. Using the same software that digitized the film, measure average pixel value in the center of each exposed region (e.g., in a 1 cm x 1 cm square), as well as in the background region of the film (0 cGy).
4. Prepare the calibration file to relate film values to dose, in a format suitable for your third party patient film analysis tools.

# Film Profiles for Completion Procedure Tests

This section provides instructions for drawing profiles in RITg148+ so that they can be analyzed in *Microsoft Excel*.

- ◆ Test Procedure ..... 522



**TIP:** RITg148+ also advertises an automated tool for the evaluation of completion procedure films; this module has not been evaluated by Accuray.

## ◆ Test Procedure

After developing both films, digitize them with an approved scanner and save the digitized film files. Be sure to label the films and film files appropriately (i.e., HU for Helical Uninterrupted). Make sure to repeat the steps below for each new film opened, since the RIT software will reset some of the parameters to their default values when a new film is opened.

1. Using the RIT software, open the **Uninterrupted Procedure - Helical** film file.
2. If the exposed regions of your image have lower numerical values than the background:
  - Turn off the image filter (if you invert and save with the filter on, you will not be able to remove the filter later).
  - From the **Edit** menu, choose **Invert and Save**, then choose **invert only**.
3. Choose a pallet of colors to work with and use the window leveling box to try to find the laser marks.
4. If you can't see the laser marks, turn off the image filter. Then, enhance the laser marks with the pin prick and erase tool. Ensure that the **pin prick value** is set to **min** (to avoid impacting the profile normalization in *Excel*, which is based on the max value in the image).
5. To compare two films correctly, make sure you are applying the same filter parameters for both films for this analysis. If the profiles are noisy, you can consider turning on the median 3x3 or 5x5 filters.

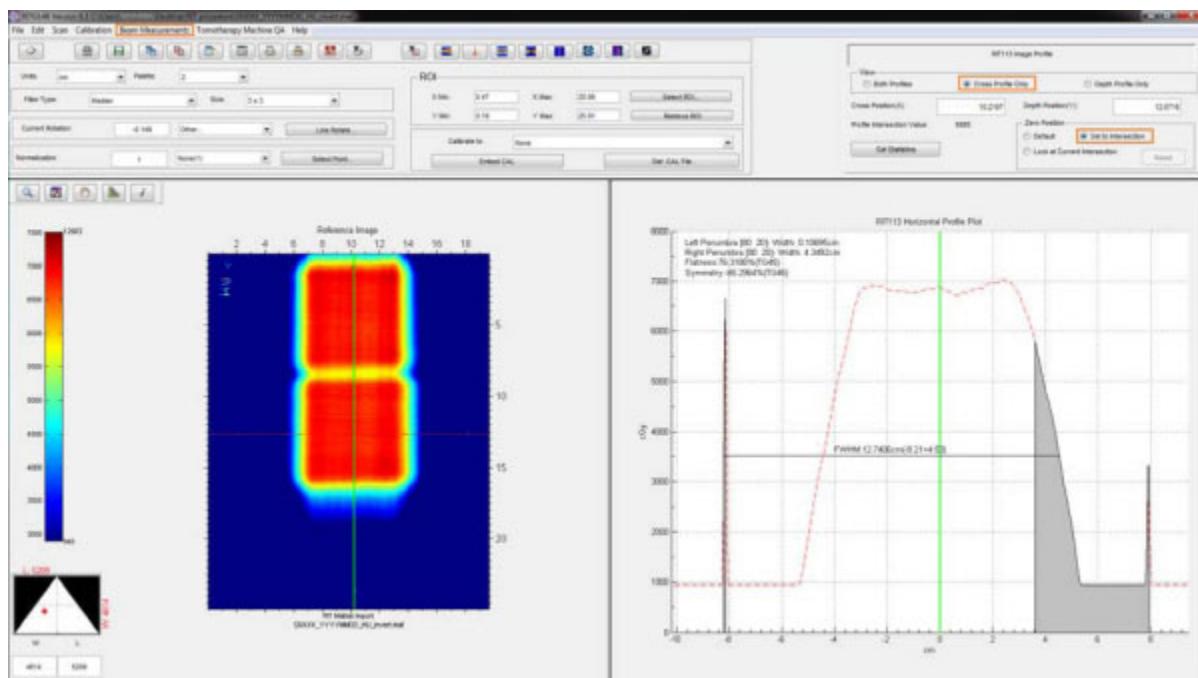


**NOTE:** Changing the filter settings makes you lose all your profile analysis settings as well as the position of the profile.

6. Since RIT measures profiles in the horizontal and/or vertical directions, it is okay if the film is rotated 90°. However, the laser lines need to run horizontally and vertically on the screen. Use the "line rotate" tool if the film is close to the alignment position. If you need to rotate the film by 90°,

consider using the **Non-Cropping Image Rotation and Resize** from the **Edit** menu. Keep the **scale factor** at 1.0.

7. Use the ROI selection tool to crop out any bright edges of the image.
8. From the **Beam Measurements** menu at the top of the window, choose orthogonal profiles.
9. Click and drag the lines in the Reference Image to move the profiles to the position of the laser marks. The directional arrows on the keyboard may also be used for this purpose.
10. Select **set to intersection** for the zero position setting. (This ensures that positions listed and saved in the interrupted and uninterrupted profile data will be referenced to the green lasers.)
11. Right-click on the profile lines in the Reference Image to adjust their color or line style, to more easily distinguish between the horizontal and vertical profiles.
12. In the upper right corner of the screen, display only the profile that corresponds to the IEC Y axis (“cross profile” or “depth profile,” depending on how the film was oriented).



The profile lines pass through the laser marks. In this orientation, the IEC Y profile is the horizontal (“cross profile”) on the screen, which we chose to display with a dashed red line. Note that although the vertical axis of the plot is labeled as “cGy,” since no calibration has been applied, the actual data is in scanner units.

13. From the **File** menu, select **Export Plot ASCII data** to get the list of data values for the profile. Click the **Save** button to save the profile data in **.txt** format. Make sure to give a consistent name to this profile data and change the file extension from **.txt** to **.csv**.



## Appendix C

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### Create Machine QA

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# Getting Started

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## ◆ About System Parameters and Machine QA Procedures

The **Create Machine QA** workflow is used to create custom machine quality assurance procedures.

Although it is possible to create a procedure that uses the imaging beam, delivering these procedures on the **Run** tab will not result in a reconstructed image volume. Only procedures generated on the **Scan** tab may be reconstructed by the treatment system software.

You can review machine QA images by choosing **Review Machine QA Registration** from the TDC Tools menu.



**NOTE:** Machine QA procedures are purged nightly. Only the most recent several images are retained. You can set the Maximum number of Machine QA Procedures to Keep in the Policies tab of the System Administration task on the Accuray Precision software.



**IMPORTANT:** If you load a procedure XML that was created on a previous version of Accuray software or a previous generation of Accuray products, the TDC will attempt to update the file format to be compatible with your current software. Due to changes in data architecture over major software versions and generations of product models, Accuray Incorporated recommends that you review the parameters of any XMLs loaded into your system to ensure that the procedure settings meet your needs.

## Modifications to Machine Data

Click on the **Machine QA** workflow button to view parameters on the **Edit Machine** tab. You may also access the **Edit Machine** tab from the **Tools** menu.

Inappropriate changes in the **Edit Machine** area could lead to treatment error. The site physicist may use the **Edit Machine** area to calibrate the monitor unit display as discussed in “Monitor Unit Display Calibration” (page 257), but should not make any other changes to the **Edit Machine** area.

Task	Path
View or Edit Machine Data	Tools > Edit Machine Machine QA > Edit Machine



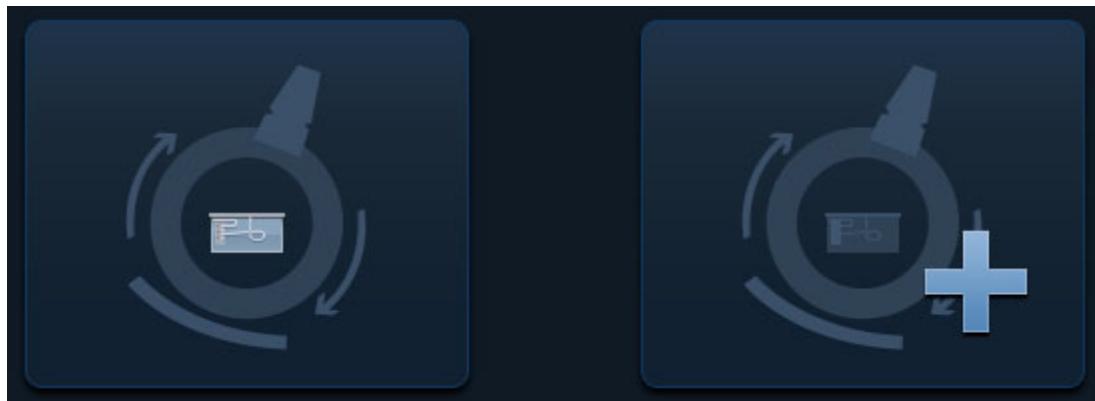
**WARNING:** Modifications to machine data, performed by unqualified personnel, can result in serious injury to the patient during treatment. Modification of data is to be done by qualified personnel in accordance with accepted practices and protocols, relevant to specific machine applications and usage. Understand the following:

- The quality of treatment delivered to the patient is critically dependent upon the accuracy of the data representing the properties of the delivery system.
- If machine data is modified, the new machine definition must be representative of the machine properties.
- Safety-related features associated with the machine definition, such as radiation output checking, should NEVER be disabled in machine data that is to be used in clinical deliveries. Such changes can result in inaccurate delivery of radiation and serious injury to the patient.

## ◆ Procedure and Run Tabs

From the TDC home screen, two workflow buttons are used for machine quality assurance. Click on the **Machine QA** workflow button to deliver machine quality assurance procedures or to view parameters on the **Edit Machine** tab. You may also access the **Edit Machine** tab from the **Tools** menu. Click the **Create Machine QA** workflow button to view, modify, or create machine quality assurance procedures.

Task	Path
Create or View Machine QA Procedures	Create Machine QA > Basic Create Create Machine QA > Create Create Machine QA > Create From Patient Plan Create Machine QA > View



Machine QA and Create Machine QA workflow buttons

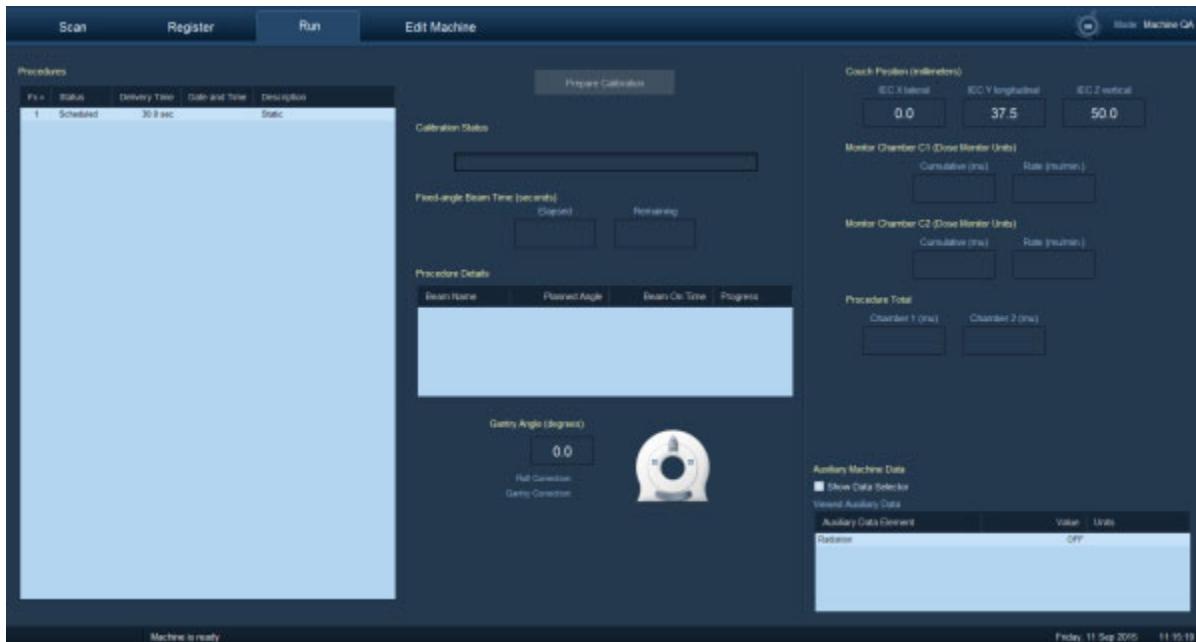
## Procedure Tab

Use the **Procedure** tab to view and create procedures.

- Click **View** to see parameters for procedures on the data server or to open a procedure **XML** file located from the data server or from a local file.
- Click **Basic Create** to make a new procedure **XML** file by selecting options and specifying parameters in a simplified data-entry form.
- Click **Create** to make a new procedure **XML** file based on an existing procedure on the data server or a local **XML** file. This advanced view allows you to view and define all parameters.
- Click **Create From Patient Plan** to make a new procedure **XML** file based on the parameters of an existing patient plan.
- Click **Delete** to select a procedure to remove.

## Run Tab

Use the **Run** tab to perform machine QA procedures to collect measurements used for system quality assurance. The procedures available in the **Procedures** list vary depending on the selected workflow.



Run Tab

## ◆ Edit Machine Tab

Use the **Edit Machine** tab to view machine data parameters.

- Click **View** to see data parameters on the data server or in an XML file.
- **Create**, **Supersede**, and **Decommission** buttons are used by Accuray Incorporated for factory calibration and service purposes.



**NOTE:** For additional descriptions and warnings related to the Edit Machine tab, see “Machine Data” (page 99).

## ◆ Open and View a Data Structure

The **Procedure** and **Edit Machine** tabs allow you to open and view machine parameters on the data server, or from an XML file located on the data server, a network-connected device, or a local device. After procedure data is loaded, click a triangle, double-click a folder, or right-click on a folder to **Expand** or **Collapse** sets of data parameters.

Procedure	
<b>View</b>	Query the Data Server or load a Procedure to view all its parameters.
<b>Basic Create</b>	Define the basic parameters to create a Procedure.
<b>Create</b>	View all parameters to define one or more as required to create a Procedure.
<b>Create From Patient Plan</b>	View all parameters as taken from a patient plan to redefine one or more as required to create a Procedure.
<b>Delete</b>	Delete selected procedure

#### Open and View a Procedure

Scan	Register	Run	Edit Machine
Save	Import	Export	Revert
<ul style="list-style-type: none"> <li>📁 TechPubs           <ul style="list-style-type: none"> <li>📄 Machine Settings</li> <li>📄 Dose Control</li> <li>▶️📁 Couch Settings               <ul style="list-style-type: none"> <li>📄 MVCT Settings</li> <li>📄 Airscan Settings</li> <li>📄 Linearity Settings</li> <li>📄 Detector Settings</li> <li>📄 Gantry Settings</li> <li>📄 Jaw Settings</li> <li>📄 MLC Settings</li> </ul> </li> <li>▶️📁 Monitored Signals</li> <li>▶️📁 Beams</li> </ul> </li> </ul>			

#### View Machine Parameters

## Command Buttons

Button	Description
<b>Query</b>	Click to search and select information on the data server.
<b>Load File</b>	Click to open an XML file.
<b>Load Default</b>	Click to view the default parameters. Default values provide you with a starting point to work from.

Button	Description
<b>Cancel</b>	Click to choose a different task.
<b>Save</b>	Click to save data as an XML file to any network-connected storage media or drive.
<b>Save to XML File</b>	Click to save data as an XML file to any network-connected storage media or drive.
<b>Save to Data Server</b>	Click to save data as an XML file to the data server.
<b>Import</b>	Click to load data from any network-connected storage media or drive.
<b>Export</b>	Click to save data to any network-connected storage media or drive.
<b>Revert</b>	Click to reset data parameters to the previously saved state.



**NOTE:** The procedures must be submitted to the data server before they can be run.

## Query the Data Server

1. From the **Procedure** tab, click **View**.
2. Click **Query**. The **Machine QA Selection Dialog** is displayed.
3. Select an item from both lists, and click **OK**.
4. The data parameters of the file are displayed.

## Load an XML File

1. From the **Procedure** tab, click **View**.
2. Click **Load File**. The **Open** dialog box is displayed.
3. Select the file that you would like to work with and click **Open**.
4. The data parameters of the file are displayed.

## Load the Default Parameters

Default values are not intended for clinical use. Rather, they provide you with a starting point to update field values.

1. From the **Procedure** tab, click **View**.
2. Click **Load Default**.
3. The default data parameters are displayed.

## Save a Procedure XML file

If you want to use the procedure that you are working with to create additional procedures later, save the procedure to an XML file.



**IMPORTANT:** Once you commit a procedure to the data server, the procedure cannot be edited. Accuray Incorporated recommends that you save XML files to disk before they are committed to the data server. However, if required, you can edit a copy of the procedure that is on the data server and re-submit it.

1. Click **Save**. The **Save** dialog box appears.

If you want to save the binary files associated with the procedure, select the **Save Binaries** check box in the **Save** dialog box. A folder (with the same name as your file) is created to store the binary files.



**NOTE:** The binary files include the MLC sinogram instructions, which are needed to run a procedure.

2. Type a file name, and click **Save**.

# The Basic Create & Sinogram Editor Interface

- ◆ Basic Create Interface ..... 533
- ◆ Sinogram Editor Interface ..... 539

## ◆ Basic Create Interface

Use **Basic Create** to make a new procedure XML file by selecting options and specifying parameters in a simplified data-entry form.

Procedure Tab - Basic Create

## Basic Procedure Data

Item	Description
<b>Machine QA Name</b>	Type a name to label the procedure stored in the data server. The default name is <b>Machine QA procedures</b> .
<b>Procedures</b>	This list displays the procedures that you can clone or delete.
<b>Clone</b>	Click this button to copy a procedure from the <b>Procedures</b> list. See “Clone a Procedure” (page 546) for more information.
<b>Delete</b>	Click this button to remove a procedure from the Procedures list.
<b>Description</b>	This field is automatically populated with information about the procedure based on your selections. You may type a new description and press <b>Enter</b> to update the description of the selected procedure in the <b>Procedures</b> list.
<b>Setup to Ready Longitudinal Distance</b>	The setup to ready position distance is the longitudinal distance that the couch will travel into the gantry bore when the <b>Ready</b> button on the <b>Positioning Control Panel</b> is pressed. The value for this parameter is typically based on where you want a phantom to be positioned prior to the start of irradiation. The default value is 700 mm, which is the normal distance from the virtual isocenter to the machine isocenter.
<b>Compression Factor and Compression Type</b>	This setting determines the amount of detector data that is saved immediately after irradiation. There are no consumers of the data stored on the data server for machine QA procedures, so these settings have no relevance.
<b>Beam</b>	Select a <b>Scan</b> or <b>Treatment</b> beam from the drop-down list.

## Fragment Settings

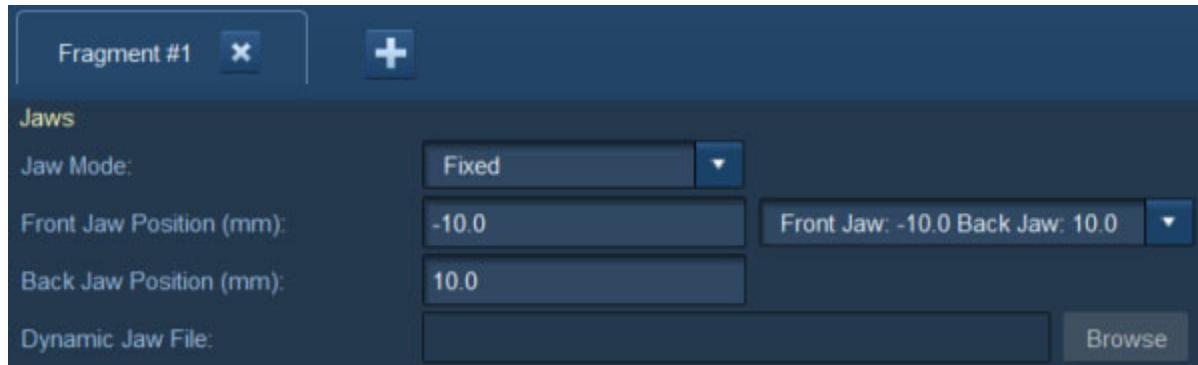
Each procedure consists of one or more fragments. A fragment is a set of instructions for the jaws, gantry, multileaf collimator and couch. The couch speed is constant within each fragment, but may vary from one fragment to another. The couch moves in the IEC +Y direction only when the beam is on. After turning the key to **Treat** and starting a multi-fragment procedure, the machine automatically steps through the series of fragments. Between fragments, the beam turns off, and the couch returns to the ready position.



**IMPORTANT:** Use the multiple fragment feature to create static-gantry procedures only.

## Jaws

Determine the **Jaws** options that you want to use to create the procedure. Based on the **Jaw Mode** that you select, various fields become available for data entry.



Item	Description
<b>Jaw Mode</b>	Select <b>Fixed</b> or <b>Dynamic</b> from the drop-down list. <ul style="list-style-type: none"><li>In a fixed jaw delivery, the jaw position is constant throughout the delivery.</li><li>In a dynamic jaws delivery, the jaws move as specified by the dynamic jaws file. See “Determining Dynamic Jaws Motion” (page 438).</li></ul>
<b>Front Jaw Position (mm)</b>	XML files that specify dynamic jaw positions may be run on machines that do not have dynamic jaws, but the jaw positions will be fixed throughout the delivery at the positions indicated by the <b>Front Jaw Position</b> and <b>Back Jaw Position</b> parameters.
<b>Back Jaw Position (mm)</b>	The <b>Front Jaw Position (mm)</b> displays the front jaw size in jaw numbers. Use the drop-down list next to the <b>Front Jaw Position (mm)</b> field to select a setting. If you select <b>Custom Settings</b> , you can type the value of the front jaw size that you want to use. See “Jaw Numbers” (page 15) for an explanation of the front and back jaw position values.
<b>Dynamic Jaw File</b>	Click <b>Browse</b> to select a dynamic jaw file to load.

## Gantry

Determine the **Gantry** options that you want for the procedure. Based on the **Gantry Mode** that you select, various fields become available for data entry.

Gantry	
Gantry Mode:	Fixed
Gantry Start Angle (degrees):	0.0
Projections Per Gantry Rotation:	
Time Per Gantry Rotation (seconds):	
Projections Per Second:	1.0

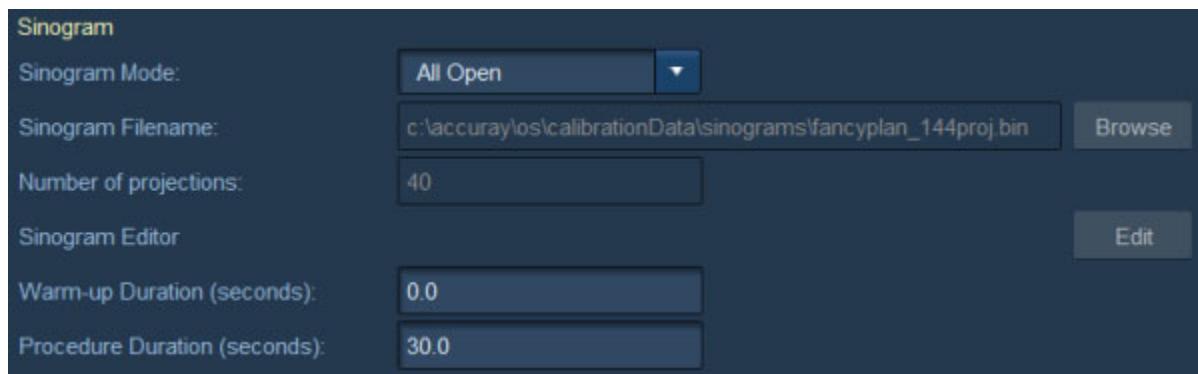
Item	Description
Gantry Mode	Select <b>Fixed</b> or <b>Rotating</b> based on whether you want the gantry to rotate during the procedure.
Gantry Start Angle (degrees)	When the gantry is rotating, type the gantry start angle at which the first projection delivers radiation. The default value is 0. The first projection will be centered on <b>Gantry Start Angle</b> + (Projection Size in degrees/2)
Projections Per Gantry Rotation	Type the number of projections for each gantry rotation. This value determines the number of projections during a single rotation. The default value is 1.
Time Per Gantry Rotation (seconds)	Type the number of seconds that one gantry rotation should last. The default value is 12. The gantry period is limited by the commissioned rotating periods setting in <b>Gantry Settings</b> in the machine record  Note the following for this parameter: <ul style="list-style-type: none"><li>• Minimum = 6.0 seconds (10 rotations per minute).</li><li>• Maximum = 60.0 seconds (1 rotation per minute).</li></ul>
Projections Per Second	Type the number of projections that are delivered per second. The default value is 1 for Fixed gantry mode. In Rotating Gantry Mode the number of projections per second is determined by the Time Per Gantry Rotation and the Projections Per Gantry Rotation.

## Sinogram

A sinogram is an array of instructions for the multileaf collimator (MLC). It indicates which leaves should open, when, and for how long. The columns of the sinogram represent the 64 leaves, and the rows represent projections. A projection corresponds to a time increment. During the procedure, the MLC steps through the instructions in the sinogram, one row at a time. For helical treatment procedures generated in the planning software, there are 51 projections per rotation, so each row corresponds to 7.06 deg of gantry rotation. For machine quality assurance procedures, the user specifies the number of projections and time per projection.

Each cell (beamlet) of the sinogram indicates the percentage of a projection for which a certain leaf should be open. A leaf can be open for 0 to 100% of the projection time increment.

You can choose the type of sinogram that controls the MLC (leaf control sinogram). Based on the **Sinogram Mode** that you select, various fields become available for data entry.

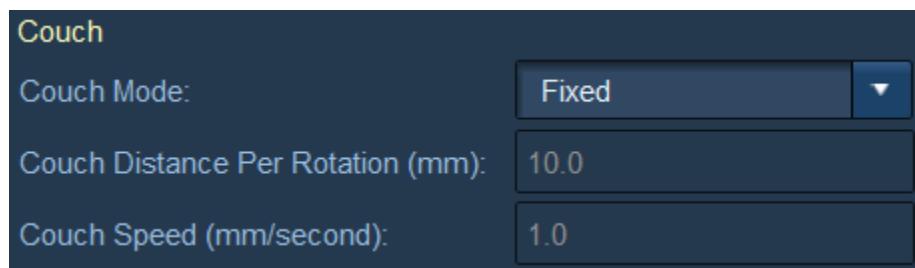


Item	Description
<b>Sinogram Mode</b>	<ul style="list-style-type: none"><li>Select <b>All Open</b> or <b>All Closed</b> if you want to use the same leaf pattern for each projection in the procedure. A static sinogram can only have open or closed leaves.</li><li>Select <b>Dynamic</b> to use a sinogram that specifies the leaf patterns and intensity for projections (the leaf pattern changes as the procedure is delivered). A dynamic sinogram is used for any procedure that does not use leaves that are all open or all closed.</li></ul>
<b>Sinogram Filename</b> (Dynamic only)	The file name and path of the loaded sinogram is displayed. The default sinogram loaded is: <b>C:\accuray\tdc\calibrationData\sinograms\fancyplan_144proj.bin</b> Click <b>Browse</b> to select another sinogram to load.
<b>Number of projections</b> (Dynamic only)	Type the number of projections for the fragment. The default value is 40.

Item	Description
<b>Sinogram Editor</b> (Dynamic only)	Click <b>Edit</b> to open the <b>Sinogram Editor</b> and edit the loaded sinogram.
<b>Warm-up Duration</b> <b>(seconds)</b> (Static only)	Type the number of seconds that the warm-up should last. The default value is 10. <b>Warm-up Duration</b> is not included in the <b>Procedure Duration</b> .
<b>Procedure Duration</b> <b>(seconds)</b> (Static only)	Type the number of seconds that the procedure should last. The default value is 30.

### Couch

Select the **Couch** options that you want to use to create the procedure. These options control the longitudinal movement of the couch. The couch moves at a constant speed throughout the beam-on procedure, including during any warm-up time (time with the beam on and leaves closed) that may be specified in the leaf sinogram.



Item	Description
<b>Couch Mode</b>	Select <b>Fixed</b> or <b>Moving</b> based on whether you want the couch to move during the procedure. If you select <b>Moving</b> , the <b>Couch Speed</b> field becomes available for data entry.
<b>Couch Distance Per Rotation (mm)</b>	Type the distance in millimeters that the couch will travel in one gantry rotation. The default value is 10.
<b>Couch Speed</b> (mm/second)	Type the distance in millimeters that the couch will travel per second. The default value is 1.

### Fragment Summary

The **Fragment Summary** lists the selections made for a given fragment. Depending on the fragment settings you choose, the **Type of delivery** field will display **Static** (static gantry), **Axial** (static couch, moving gantry), or **Helical** (moving couch and gantry).

### Fragment Summary

Type of delivery: Static  
Total number of projections: 30  
Projections per second: 1.00  
Gantry Rotations: None  
Projections per rotation: 6.00  
Total Couch Distance: 0.00 mm  
Procedure Time: 30.00 seconds

### Status

Information appears in the **Status** area if there is a warning generated by the fraction settings you have entered or selected. The following image contains sample status messages.

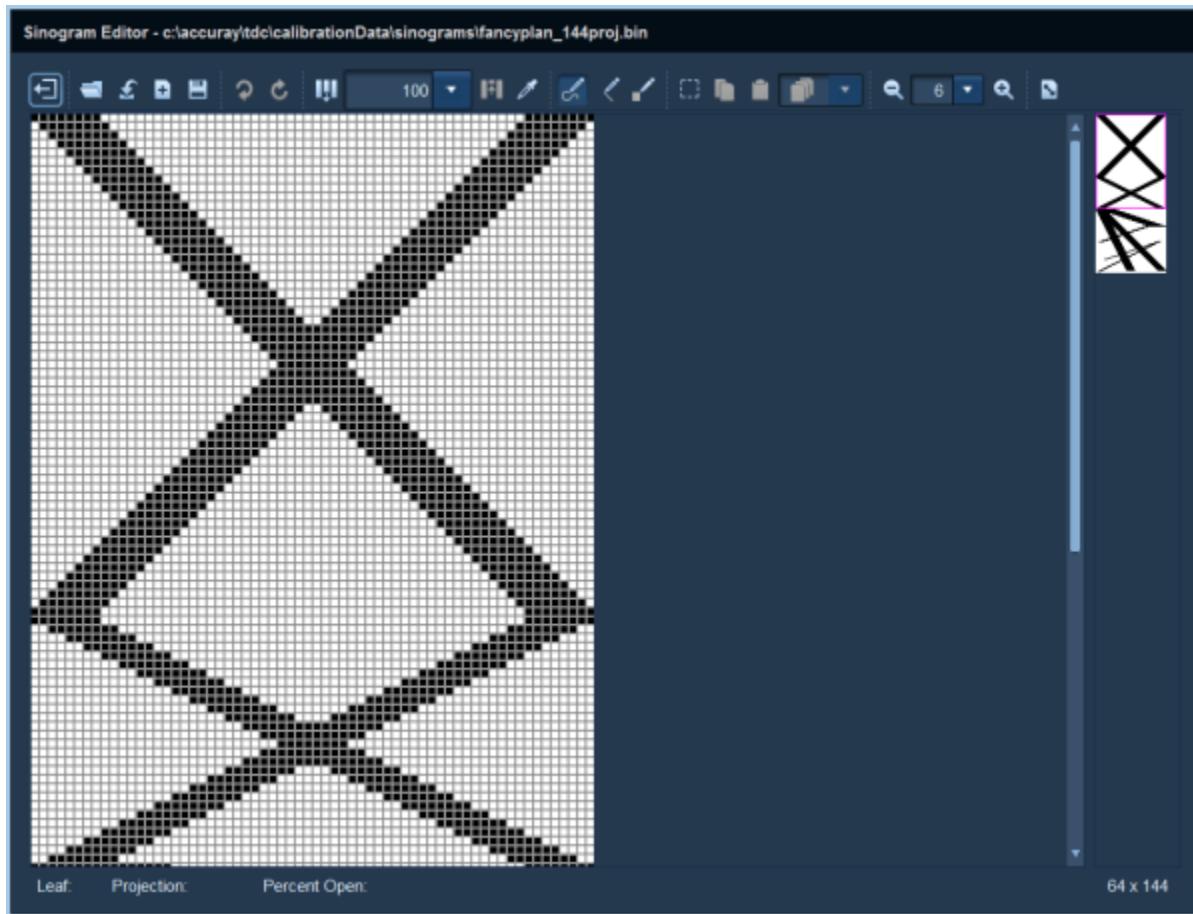
### Status

**Form Error Examples:** Compression factor must be greater than or equal to 1  
The projection count is greater than the maximum allowed value of 100000.  
**Fragment #1 (Delivery: Helical, Sinogram: Static):** Projections per gantry rotation cannot be achieved exactly with the current machine record settings.  
**Fragment #2 (Delivery: Helical, Sinogram: Static):** Projections per gantry rotation cannot be achieved exactly with the current machine record settings.  
**Fragment #2 (Delivery: Helical, Sinogram: Static):** Couch distance per gantry rotation cannot be achieved exactly with the current machine record settings.

## ◆ Sinogram Editor Interface

Use the **Sinogram Editor** to create and edit sinograms. The title bar includes the name of the sinogram file that you are working with.

## About the Sinogram Editor Work Area



Sinogram Editor

The **Sinogram Editor** work area has the following components:

Component	Description
Sinogram Editor Toolbar	The toolbar at the top of the window contains various tools to create, modify, and save a sinogram.
Edit Area	The edit area in the center of the window displays the sinogram pixel-by-pixel.
Navigator	<p>The navigator on the right side of the window is used to quickly change the edit area view.</p> <ul style="list-style-type: none"><li>To move the view of an image, drag the colored box in the navigator.</li><li>You can also click anywhere in the navigator to designate the viewable area.</li></ul>

Component	Description
Information Bar	<p>The information bar is located at the bottom of the window and displays:</p> <ul style="list-style-type: none"> <li>• The leaf number, projection number, and percent open (leaf open percent) for the current position of the cursor within the edit area.</li> <li>• The sinogram's number of leaves and number of projections.</li> </ul>

### Leaf Open Percent

Leaf open time is defined as the percentage of time that the leaf is open for a projection. For example, if a projection lasts four seconds and the leaf open percent is 50%, then the leaf is open for two seconds in that projection. Leaf open times are also centered on the projection.

### Sinogram Editor Toolbar



Item	Description
	<b>Exit</b> Click this button to end edit mode and close the <b>Sinogram Editor</b> . If you have not saved your changes, a dialog box prompts you to save or discard your changes.
	<b>Open</b> Click this button to load a sinogram from file.
	<b>Import Image</b> Click this button to import an image as a sinogram. You can only import .jpg, .gif, and .png files.
	<b>Create New Sinogram</b> Click this button to create a new sinogram. The number of projections defaults to 100.
	<b>Save</b> Click this button to save any changes.
	<b>Undo</b> Click this button to reverse the last action you performed. You can undo up to the last 20 actions.

Item	Description
	<p><b>Redo</b> Click this button if you decide you did not want to undo an action. You can redo up to the previous 20 actions.</p>
	<p><b>Decrease Leaf Open Percent</b> Click this button to decrease the leaf open percent value by increments of 1%.</p>
	<p><b>Leaf Open Percent</b> Type a Leaf Open Percent (0-100) or select a percent value from the drop-down list.</p> <ul style="list-style-type: none"> <li>• 0%</li> <li>• 25%</li> <li>• 33%</li> <li>• 50%</li> <li>• 66%</li> <li>• 75%</li> <li>• 100%</li> </ul>
	<p><b>Increase Leaf Open Percent</b> Click this button to increase the leaf open percent value by increments of 1%.</p>
	<p><b>Select Current Open Percent</b> Click this button to select a percent value from any pixel in the edit area.</p>
	<p><b>Draw Freehand</b> Click this button to create freehand shapes in the edit area.</p>
	<p><b>Draw Line</b> Click this button to create lines in the edit area.</p>
	<p><b>Draw Rectangle</b> Click this button to create rectangles in the edit area.</p>
	<p><b>Select Area</b> Click this button to select an area of the sinogram. The selected area is outlined by a blue border.</p>
	<p><b>Copy</b> After selecting an area, click this button to copy the selection.</p>
	<p><b>Paste</b> Click this button to paste the selection you have copied.</p>

Item	Description
	<b>Repeat Current Selection</b> Click this button to copy the selected area. Refer to the following table, "Repeat Selection Options and Descriptions" (page 543) for more information about the drop-down options.
	<b>Zoom Out</b> Click this button to reduce the view of the sinogram edit area.
	<b>Set the Zoom Level</b> Click this button to magnify or reduce the view of the sinogram edit area.
	<b>Zoom In</b> Click this button to magnify the view of the sinogram edit area.
	<b>Resize Sinogram</b> Click this button to resize the sinogram by changing the number of projections. You can have up to 100,000 projections in a sinogram.

### Repeat Selection Options and Descriptions

Item	Description
	Select Up to copy the selection to the beginning of the sinogram.
	Select Down to copy the selection to the end of the sinogram.
	Select Left to copy the selection to the left.
	Select Right to copy the selection to the right.
	Select Up and Down to copy the selection to the beginning and end of the sinogram.
	Select Left and Right to copy the selection to the left and right of the sinogram.

# Using Basic Create & Sinogram Editor

- ◆ Create a Procedure with Basic Parameters ..... 544
- ◆ Load and Edit a Sinogram ..... 547

## ◆ Create a Procedure with Basic Parameters

### Define Basic Parameters

1. From the home screen, click **Create Machine QA**.
2. On the **Procedure** tab, click **Basic Create**. The default parameters load.
3. Type a new **Machine QA Name** if necessary. This is the name that appears in the plan list.
4. Type a new procedure **Description** if necessary.
5. Verify that the **Setup to Ready Longitudinal Distance** value is correct.
6. Select a **Beam** from the drop-down list.

### Define Fragment Parameters



**IMPORTANT:** To perform a helical calibration procedure, only one fragment is required.

You can create multiple fragment procedures with different settings for jaws, gantry, sinogram, and couch. Depending on your procedure objectives, update the following parameters as necessary:

- “Jaw Parameters” (page 545).
- “Gantry Parameters” (page 545).
- “Sinogram Parameters” (page 545).
- “Couch Parameters” (page 546).

Once you have created the procedure(s), do one or more of the following:

- Clone the procedure if you want to make a copy of the procedure and update it with different parameter values. Continue to “Clone a Procedure” (page 546).
- Save the procedure to an **XML** file if you want to use this procedure to create additional procedures at a later date.
- Create the procedure on the data server to make it deliverable. Continue to “Save a Procedure on the Data Server” (page 546).

## Jaw Parameters

Select a **Jaw Mode** from the drop-down list.

Selection	Required Settings
Fixed	Select jaw position settings from the drop-down, or manually enter jaw position values for: <ul style="list-style-type: none"><li>• <b>Front Jaw Position (mm)</b></li><li>• <b>Back Jaw Position (mm)</b></li></ul>
Dynamic	Click <b>Browse</b> to select a dynamic jaw file to load and click <b>Open</b> .

## Gantry Parameters

Select a **Gantry Mode** from the drop-down list.

Selection	Required Settings
Fixed	<ul style="list-style-type: none"><li>• Enter a value for <b>Gantry Start Angle (degrees)</b>.</li><li>• Enter a value for <b>Projections Per Second</b>.</li></ul>
Dynamic	<ul style="list-style-type: none"><li>• Enter a value for <b>Gantry Start Angle (degrees)</b>.</li><li>• Enter a value for <b>Projections Per Gantry Rotation</b>.</li><li>• Enter a value for <b>Time Per Gantry Rotation (seconds)</b>.</li></ul>

## Sinogram Parameters

Select a **Sinogram Mode** from the drop-down list.

Selection	Required Settings
All Open or All Closed multileaf collimator and <b>Fixed</b> gantry	<ul style="list-style-type: none"><li>• Enter a value for <b>Warm-up Duration (seconds)</b>.</li><li>• Enter a value for <b>Procedure Duration (seconds)</b>.</li></ul>
All Open or All Closed multileaf collimator and <b>Rotating</b> gantry	<ul style="list-style-type: none"><li>• Enter a value for <b>Number of projections</b></li></ul>
<b>Dynamic</b> multileaf collimator	<ul style="list-style-type: none"><li>• Select a sinogram to load or use the Sinogram Editor to edit or create a sinogram (refer to “Create or Edit a Sinogram” (page 548) for more information).</li><li>• Enter a value for <b>Number of projections</b></li></ul>

## Couch Parameters

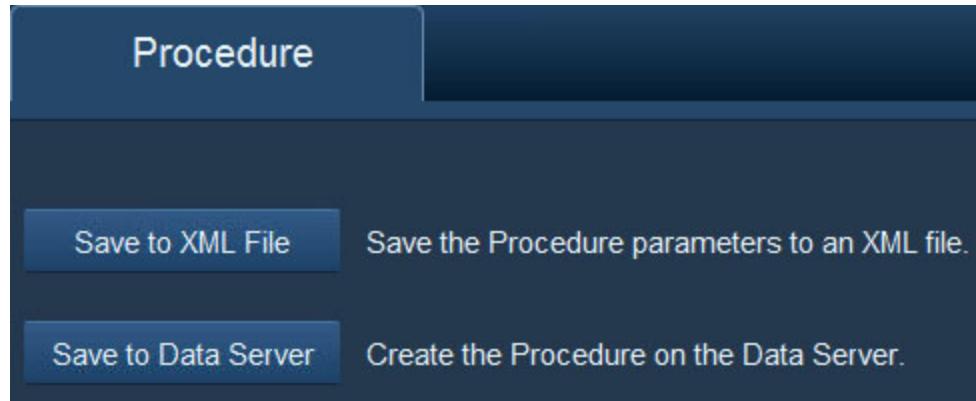
Select a **Couch Mode** from the drop-down list.

Selection	Required Settings
Fixed	No additional settings required. The couch will be stationary.
Moving	<ul style="list-style-type: none"><li>If you selected <b>Fixed</b> for <b>Gantry Mode</b>, enter a value for <b>Couch Speed (mm/second)</b>.</li><li>If you selected <b>Rotating</b> for <b>Gantry Mode</b>, enter a value for <b>Couch Distance Per Rotation (mm)</b>.</li></ul>

## Clone a Procedure

1. Select a procedure in the **Procedures** list.
2. Click **Clone**. The cloned procedure **Description** appears in the **Procedures** list.
3. Edit the parameters for the cloned procedure if necessary.
4. Once you have cloned the procedure(s), do one or more of the following:
  - Save the procedure to an **XML** file if you want to use this procedure to create additional procedures at a later date.
  - Create the procedure on the data server. The procedure(s) will be listed under the **Machine QA Name** you entered.

## Save a Procedure on the Data Server



### Save a Procedure on the Data Server

1. When you are ready to save the parameters to the data server, click **Save to Data Server**. The **Saving Machine QA Procedure to Data Server** dialog box appears.
2. Were your procedures validated?

- If yes, click **Close**.
- If no, edit the necessary parameters and go back to step 1.

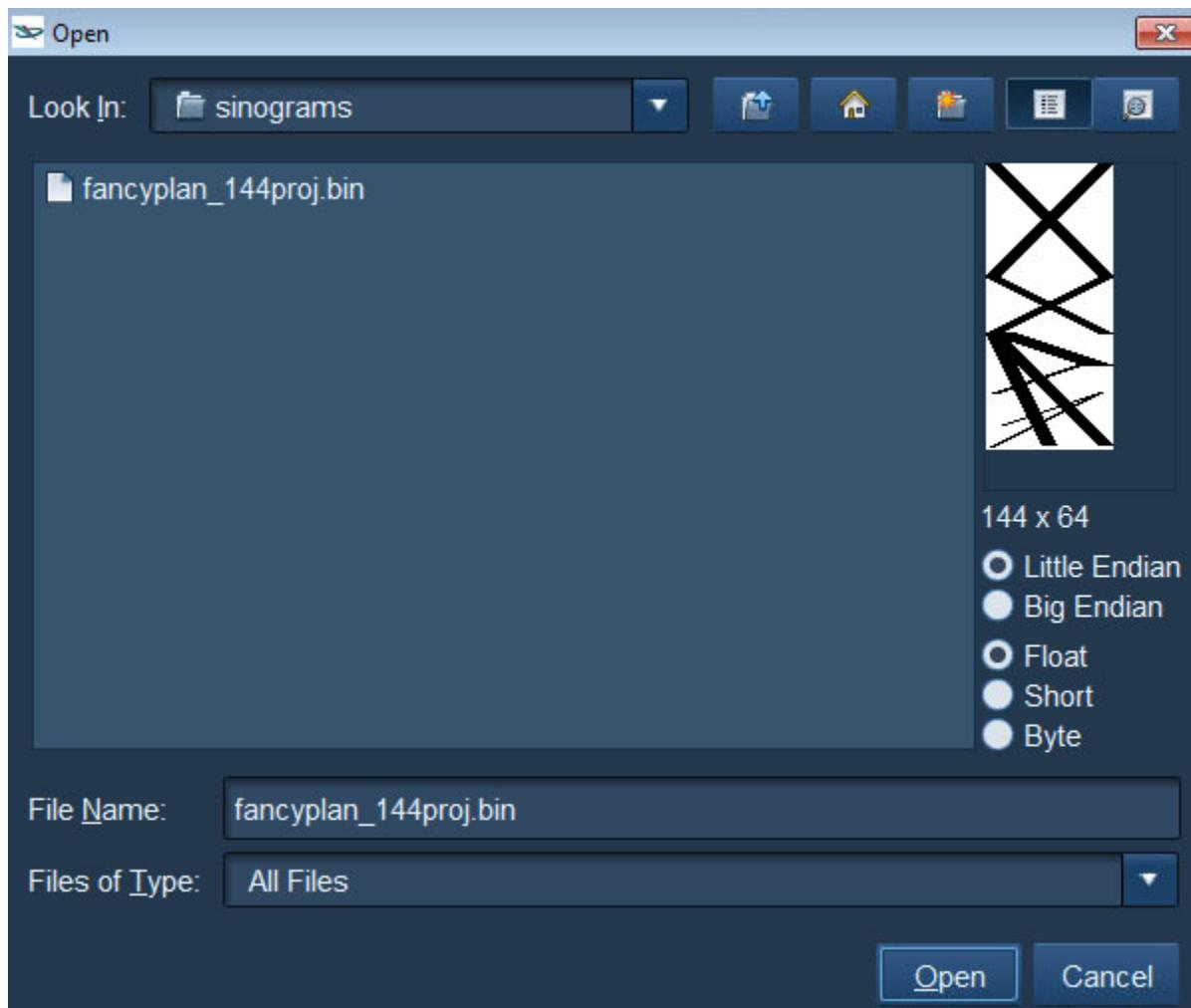
## ◆ Load and Edit a Sinogram

### Load a Sinogram



**TIP:** If you have already loaded a sinogram and you would like to use a different one, complete the following steps to load a new sinogram.

1. After you have selected a dynamic sinogram, click **Browse**. The **Open** dialog box appears.



Select a Sinogram Using the Open Dialog Box

2. Select the sinogram that you want to load.

3. If you can preview the sinogram in the preview window on the right side of the dialog box, click **Open** to load the sinogram.

If you cannot preview the sinogram, select different data settings below the preview pane until you can preview the sinogram. If you cannot preview the sinogram, the sinogram cannot be loaded.

4. If you need to edit the sinogram, continue to “Create or Edit a Sinogram” (page 548).

## Create or Edit a Sinogram

1. Do one of the following:

- Click **Edit** to edit the current sinogram.
- Click **Create** to create a new sinogram to use.

The **Sinogram Editor** appears.

2. Set the leaf open percent value. See “Set the Leaf Open Percent Value” (page 549) for more information.
3. Use one or more methods to create or edit the sinogram:
  - “Use the Drawing Tools” (page 550).
  - “Select and Duplicate an Area” (page 550).
  - “Zoom In or Out” (page 551).
  - “Resize Sinogram” (page 551).
4. Save your changes. See “Save” (page 549) for more information.
5. Click the **Exit** button to close the **Sinogram Editor**.

## Sinogram Editor Options

### Open a File

1. Click the Open button. The **Open** dialog box appears.



**NOTE:** If the **Unsaved Sinogram** dialog box appears before the **Open** dialog box, click **OK** to continue or click **Cancel** to save the sinogram.

2. Select the sinogram that you want to load.
3. If you can preview the sinogram in the preview window, click **Open** to load the sinogram.

If you cannot preview the sinogram, select different data settings until you can preview the sinogram. If you cannot preview the sinogram, you cannot load the sinogram.

## Import an Image

If you cannot use the **Sinogram Editor** to create a sinogram, you can create an image with any image-editing software and use it as a sinogram for a procedure. Make sure to save your image as a **.jpg**, **.jpeg**, **.gif**, or **.png** file in order to import it.

The image is scaled to 64 pixels wide to match the MLC leaf count. If the image is not 64 pixels wide, some image detail may be lost.

1. Click the Import an Image button. The **Open** dialog box appears.



**NOTE:** If the **Unsaved Sinogram** dialog box appears before the **Open** dialog box, click **OK** to continue or click **Cancel** to save the sinogram.

2. Select the image that you want to import. The preview window displays the image that you selected.
3. Click **Open**. The image file appears as a sinogram in the edit area.

## New Sinogram

Click the New Sinogram button to start creating a new sinogram.



**NOTE:** If the **Unsaved Sinogram** dialog box appears before the **Open** dialog box, click **OK** to continue or click **Cancel** to save the sinogram.

## Save

1. Click the Save button. The **Save** dialog box appears.
2. Create a new directory to save the sinogram in.



**NOTE:** Accuray Incorporated recommends that you save new and edited sinograms in a different directory from the sinograms folder.

3. Open the new directory that you just created.
4. Type a file name for the sinogram and click **Save**.

## Undo/Redo

Click Undo to reverse the last action you performed. You can undo up to the last 20 actions.

Click Redo if you decide you did not want to undo an action. You can redo up to the previous 20 actions.

## Set the Leaf Open Percent Value

Use any combination of the following tools to set the leaf open percent value.

Item	Description
	Click the Decrease Leaf Open Percent button. The leaf open percent value decreases incrementally by 1% with each click of the button.
	Type a Leaf Open Percent (0-100) and press <b>Enter</b> . You can also select a preset percent value from the drop-down list.
	Click the Increase Leaf Open Percent button. The leaf open percent value increases incrementally by 1% with each click of the button.
	Click the Select Current Leaf Open Percent button and click a pixel in the sinogram edit area to set the leaf open percent value.

## Use the Drawing Tools

Use any combination of the drawing tools to create or edit open leaf percent values.

- Click the Draw Freehand button, and drag the pointer to create a free-form line in the sinogram. This drawing tool is one pixel wide.
- Click the Draw Line button, and drag the pointer to create a line in the sinogram. This drawing tool is one pixel wide.
- Click the Draw Rectangle button, and click in the sinogram. Drag the pointer to draw the desired shape and size.

## Select and Duplicate an Area

You can copy and paste a selected area, or you can repeat a selected area.

1. Click the Select Area button and select the area of the sinogram that you want to duplicate.
2. Do one of the following:
  - To copy and paste a selection, click the Copy button. Click Paste and click in the sinogram where to place the copied selection. Once an area has been copied, the Paste button will continue to paste the copied selection until a new area is selected and copied.
  - To repeat the selection, click the Repeat Selection button and select an option. The selected area is copied to the sinogram as the option dictates. You do not need to copy a selected area to repeat the selection in the sinogram.

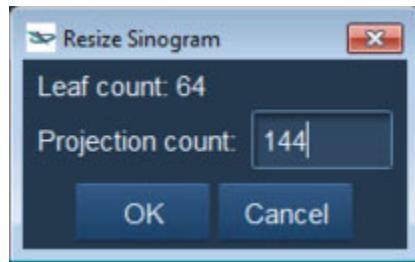
## Zoom In or Out

Click the Zoom In button to magnify the view of the sinogram edit area. Click Zoom Out to reduce the view of the sinogram edit area. When you use the Zoom In or Zoom Out tool, each click magnifies or reduces the image to the next preset level.

You can also select a preset zoom level from the drop-down list.

## Resize Sinogram

1. Click the Resize Sinogram button. The **Resize Sinogram** dialog box appears.



Resize Sinogram Dialog Box

2. Type a new number in the **Projection count** text box to change the number of projections in your sinogram.
3. Click **OK**. The sinogram updates to reflect the number of projections you entered.

# Using the Create XML Interface

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## ◆ Create XML Interface

### Navigate the Data Structures

Each tab is organized in a tree-like structure of folders that contain data parameters that can be edited. When you view the data parameters, use the following techniques to navigate:

- “Expand” (page 553)
- “Expand Edited” (page 553)
- “Collapse” (page 554)
- “Collapse To Root” (page 554)
- “Clone” (page 554)
- “Delete” (page 554)



Procedure Tab Directory

### Expand

When you expand a folder, all sub-folders and parameters in the folder are displayed. To expand a folder, do one of the following:

- Click the navigator icon next to the folder that you want to expand.
- Right-click the folder that you want to expand, and click **Expand** from the shortcut menu.
- To expand all folders at once, right-click anywhere in the folders area and click **Expand** from the shortcut menu.

### Expand Edited

Select **Expand Edited** to open all folders with data that you edited and close all folders with non-edited data. To expand folders with edited data, do one of the following:

- Right-click the folder that you want to expand, and click **Expand Edited** from the shortcut menu.

- To expand all edited folders at once, right-click anywhere in the folders area and click **Expand Edited** from the shortcut menu.

### Collapse

When you collapse a folder, all sub-folders and parameters in the folder are closed. To collapse a folder, do one of the following:

- Click the navigator icon next to the folder that you want to collapse.
- Right-click the folder that you want to collapse, and click **Collapse** from the shortcut menu.
- To collapse all folders at once, right-click anywhere in the folders area and click **Collapse** from the shortcut menu.

### Collapse To Root

To collapse an expanded folder to its root folder, right-click any item below it and click **Collapse To Root** from the shortcut menu.

### Clone

Use **Clone** to copy the procedure and update it with different parameter values. Use this option to create additional fragments for multi-fragment procedures.

Right-click the **Procedure** folder that you want to clone and click **Clone** from the shortcut menu.

### Delete

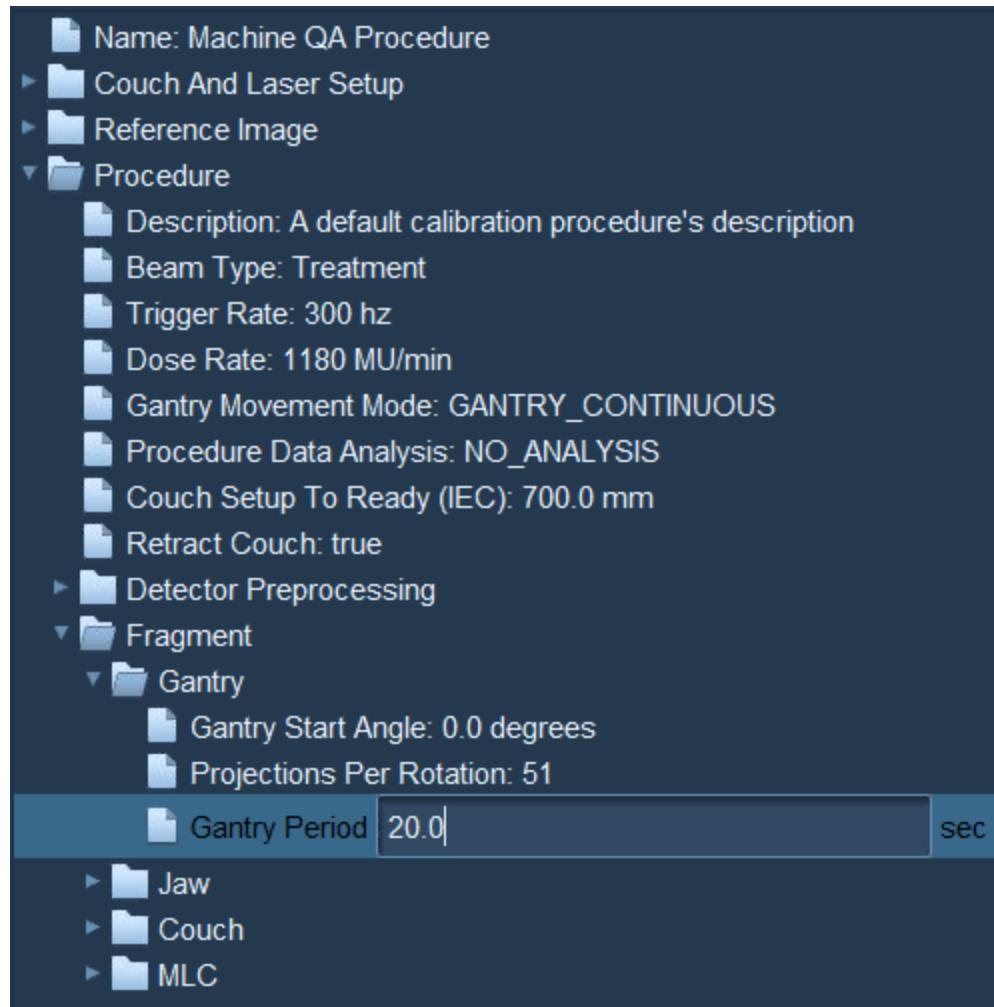
Right-click the **Procedure** folder that you want to delete and click **Delete** from the shortcut menu.

## Edit Parameters

You can edit the parameters that are stored in the data server or stored on any network-connected media or drive.

### Enter a Value

Most parameters have one or more values that you manually enter. Note that some values require that they be formatted correctly, such as floating point values.



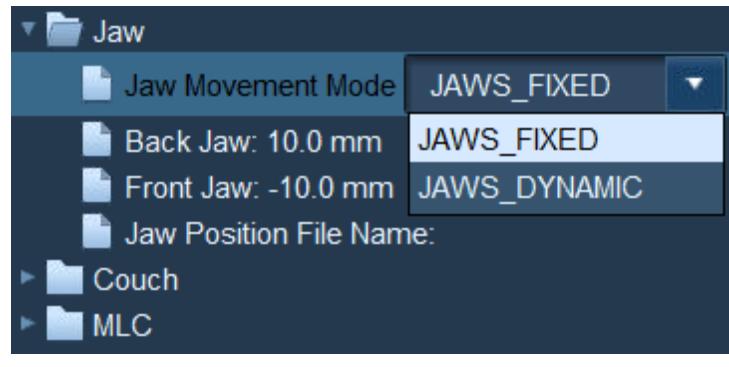
Enter a Value

To enter a value in a parameter:

1. Locate the parameter that you want to change.
2. Double-click the parameter to edit it. An editable text box appears.
3. Type a new value, and press **Enter**. The parameter is updated with the new value.

#### Update Parameters with Specific, Predefined Values

Some parameters display a selection of specific values that are predefined. For these parameters, a drop-down list displays the values you can choose from when the parameter is selected.



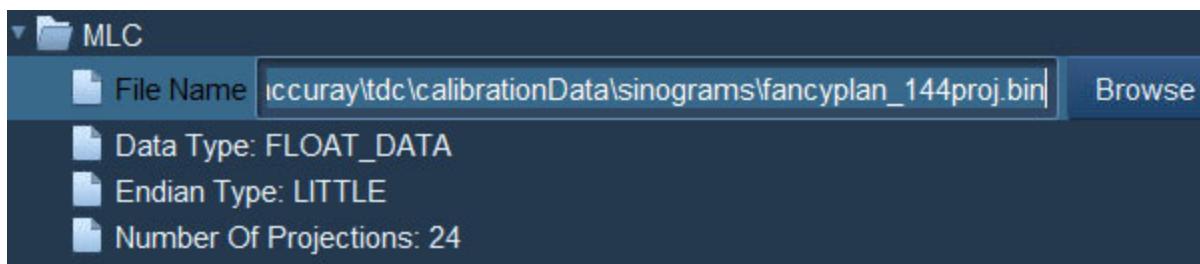
**Update with Predefined Values**

To update a parameter with predefined values:

1. Locate the parameter that you want to change.
2. Double-click the parameter to edit it. The drop-down list appears.
3. Click the drop-down list, and select a new value. The parameter is updated with the new value.

### Update Parameters Using a Binary File

Some parameters allow you to import data from a binary file (such as leaf control sinograms). When you open the parameter for a structure that permits this option, a **Browse** button appears to allow you to locate the binary file.



**Update with a Binary File**

To update a parameter with a binary file:

1. Locate the parameter that you want to change.
2. Double-click the parameter to edit it. The **Browse** button appears.
3. Click **Browse**. The **Open** dialog box appears.
4. Select the file that you would like to work with, and click **Open**. The parameter is updated with the new value.
5. Select the correct **EndianType** for the file you just uploaded.

## ◆ Create a Procedure

### Description of Procedure Parameters

The following table lists and briefly describes the common parameters that are used to create procedures.

Parameter	General Value
<b>Name</b>	This value identifies the procedure stored in the data server.
<b>Couch And Laser Setup &gt;</b> <b>Use Default Couch Setup Positions</b> <b>Couch Setup Y Position (IEC)</b> <b>Couch Setup Z Position (IEC)</b>	These values set the position the couch travels to if the <b>Setup</b> button on the <b>Positioning Control Panel</b> is pressed. When set to <b>True</b> , <b>Use Default</b> will cause the procedure to use the <b>Out of bore setup positions</b> in <b>Couch Settings</b> in the machine record every time it runs. When set to <b>False</b> , the procedure will use the <b>Couch Setup</b> positions specified here.
<b>Couch And Laser Setup &gt;</b> <b>Moveable Laser X Position (IEC)</b> <b>Moveable Laser Y Position (IEC)</b> <b>Moveable Laser Z Position (IEC)</b>	These values set the moveable lasers relative to the virtual isocenter. <ul style="list-style-type: none"><li>• <b>Moveable Laser X Position (IEC)</b> sets the IEC X offset of the red lasers.</li><li>• <b>Moveable Laser Y Position (IEC)</b> sets the IEC Y offset of the red lasers.</li><li>• <b>Moveable Laser Z Position (IEC)</b> sets the IEC Z offset of the red lasers.</li></ul>
<b>Reference Image &gt;</b> <b>File Name</b> <b>Data Type</b> <b>Endian Type</b> <b>Element Size (IEC)</b> <b>Dimensions</b> <b>Start (IEC)</b>	These values describe the selected binary file (KVCT image). For a machine QA procedure, this would typically be the desired phantom CT image. On the <b>Register</b> tab, this reference image is the <b>Plan</b> image that is compared to a <b>Scan</b> image to position the phantom.
<b>Procedure &gt;</b> <b>Description</b>	This value describes the contents of the procedure.

Parameter	General Value
Procedure > <b>Beam Type</b> <b>Pulse Rate</b> <b>Nominal MU</b>	<p>The combination of beam type, trigger rate, and dose rate specify the output used in the procedure:</p> <ul style="list-style-type: none"> <li>For <b>Beam Type</b>, select a beam from the pull-down menu.</li> <li>For <b>Pulse Rate</b>, enter the accelerator pulse frequency value that matches the <b>Beam Type</b>.</li> <li>For <b>Nominal MU</b>, enter the value that matches for the selected <b>Beam Type</b>.</li> </ul>
Procedure > <b>Gantry Movement Mode</b>	<p>Select one of the following:</p> <ul style="list-style-type: none"> <li><b>GANTRY_CONTINUOUS</b> (rotating)</li> <li><b>GANTRY_DISCRETE</b> (fixed-angle)</li> <li><b>GANTRY_NONE</b> (static). If you select this parameter, you must also set the <b>Gantry Period</b>, as it is required to calculate the couch speed.</li> </ul>
Procedure > <b>Couch Setup to Ready (IEC)</b>	<p>Enter the translational distance (mm) that the couch will travel from the virtual isocenter into the gantry bore when the <b>Ready</b> button on the <b>Positioning Control Panel</b> is pressed. The value for this parameter is typically based on where you want a phantom to be positioned prior to the start of irradiation.</p>
Procedure > Detector Preprocessing > <b>Type</b> <b>Compression Factor</b>	<p>For <b>Type</b>, use <b>BY_COMPRESSION_FACTOR</b> (default). This value determines how detector data is stored in the data server.</p> <p>The <b>Compression Factor</b> determines the amount of detector data that is saved immediately after irradiation. When you increase the <b>Compression Factor</b> value, less detector data is collected by the system. This results in a smaller detector data file.</p>

Parameter	General Value
Procedure > Fragment > Gantry > <b>Gantry Start Angle</b> <b>Projections Per Rotation</b> <b>Gantry Period</b>	<p><b>Gantry Start Angle</b> specifies the angle (degrees) where the procedure begins (the angle at the start of the first projection).</p> <p><b>Projections Per Rotation</b> determines the number of MLC changes during a single rotation. For optimized IMRT plans, the value is 51. The minimum value for this parameter is 1.</p> <p><b>Gantry Period</b> and the total number of projections are used to determine the duration of the procedure. This parameter specifies the duration, in seconds, for 1 gantry rotation. Note the following for this parameter:</p> <ul style="list-style-type: none"> <li>Default = 20.0 seconds</li> <li>Minimum = 6.0 seconds (10 rotations per minute)</li> <li>Maximum = 60.0 seconds (1 rotation per minute)</li> </ul>
Procedure > Fragment > Jaw > <b>Jaw Movement Mode</b>	<p>This parameter defines the jaw movement type. Select one of the following:</p> <ul style="list-style-type: none"> <li><b>JAWS_FIXED</b>.</li> <li><b>JAWS_DYNAMIC</b>. If you select this parameter, you must also select a file for the <b>Jaw Position File Name</b>.</li> </ul>
Procedure > Fragment > Jaw > <b>Back Jaw</b> <b>Front Jaw</b> <b>Jaw Position File Name</b>	<p>These parameters determine the jaw width in jaw numbers:</p> <ul style="list-style-type: none"> <li>For <b>Back Jaw</b>, enter a value in the range of -25 to 25 (mm).</li> <li>For <b>Front Jaw</b>, enter a value in the range of -25 to 25 (mm).</li> </ul> <p>For dynamic jaw movement, provide the path of the data file for the procedure. The dynamic jaw data file defines the jaw position and projections for the procedure.</p>
Procedure > Fragment > Couch > <b>Movement Mode</b> <b>Distance Per Rotation</b>	<p>For <b>Movement Mode</b>, select one of the following:</p> <ul style="list-style-type: none"> <li><b>COUCH_FIXED</b>. The couch speed will automatically be set to 0 (zero).</li> <li><b>COUCH_MOVING</b>. The couch speed will be set according to the following parameter.</li> </ul> <p><b>Distance Per Rotation</b> specifies the distance the couch will travel per one gantry rotation. Note the following for this parameter:</p> <ul style="list-style-type: none"> <li>Couch speed (mm/sec) = <b>Distance Per Rotation</b> (mm) / <b>Gantry Period</b> (sec).</li> </ul>

Parameter	General Value
Procedure >	
Fragment >	
MLC >	
<b>Filename</b>	<b>Filename</b> defines the path of the leaf control sinogram file for the procedure. Right-click the filename to access the <b>Sinogram Editor</b> .
<b>Data Type</b>	The default value <b>FLOAT_DATA</b> is appropriate for most sinograms.
<b>Endian Type</b>	For <b>Endian Type</b> , select one of the following:
<b>Number Of Projections</b>	<ul style="list-style-type: none"> <li>• The default value <b>LITTLE</b> is appropriate for files with PC-byte order and most sinograms provided by Accuray Incorporated.</li> <li>• The value <b>BIG</b> is appropriate for sinograms created with Sun and Java applications, such as sinograms from <i>H-Series</i> systems or other legacy Accuray archives.</li> </ul>
	<p><b>Number of Projections</b> specifies the number of projections for the procedure. The value must be equal to or less than the total number of projections specified by the leaf control sinogram. For example, if the leaf control sinogram contains 25 projections, and you enter 20, only the first 20 projections will be used to create and run the procedure.</p>

## Identify Important Procedure Parameters

Before you create a procedure, complete the following instructions to identify values for significant parameters used in all procedures. This information is also used to “Calculate Beam-on Time and Dose” (page 561). These steps do not have to be performed in the order given:

1. Choose the sinogram that will be used to build the procedure.
2. Enter the **Number of projections**.
3. Enter the **Time Per Gantry Rotation**.



**TIP:** When determining the number of projections per rotation based on a sinogram that specifies all leaves open, set the number of projections (**Number of projections**) equal to the gantry period (**Gantry Period**). Doing so will simplify the beam-on time and dose calculation because the number of seconds per projection will be 1.

4. Determine the number of projections for each gantry rotation (**Projections Per Gantry Rotation**).

## Calculate Beam-on Time and Dose

You can calculate beam-on time and dose for a procedure using the parameter values.

### Beam-on Time Equation

The following parameters used to calculate beam-on time are described under “Description of Procedure Parameters” (page 557):

- Total number of projections
- Gantry Period
- Projections Per Rotation

Using the above parameters, beam-on time is calculated as follows:

$$[\text{Total number of projections} \times \text{Gantry Period}] / \text{Projections Per Rotation}$$

### Example: Calculate Beam-on Time and Dose

For this example, a leaf-control sinogram with the following specifications is used:

- The first 10 projections will be with leaves closed.
- The next 70 projections will be with leaves open.

Based on the leaf-control sinogram and procedure definitions, the following table gives the beam-on times for leaves closed (10 seconds) and leaves open (20 seconds). With this example, an output of 900 cGy per minute should produce a dose of 300 cGy in 20 seconds of leaf open time.

Parameter	Value	Leaves Closed	Leaves Open
Sinogram Filename	Leaf sinogram used	10 projections	70 projections
Number Of Projections	30 projections	10 projections	20 projections
Gantry Period	20 seconds	*Beam-on Times	
Projections Per Rotation	20 projections	<ul style="list-style-type: none"><li>• Total Time: <math>[30 \times 20] / 20 = 30</math> seconds</li><li>• Leaves closed: <math>[10 \times 20] / 20 = 10</math> seconds</li><li>• Leaves open: <math>[20 \times 20] / 20 = 20</math> seconds</li></ul>	

\*Beam-on Time = [Number of Projections x Gantry Period] / Number of Projections Per Rotation

## View All Parameters and Define as Needed

1. From the home screen, click **Create Machine QA**.
2. On the **Procedure** tab, click **Create**.

3. Click **Load File** and browse to an **XML** procedure file. Click **Open**.
4. Expand the **Procedure** folder, and edit parameters as necessary. The following beam parameters must match a calibrated beam.
  - **Trigger Rate**
  - **Dose Rate**



**IMPORTANT:** If you use an uncalibrated beam, the validation will be unsuccessful when you try to create a procedure on the data server.

5. Verify that the value of **Couch Setup To Ready (IEC)** is correct.
6. Double-click **Name**, and type a new procedure name.
7. Once you have created the procedure(s), do one or more of the following:
  - Clone the procedure. Continue to “Clone a Procedure” (page 562).
  - Save the procedure to an **XML** file if you want to use this procedure to create additional procedures at a later date.
  - Create the procedure on the data server. The procedure will be listed on the data server under the patient name you created in step 6.

## Clone a Procedure

1. Do one of the following:
  - Right-click the procedure you want to clone.
  - For a multi-fragment procedure, right-click the **Procedure** you want to clone to add a fragment.
2. Click **Clone** from the shortcut menu. The cloned procedure appears in the **Procedure** tab.
3. If needed, edit parameters for the procedure.
4. If needed, click the **Machine QA Name** folder, type a procedure name, and press **Enter**.
5. Once you have cloned the procedure(s), do one or more of the following:
  - Save the procedure to an **XML** file if you want to use this procedure to create additional procedures at a later date.
  - Create the procedure on the data server. The procedure(s) will be listed under the name you created in step 4.



## Appendix D

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### Create and Deliver Phantom Plans

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## About Phantom Plans

A phantom plan is a treatment plan optimized and calculated on a phantom image. When importing the image to Accuray Precision, the Type is set to Phantom.

On the Treatment Delivery Console, lists of phantom plans and patient plans are maintained separately.

Phantom plans can be used for research or QA, such as absolute dose calibration (*TomoHelical*-phantom, *TomoDirect*-phantom). The number of available fractions for delivery is fixed in the plan. If a phantom plan is interrupted, you can create a completion procedure.

A phantom plan (also known as a "phantom template plan" or "QA template plan") is required as an input for creating a patient QA plan.

# Create a Phantom QA Plan

To create a Phantom QA plan, select a phantom image, create contours, and complete plan set up tasks. Optimize QA plan and save it as Make Deliverable.

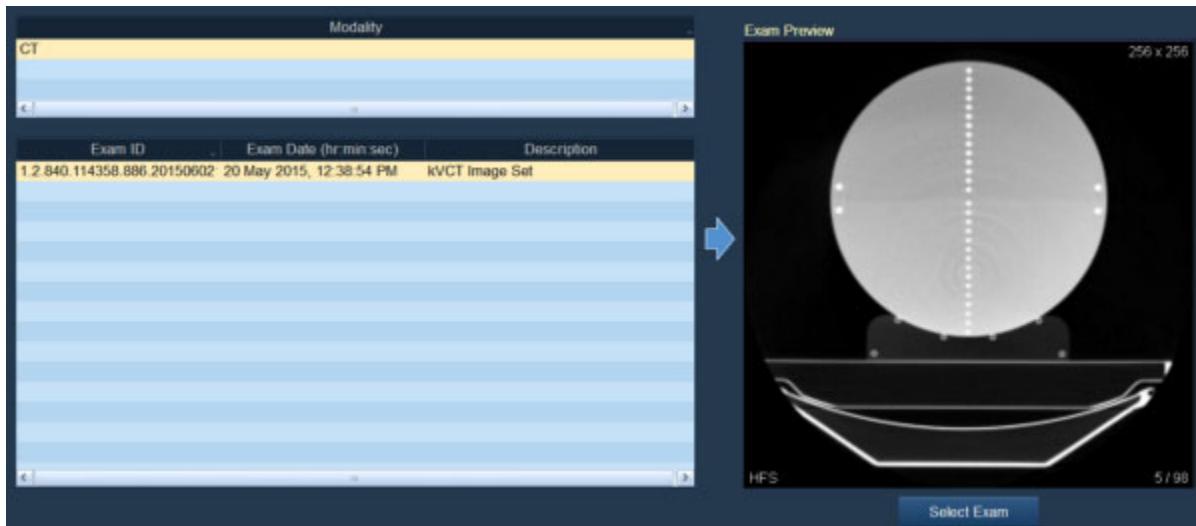
- ◆ Select a Phantom Image and Create VOIs ..... 565
- ◆ Setup and Save the Phantom QA Plan ..... 566

Detailed instructions for selecting and creating plans can be found in the *Treatment Planning Manual*.

## ◆ Select a Phantom Image and Create VOIs

Complete the following instructions to select a phantom as the primary image for the **Phantom QA** plan and create VOIs.

1. Click the **New Plan** icon in the **Patients and Plans** section of the *Precision* system home page.
2. From the list of patients on the **New Plan** page, click the phantom that will be used to create the QA Template plan. The plan you select must be listed as a **Phantom** in the **Type** column.
3. Under **Select Type**, click the **Standard** icon
4. Click **Next>>** to display the **Select Exams** screen.
5. Under **Modality**, click the CT image that will be used to create the QA Template Plan.
6. The image you selected is shown in the **Exam Preview** area of the screen.
7. To include the phantom image in the QA plan, click **Select Exam**.
8. Under **Selected Exams**, the CT image you have chosen is listed. Make sure that the **Pri.** check box is selected for the primary CT.
9. Click **Next >>**. The **Select Optional Plan Template** screen is shown. Click **Ignore Template** to display the **Contour > Manual > Tools** screen.
10. Use the contour **Tools** to create at least one VOI for the phantom. For example, contour an ion chamber collection volume.

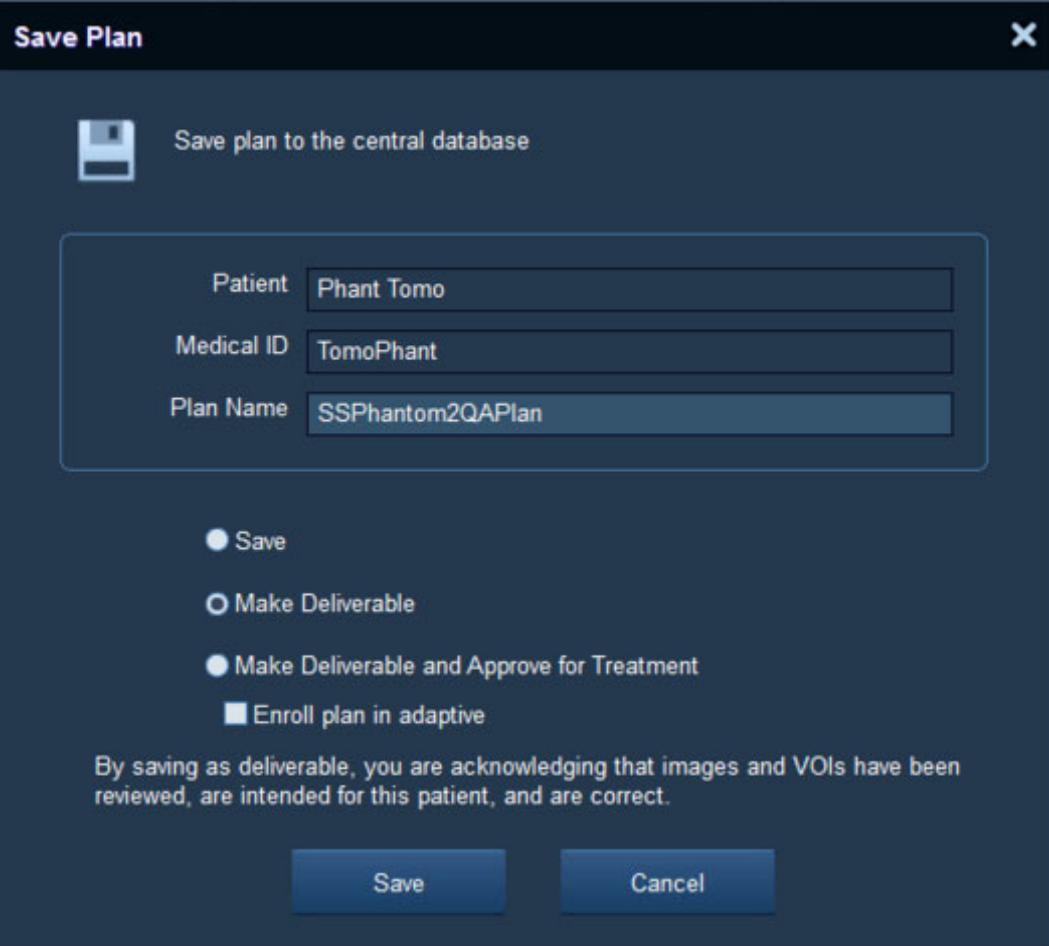


Select Exam Preview

## ◆ Setup and Save the Phantom QA Plan

Complete the following instructions to enter machine parameters, replace the couch in the phantom image, position the red lasers, and then optimize the plan. Save the Phantom QA plan as **Make Deliverable**.

1. Select **Setup > Machine > Tools** and enter the following **Machine Parameters**:
  - Treatment Machine
  - Delivery Mode
  - Plan Mode
  - Jaw Mode
2. Replace the couch in the phantom CT image. Click **Accept** when finished.
3. Click **Setup > Patient > Tools** to adjust the position of the phantom image and the red lasers. Click **Accept Red Lasers** when finished.
4. Click **Plan > Tools** to define plan parameters for the QA Template.
5. Optimize the plan and perform **Final Dose** calculations.
6. Click **Evaluate** to review the plan.
7. Click **Save Plan**.
8. Save the QA Template as **Make Deliverable**.



## Perform a Treat Phantom Plan QA Workflow

For instructions to position, scan, and register the phantom, as well as position point dosimetry devices and films, refer to “Patient QA Plans” (page 390).



## Appendix E

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### Dose Calculation Results for Typical Treatments

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## Introduction

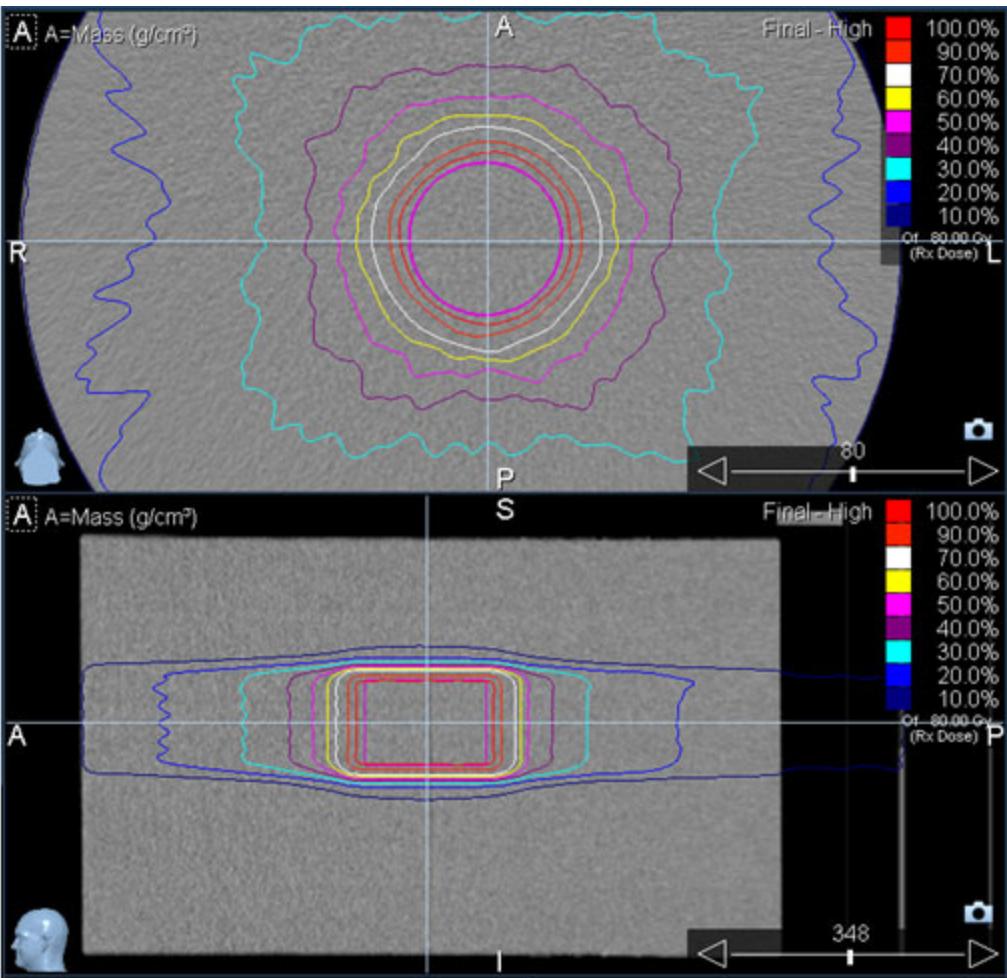
This appendix describes dose calculation results for typical treatments using the treatment delivery system. Four treatment cases are provided to illustrate typical results from GPU implementation of the Optimizer and the Convolution/Superposition algorithm described in “Chapter 6” (page 411). The four cases are:

- A Helical-mode Treatment on Homogenous Phantom with a Cylindrical target
- A Direct-mode Treatment on Homogenous Phantom with a Cylindrical target
- A Helical-mode Head & Neck Treatment
- A Helical-mode Prostate Treatment

## A Helical-mode Treatment on Homogenous Phantom with a Cylindrical Target

This case shows the typical dose distribution for a helical treatment optimized to a central cylindrical target. The jaws are configured in Dynamic mode, the field width is 2.5cm, the pitch is 0.3, and the modulation factor is 2.0. The prescription dose was set to 80 Gy. The dose distribution was optimized for 50 iterations and the final dose was calculated at high resolution.

The figure below shows the dose distribution through the center of the target in the axial and sagittal planes with the 10% increments of the isodose lines. The table below the dose distributions shows the target objectives for the optimizer.



Prescription % Volume For PTV 100.00 % will receive 80.00 Gy in 40 Fractions

#### Target Objectives

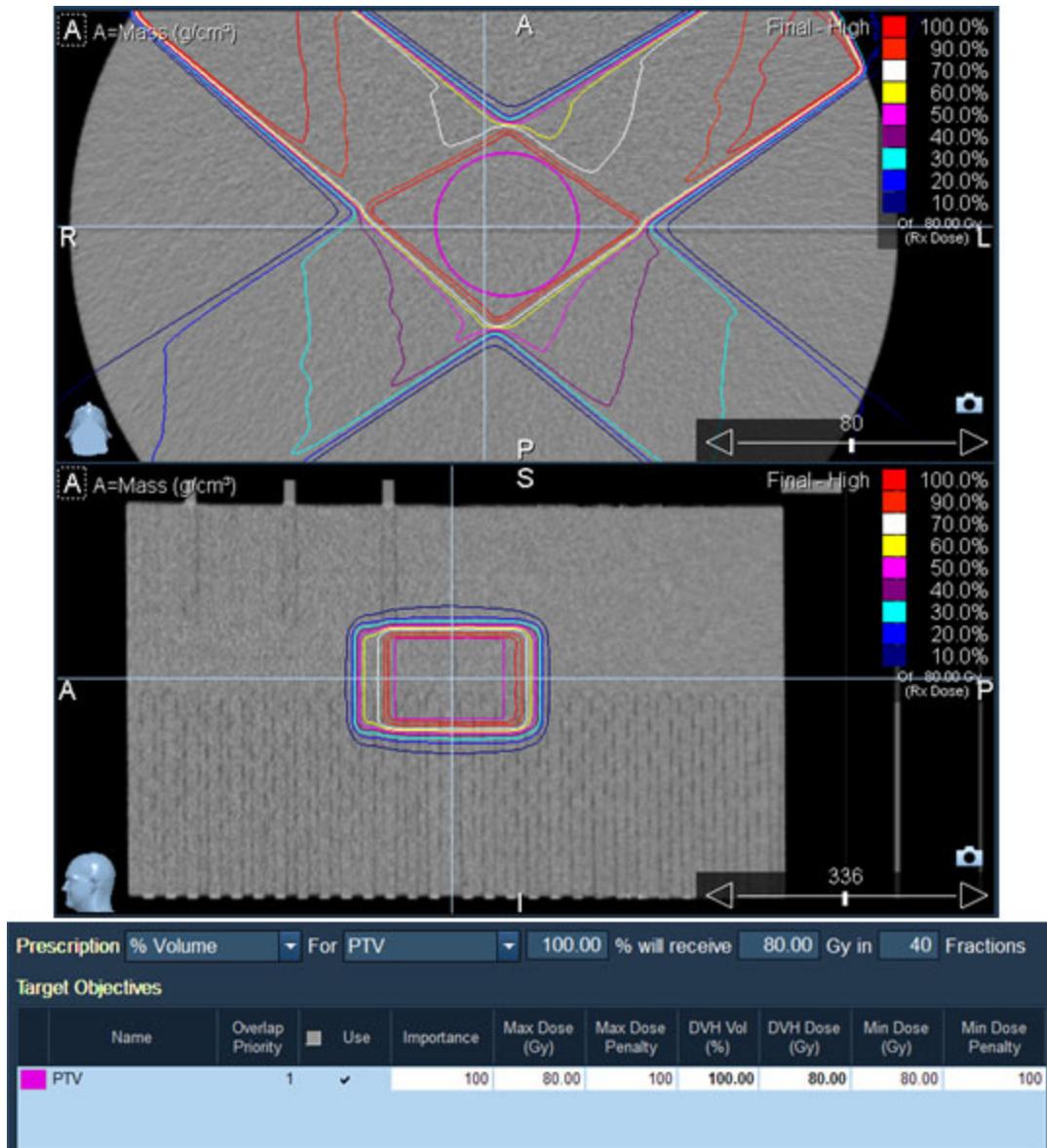
Name	Overlap Priority	Use	Importance	Max Dose (Gy)	Max Dose Penalty	DVH Vol (%)	DVH Dose (Gy)	Min Dose (Gy)	Min Dose Penalty
PTV	1	<input checked="" type="checkbox"/>	100	80.00	100	100.00	80.00	80.00	100

**Dose Distribution and Target Objectives**

## A Direct-mode Treatment on Homogenous Phantom with a Cylindrical Target

This case shows the typical dose distribution for a dual beam Direct-mode treatment optimized to a central cylindrical target. The jaws are configured in Dynamic mode, the field width is 2.5cm, and the modulation factor is 2.0. The prescription dose was set to 80 Gy. The dose distribution was optimized for 50 iterations and the final dose was calculated at high resolution.

The figure below shows the dose distribution through the center of the target in the axial and sagittal planes with the 10% increments of the isodose lines. The table below the dose distributions shows the target objectives for the optimizer.



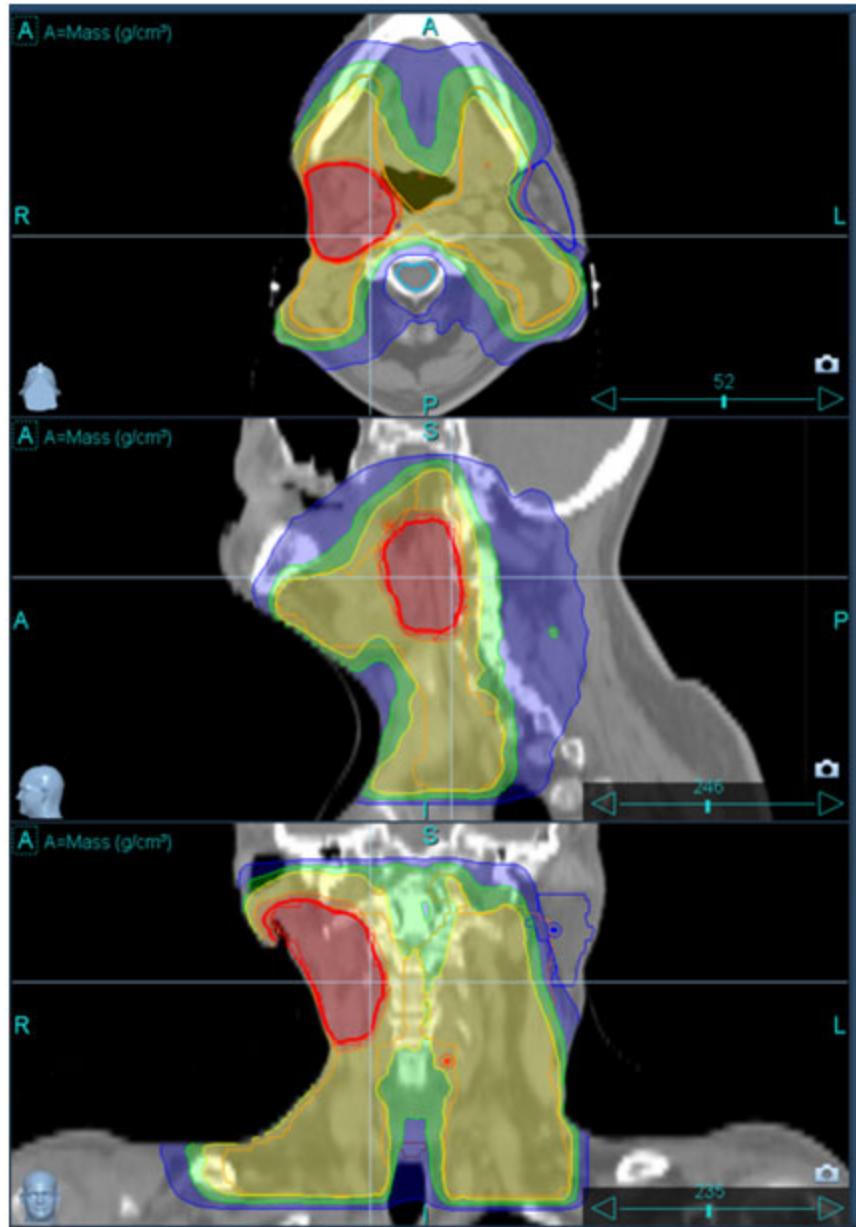
**Dose Distribution and Target Objectives**

## A Helical-mode Head & Neck Treatment

This case shows the typical dose distribution for a Head & Neck case. The jaws are configured in Dynamic mode, the field width is 5cm, the pitch is 0.303, and the modulation factor is 2.0. The prescription dose was set to 66 Gy in 30 fractions. The optimization and final dose were calculated at high resolution.

The first figure below shows the dose distribution through the center of the target in the axial, sagittal, and coronal planes with isodose lines at xx, yy, and zz.

The second figure below shows the Target Objectives and Critical Constraints used in the optimization along with the final DVHs for the indicated structures.





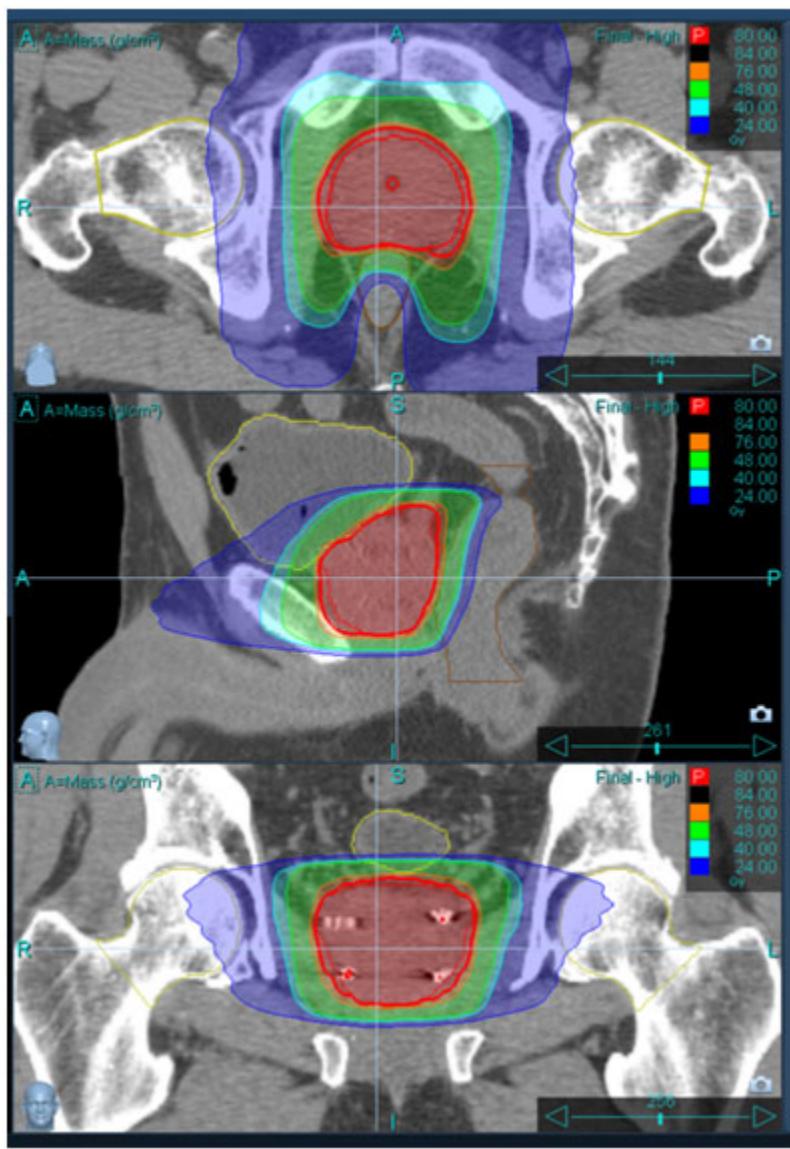
Target Objectives and Critical Constraints

## A Helical-mode Prostate Treatment

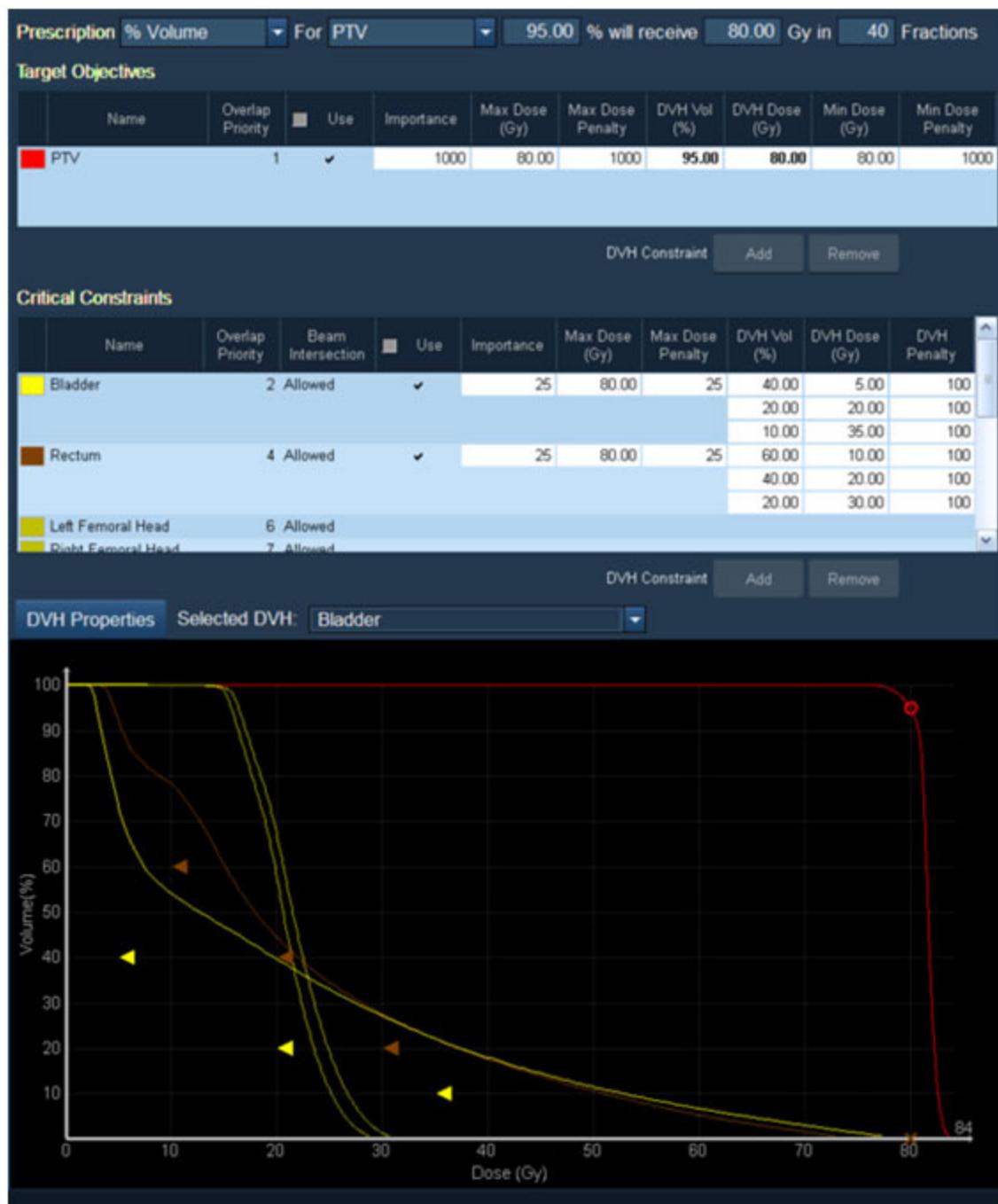
This case shows the typical dose distribution for a Prostate case. The jaws are configured in Dynamic mode, the field width is 2.5cm, the pitch is 0.303, and the modulation factor is 1.7. The prescription dose was set to 80 Gy in 40 fractions. The optimization and final dose were calculated at high resolution.

The first figure below shows the dose distribution through the center of the target in the axial, sagittal, and coronal planes with isodose lines at 80, 76, 48, 40, and 24 Gy.

The second figure below shows the Target Objectives and Critical Constraints used in the optimization along with the final DVHs for the indicated structures.



Dose Distribution



Target Objectives and Critical Constraints





## Appendix F

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### Acronyms and Definitions

Acronym or Abbreviation	Full Name	Definition
3DCRT	3D Conformal Radiation Therapy	A treatment plan in which the MLC pattern is determined by the TPS to attempt to achieve a homogeneous target dose without optimization constraints.
Accuray Precision	Accuray Precision Planning System	Brand name for the Accuray planning system
Advanced Delivery		Treatments with dynamic jaws.
ATP	Acceptance Test Procedures	A demonstration of the system performance that culminates in the acceptance of the machine by the customer.
AutoSegmentation		The AutoSegmentation tools on the Precision Planning System can be used to automatically contour skin or structures for male pelvis, head and neck, and brain. Brain AutoSegmentation requires a T1-weighted MR image.
Back Jaw		The jaw on the +IEC Y side of the gantry.
Basic Dosimetry		A rotational variation procedure analyzed by the TQA software.
Beam expansion		For <i>TomoDirect</i> plans, leaves opened beyond the target, to help achieve full coverage if the target moves slightly.

Acronym or Abbreviation	Full Name	Definition
Beamlet		The radiation through a given MLC leaf in one projection of delivery.
BEV	Beam's Eye View	A visualization of patient image data where the viewing position is located at the radiation source and points toward isocenter.
Beam Revision Number		A counter that is incremented whenever changes are made to the machine data that could impact plan calculations.
CAX-Y	Central Axis Y-Axis Divergence Test	A QA film test to verify that the beam is pointed in the plane of gantry rotation.
CCK	Couch Control Keypad	Buttons on the couch for adjusting the couch position.
CCCS	Collapsed Cone Convolution Superposition	The dose calculation algorithm used by the Planning System.
<i>Tomo</i> Phantom		Informal name for the cylindrical Virtual Water phantom included in the purchasable Standard QA kit. See also, <i>Tomo</i> Phantom.
Commissioning		The site physicist's preparation and approval for treating patients on a new or updated system. Includes verification that the machine is performing consistently with the pre-installed beam model.
Cone profile		A transverse profile or associated data in the beam model.
CSV	Comma-Separated Variable	A data storage format that can be opened in a spreadsheet program such as Microsoft Excel.
CTrue Image		MVCT image acquired on the system.
DCS	Dose Control System	Servo feedback loop on the monitor chamber data and gun current to keep the beam stable.
DRR	Digitally Reconstructed Radiograph	A digitally reconstructed X-ray image of the patient; available in the Beam's Eye View for <i>TomoDirect</i> plans.
DTA	Distance To Agreement	The closest distance from a measured data point to a point with the same value in the calculated dose profile or dose distribution.

Acronym or Abbreviation	Full Name	Definition
Dynamic Jaws	<i>TomoEDGE</i> Dynamic Jaws	Treatment delivery modality in which the jaws gradually open and close at the superior and inferior ends of the target to improve the superior and inferior dose fall-off.
Edit Machine		A task accessible from the TDC that allows viewing and editing of machine and beam model parameters, for users with appropriate credentials.
Flash		See beam expansion.
Fragment		A sub-division of a treatment procedure with instructions for the gantry, couch, jaws, and leaves. For example, one beam angle within a <i>TomoDirect</i> plan.
Front Jaw		The jaw on the - IEC Y side of the gantry.
FSE	Field Service Engineer	Trained personnel who service the Accuray machine. See also, service representative.
FWHM	Full-Width at Half Maximum	The size of a profile, as represented by the distance between the 50% values of the profile.
FWQM	Full-Width at Quarter Maximum	The size of a profile, as represented by the distance between the 25% values of the profile.
Gamma		A comparison metric for profiles or dose distributions; see Low 1998.
GPU	Graphics Processing Unit	Computing hardware for the dose calculator.
iLink		Secure remote connection to the treatment system for remote system service and support.
IMRT	Intensity Modulated Radiation Therapy	A treatment plan with leaf modulation determined through optimization.
Isocenter		The common point which is the mechanical and radiation isocenter of the Accuray system. (treatments do not use a target isocenter, because the couch moves during the delivery).
J##	Jaw Number	An internal system of specifying the jaw positions.

Acronym or Abbreviation	Full Name	Definition
JFOF	Jaw Fluence Output Factor	Relative factors in the beam model to account for the dependence of the output on the field size.
Latency		Small differences between how long the leaves are programmed to be open and how long they are actually open.
LDA	Lateral Drive Assembly	Electronics built into the head and foot of the couch, used for mechanical adjustment of the X position of the couch.
Leaf filter		Data in the beam model to account for the fluence distribution across a leaf in the transverse direction.
LFOF	Leaf Fluence Output Factor	Ratio of the fluence measured if a leaf and its neighbor(s) are opened simultaneously versus consecutively.
LINAC	Linear Accelerator	The hardware that accelerates electrons to interact in a target that produces a photon beam.
Longitudinal Profile		Beam profile in the Y direction.
LOT	Leaf Open Times	
Machine Transfer		A workflow within the Plan Transfer task on the Precision Planning System that can be used to generate a similar plan for delivery on a different system.
MLC	Multi-Leaf Collimator	The secondary collimator of the system, consisting of 64 leaves that can be independently opened or closed to shape the fluence distribution in the transverse direction.
Modulation Factor		The ratio of the maximum to average beamlet open time in a sinogram; a larger Modulation Factor may provide more flexibility to vary the beamlet weights and achieve plan goals, at the expense of longer delivery times.
MU	Monitor Unit	A unit of raw counts on the monitor chambers; typically calibrated so that 1 MU corresponds to 1 cGy at isocenter at 1.5 cm depth.
MVCT	MegaVoltage Computed Tomography	CT images acquired using the LINAC as the radiation source.

<b>Acronym or Abbreviation</b>	<b>Full Name</b>	<b>Definition</b>
PAC	Pulse Amplitude Control	An input to the LINAC that influences the output rate of the machine.
PCP	Positioning Control Panels	Screens on the front of the gantry for adjusting the couch position.
PDD	Percent Depth Dose	Beam profile along the beam direction for characterizing the system energy.
Penumbra		Sometimes used to refer to longitudinal profiles.
Pitch ( <i>TomoDirect</i> )		Couch travel in cm per sinogram projection.
Pitch ( <i>TomoHelical</i> )		Couch travel per gantry rotation, divided by the nominal field width (unitless).
PreciseART		Previously Enhanced Adaptive.Purchasable software for evaluating the dosimetric impact of anatomy changes over the course of treatment, using the daily MVCT images.
Projection		An increment of time in which there is an opportunity for each leaf to independently open and close up to one time.
QA	Quality Assurance	Tests to verify the machine performance and consistency between plan calculations and delivery.
RIT	Radiological Imaging Technology	Third party vendor that provides film analysis for Accuray.
RITg148+		Product name of the RIT custom-designed film analysis package for tomotherapy-based Accuray products.
RotVar	Rotational Variation Procedure	A beam-on procedure with rotating gantry, all leaves open, and no object in the bore.
RSS	Running Start and Stop	See dynamic jaws.
SAD	Source to Axis Distance	Distance from the radiation source to the mechanical and radiation isocenter of the machine. A "SAD" setup involves placing the measurement device at isocenter.
Sag		The deflection of the couch as it travels into the bore.

Acronym or Abbreviation	Full Name	Definition
SBRT	Stereotactic Body Radiation Therapy	
Self Transfer		A workflow within the Plan Transfer task on the Precision Planning System that can be used following changes to beam data, to generate a similar plan that accounts for the new machine properties (the original plan is discontinued).
Serpentine PDD		A "snake-like" PDD that involves acquiring a small longitudinal profile at each depth, to ensure that the maximum of the profile is identified at each depth.
Service Representative		Trained personnel who service the Accuray machine. See also, FSE.
Sinogram		A data array in which the columns represent leaves or detector channels and the rows represent time increments (projections).
Specification Conformance Verification		Pre-ATP on-site testing of a new machine by Accuray personnel to ensure that it meets Accuray specifications for system alignment, profiles, dose rate, and image quality.
SRS	Stereotactic Radiosurgery	
SSD	Source to Surface Distance	Closest distance from the radiation source to the surface of the phantom or water.
Super-Sampling		Dose calculations performed at multiple discrete positions per sinogram projection.
TAG-P	Tongue and Groove Penumbra	LFOF - 1. The beam model stores LFOF values minus 1, and calls it TAG-P.
TCOM	Treatment Commissioning	A spreadsheet provided by Accuray that lists the profile data included in the beam model: transverse profiles, longitudinal profiles, and PDDs.
TDC	Treatment Delivery Console	Computer workstation from which the user can run the treatment machine.
TDC Couch Control		Controls on the TDC for couch positioning outside the treatment room.

Acronym or Abbreviation	Full Name	Definition
TEMS	Tomo Electrometer Measurement Software	Accuray software that interfaces with the Standard Imaging <i>Tomo</i> Electrometer and water tank, for plotting beam profiles.
TG-### (e.g., TG-148)	Task Group ###	Report of the AAPM Task Group.
<i>TomoDirect</i>		Treatment modality with user-selected static beam angles, moving couch, and leaf modulation.
<i>TomoDirect-phantom</i>		Test patient provided by Accuray for dosimetric verification of the <i>TomoDirect</i> feature.
TomoEDGE		Brand name for the dynamic jaws feature.
<i>TomoHelical-phantom</i>		Test patient provided by Accuray for dose calibration.
<i>Tomo-phantom</i>		Formal name for the cylindrical Virtual Water phantom included in the purchasable Standard QA kit.
Topo	Topographic Profile	A beam-on procedure with a static gantry and a moving couch; e.g., for using an ion chamber in Virtual Water to collect longitudinal profiles.
TPS	Treatment Planning System	Informal acronym for the Precision™ Treatment Planning System
TQA	Total Quality Assurance	A purchasable software that collects data from the on-board monitor chambers and detectors for machine QA, or receives data imported manually by the user, and creates reports and provides trending tools.
Transverse Profile		Beam profile along a line perpendicular to the direction of the beam; if the LINAC is at 0°, the transverse profile is along the X axis.
Virtual Isocenter		A reference point located -700 mm in Y from the machine and radiation isocenter; marked by the intersection of the green lasers.
VOI	Volume of Interest	A contoured target or avoidance structure.
Warm-up (5-minute)		A 5-minute procedure that should be run at the beginning of the treatment day and whenever the machine has been idle for an hour or more.

Acronym or Abbreviation	Full Name	Definition
Warm-up (10-second)		For all treatment plans, leaves are closed for at least the first 10 seconds of beam-on time to allow for output ramp-up.
Xg	g = gantry	Rotational coordinate system used to specify the leading edge of the MLC for assigning leaf expansion for <i>TomoDirect</i> plans.
XML	eXtensible Markup Language	Programming language for machine procedures in the system.



## Appendix G

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### References



**NOTE:** The following references are useful in describing aspects of the *TomoTherapy* style of treatment system. However, not all references provide machine and algorithmic information that is consistent with the current product model.

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