

MicroCT 35

User's Guide

Revision 4.05



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Warranty

Limited Warranty Statement

This Limited Warranty defines the restrictions and warranty period that apply to the SCANCO Medical AG μ CT Products that you have purchased. Contact SCANCO Medical AG if you have questions about this Limited Warranty.

Terms of the Warranty

SCANCO Medical AG warrants that the product you have purchased from SCANCO Medical AG or from a SCANCO Medical AG authorized reseller is free from defects in materials or workmanship under normal use during the Warranty Period. The warranty period commences on the date of installation and ends 12 month after the date of installation. Your installation protocol, showing the date of installation of the product is your proof of the date of installation. This warranty is transferable to anyone who subsequently purchases the product from you.

This Limited Warranty does not include expendable parts.

Should the product require service during the term of the Limited Warranty, SCANCO Medical AG will repair or replace the defective part(s) with new part(s), or at SCANCO Medical AG's discretion a used part(s) that meets or exceeds the performance specifications for new parts. In some cases, SCANCO Medical AG will ship a new user replaceable part(s) directly to you, or at SCANCO Medical AG's discretion a used part(s) that meets or exceeds the performance specification for new parts. All exchanged parts and products replaced under this warranty will become the property of SCANCO Medical AG.

SCANCO Medical AG is not responsible for any handling fees, import duties, or tariffs. This Limited Warranty extends only to products initially purchased from SCANCO Medical AG or from a SCANCO Medical AG authorized reseller.

This Limited Warranty does not extend to any product that has been damaged or rendered defective

- as a result of accident, misuse, or abuse
- by operation outside the usage parameters stated in the product's user documentation
- by the use of parts not manufactured or sold by SCANCO Medical AG
- by modification of the product
- as a result of service by anyone other than SCANCO Medical AG or a SCANCO Medical AG authorized service provider

SCANCO Medical AG is not responsible for damage to or loss of any programs, data, or removable storage media. SCANCO Medical AG is not liable for any damages caused by the product or the failure of the product to perform, including any lost profits, lost savings, incidental damages, or consequential damages. SCANCO Medical AG is not liable for any claim made by a third party or made by you for a third party.

Limitations of Remedy:

EXCEPT AS EXPRESSLY SET FORTH IN THIS WARRANTY, SCANCO MEDICAL AG MAKES NO OTHER WARRANTIES, EXPRESS OR IMPLIED, INCLUDING ANY IMPLIED WARRANTIES OF MERCHANTABILITY AND FITNESS FOR A PARTICULAR PURPOSE. SCANCO Medical AG EXPRESSLY DISCLAIMS ALL WARRANTIES NOT STATED IN THIS LIMITED WARRANTY. ANY IMPLIED WARRANTIES THAT MAY BE IMPOSED BY LAW ARE LIMITED TO THE TERMS OF THIS EXPRESS LIMITED WARRANTY.

This limitation applies whether damages are sought, or a claim made, under this warrant by or as a tort claim (including negligence and strict product liability), a contract claim, or any other claim. This limitation cannot be waived or amended by any person. This limitation of liability will be effective even if SCANCO Medical AG or an authorized representative of SCANCO Medical AG has been advised by you of the possibility of any such damages. This limitation of liability, however, will not apply to claims for personal injury.

Safety Information

Description of Warning symbols



X-Rays!

X-Rays may be present



Caution!

This warning symbol defines important warning information regarding the instrument or operator action. Disregarding these informations may lead to damage to the instrument or loss of data.



Electric Shock!

Disregarding this kind of provisions may lead to electric shock and serious health risk.

Product description

Intended use

This instrument μ CT 35 is intended to be used as an analytical instrument to measure, visualize and quantify the structure of small objects.

Abuse

This instrument is not intended to be mis-used as an in-vivo medical device or in-vitro diagnostic device.

User's responsibility

The user is obliged to read the following safety instructions before operating the instrument.

Safety precautions

Warning labels attached to the instrument

The following warning labels are attached to the instrument:



Caution!

Scanned objects must be COMPLETELY contained in the sample holder-tubes. Make sure absolutely no fluid can drip on scanner mechanics.



Caution!

Do not apply vertical force on open door. Scanner might dip!

Safety provisions



Caution!

Your instrument is equipped with various safety provisions. It is prohibited to modify, suspend or remove these safety provisions under all circumstances!

Ionizing radiation



X-Rays!

This μ CT instrument generates X-rays. The system was tested for radiation leakage at the factory and conforms with regulatory requirements under normal operating conditions.

Do not operate your instrument if it is physically damaged. The damage of the scanner-housing may lead to emitted stray-radiation!

In this case, the system must be inspected by SCANCO Medical AG authorized personnel prior to using it again.

Sample holder



Caution!

Only use sample holders supplied by Scanco Medical AG or other manufacturers which exactly match the size of the original sample holder. Using sample holders of different shape may damage your scanner!

Electric connections and damaged cables



Electric Shock!

Touching electrical connections inside the instrument or damaged cables may lead to electric shock and serious health risk! In case of damaged cables, switch off the instrument and call SCANCO Medical AG for service.

Sample size



Caution!

Make sure that the sample fits completely inside of the sample holder! If samples extend out of the sample holders, your measurements will be negatively affected or you can damage your instrument!

Chemical compatibility of the sample holder tubes.



Caution!

The supplied sample holder tubes are made of PMMA (Poly-Methyl-Methacrylat, clear whitish) or PEI (Poly-Ether-Imid, yellowish, translucent). The chemical and physical resistance of each material differ considerably.

Please consider the specific material properties for your intended use.

Note: Please check "Sample holder: Thermal and chemical compatibility" in the section "General Information" for your intended use.

Instrument positioning



Caution!

To avoid personal injury due to sharp-edged MicroCT sample door, place the instrument about 35 cm away from the tables front edge.

Safety measures

1. Capture Key



The scanner works only if the capture key is present and both main switch and capture key are activated!

2. Emergency Stop

Pushing the emergency stop button will immediately interrupt the main power.

3. Door locked indicator



While the door locked indicator is lit, the sample door can not be opened.

Important Information

Manufacturer and Contact for Service or Support

SCANCO Medical AG
Fabrikweg 2
CH-8306 Bruettisellen
Switzerland

Telephone	+41-(0)44-805 98 00
Telefax	+41-(0)44-805 98 01
URL	www.scanco.ch
e-mail general	info@scanco.ch
e-mail support	support@scanco.ch
e-mail sales	sales@scanco.ch

User's responsibility

The user is obliged to read the following safety instructions before operating the instrument.

Software licence agreement

The software described in this document is a part of the MicroCT 35 and may not be copied onto a computer other than that delivered with the instrument.

The operating system software OpenVMS/DECwindows Motif is licensed for this computer only, and may only be copied for safeguarding purposes!

Installation

Installation of the equipment may only be carried out by SCANCO Medical AG or SCANCO Medical AG authorized personnel.



Caution

To assure adequate circulation of air for cooling, make sure that the instrument is located at least 20 cm away from walls on each side of the instrument.

Maintenance

Maintenance of the equipment, transportation and re-installation in a different place may only be carried out by SCANCO Medical AG or SCANCO Medical AG authorized personnel. Never remove or open any covers or parts of the housing of the equipment. A yearly maintenance by SCANCO Medical AG or SCANCO Medical AG authorized personnel is recommended.

Cleaning

For outside cleaning use soft materials moistened with water or ethanol only. Shut down properly and unplug instrument before cleaning. Never spill liquids on or in the instrument.

Sample Holders

Sample size



Caution

Please make sure that the sample size corresponds with the sample holder and that the objects are COMPLETELY contained in the sample holder-tube. Unsuitable sample size may lead to damages on instrument and/or sample.

Sample holder compatibility

Sample holders are available in two different materials. The standard holders are made of PMMA (Poly-Methyl-Methacrylat clear, whitish). In case of superior chemical or physical requirements, sample holders made of PEI (Poly-Ether-Imid, yellowish) are available.

Thermal and chemical compatibility

Table 1.

Resistance Properties	PMMA	PEI
max. Temperature Sterilisation steam autoclave:	+ 85°C N ¹	+ 170°C R ²
Water	R	R
Inorganic Acids	r	R
Inorganic Bases	N	r
Ketone	N	N
Aldehydes (Formaldehyde)	r ³	R
Alcohols	r	R
Ether	N	R
Ester (e.g. Ethyl-Acetate)	N	r
Chlorofluorocarbons (CFC)	N	R
Aliphatic Hydrocarbons	N	R
Aromatic Hydrocarbons	N	r
Chlorinated Hydrocarbons	N	N
R resistant r limited resistance N non resistant		

1. not possible

2. 138°C/20 Min. / 1 bar

3. limited resistance only in diluted form!

Physical resistance of PMMA sample holder



Caution

After prolonged exposure to certain solvents, physical stress or surface scratches, PMMA may show hairline cracks. Please check the compatibility table before using solvents.

These hairline cracks may lead to leaking of fluid, which must be strictly avoided. The instrument can be seriously damaged. Please check the sample holder before each use.

Disposal



Caution

The instrument contains low quantities of several materials which may be hazardous to the environment if not disposed correctly. Please contact SCANCO Medical AG before disposal of instrument or X-Ray tube

Disclaimer

SCANCO Medical AG will not accept any claims for compensation for any damages incurred in connection with this instrument and software. SCANCO Medical AG will not be liable for technical or editorial errors or omissions contained herein; nor for incidental or consequential damages resulting from the furnishing or use of this material.

Setup and Operation

Connections

Mains Connection and Main Power Switch

Only use suitable power cords for mains connection. Use Main Power Switch to switch instrument on or off.



SCSI

The SCSI connection is to be used for connection to the computer only.

Optical signals



1. X-Ray indicator lamp



2. Door locked.
Measurement in progress



3. Power on
(capture key and
main switch must
be turned on)



4. Change Sample



1 Startup Procedure MicroCT 35

Turning on equipment

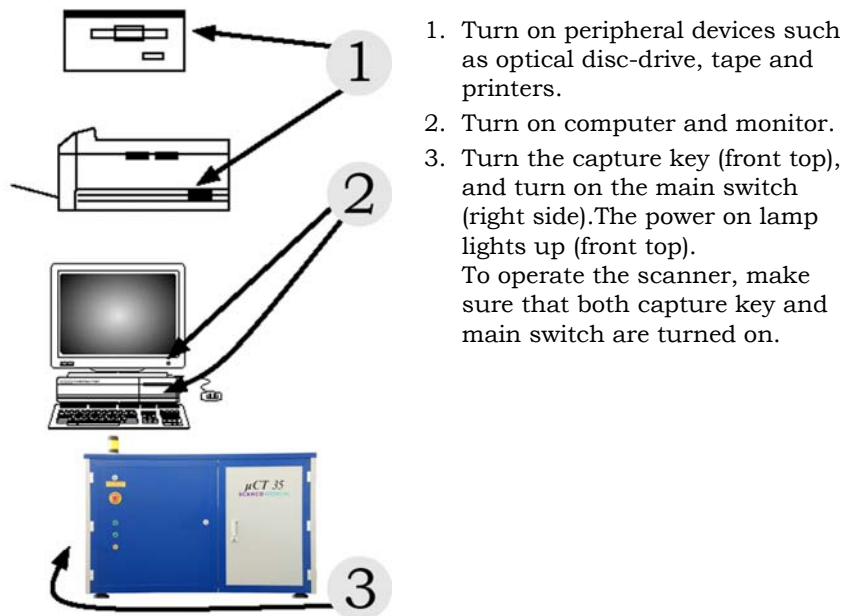


Figure 1. Turning On Equipment

It takes about 5 minutes before your computer is ready to start.

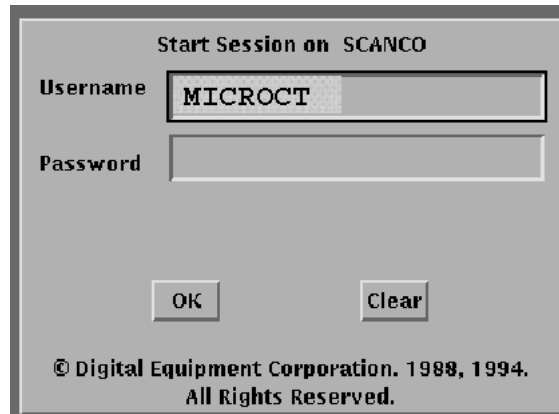


Notice

The scanner must be switched on for at least 20 minutes before starting a measurement; otherwise an error message will appear, if the measurement program is open.

Starting Main Program MicroCT

Enter MICROCT as USERNAME and press the RETURN key. Then enter the required password and press the RETURN key again or click on the OK-Button.



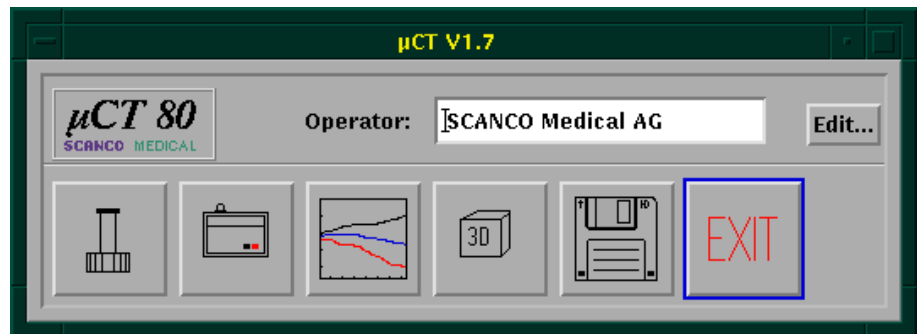
The image shows a graphical user interface for a login window titled "Start Session on SCANCO". It features two input fields: "Username" and "Password". The "Username" field contains the text "MICROCT". Below the input fields are two buttons labeled "OK" and "Clear". At the bottom of the window, there is a copyright notice: "© Digital Equipment Corporation. 1988, 1994. All Rights Reserved."

Figure 2. Login-Box

2 Shutting Down MicroCT 35

Exiting Main Program MicroCT

To exit the control box click on the EXIT-Button:



To exit completely, use the END SESSION button of the Session Manager.

Shutdown of Computer

Enter SHUTDOWN as USERNAME and click on OK.

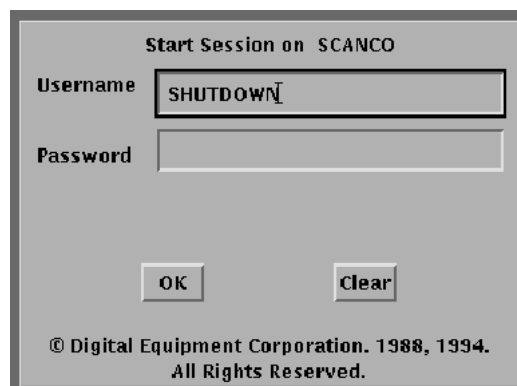


Figure 3. Login-Box for Shutdown

The computer closes all databases and programs, so that you can use all the programs again without problems the next time.



Notice

Never switch off the computer without performing a correct SHUTDOWN! Only in this way it can be guaranteed that all data can be read again without problems.

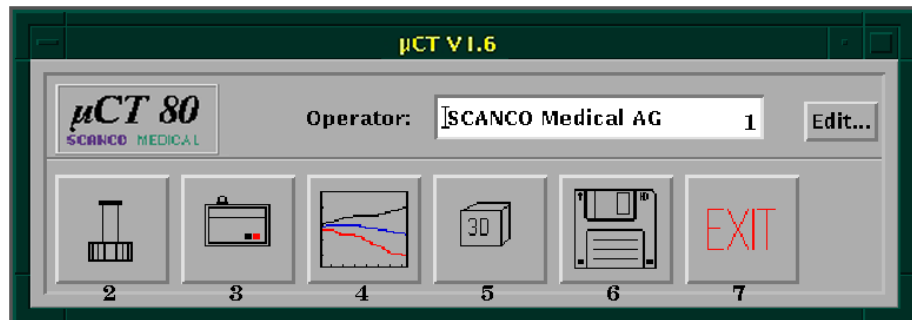
Only after the information SYSTEM SHUTDOWN COMPLETE - USE CONSOLE TO HALT SYSTEM

or the prompt >>> appears, you can turn off the equipment as follows:

Turning Off Equipment

1. Monitor
2. Computer
3. Tape Drive
4. Printer
5. Scanner

3 Program Overview

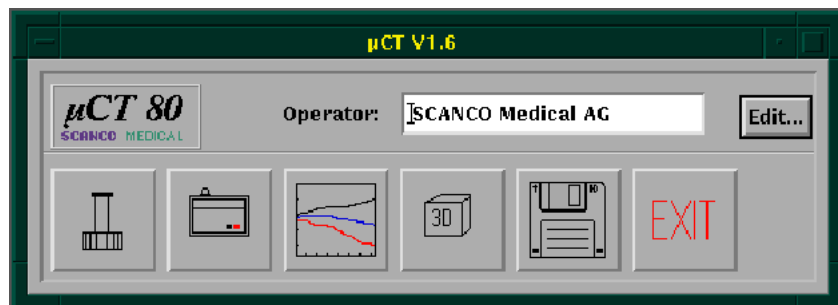


With the program MicroCT, the following can be done:

1. Recording or changing operator data (Editing).
2. Recording or changing sample data (Editing).
3. Perform Measurements
4. Evaluate Measurements
 - d Slicewise evaluation
 - e 2D-Histomorphometry
 - f 3D-Histomorphometry
 - g Image Documentation
5. 3D-Display and 3D-Documentation
6. Data-Management
 - a Move measurement data to/from optical disk or tape
 - b Delete measurement data
 - c Backup copy of harddisk
 - d Initialize tapes (format)
7. Exit MicroCT Main Program

4 Edit Operator Data

Start Program



On the main menu click on the framed button EDIT.

The screenshot shows the "Operator registration" form within the software. The title bar at the top says "Operator: V1.21". The form is titled "File" and contains several input fields and checkboxes. The "Patient Number:" field is set to "4". Below it are checkboxes for "Address Group:" with options "Patient", "Physician", "Insurance", and "Staff". The "Title:" field is followed by buttons for "Mr", "Mrs", "Messrs", and "Other". The "Name:" field contains "SCANCO Medical". Below this are fields for "Address (1):", "Address (2):", "Zip-Code:", "City:", and "Country:". Further down are fields for "Tel Private (1):", "Tel Private (2):", "Tel Business:", "FAX:", "Profession:", and "Remarks:". At the bottom of the form are four buttons: "Find..." (which is highlighted with a blue border), "Find Next", "New", and "Update".

Figure 4. Operator registration program

Enter the operator data. Each field can be selected directly by using the mouse, using the RETURN key brings you to the next field.

The operator number is automatically allocated by the program and cannot be changed.

Upon finishing the data input, the data can be saved by clicking the SAVE/UPDATE button.



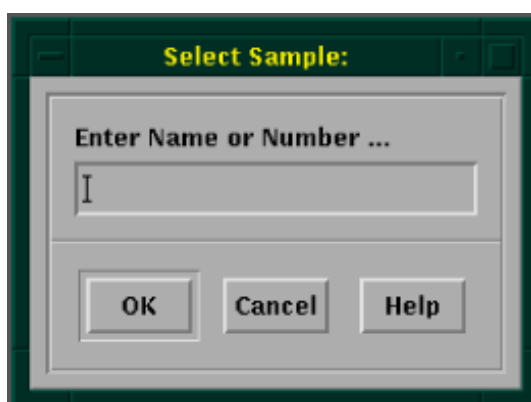
Notice

For a measurement, the program requires at least a name. The data can, however, be completed or changed at any time (i.e. address change, change of name because of marriage, etc.) by using FIND..., changing the data and then finally using UPDATE.

Possibilities

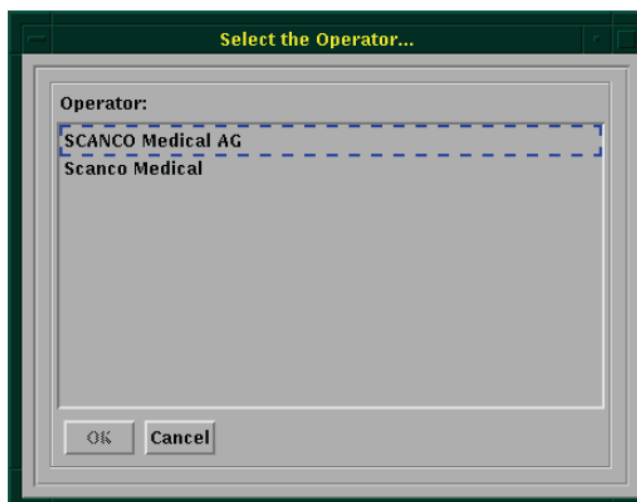
Find

The following data window appears after clicking the FIND... button:



The 'Select Sample' dialog box has a title bar with the text 'Select Sample:'. Inside, there is a label 'Enter Name or Number ...' above a text input field. The input field contains the letter 'I'. Below the input field are three buttons: 'OK', 'Cancel', and 'Help'.

Click the data input field and fill it in as required. Confirm your input by clicking the OK-button. Upon entry of a number or of the complete entry of the operator's name, the data will appear in the fields. If only the first few letters of a name are entered, then a list showing all operators starting with these letters will appear. Thus, if "S" is entered, the list will show all operators whose name starts with S, such as Sample 1, Sample 2, etc.



The 'Select the Operator...' dialog box has a title bar with the text 'Select the Operator...'. Inside, there is a label 'Operator:' above a list box. The list box contains two entries: 'SCANCO Medical AG' and 'Scanco Medical'. The first entry is highlighted with a dashed blue border. Below the list box are two buttons: 'OK' and 'Cancel'.

Click on the desired name and confirm the entry by clicking OK.

**Notice**

Always use the same spelling because the program is case sensitive!

The possibility now exists of changing or completing data. Always use the same spelling!

Find Next

By clicking the FIND NEXT button, the next operator in alphabetical or numerical search order will appear, depending on whether you entered the operators name or number while using FIND...

New

If you click on the NEW button, all fields become free, to enable a new operator data to be entered.

Save/Update

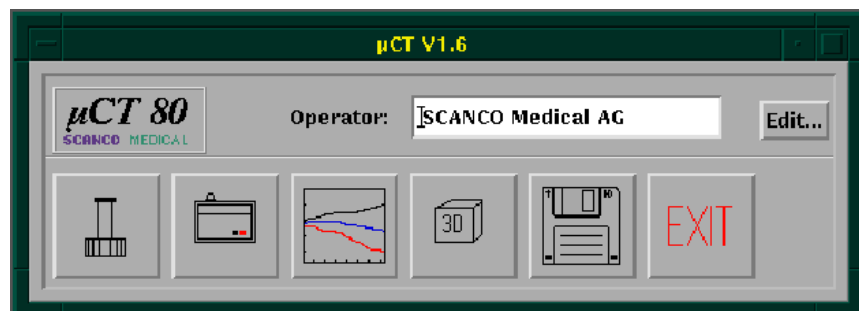
If you click on the SAVE button (labeled UPDATE in modifying mode), all input data for this operator will be saved/updated.

Exiting Operator Program

Click on the FILE button followed by either QUIT or EXIT. This will lead you back to the main menu. Using EXIT, any changes will be automatically saved, whereas with QUIT you can return to the main menu without saving the edited data.

5 Edit Samples Data

Start Program



On the main menu click on the framed button.

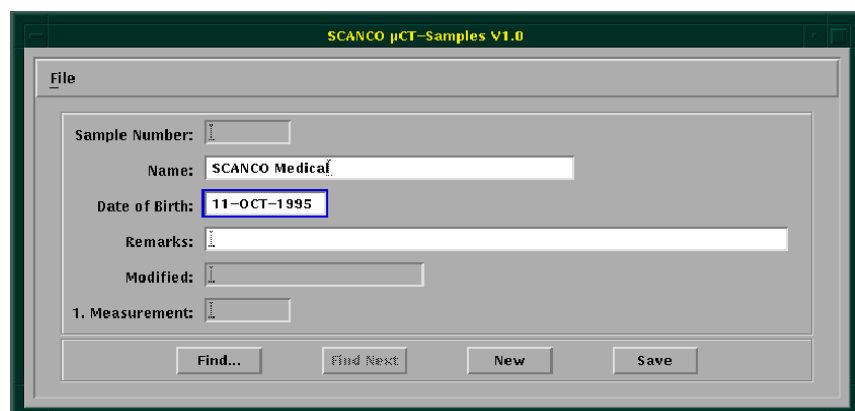


Figure 5. Sample registration program

Enter the sample data. Each field can be selected directly, using RETURN brings you to the next field.

The sample number is automatically allocated by the program and cannot be changed.

Upon finishing the data input, the data can be saved by clicking the SAVE button.



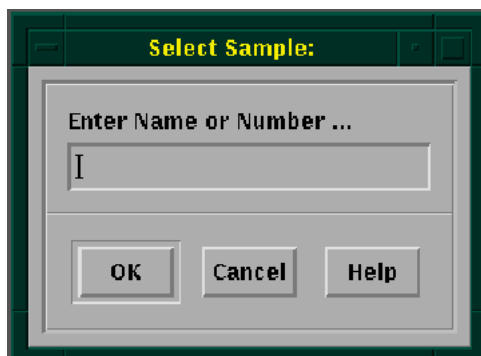
Notice

For a measurement, the program requires at least a name. The data can, however, be completed or changed at any time by using FIND..., changing the data and then finally using UPDATE.

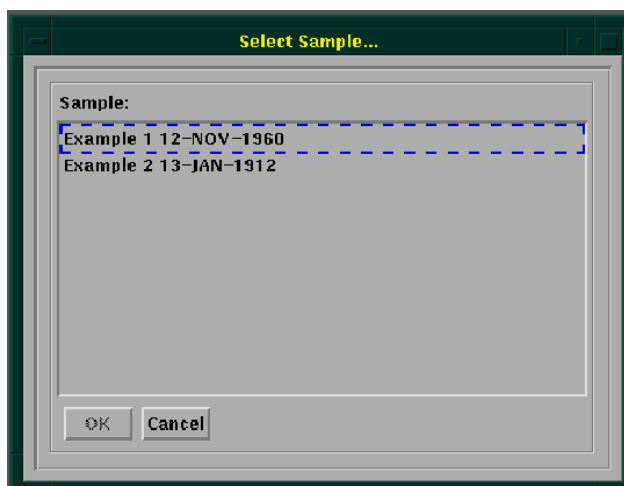
Possibilities

Find

The following data window appears after clicking the FIND... button:



Click the data input field and fill it in as required. Confirm your input by clicking the OK-button. Upon entry of a number or of the complete entry of the sample's name, the data will appear in the fields. If only the first few letters of a name are entered, then a list showing all samples starting with these letters will appear. Thus, if "E" is entered, the list will show all samples whose name starts with E, such as Example 1, Example 2, etc.



Click on the desired name and confirm the entry by clicking OK.



Notice

Always use the same spelling because the program is case sensitive!

The possibility now exists of changing or completing data. Always use the same spelling!

Find Next

By clicking the FIND NEXT button, the next sample in alphabetical or numerical search order will appear, depending on whether you entered the samples name or number while using FIND...

New

If you click on the NEW button, all fields become free, to enable a new sample data to be entered.

Save/Update

If you click on the SAVE button (labeled UPDATE in modifying mode), all input data for this sample will be saved/updated.

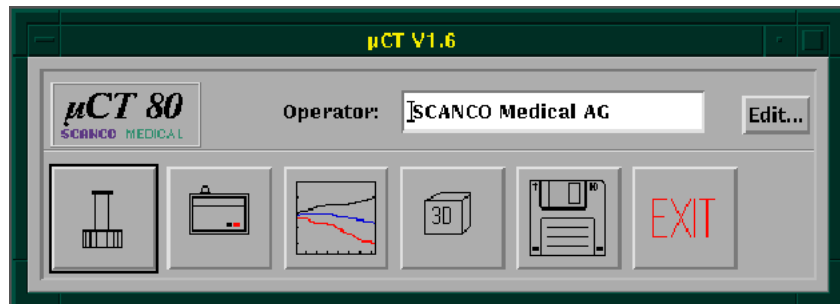
Exiting Sample Program

Click on the FILE button followed by either QUIT or EXIT. This will lead you back to the main menu. Using EXIT, any changes will be automatically saved, whereas with QUIT you can return to the main menu without saving the edited data.

6 Sample Measurements

Starting the Measurement Program

To start the measurement program, you must first enter your name in the field OPERATOR. Then, on the main menu, select the icon with the scanner symbol by clicking on it:



Selecting the Sample

In the middle of your screen, the following input window appears:

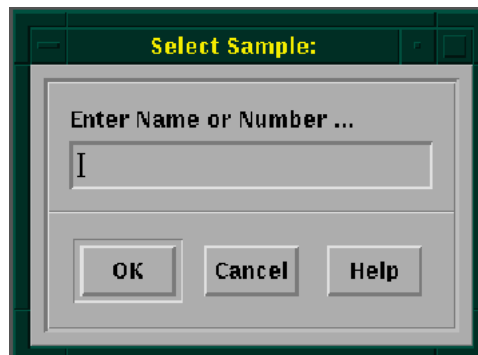


Figure 6. Input of Sample's Name or Number

Click on the input field and fill it in accordingly. Confirm your input by clicking the OK button.

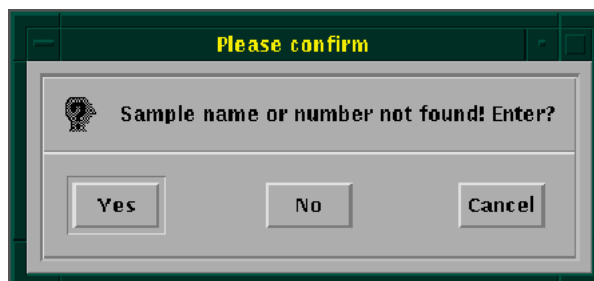


Notice

The program is case sensitive! (See p. 10)

As in the sample registration program, a list now appears of all samples who correspond to your entry. Click on the sample that you require in the list and confirm with OK.

If the desired name cannot be found in the database, the following question will appear:



You should now click on YES if you wish to enter the sample. The input page of the sample registration program appears. See “Sample registration program” on page 9. Enter the corresponding data. See “Edit Samples Data” on page 9.

After you have chosen or entered a sample, the main measurement window appears. If the sample is not being measured for the first time, its earlier measurements will be displayed, with date and number of slices performed.

You can now mount the sample holder. Open the door, place the sample holder on the support in the measurement chamber and close the door afterwards.



Caution

Be extremely cautious about putting only sample holders into the machine corresponding to the diameter selected in the controlfile! A sample holder with a diameter which is too large for the measurement protocol can be destroyed and may also damage the MicroCT!

Controlfiles (Measurement Protocol)

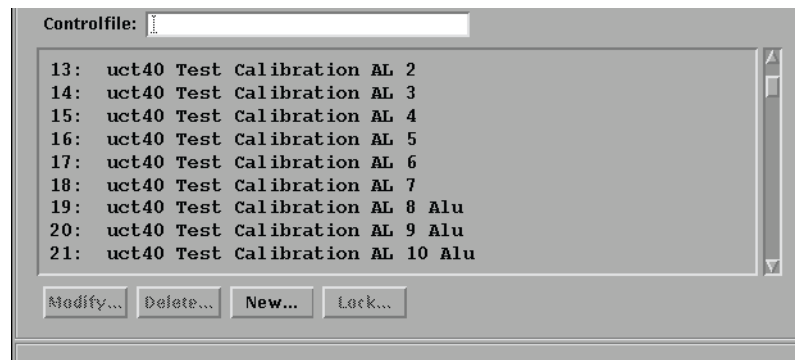
Controlfile Types

There are two types of controlfiles:

- System-Defined (with fixed measurement protocols)
- User-Defined types (can be altered by user)

Selecting a Controlfile

Select the correct measurement protocol (Controlfile) by clicking on one item of the list.



After the controlfile is selected, you can perform a Scout-View measurement or a Slice-Measurement by clicking on either SCAN or SCOUT.

Creating a new Controlfile

If you want to define a new controlfile, click on NEW... and the controlfile definition box appears. For details on how to create a controlfile see “Modifying a Controlfile” p. 15.

Deleting a Controlfile

If you have selected a user-defined controlfile, you can delete it by clicking on DELETE... You have to confirm the deletion of a controlfile.

The controlfile is not actually deleted, but marked as invalid and does no longer appear in the list of controlfiles.

Locking a Controlfile

If you have created or modified a user-defined controlfile, you can lock it (change its type to system-defined) and hereby prevent its further modifications or deletion. Click on LOCK... for this purpose and confirm your action.



Notice

Note: Locked controlfiles can not be viewed anymore by clicking on the “Modify” button.

Modifying a Controlfile

If the controlfile you have selected is a user-defined one, you can alter its protocol before starting the measurement by clicking on MODIFY...:

Definition of Controlfiles...

Controlfilename: 1.

Scout-View: ☒ enabled ☐ disabled ☐ Narrow Angle 2.

Start Position (mm): 3.

End Position (mm): 4.

Increment (µm): 5.

Angle (°): 6.

E (kVp): ☒ 45 ☐ 55 ☐ 70 I (µA): ☒ 88 ☐ 177 7.

Resolution: ☒ Standard ☐ Medium ☐ High ☐ Custom 8.

Samples: Proj/180°: 9.

Mode: ☐ Conebeam 10.

Diameter [mm]: ☒ 12.3 ☐ 16.4 ☐ 20.5 ☐ 30.7 ☐ 36.9 11.

Number of Slices: 1.25 mm (1x104) 12.

Increment (µm): ☐ Isotropic 13.

Rel. Position of First Slice to Ref. Line (mm): 14.

Integration Time (ms): 15.

Average Data: 16.

Tot. No. of Slices: 104 Meas. Time: 3.5 min (11 mAs)

Calibration: 17.

Evaluation: 18.

Explanation:

1. Enter a meaningful name describing the Measurement Protocol
2. Choose enabled for measurements with a Scout-View, which means that the Rel. Pos. of First Slice is relative to the line set with the mouse. If you disable the Scout-View, the position of the first slice is relative to Position 0 mm of the scanner (top of sample holder).
3. Start Z-Position of Scout-View. This value appears in the Scout-View-Dialog Box as the default value and can be altered for each measurement individually.
4. End Position of Scout-View. This value appears in the Scout-View-Dialog Box as the default value and can be altered for each measurement individually.

5. Scout-View Increment. This value is calculated automatically when you change the Start- or End-Position, so that 256 Scout-View-Lines are performed at maximum. If you choose a small Scout area, the increment can be chosen smaller, this way, the resolution is improved.
6. Scout-View Modus only, moving of the object for a better visual presentation of an uneven object.
7. Choose Energy and Current Settings
8. There are 4 modes of the resolution option:

Resolution:	Acquisition:	Reconstruction:
<i>Standard:</i>	250 projections with 1024 samples each	1024 x 1024 pixels
<i>Medium:</i>	500 projections with 1024 samples each	1024 x 1024 pixels
<i>High:</i>	1000 projections with 2048 samples each	2048 x 2048 pixels
<i>Custom:</i>	userdefined, up to 2000 projections / 2048 samples each	2048 x 2048 pixels

9. Conebeam: we recommend not to change this setting.
10. Choose the diameter of the sample holder (The number indicated is the size of the reconstruction area which is slightly larger than the sample holder).
11. Choose the number of slices wished. The indicator shows the covered range in [mm] resulting from number of slices and current slice increment.
12. Slice increment. Isotropic voxel size is mandatory.
13. Relative Position to Scout-View-Reference Line (set with mouse, see 2) or the absolute position 0 mm (if Scout disabled).
14. Integration Time: Adapt the Integration Time on the sample density. If you want nice 3D-displays, choose longer integration time. The reconstruction time is not affected by this value, but the measurement time.
15. Average Data: Multiply the datas of the integration time with the choosen Factor (1-10 x). It is useful for non-standard measurements with integration times over maximum value.
16. Calibration: For an alignment of the scanners and the Phantom.
Change: Opens the Script Selection-Box, there choose a controlfile corresponding to the measurement energy.
Evaluation: we recommend not to change this setting.

If you have set up your measurement protocol, you have to test it before you can use or save it by clicking on TEST.

If this is successful, the buttons OK, SAVE AS NEW and SAVE get sensitive and you now can use the modified protocol for the next measurement only (by clicking on OK) or save it first (clicking on SAVE) and the clicking on OK to return to the main screen.

SAVE AS NEW can be used to store a slightly modified protocol under a different name and number.

You now can perform either the SCOUT or SCAN procedure.



Notice:

Controlfiles have to be saved (or saved as new) if you intend to do a batch measurement with them afterwards (See “Batch Measurement” on page 19).

Unload

Use this button to bring a specimen to the position for removing it if it is not in the loading position. It also shuts down the X-Ray tube and then unlocks the door.

Scout-View

General

The scout-view, comparable with a conventional radiograph, is used to determine the measurement area. On the scout-view, a reference line has to be set. This reference line determines the position of the first slice and must therefore be selected very carefully.

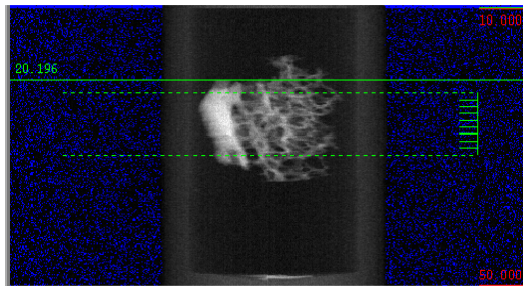
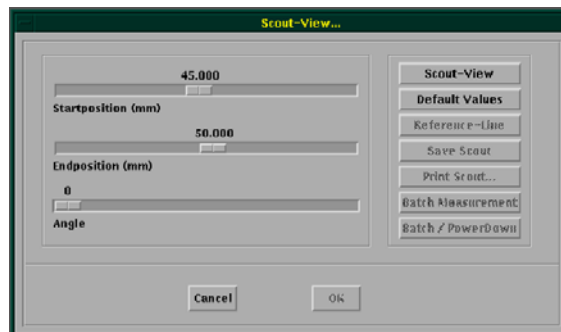


Figure 7. Scout-View of Bone Biopsy with Reference Line

Select SCOUT-VIEW... . The following window will appear:



You can now:

- Determine start- and end-position for the Scout-View
- Perform the Scout-vView
- Set the reference-line
- Save the Scout-View (this is done automatically for the first Scout-View of each sample (=reference Scout-View of reference measurement))

Start- and Endposition

With the two scalers you can determine the extent of the Scout-View. The controlfile gives you default values, which you can change for a specific sample. The smaller the range the better you will see the details of the specimen.

Angle

Using this scaler you can rotate the specimen (Scout-View only!) This allows to better visualize structures not visible from one angle but from another (e.g. baseplate of a joint)

Default Values

Sets the scalers to their initial positions.

Start Scout-View

Click on the SCOUT-VIEW button. The MicroCT now starts measuring the overview image. It will first show half of the radiograph, then continue with the second half of the image.

You can interrupt the scout-view at any position by clicking on the CANCEL button. If it is scanning the first half, it will continue immediately with the second half, if you click while scanning the second half, it will stop.

This means you may have to click twice to interrupt the scout-view completely.

Reference Line

Click on the REFERENCE LINE button and then move the pointer to the current Scout-View at the upper right. The green reference line now follows the pointer. As soon as the left mouse button is pressed, the line is fixed. You can correct the positioning of the line as often as you wish, by again clicking on the REFERENCE LINE button.

As you move the reference line, you also can adjust the number of slices by pressing and holding the SHIFT key. Moving the pointer then adjusts the end of the scan (scan length, scan area). By releasing the SHIFT key, you can move the start line again. Clicking with the mouse sets both start and end position.

To center a certain number of slices, move the reference line to the top of the specimen, than, press the ALT key and move the mouse-pointer to the bottom. The reference line will be centered in between. Click to fix this centered reference line.

Print Scout-View

Use this button to make a hardcopy of the image on the top right of your screen. You can choose between PostScript (sheet including sample name, number etc.) or Encapsulated PostScript and TIFF format (image data only, file only).

Save Scout-View

The reference Scout-View (first measurement) is automatically saved, and is shown for every follow-up measurement of the same sample. The function SAVE therefore is only used if the reference Scout-View for some reason cannot be used.

Batch Measurement

This button will put the measurement at the reference line you have just defined into the measurement queue. You can define multiple measurements, then as soon as you exit the program, one after the other will start. As soon as the measurement job is put into the queue, you will get an information telling you the job-number of the measurement.

You can put multiple specimens in one sample holder. Please be aware that if you have multiple specimens and batchmode measurements on all of those different specimens, do choose the appropriate Number/Name for each specimen **before** you click the BATCH MEASUREMENT button. You can modify the sample by clicking on OTHER... or NEW....



Notice

If you want to apply different Controlfiles for different measurements, you have to redo the Scout-View!

OK

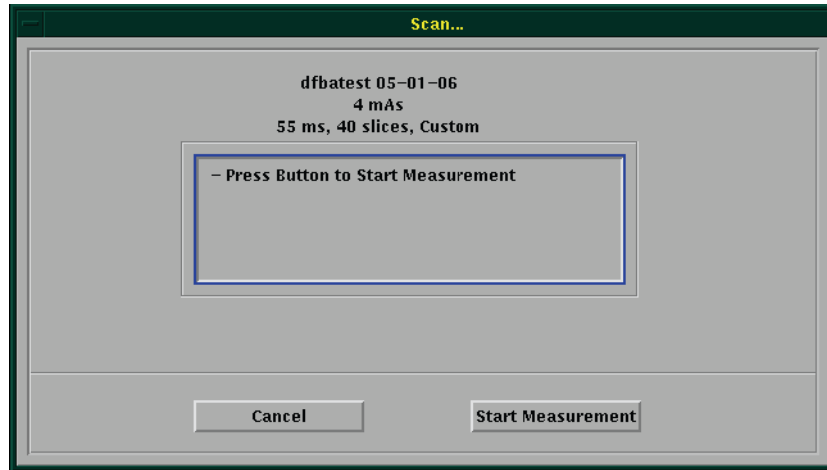
When you have positioned the reference line as prescribed (See p. 17), click on the OK button to start an interactive measurement (not needed if you have already started a batch measurement). This button also saves the Scout-View to disk if it is the first Scout-View for that specimen.

Cancel

If you notice an error in your inputs (for example, wrong measurement protocol, wrong sample etc.), or if the Scout-View is unusable and you need to reposition the sample, you can use this function to return to the main page. Correct the errors and start again with the Scout-View.

Measurement

Click on the SCAN... button. The following window will appear:



Start Measurement

Click on the START MEASUREMENT button. The computer system first allocates the disk space needed for the measurement and then starts measuring the Reference Intensity (I₀) and continues measuring one slice after the other. The raw data (sinograms) of a measurement appear consecutively, the most recent always being shown full size at the upper right.

Cancel

See cancel (See p. 19) of Scout-View.

7 Evaluation

General

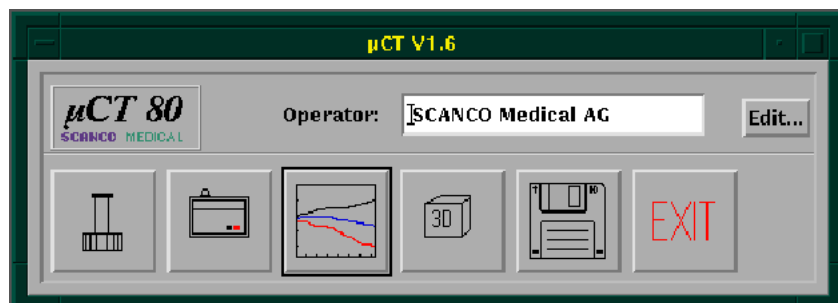
2D- and 3D-histomorphometric evaluation can be performed on either a rectangular/ cubic volume or any irregular shaped ROI/VOI (**R**egion/**V**olume **O**f **I**nterest). The ROI/VOI is defined by a set of Graphical Objects (GOBJs), which can be contours or geometric objects such as rectangles or ellipses.

The ROI/VOI has to be drawn on a slice-based method. The 3D-shape can be defined by either drawing objects on all consecutive slices or by creating a "hull" between any two slices (interpolating the intermediate slices, morphing).

The defined ROI/VOI is stored to disk and will be reloaded once the measurement data is being reloaded. Exactly the same VOI thus can be re-evaluated at a later time.

Starting the Evaluation Program

Enter your name into the operator field (See p. 12) and click with MB1 on the button with the evaluation symbol in the main program:



Overview

With the evaluation program you can carry out the following functions:

- View images
 - view/enlarge (zoom)
 - document (print)
 - convert (EPS, TIFF)
 - Distance measurements
 - view profiles (linear attenuation coefficients among lines)
 - examine linear attenuation coefficient at cursor position
- analyze ROI (**R**egion **O**f **I**nterest, 2D)
 - ROI with different shapes (rectangle, ellipse, contour)
 - analyze ROI (attenuation coefficient, determine area)
- histomorphometric evaluation (2D & 3D)
 - create data set for 3D-Display/Animation/3D-Histo

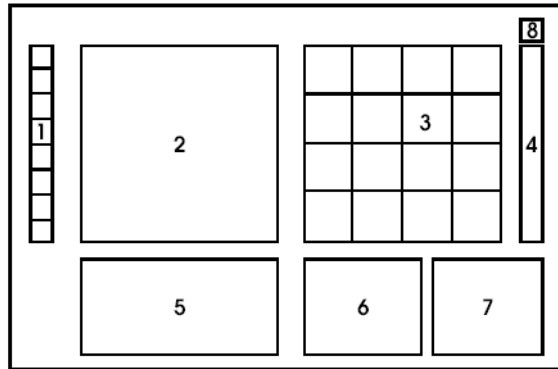


Figure 8. Evaluation Overview

1. *Drawing Symbols (Icon Box)*: By clicking on these symbols, the mouse function, which will be applied, is selected. These functions are only valid for inputs or clicks in input field 2.
2. *Drawing field*: In this field, the image being processed (current picture) is shown. As soon as the mouse pointer moves in this field, and the left mouse button is pressed and/or is held down, the drawing function selected in field 1 takes place.
3. *Overview field*: In this field a certain number of tomograms are displayed: Clicking on an image in this field, it will become the current image and is displayed large in field 2
4. *Black & white/Color scale*: Click in this field to change the colors. By repeated mouse clicks with the left mouse button you will return to the original black & white display.
5. *Image selection area*: Moving the cursor in this field and clicking with the mouse causes the indicated image to be shown in field 2. You also can enter a slice number by using the keyboard or click on arrows to more trough multiple slices one by one.
6. *2D-Evaluation Information*: Information window showing coordinates of cursor, size of ROI and distance, density and area calculations.
7. *Choose evaluation method*: Printing, 2D/3D histomorphometry, 3D distance measurements.
8. *Density scaling*: By clicking on this button causes all images to be reloaded. While being reloaded, all images are displayed at a fixed density scale, so you can compare density values visually. To return to the original display (all images at the most possible brightness), click on the button again.



Notice:

This does not affect any evaluation, but only the display on the screen!

Selection of Sample and Measurement

Selection of Non-Archived Measurements

After starting the evaluation program, you will see the following input window:

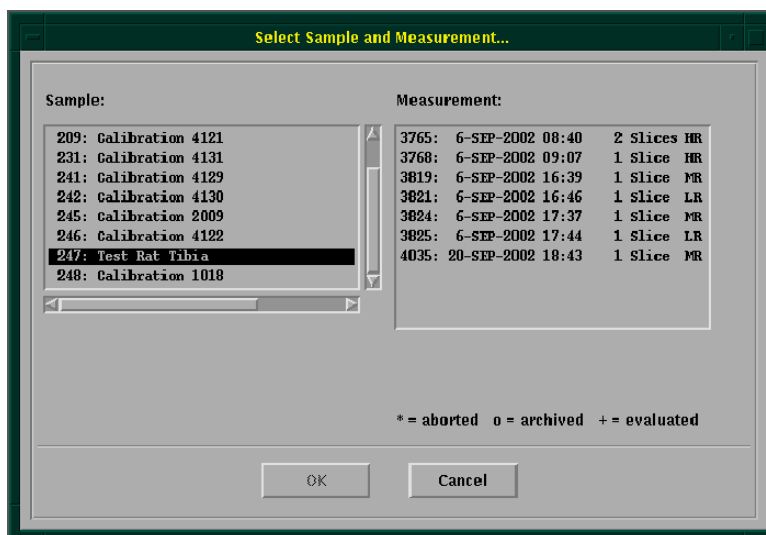


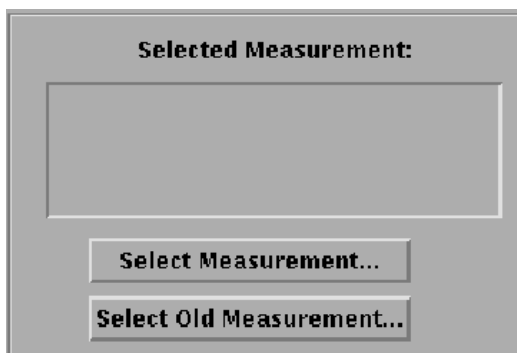
Figure 9. Evaluation: Selection of Sample and Measurement

On the left hand side you see all the samples whose measurements have not yet been archived. Click on the desired sample, and all the measurements of this sample will appear on the right-hand side. After you have clicked on a measurement, and confirmed with the OK button, all images belonging to this measurement will be loaded and appear on the screen.

If you later need to choose other measurements, click on the SELECT MEASUREMENT... button in the main window.

Selection of Measurements already Archived (saved)

If you want to select a measurement that has already been archived, interrupt the above procedure using the button CANCEL and select the SELECT OLD MEASUREMENT... button in the main window:



Enter the name or number of the sample see "Input of Sample's Name or Number" p. 12. The input window shown in fig. 7-2 now appears again. Click

the sample and the measurement as described above. You will then be asked-
to put the corresponding tape with the archived images into the disk drive.



Notice

If you stored the data to Tape, you will first have to restore the data to the harddisk before you can reevaluate it!

Zoom

If you have to correct your contour, or have to draw a mask, you can display part of the screen enlarged. To do this, click on the menu point ZOOM and choose the enlargement factor in the submenu (ZOOM 2x to ZOOM 20x). In the current image a green frame appears, which shows the screen section which will be enlarged, and which can be moved with the mouse. Click with MB1, and the section displayed will be enlarged. If you wish to have another section enlarged, choose the menu point ZOOM once more and so on. With ZOOM RESET you will return to the normal display.

SHOW FULL SIZE opens a window and shows an image in full 1024 x 1024 pixel resolution. Click on CANCEL to close it.

Density scaling

Usually, all images are shown at the maximum brightness. This prevents you from visually comparing the bone values, however. By clicking on the button above the color scale, the images will be displayed in a unified norm (fixed scale):

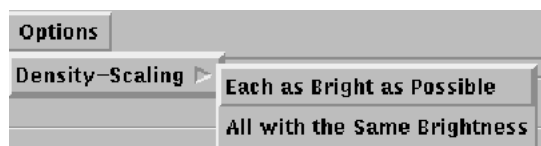


maximal

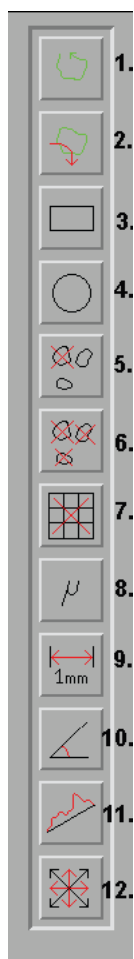


normal

You can achieve the same effect with the menu OPTIONS:



Defining the ROI or VOI



Drawing Icons

By clicking on the buttons shown alongside, you can:

1. Draw Contour: Sketch contours in the *counter clockwise* direction. All contours are automatically closed!
2. Correct: The contour to be corrected must be crossed at two places. The part lying in between these crossing points will be replaced by a new contour. (*counter clockwise* drawing direction!)
3. Draw Rectangle/Square.
4. Draw Ellipse/Circle.
5. Delete Object: Deletes one contour/rectangle/ellipse of the current image.
6. Delete All Objects: Deletes all contours/rectangles/ellipses of the current image.
7. Delete Objects of All Images: Deletes all contours / rectangles / ellipses of all images.
8. Show attenuation coefficient at cursor position.
9. Distance measurement.
10. Angle
11. Show Profile
12. Move Objects (left mouse button) / Scale Objects (right mouse button)

Figure 10. Drawing Icons

Drawing Objects

Choose the slice where you want to draw a contour by clicking on the appropriate field or by entering its number.

Then, click on one of the drawing options (CONTOUR, CIRCLE/ELLIPSE, or SQUARE/RECTANGLE Button, Button 1, 3 or 4).

By clicking into field 1 and dragging/drawing (press the left mouse button), the object appears.



Notice

You can get Circles/Squares by using SHIFT / left mouse button. **Without the SHIFT modifier, you can also draw ellipses/rectangles.**



Notice

Drawing a Contour has to be performed counter-clockwise!

Modifying Contours

You can modify contours by clicking on Button 2. Then, draw over the contour you want to modify. You have to keep the same drawing direction (counterclockwise). The original contour has to be crossed at least twice. The part between the first and last crossings will be replaced by the new drawing.

Moving/Scaling Objects

By clicking on the Button 12, you select the Scale/Move mode. You can grab the objects by moving the pointer on one of the eight handles.

By clicking and holding the left mouse button, you can move the object around.

By clicking and holding the center mouse button, you can scale the objects.



Notice

By using SHIFT / center mouse button the scaling will be constraint, which means that the scale factor will be equal for both horizontal and vertical direction.

Selecting Objects

Click on the Move / Scale Button (12). Then, use the repeated SHIFT / left mouse button to select the individual object you want to select.

By using ALT / left mouse button, you select all objects of one slice.

Deleting Graphical Objects

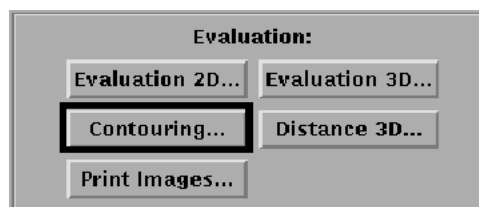
You can delete a single object by clicking on Button 5. Strike over the object you want to have deleted by using the left mouse button.

By clicking on Button 6, you delete all objects of the current active slice.

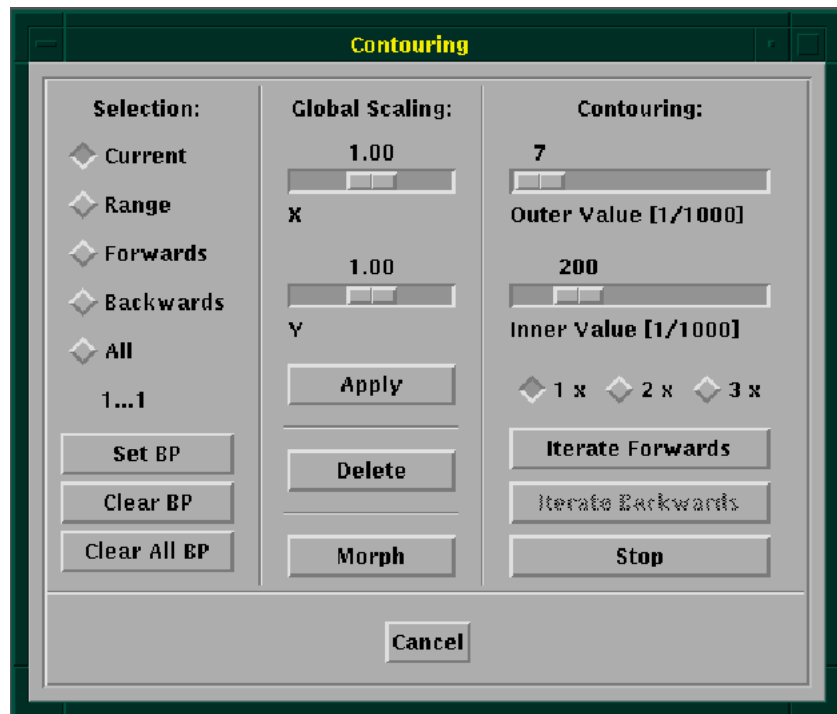
By clicking on Button 7, you can delete all graphical objects of the whole dot-tiest.

Creating a Volume

Drawing objects on all slices is very time consuming. To create a volume, you can get a quicker result by one of the following graphical methods. Click on the button CONTOURING... for these tasks:



The following window appears:



Range Selection

The following actions are performed on a RANGE. You select the range by clicking on one of the options:

- *Current*: image in main window only
- *Range*: start and end of range are defined by BPs, **B**reak**P**oints, Reference slices (green objects)
- *Forwards*: range starts at current slice and extends forwards
- *Backwards*: range starts at current slice and extends backwards
- *All*: entire volume

The slice numbers which will be affected are indicated below the range options (e.g. 17...34)

Brakepoints (BP)

If you choose RANGE in range selection, the range is defined by brakepoints. Any slice containing a hand drawn object becomes a reference slice (or BP). Slice 1 and the last slice of your volume are also considered as BPs.

You can have as many BPs as you like. The whole volume is then divided into different ranges, each extending from one BP to the next BP. You choose the range by clicking at any slice in your range.

You can modify any slice to be a reference slice by clicking on the SET BP button, you can remove a reference slice from the BP-list by clicking on CLEAR BP and you can reset all BP by clicking on CLEAR ALL BP.



Notice

The range extends from the previous BP (not included in the range) to the next BP (included)!

Global Scaling

You can scale objects in the selected range by setting the range, the X- and Y-Scale factor and then clicking on the APPLY button.

Delete

You can delete objects in a range by setting the range and then clicking on the DELETE button.

Morphing

To create a VOI, you can "morph" or extrude the missing objects between two reference slices. The program interpolates the slices in between. To create complex shapes, repeat the morphing step for different ranges. Hand-drawn contours are automatically taken as BP's, but you may use the SET BP, CLEAR BP and RANGE functions for to alter the proposed ranges.



Notice

Morphing only occurs between matching number of contours. If you have two objects in the first slice, you also need 2 objects in the last slice of your range.

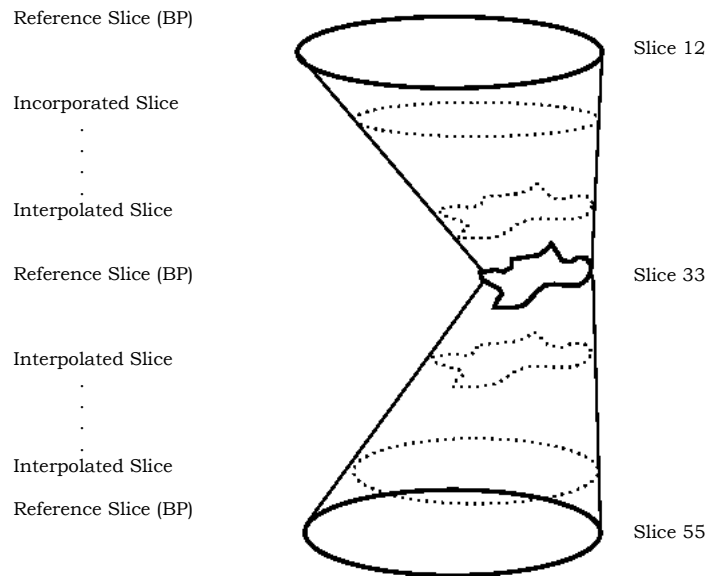
Quick Guide to Expanding a Shape into the 3rd dimension

1. Click on 1st slide which should be included in VOI
2. Draw object (hand drawn or geometric shape)
3. Click on last slice which should be included in VOI
4. Draw new object in this slice
5. Open the Contouring menu as shown above (CONTOURING...)
6. Click on RANGE (selects your VOI inside of your selected slices)
7. Click on MORPH (extends the shapes inside of your selected slices)
8. Click on CANCEL (closes the Contouring dialog box)
9. Start either 2D or 3D-Evaluation as in previous versions

Tip: Move forwards in your slices while you are morphing and the Range / BP-System automatically selects the correct range.

Following is an example of how to create a complex 3D-shape:

If you want to create the following VOL, you have to define 3 reference slices:



Automatic Contouring

Once you have drawn an object, its shape can be automatically adapted to the surface of the bone. The object to start from (hand drawn contour) should approximately match the form of the bone.

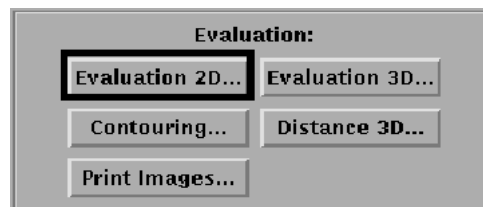
To start the automatic contouring, click on the button ITERATE FORWARDS or ITERATE BACKWARDS. The finding of the contour can be influenced by:

1. Object to start from: The closer the hand drawn object to the real contour, the better the adaption.
2. The value INNER VALUE should be set to the approximately value of bone (see threshold setting in 2D/3D Evaluation)
3. The value OUTER VALUE should be set to the approx. value of soft tissue (see threshold setting in 2D/3D Evaluation)
4. Number of Iterations: Usually, the ITERATION 1X is sufficient. If the shape of the bone changes very rapidly, choose 2X or 3X.

If you select the FORWARDS or BACKWARDS range, the program automatically moves to the next slice after it has finished the contouring on the current slice.

2D Evaluation

Click the EVALUATION 2D... button:



The following window appears at the lower right:

ROI Selection

If you have drawn any objects before, a white bounding box appears around all your objects. If you have not drawn any contours, a default-sized box appears in the middle of the image. The bounding box delimits the valid area for the evaluation.

You can **move** the ROI around by clicking (and dragging) on one of the selection points using the left mouse button, or you can **resize** it by clicking on one of the selection points using the center mouse button.

You can also set or adjust the position or size of the ROI by directly entering the coordinates and dimensions using the keyboard.

Additionally you can select the number of slices which will be analyzed. With the scaler SLICES you decide how many of them will be processed. With the START Z and DIM Z you select the range of the evaluation. 2D evaluation will start with slice START Z and continue to slice START Z + DIM Z, while processing SLICES in total, equally distributed.



Notice

If you set SLICES to 1, only the first slice will be processed, no matter how large your DIM Z is set!

Segmentation

Using the scalars SIGMA, SUPPORT and THRESHOLD, you can change the segmentation parameters. Once you have found your optimal settings, keep them constant for a series of evaluations.

Printing

The next selection affects printing. Set the NUMBER OF COPIES to how many copies of each result sheet you would like to obtain. The toggle buttons PRINT LIST and PRINT SHEET affect the result sheet output. PRINT LIST will create a summary report for all processed slices including the mean values of all slices (filename of summary report is HISTO_2D_xxx.DAT, where xxx is the measurement number. The file is located in the directory with the logical name equivalent UCT_HISTO_RESULTS, see Appendix).

PRINT SHEET creates an individual sheet for each slice showing the main image and the 2D histomorphometric values on it. Keep in mind that these sheets are very large in size and could fill your harddisk if you process all slices of your measurement (200 or more...).

Starting Evaluation

If you have checked all your settings, click on START EVALUATION.



Notice

The evaluation will only be performed inside of both:

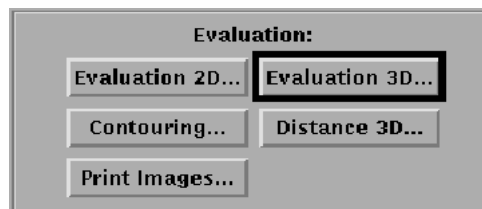
a) your objects/contours (green/red)

b) the bounding box (white)

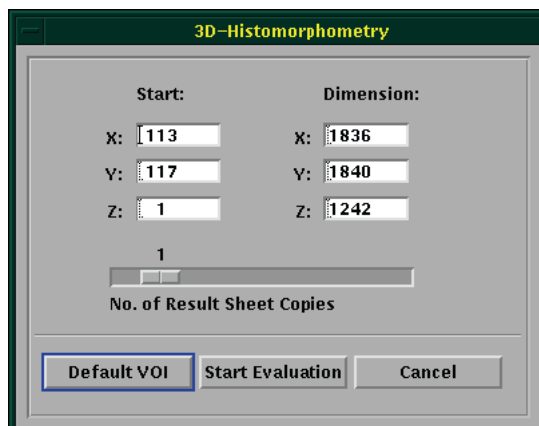
The bounding box in its default size contains all your objects and thus does not further limit the ROI/VOI.

3D-Evaluation

Click on the EVALUATION 3D... button:



The following window appears at the lower right:



Defining VOI

If you have drawn any objects before, a white bounding box around all your objects appears on the screen. If you have not drawn any contours, a default sized box appears in the middle of the image. The bounding box delimits the valid area for the evaluation.

You can **move** the VOI around by clicking (and dragging) on one of the selection points using the left mouse button, or you can **resize** it by clicking on one of the selection points using the center mouse button.

You can also define or adjust the position or dimension of the VOI by directly entering the coordinates/sizes using the keyboard.

Segmentation

See below for changing Evaluation Parameters.

Starting Evaluation

The green/red objects indicate the volume which will be used for the 3D-evaluation whereas the white circles indicate the VOI (sphere) used for the 3D-MIL-evaluation (no longer executed in the evaluation script by default).

The VOI is further delimited by the white bounding box. The volume inside of the white bounding box will be written to disk. Everything outside the bounding box will neither be evaluated nor be displayed in 3D.

If you have found your VOI, click on START EVALUATION and the evaluation immediately starts as a batch process (this means that you can now exit the program or launch a second evaluation).



Notice

The evaluation will only be performed inside of both:

a) your objects/contours (green/red)

b) the bounding box (white)

The bounding box in its default size contains all your objects and thus does not further limit the

Changing Evaluation Parameters

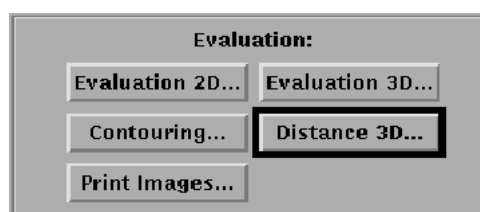
Any experienced user can modify the 3D Evaluation Procedure (e.g. change the threshold level for the segmentation or change the view parameters for the 3D-image on the result sheet) by editing the command procedure

[MICROCT.MAIN]UCT_EVALUATION_V4.COM

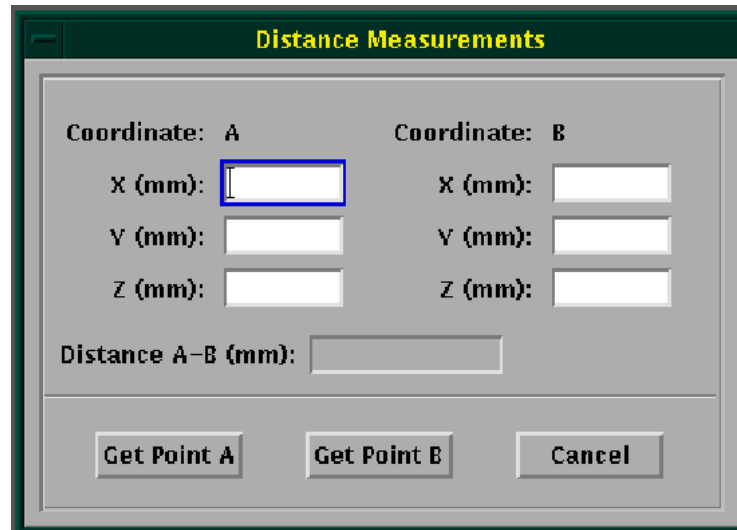
For this purpose, check the Appendix ("Modifying UCT_EVALUATION" p. 77)

Distance 3D

Click the DISTANCE 3D... button:



The following window appears:



The **Distance Measurements** dialog box is shown. It has a title bar with the text "Distance Measurements" in yellow. The main area is divided into two columns: "Coordinate: A" and "Coordinate: B". Each column has three input fields for "X (mm)", "Y (mm)", and "Z (mm)". Below these columns is a single input field for "Distance A-B (mm)". At the bottom, there are three buttons: "Get Point A", "Get Point B", and "Cancel". The "X (mm)" input field for Coordinate A is currently selected with a blue border.

Select the 1st slice you want to set a marker. Then click on GET POINT A and move the cursor to the main window. As you move the cursor, the coordinates appear in the window at A. Click, if you have found your Position A.

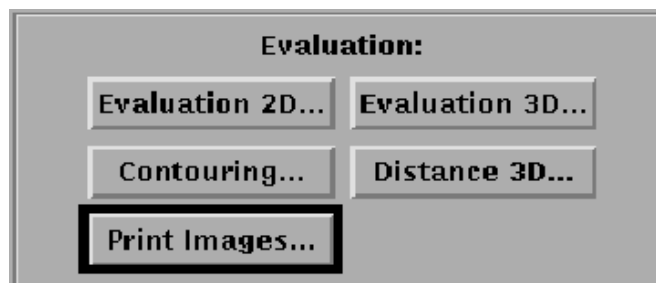
Proceed the same way for Point B. You also can manually enter coordinates using the keyboard.

The distance from Point A to Point B is displayed in the window every time you click in the main window or enter coordinates using the keyboard. Two green markers indicate the positions.

Use CANCEL to terminate 3D-Distance measurements.

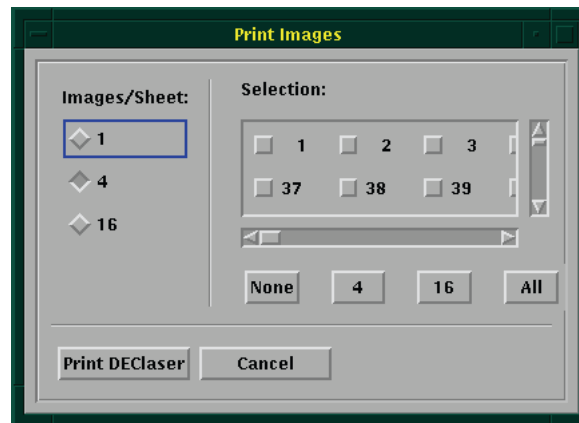
Print Images

Click on the PRINT IMAGES... button:



The **Evaluation** dialog box is shown. It has a title bar with the text "Evaluation:". The main area contains five buttons arranged in three rows. The first row has "Evaluation 2D..." and "Evaluation 3D...". The second row has "Contouring..." and "Distance 3D...". The third row has "Print Images...". The "Print Images..." button is highlighted with a thick black border.

The following input window appears:



With the toggle buttons on the left side, you can choose how many images per sheet you want to have printed. The size of each printed image is dependent on this value.

Then, select the requested images by clicking on the button with the corresponding number.

Alternatively, if you press the button 4 or 16, either 4 or 16 images are selected, equally distributed over the whole number of slices.

The button ALL selects all images, while the button NONE clears all selections.

Confirm your selection with PRINT DEClaser. The images will appear after a few minutes.



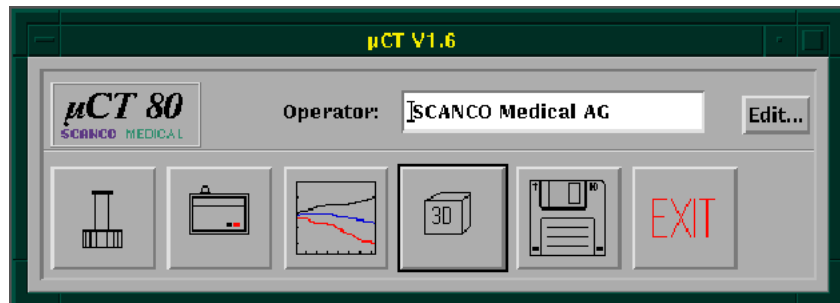
Caution

Do not switch off your computer (SHUTDOWN) before you have received all the prints!

8 3D-Display

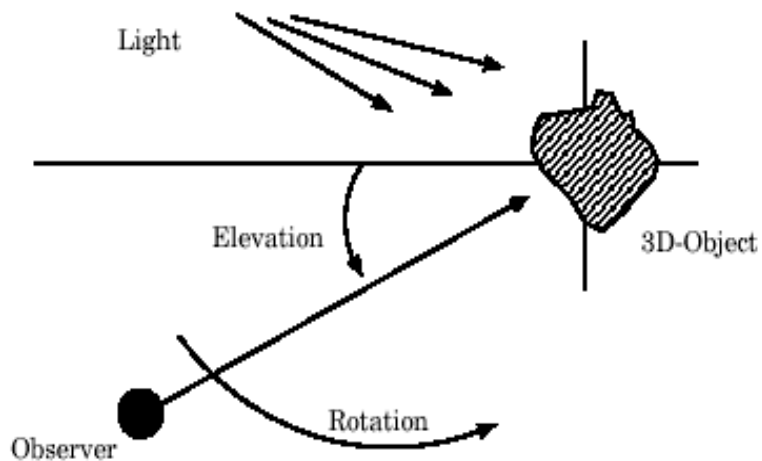
Starting the 3D-Display Program

Enter your name into the operator field (See p. 12) and click on the button with the 3D-symbol in the main program:



General 3D-Scene

The 3D-Scene is as follows:



There is an observer who moves around in the scene and looks at an object which is positioned at the origin. The observer is at a specific elevation (angle) and looking either from above, below or straight on the object. He also moves around the object, which is given by his rotation angle.

The light source is given relative to the observer. So if the observer moves, the light source also moves. Standard values are 20° higher and 20° to the right from the observer position.

If you change the perspective, that means that you move the observer closer to the object or further away from the object.

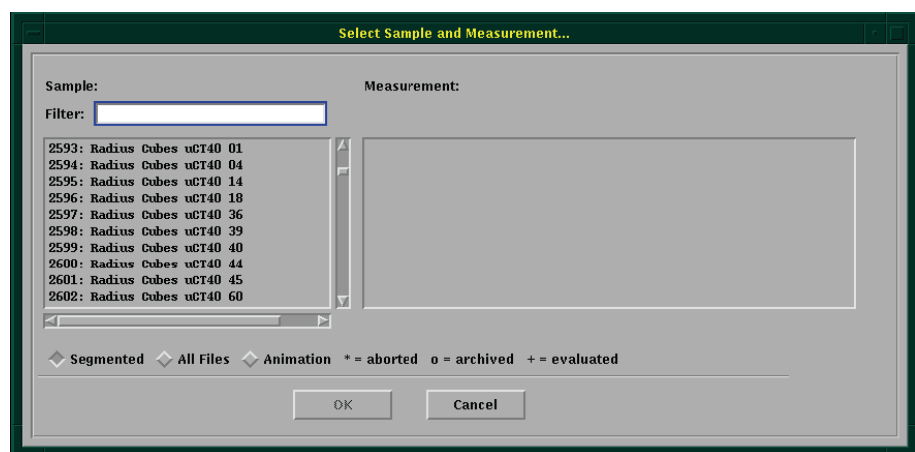
Modes of Operation

You choose the mode of operation by selecting the data type in the sample selection box:

- Interactive calculation mode (SEGMENTED, ALL FILES)
- Animation mode of precalculated views (ANIMATION)

Selecting the Sample and the Measurement

If you start the program, the selection window appears automatically. If you want to choose another sample after displaying the first one, click on the menu FILE and then OPEN.... This following window appears:



First, choose the type of data by clicking on either SEGMENTED, ALL FILES or ANIMATION. Then click on the sample you want to display. If there is data of the corresponding type available, it appears on the right side. Click on the measurement you want to display. The data is loaded after you confirmed your choice with OK.

To display the data, click on the START-button at the bottom left of the screen.

Start/Stop

Start the calculation of the 3D-Scene by clicking on the START button. You can interrupt the calculations by clicking on the STOP button.



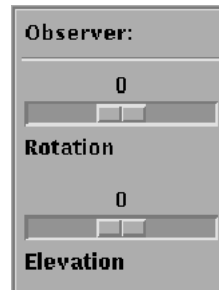
Alternatively, you also can click with MB1 into the main window to start/stop the calculation and the display.

In ANIMATION mode, they start/stop the animation.

Visual Effects

Observer

By changing the ROTATION and ELEVATION of the observer, you change the angle from which you look at the object.



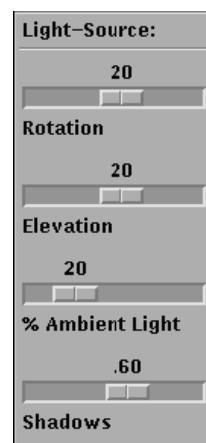
A vertical panel titled "Observer:" containing two sliders. The first slider is labeled "Rotation" and has a value of "0". The second slider is labeled "Elevation" and also has a value of "0".

Alternatively, you also can click into the main window and as you move the cursor up and down, you change the ELEVATION, if you move left or right, you change the ROTATION. If you release the left mouse button, the calculation starts.

If you click while iterating the views, you interrupt, and can then change the observer settings again by click-and-drag.

Light Source

By changing the ROTATION and ELEVATION of the light source, you change the effect of shading the object. The values are relative to the observer position.



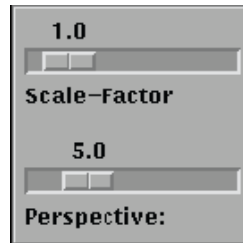
A vertical panel titled "Light-Source:" containing four sliders. The first slider is labeled "Rotation" and has a value of "20". The second slider is labeled "Elevation" and also has a value of "20". The third slider is labeled "% Ambient Light" and has a value of ".60". The fourth slider is labeled "Shadows".

The scaler AMBIENT LIGHT affects the shading of the object, where 0% means direct lighting only and 100% means ambient lighting only. The values in between are a mixture of both light source types.

SHADOWS affects the intensity of the shadow (lighter/darker).

Other Effects

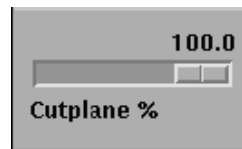
By changing the SCALE-FACTOR, you enlarge the object or make it appear smaller. The PERSPECTIVE scaler lets you change the visual effect as if you moved to the object or further away. The scale hereby is modified in a way that the size is not affected.



Center mouse button for scaling within window

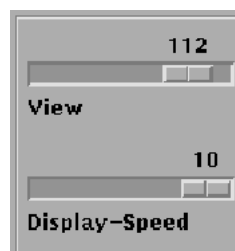
Cutplane %

To perform a virtual cut through the displayed object, align the scaler between 0 and 100 %. 0 % is an exact cut through the middle of the object, parallel to the monitor layer.



Display Options for Animation-Mode

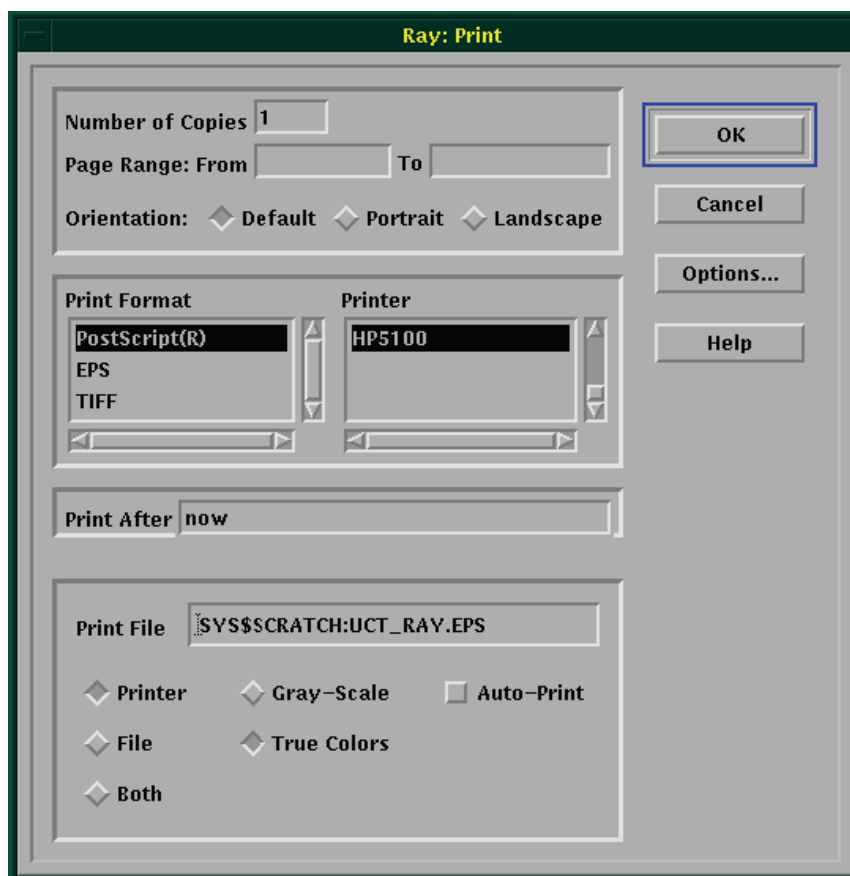
If you choose the Animation-mode, the above effects cannot be set. In this mode you can change the speed of the animation and also choose the view by clicking on the appropriate scalers.



Printing of 3D-Scenes

After you have a 3D-Display on the screen, you also can print a result sheet containing the sample data and the 3D-display. Choose the menu FILE and PRINT...

The following window appears:



First, choose the type of printout you want by clicking on one of the PRINT FORMAT options: PostScript®, EPS or TIFF if available. Then, choose the printer attached and the corresponding button PRINTER, FILE or BOTH.

The color of the output can be set to different values. Choose GRAY SCALE or TRUE COLORS for the object, and PRINTER or FILE for printing or saving as a document of the data.

Then, set the PRINT FILE to your wishes and click on OK.

Calculating Animated 3D-Sequences

In the DECterm window, type

\$ ANIMATION * or

\$ ANIMATION xxx, where xxx is the sample number

Then enter the other requested information. The input file is one of those which are listed, all other parameters are given by default and can be altered at wish.

The resulting animated sequence can then be displayed using the 3D program as described above.

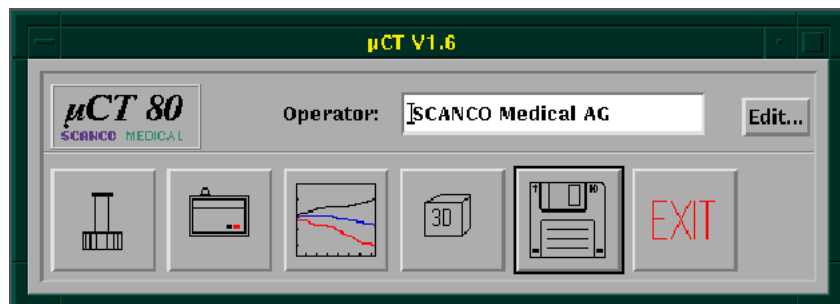
9 Archiving Program

Overview

- Archive images to optical disk or tape
- Delete measurement data
- Formatting (initializing) of tapes
- Determining capacity (free blocks) of the hard disk, optical disks and diskettes
- Backup of all databases and programs to optical disk or tape (full backup)

Starting Program

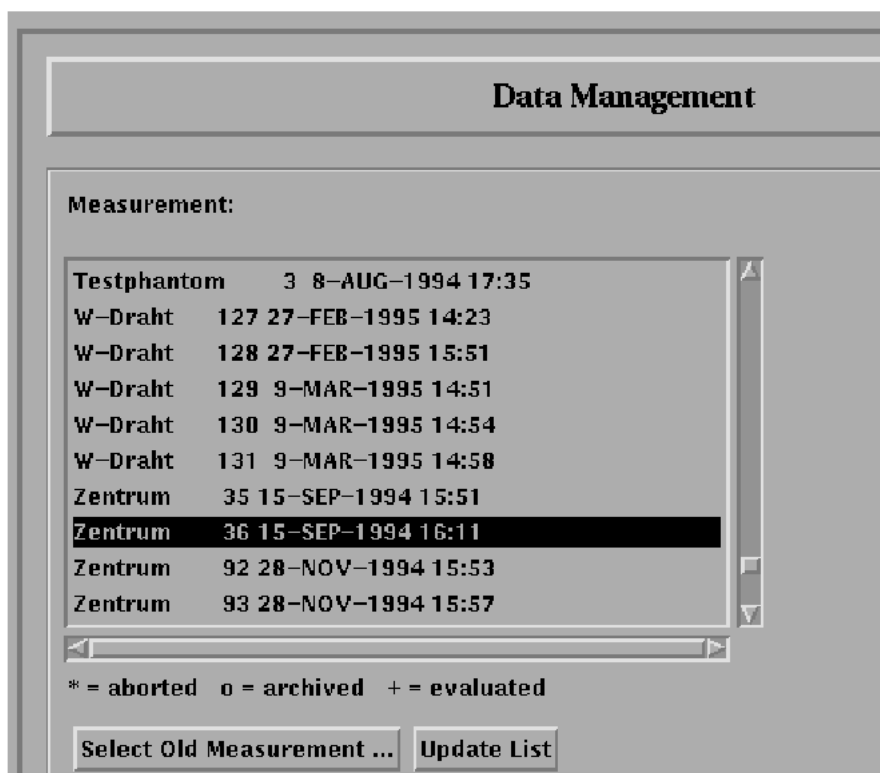
Click on the diskette symbol:



Archiving / Deleting Images

Selecting the measurement

In the upper left hand side, all samples are listed who either have measurements that have not yet been archived, or whose measurements have not yet been deleted:



Choose the corresponding measurement by clicking. You can now either archive these measurements or delete them.

To get the data of archived measurements back to your local hard disk, click on SELECT OLD MEASUREMENT... and then you are prompted to enter the name or number of the sample you want. Enter its name or number and all measurements of that sample appear. Select the desired measurement by clicking on it.

After you have performed a copy/move operation, you can click on UPDATE LIST, as this is not performed immediately because of performance reasons.

Selecting the file type

If you have selected the measurement, you have to select the files you want to copy or move. Click on the button RAW (raw data, *.RSQ) or IMA (Images, *.ISQ, GOBJs, *.=GOBJ and VOI, *.AIM) on the left.

Depending on the destination device, with IMA selected, you also have to select images, AIMS or everything (except RAW, which are handled separately) for the following operation.

Selecting the Destination Device

Click on the DEVICE button, and the list of all available devices appears. Select the appropriate:



1. HardDisk

2. Tape (Streamer)

3. Waste basket

Depending on where the source files reside, you cannot choose all devices, e.g., if the files are on the harddisk, you cannot choose the harddisk as a destination device.

If you want to delete any measurements, you choose the wastebasket as the destination device.

If you want to archive or copy some files, choose the tape device.

Selecting the Copy/Move Operation

If you choose the COPY function, the files are copied to the destination device, but the original still exists and the database still points to this original.

If you choose MOVE, the original is deleted after successful copy operation and the database entry is changed to the new location.

If you want to delete any measurement data, choose MOVE and WASTEBASKET. If a **COPY** of the data does exist on the Harddisk (original still on tape or MO), then the **COPY** will be deleted first. If you redo the command, then the data where the database is pointing to (e.g. Tape) will be deleted and then the DB will be updated.

General Guidelines for daily operations

Archiving: use MOVE to Tape

Restore use COPY to Hard Disk (from Tape)

Starting the move/copy function

If your destination device is a harddisk or an optical disk, just click on the START... button to execute the desired function. If your destination device is a tape, you first have to mount the corresponding tape manually see "Mount/Dismount" p. 45.

After your confirmation, the images of the selected measurement will be copied/ moved to the destination device. If you later want to view these images again (in the evaluation program), you will be asked to input the appropriate optical disk. If you store the images on tapes, you first have to copy or move them back from tape to disk to be able to reevaluate them.

Backup

Under some circumstances it is possible that a hard disk can crash, which makes it impossible to read sample data, old measurement results or Scout-Views again. Such defects are extremely unlikely, but are disastrous for follow-up studies, as previous measurement results cannot be read any more.

You should therefore regularly make a copy of your databases (data security), preferably once a week.

You can backup your data to either optical disk or tape.

If you use the tape drive, you can add many backups to the same tape.

You should use an **optical disk or tape specially reserved for this purpose**.

With optical disks, one week use side A and the following week side B, so that you always have two copies available!

With tapes, we recommend you to use two tapes, alternating between them!



Notice

Use a new optical disk for this purpose. Only new disks without a label and disks initialized with label BACKUP will be accepted

Tapes have to be initialized (with free chosen label name with a length of 6 letters)

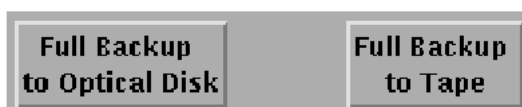


Notice

Do not store your backup disks or tapes in the same room as the equipment, better still, not in the same building! (Danger of fire, water damage etc.)

Before you start a backup procedure, you should terminate all other programs or applications (such as measurement program, evaluation program etc.). Otherwise, some files might be locked by those applications and therefore not be saved.

To start the backup operation, insert the optical disk or the tape and click on the FULL BACKUP TO OPTICAL DISK or FULL BACKUP TO TAPE button:



Then confirm the following question whether you inserted the appropriate disk or tape. A safety copy of all databases and programs will then be made.



Notice

In doing this, everything that was previously on the optical disk will be over-written, and thereby deleted. In no case use a sample disk as the back-up disk!

Device-Information

Disk Information	
Harddisk:	mounted
Free (MB):	203965.68
Free Slices (1kx1k):	62815
Optical Disk:	dismounted
Free (MB):	0.00
Free Slices (1kx1k):	0
<div>MountDismountInitialize...</div>	
Tape:	dismounted
<div>MountDismountInitialize...</div>	
Floppy-Disk:	
Free (MB):	
Sample:	
<div>MountDismountInitialize...</div>	

Initialize

All media (data carriers) must be initialized (formatted) **before they can be used for the first time**. In doing this, every diskette, tape or optical disk will be given a label.

The optical disks must be initialized before they are used for the first time. We recommend that, **as soon as you receive a new packet, you should immediately initialize both sides of all disks** (so that later, by mistake, you do not initialize a disk which has already had sample data written to it). Give the individual sides names with consecutive numbers (for example, UCT001, UCT002, UCT003...), The name **must not contain a space or special characters** and is limited to 15 characters.

The same as above has to be performed for tapes as well, but tapes are one-sided media only and the label is limited to 6 letters.



Notice

When initializing, all data which could already be on the medium will be lost!

Mount/Dismount

Before diskettes, tapes or optical disks can be used, they must first be mounted by the system (made accessible to the user), and, after use, they will be dismounted. This is carried out automatically by the program for optical disks, but has to be done manually for tapes because of performance reasons.

If you once need to check how many measurements can still be fitted onto an optical disk, or which name the disk has, you must mount the disk by clicking on the MOUNT button. The name of the disk appears next to the "mounted", for example, "Mounted as UCT001". Also the number of free MB and the corresponding number of slices and raw data appears (calculated as images taken at high resolution mode). Afterwards, the optical disk must be dismounted again.

- Checking the available remaining space on a tape is not possible.

10 DECterm based Programs

General Guidelines

To start one of the following programs, you need access to a terminal session window either directly on the machine or via the network (telnet, rlogin, set host etc.)

You can start the programs by typing a shortcut (or symbol). The following table summarizes the names, functions and location of the programs.

Symbol/Command	Program Name/Location	Function
\$ R UCT_RECONSTRUCTION	UM:FAN_RECONSTRUCTION.EXE	2D-Slice-Reconstruction
\$ ANIMATION	UM:ANIMATION.COM	Create Animation File
\$ IPL	UM:IPL_SCANCO_M.EXE	3D-Segmentation / MIL Calculation
\$ UCT_THREEDEE_BATCH	UM:UCT_RAY_BATCH.EXE	Program to print 3D-Result-sheet
\$ UCT_LIST	UM:UCT_LIST.EXE	DB-Query (3D-Histo)
\$ WRITE_INFO	UM:UCT_WRITE_INFO.EXE	DB-Query (Sample-Info)

2D-Reconstruction

If for any reason (e.g. insufficient disk space) the slice-reconstruction is not finishing, or you have destroyed the 2D-Slice-data (*.ISQ) but still have the RAW-data (*.RSQ) somewhere, you can reconstruct the missing slices with this program. There is no shortcut for this program. Start it using the following command:

```
$ RUN UCT_RECONSTRUCTION
```

Raw-Data-File:

```
DISK3:[BRUNO.DATA.00000033.00000680]C0000372.RSQ
```

SliceSelection: N (1 slice) or N:M (from:to) or A (all)

SliceNr. [0...222] (Neg. to stop):17:34

You first have to give the input filename, which is the *.RSQfile. Then, you define which or how many slices to reconstruct. You can give the following values:

- **A** This means, reconstruct ALL slices
- **N** Enter one value, then this slice will be reconstructed and you will be asked again. To end the program, enter a *negative value*.
- **N:M** Reconstruct a range (from slice n to m), so enter e.g. 5:19.



Notice

Most programs operated in the terminal start counting the slices at 0, while the standard user programs start counting at slice 1. You might have to adjust for this difference of 1.

IPL (Image Processing Language)

This program is used to execute the 3D-segmentation and different morphometric evaluations, e.g. MIL (Mean Intercept Length), DT (Distance Transformation), TRI (Triangulation), SMI (Structure Model Index) etc.

The concept of this program is: You work with multiple objects in memory. One object is usually the input for a procedure, whereas the result will be the next object. You can delete objects (internally, in memory only).

You can also read and write objects from/to disk. Each object has to be given an internal name, such as *input*, *output*, *segmented* or just *a*, *b*, *c* etc.

Once launched in interactive mode, you can execute the commands below. Each command takes a few arguments which usually have a default value. By pressing the return key, the value is entered. If you have to enter values for all coordinates (x, y and z), you can either give all three values separated by a space or just enter one value, which is then applied to all coordinates. If the order of the arguments is known by heart, you can supply them in the correct order together with the command, e.g. 'gauss in out' and then press return to be asked the next arguments.

IPL commands may be abbreviated. The procedure name list is searched against your input, and IPL takes the first command that matches the abbreviation (execute 'he lp' to see the list and search order). There is no 'ambiguous command' warning.



Notice

IPL only accepts lower case input!



Notice

In the standard evaluation (Start Evaluation 3D...), IPL is operated in batch mode. Then the two dots (..) in the last IPL line of the batch-command file are very important. DO NOT DELETE OR FORGET THEM! At the IPL startup in 'batch mode', the whole string is read up to the two dots, and then commands in the string are executed one by one.

On the other hand, in interactive mode IPL executes the commands immediately. To exit interactive IPL, use 'quit'.

help

Gives the list of all available procedures or a short description of a procedure if `ipl> 'help xxxx'` is typed.

quit

Quits the program

`ipl> quit` (or `q`)

list

Lists all objects currently in memory or lists all procedures, optionally only items starting with `beginning_with`.

```
iopl> list
-objects           [true] >
-procedures        [false] >
-beginning_with    [] >
```

read

Reads an object from disk. The file type has to be *.aim. By reading an object from disk, you have to give it an internal name.

```
iopl> read
-name              [in] > a
-filename          [default_file_name] > DISK3:[DATA]C0000372.AIM
-type              [aim] >
-uncompress        [true] >
```

aim_read

Shortcut for reading an AIM from disk. The file type has to be *.aim. By reading an object from disk, you have to give it an internal name. Same function as `read`, but type and uncompress are assumed to be aim and true.

```
iopl> aim
-name              [in]> a
-filename          [default_file_name] > DISK3:[DATA]C0000372.AIM
```

or on one line only:

```
iopl> aim in DISK3:[DATA]C0000372.AIM
```

isq_to_aim

Reads an .ISQ from disk and puts the requested volume of interest into memory as an aim object. The volume of interest is given by `pos` (upper left corner) and `dim` (dimension of aim object).

```
iopl> isq
-aim_name          [in] > a
-isq_filename      [default_file_name]>DISK3:[DATA]C0000372.ISQ
-pos               [0 0 0] >150 240 0
-dim               [-1-1-1] >210 210 210
```

write

Writes an object to disk. The file type should be *.aim. You can compress segmented

files using `run_length` or `binary` compression. Default is `binary`, but for gray scale images the compress type is always switched internally to `none`.

```
iopl> write
-name              [default_name] > a
-filename          [default_file_name] > DISK3:[DATA]XYZ.AIM
-compress_type     [bin] > r
```

delete

This command is used to delete an internal object, i.e. to free memory.

```
iopl> delete
-name              [] > a
```

examine

Use this command to examine different things of an object and show the results on the screen. Possible values are: geometry, histogram, statistics, number, log, and z_mean_max (mean and max values of each slice along z-axis).

```
ipl> examine
-input                [default_name] > a
-item                 [geometry] >

!> dim                504 122 223
!> off                0 0 0
!> pos                266 308 0
.
.
```

sup_divide

This command is used to subdivide an object into smaller objects. This is helpful in examining only a small part of the complete object or for segmenting the whole object using small subobjects to save memory. You can either define the subvolume(s) by entering the number of subvolumes (supdim, in all directions) or their size in pixels (subdim). suppos is the offset of the object in pixels in local coordinates. If you leave the value at -1, the object(s) will be centered. testoff is used for overlapping the small subobjects in case of a procedure such as a gauss-filter. If supdim_numbers is not a divisor of the original object's dimensions, a few voxels may be discarded, at most subdim_number voxels per direction x, y or z.

```
ipl> sup_divide
-input                [in] > a
-supdim_numbers       [-1-1-1]> 4
-testoff_pixels       [0 0 0] > 2
-suppos_pixels_local  [-1-1-1]>
-subdim_pixels        [-1-1-1]>
```



Notice

If you plan to subsequently use a gauss-filter on the object, testoff must be equal to the support in the gauss-filter

sub_get

Extracts a sub volume that has the position and size as entered by pos and dim. The flag global_pos_flag controls whether pos is the global position (given by the original measurement) or the local position in the input object.

```
ipl> sub_get
-input                [in] > a
-output              [sub] > s
-pos                 [0 0 0] >10 30 10
-dim                  [0 0 0] >120
-global_pos_flag      [false] >
```

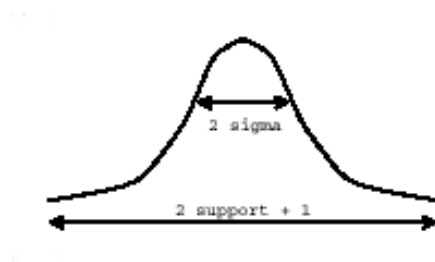
sub_pick

Is an older version of sub_get, that needs previous execution of sup_divide to enter the positions and sizes in the grid. subpos_numbers is the (0-based) position in numbers in the suppos-grid.

```
ipl> sub_pick
-input          [in] > a
-output         [sub] > s
-subpos_numbers [0 0 0] >
```

gauss_lp

This is the command to gauss-filter an object. The shape of the filter can be given using sigma and support. You have to give an internal name for the output object.



```
ipl> gauss
-input          [in] > a
-output         [gauss] > b
-sigma          [1.000000] > 1.2
-support        [2] >
```

threshold

Using this command, you can binarize an object. All voxels below lower_in_perm and above upper_in_perm will be set to value 0, the rest (the object) will be given a value of value_in_range, usually 127. The values for the lower and upper threshold are given in 1/1000, covering the whole range of the data values (0 to 32767 for gray scale AIMS, -128 to 127 for char AIMS).

```
ipl> thresh
-input          [gauss] > b
-output         [th] > c
-lower_in_perm  [300] > 220
-upper_in_perm  [1000] >
-value_in_range [127] >
```

gauss_seg and seg_gauss

Use this command to do the gauss_lp and the threshold in one step. This saves memory and reduces the computing time. However, you have no access to the intermediate object.

```
iopl> gauss_seg (or seg)
-input          [in] > a
-output         [seg] > b
-sigma          [1.000000] > 1.2
-support        [2] >
-lower_in_perm  [300] > 220
-upper_in_perm  [1000] > 1000
-value_in_range [127] >
```

adaptive_threshold

Using this command, you can find out which threshold leads to the best segmentation of the bone. The program examines the BV/TV parameter at different threshold values (given by first_threshold, last_threshold and nr_steps). It then tries to find the threshold with the least change, which it considers to be the best choice. At the end, this value is applied to the input and written to the output object using the value_in_range as in threshold.

```
iopl> adaptive_thresh
-input          [gauss] > a
-output         [th_adp] > c
-first_threshold [400] > 300
-nr_steps       [30] > 50
-value_in_range [127] >
```

fft_laplace_hamming

Segmentation of an object based on zero crossing of second derivative. The second derivative is calculated in the fourier domain by applying a ω^2 filter, for noise smoothing a Hamming filter is simultaneously applied. To ensure that regions with high attenuation are segmented as foreground, the original image is added with variable weight 1-laplace_epsilon. The result is an object of type 'float' that has to be normed to 'short' again with norm_max.

Redim_pow2 can be used to simultaneously interpolate the object to a new voxel size by fourier interpolation in powers of 2 (redim_pow2 = 2 -> 4 times interpolation). Laplace_epsilon controls the weight of the curvature image, the higher the epsilon, the more 'edge enhanced' the image appears.

Lp_cut_off_freq is the Hamming filter lowpass frequency in units half the Nyquist frequency: 0.5 is a filter rolling off to 0 just at the Nyquist boundary. Hamming_amp is the amplitude of the Hamming filter, its default is best not varied.

```
iopl> fft_laplace
-input          [in] > in
-output         [lh] > out
-redim_pow2     [0 0 0] >
-laplace_eps    [0.900000] >
-lp_cut_off_freq [0.400000] >
-hamming_amp    [1.000000] >
```

norm_max

Norm_max has to be applied after fft_laplace_hamming to convert the 'float' values to 'short' again. max in the input will be set to the maximal possible value of the chosen data output type type_out (32767 for short), as will all values above max. The values from zero to max will be scaled to the data range available for the output data type. With 'examine lh histo' the histogram of the fft_laplace output can be viewed, and a suitable max can thus be chosen, normally a value at the upper end of the main distribution. The range of the

fft_laplace output can vary greatly for different types of objects, since the curvature can be very different. It is advised, however, to use the same value for max for one type of sample, i.e. within one study population. The value is not very crucial, as long as it is above the respective value that is thresholded afterwards to produce a binary image.

```
ipl> norm
-input          [lh] >
-output         [norm] >
-max            [50000.000000] >
-type_out       [short] >
```

gobj_maskaimpeel_ow

Performs a masking of an object with a GOBJ (or a AIM-mask, needs more memory and time with AIM, though). Voxels outside the mask are set to Zero. Peel_iter gives the number of two-dimensional peel iteration applied to the contours. The operation is working directly on the object, i.e. it is overwriting Zeros on it. NB: Gobj_maskaimpeel_ow may be repeatedly used on the same object, but using a smaller peel_iter number does not restore the region set to Zero anymore, i.e. while trying out different peel_iters, go from small numbers upwards. The relative volume of the mask is stored in the proceeding log, which may be shown with 'examine in log' afterwards.

```
ipl> gobj_mask
-input_output    [in] >in
-gobj_filename   [default_file_name] >u0001977.GOBJ
-peel_iter       [0] >
```

cortex_maskoff

Expert function.

Combines a GOBJ contour (e.g. the outer bone contour) with a cortex-segmentation mask. The resulting AIM-mask is then the region inside the GOBJ, but without the cortex, i.e. only the trabecular region. The input is a GOBJ file and a volume that should represent the cortex: input_mask. This input_mask has to be produced with seg_gauss beforehand (e.g. with a high sigma 10.0 and support 6, and an appropriate threshold 150 or 300.) cortex_peel_iter gives a minimal cortex thickness, i.e. the minimal boundary of the outer contour that is excluded in the mask. A component labeling is performed for every slice for the cortex ($\Rightarrow$ cl_cortex in percent) and then for the inner mask ($\Rightarrow$ cl_inner in percent), in the example below, for every slice only parts of the cortex that take up more than 50% are considered for the slice-wise exclusion, and then only parts making up more than 60% are taken for the mask.

```
ipl> cortex_mask
-input_mask      [in] >
-gobj_filename   [default_file_name] >u0001234.GOBJ
-output          [out] >
-cortex_peel_iter [5] >
-cl_cortex       [10.000000] >50.
-cl_inner        [10.000000] >60.
```

gobj_to_aim

Produces a solid, filled volume from a GOBJ file, i.e. the inside of the GOBJ mask. This function is needed if the element-size (voxel size) of the original volume or segmented volume has been changed with scale_el_size, e.g. to make the voxels cubic. Then the GOBJ produced on the original ISQ file does not match anymore, but the AIM-mask produced with gobj_to_aim can be scaled to the appropriate voxel size (scale with integrate false), written to disk and then used in gobj_maskaimpeel_ow. Also any other IPL commands can be applied to the AIM-mask like to any other binary volume.

```
ipl> gobj_to_aim
```

```
-gobj_filename      [default_file_name] >U0001977.GOBJ
-output             [out] >out
-peel_iter          [0] >
```

cut2d_shape_ow

Cut a two-dimensional ellipse, circle, or rectangle extended along the z-axis from an object and set all points lying outside to zero. The size of the shape `type_of_shape` is adjusted to the biggest size lying within the x-y plane, if -1 is chosen for `halfaxes_x_y`, otherwise to the given size (may overlap the boundary). `cutborder` controls whether the border of the shape is set to zero (true) or not (false). The operation is overwriting, i.e. the input object is altered!

```
ipl> cut2d_shape
-input_output       [in] >
-type_of_gobj       [circle] >
-halfaxes_x_y       [-1-1] >
-midpos_x_y         [-1-1] >
-cutborder          [false] >
```

cl_ow_rank_extract

Component labeling (CL) of a segmented image. Faces have to touch for voxels to be considered connected, i.e. a voxel can have 6 connected neighbours. Extracts the regions with the given rank in the size ordered table. Overwrites the input. Usually used with rank 1 to 1 to remove any small noisy speckels not connected to the main structure. `connect_boundary` controls whether the whole boundary of the box containing the object acts as a connector of surface points.

```
ipl> cl
-input_output       [seg] > a
-first_rank         [1] >
-last_rank          [1] >
-connect_boundary    [false] >
-value_in_range     [127] >
```

cl_rank_extract

Same as above, but not overwriting the input. Uses more memory.

```
ipl> cl_rank
-input              [seg] >
-output             [cl] >
-first_rank         [1] >
-last_rank          [1] >
-connect_boundary    [false] >
-value_in_range     [127] >
```

cl26_rank_extract

Similar as above, but also voxels only touching by an edge are considered connected.

```
ipl> cl26_rank
-input              [seg] >
-output             [cl] >
-first_rank         [1] >
-last_rank          [1] >
-connect_boundary    [false] >
-value_in_range     [127] >
```

cl_extract

Same as `cl_rank_extract`, but extracting according to fractional volume of components. Not available with `connect_boundary` flag.

```
ipl> cl_extract
-input                [seg] >
-output               [cl] >
-lo_vol_fract_in_perc [1] >
-up_vol_fract_in_perc [1] >
-value_in_range       [127] >
```

cl_nr_extract

Same as `cl_rank_extract`, but extracting according to number of voxels of components. Not available with `connect_boundary` flag.

```
ipl> cl_nr_extract
-input                [seg] >
-output               [cl] >
-min_number           [10] >
-max_number            [0] >
-value_in_range       [127] >
```

cl_image

Gives the component labeled image as output, with value 127 for biggest connected part, 126 for second biggest etc.

```
ipl> cl_image
-input                [seg] >
-output               [cl] >
```

db_sanco_activate

Activates (or deactivates) the database for writing all subsequent evaluation results into it. It stays activated until `db_sanco_activate false` is entered.

```
ipl> db_sanco_activate
-write                [true] >
```

tri_da_metric_db

This command triangulates a segmented object and calculates object volume and surface as well as the structure model index (SMI). Using the plate model, trabecular number, thickness and separation are derived.

`Tri_da_metric_db` uses the contours of a GOBJ or AIM-mask if it finds the GOBJ filename in the proceedings log. Otherwise, the whole box region is evaluated. The results are written into the database ($\Rightarrow$ db), if the database was activated, see `db_sanco_activate`. You should usually not modify the default values of the arguments `ip_sigma`, `ip_support`, `ip_threshold`, `interpolate`, `nrave_iter`, `t_dir_radius`, `epsilon`. The output is an object with `nr_views` different 3D views of the triangulated object. This output may be written to disk with '`msq_from_aim`' and viewed with the 3D-Display program.

```
ipl> tri
-input                [th] >seg
-output               [tri] >
-gobj_filename        [gobj_from_log] >
-peel_iter             [-1] >
-ip_sigma              [2.000000] >
-ip_support            [1] >
-ip_threshold          [64] >
-interpolate           [true] >
-nrave_iter            [0] >
-t_dir_radius          [2] >
```

```

-epsilon          [1.200000] >
-size_image       [512 512] >
-scale_image      [0.700000] >
-edges            [false] >
-nr_views         [0] >

```

dt_object_param

Calculates the mean thickness of the structure with the distance transformation (DT) method by filling largest spheres into the object and calculating their mean diameter (volume weighted mean). Mean thickness and standard deviation are written to the database, if activated. The output object shows the spheres fitting inside the structure with the voxel values being their diameter in voxel units. `Dt_object_param` uses the contours of a GOBJ or AIM-mask if it finds the GOBJ filename in the proceedings log. `Roi_radius_factor` controls whether only a sphere is evaluated or the whole region (default). DT also works with GOBJ-masked objects. The epsilons are used for suppressing artefacts due to rough surfaces. You should usually not modify the default values. (For very coarse voxel sizes above 100 μm , `assign_epsilon 0.9` may be chosen.) `Histogram_or_screen` controls whether a histogram of the thickness distribution is written to a text file and/or shown on the screen.

```

ipl> dt_obj
-input          [in] >
-output         [out] >
-gobj_filename  [gobj_from_log]
-peel_iter      [-1]
-roi_radius_factor [10000.0] >
-ridge_epsilon  [0.900000] >
-assign_epsilon [1.800000] >
-histofile_or_screen [none] >samp012_thickness.tab

```

dt_background_param

Calculates the mean separation of the structure with the distance transformation (DT) method by filling largest spheres into the background of the object and calculating their mean diameter (volume weighted mean). Mean separation and standard deviation are written to the database, if activated. The output object shows the spheres fitting inside the background with the voxel values being their diameter in voxel units. Dt_background_param uses the contours of a GOBJ or AIM-mask if it finds the GOBJ filename in the proceedings log. *Roi_radius_factor* controls whether only a sphere is evaluated or the whole region (default). DT also works with GOBJ-masked objects. The *epsilons* are used for suppressing artefacts due to rough surfaces. You should usually not modify the default values. (For very coarse voxel sizes above 100 μm , *assign_epsilon* 0.9 may be chosen.) *Histogram_or_screen* controls whether a histogram of the thickness distribution is written to a text file and/or shown on the screen.

```
ipl> dt_back
-input                      [in] >
-output                     [out] >
-gobj_filename              [gobj_from_log]
-peel_iter                  [-1]
-roi_radius_factor          [10000.0] >
-ridge_epsilon              [0.900000] >
-assign_epsilon             [1.800000] >
-histofile_or_screen        [none] >
```

dt_mat_param

Calculates the mean trabecular number of the structure with the distance transformation (DT) method by filling largest spheres into the background of the mid axis transformed object (-> mat) and calculating their mean diameter (volume weighted mean). Mean number and standard deviation are written to the database, if activated. The output object shows the spheres fitting in between the mid axis structure with the voxel values being their diameter in voxel units. Dt_mat_param uses the contours of a GOBJ or AIM-mask if it finds the GOBJ filename in the proceedings log. *Roi_radius_factor* controls whether only a sphere is evaluated or the whole region (default). DT also works with GOBJ-masked objects. The *epsilons* are used for suppressing artefacts due to rough surfaces. You should usually not modify the default values. (For very coarse voxel sizes above 100 μm , *assign_epsilon* 0.9 may be chosen.) *Histogram_or_screen* controls whether a histogram of the thickness distribution is written to a text file and/or shown on the screen.

```
ipl> dt_mat
-input                      [in] >
-output                     [out] >
-gobj_filename              [gobj_from_log]
-peel_iter                  [-1]
-roi_radius_factor          [10000.0] >
-ridge_epsilon              [0.900000] >
-assign_epsilon             [1.800000] >
-histofile_or_screen        [none] >
```

dt_mat_output

Performs the mid axis transformation of the structure and saves the mid axes in the output.

```
ipl> dt_mat_output
-input                      [in] >
-output                     [out] >
-ridge_epsilon              [0.900000]>
```

connectivity

Calculates the connectivity density of a segmented object, according to Odgaard and Gundersen (Bone 14:173182; 1993). The insure that only one connected object and one connected background is evaluated, a component labeling and extraction of the dominant component is performed for both the foreground and the background. Use `conn_nocl` and `conn_bgcl` if you wish no component labeling or only a background component labeling/extraction, e.g. if a component labeling is already incorporated into the segmentation.



Notice

The component labeling and extraction changes the input volume!

```
ipl> connectivity
- in_out          [in] >
```

conn_nocl

Calculates the connectivity density of a segmented object without prior component labeling. If the object consists of more than one unconnected part, you would have to add the number of components minus one to the connectivity, and then calculate the connectivity density. Likewise, if the background is made up of more than one part, you would have to add the number of background components minus one.

```
ipl> conn_nocl
- in_out          [in] >
```

conn_bgcl

Calculates the connectivity density of a segmented object with only component labeling and extraction of the background. If the object consists of more than one unconnected part, you would have to add the number of components minus one to the connectivity, and then calculate the connectivity density.



Notice

The component labeling and extraction changes the input volume!

```
ipl> conn_bgcl
- in_out          [in] >
```

voxbobj_sanco_param

Evaluates a segmented image for the fraction of voxels set and writes result to the database (if activated). For gray scale (original) images, mean attenuation coefficient is written to database. The object is masked again with the given GOBJ or AIM-mask. By default, the GOBJ filename is taken from the proceedings log (last occurrence of a GOBJ filename). If the GOBJ file is not found, vox_sanco_param (see below) is applied. Peel_iter controls the number of 2D peel iterations for the mask. By default, peel_iter is taken from the proceedings log.

```
ipl> vox
-input          seg
-gobj_filename  gobj_from_log
-peel_iter      -1
```

vox_sanco_param

Evaluates a segmented image for the fraction of voxels set and writes result to the database (if activated). For gray scale (original) images, mean attenuation coefficient is written to database. If the proceedings log of the object contains a GOBJ mask operation, the relative volume of the masked region is incorporated into the calculation.

```
ipl> vox_sanco seg
```

mil_param

This command executes the MIL-calculations (Mean Intercept Length, Parfitt). You should usually not modify the default values. If the database is activated, the result of the calculations are written to the evaluation-database.

```
ipl> mil_param
-input          [default_name] > a
-ray_plane_scale [2.000000] >
-roi_radius_factor [1.000000] >
-t_dir_ortho     [no] >
-t_dir_ortho_nr   [8] >
-t_dir_radius     [2] >
-fabric_tensor    [yes] >
```

milv1_param

This command executes the MIL-calculations in its first version (different border handling). You should usually not modify the default values. If the database is activated, the result of the calculations are written to the evaluation database.

```
ipl> milv1
-input          [default_name] > a
-ray_plane_scale [2.000000]>
-roi_radius_factor [1.000000]>
-t_dir_ortho     [no] >
-t_dir_ortho_nr   [8] >
-t_dir_radius     [2] >
-fabric_tensor    [yes] >
```

histo

Gives a histogram of an object. With the default arguments same effect as 'examine in histo'. Optionally, the histogram is shown from from_val to to_val, default from minimal value to maximal value found in input volume. Optionally, a tabulated version of the histogram is printed to a file (given with fileout_or_screentab) or the screen (fileout_or_screentab screen, in addition to the bar-column representation) with the number of bins given with nr_bins_in_tab. The number of bins in the bar-column representation is not affected by nr_bins_in_tab!

```
ipl> histo
-input [in] > rat
-fileout_or_screentab [none] > my_histo.tab
-from_val [-1] > 1500
-to_val [-1] > 3000
-nr_bins_in_tab [-1] >
```

scale_elsize

Using this command you can change the voxel size of your object. down_scale enlarges the voxel size (reduces the resolution), up_scale makes the voxel size finer. Non-integer scaling can either be given directly, e.g. with down_scale 1.5; or with a combination of down_scale 3 and up_scale 2. The effect is exactly the same, the latter may just save you a division by hand. The integrate flag controls whether averaging of voxels is done in down-scaling (and potential interpolation of partial voxels) and whether interpolation is done in up-scaling. It is suggested to use integrate true for gray-scale images, but integrate false for binary segmented images to preserve the binary status. Otherwise a subsequent thresholding operation may be needed to ensure a binary image again.

Scale_elsize automatically selects among the below described procedures ipscale_elsize and noipscale_elsize, according to whether there are fractional voxels who may then be interpolated ($\Rightarrow$ ip): For integer down-scalings noipscale is chosen, for non-integer down-scalings and any up-scalings ipscale is chosen. The exception is non-averaging scaling of binary objects always with noipscale to maintain the binary status, if the integrate flag is put on false. If a GOBJ mask is used for the evaluation of an object, the GOBJ mask has to be transformed into an AIM-mask with gobj_to_aim, and this AIM-mask can then be scaled to the same voxel size as the original object. Use integrate false for the mask scaling to preserve the binary status of the mask (alternatively, after masking with integrate true, perform a threshold operation to produce a binary mask again).

```
ipl> scale
-input [in] > a
-output [sca] > x
-down_scale [2.000 2.000 2.000] >
-up_scale [1.000 1.000 1.000] >
-integrate [true] >
```

ipscale_elsize

One constituent of `scale_elsize`. If the new voxel grid is not a integer multiple of the original voxel grid, then the new values lying between old voxels points are interpolated ($\Rightarrow$ ip), and depending on the `integrate` flag also averaged over the voxel volume. The `center` flag controls whether the center of the object is still in the center of the scaled object, or whether the upper left top corner is also the beginning of the scaled object (`center false`). The computation time and memory needed is larger than for `noipscale_elsize`.

```
ipl> ipscale_elsize
-input                [in] >a
-output              [sca] >b
-down_scale          [2.000 2.000 2.000] >1
-up_scale            [1.000 1.000 1.000] >2
-center              [false] >
-integrate            [true] >
```

noipscale_elsize

Scales the objects without interpolating non-integer voxel locations in the scaled object, but takes nearest neighbour approach. Computational faster and uses less memory, but nearest neighbour choice may create less accurate scaling. Does not account for fractional voxels for non-integer scaling, even if `average` flag is true, e.g. for `down_scale` 2.6 and `average true`, only 2 voxels are averaged (per direction).

```
ipl> noipscale
-input                [in] > a
-output              [sca] x
-down_scale          [2.000 2.000 2.000] >
-up_scale            [1.000 1.000 1.000] >
-average              [true] >
```

scale_ow_elsize_noip

Same as `noipscale_elsize`, but overwrites input. Saves memory. Does not work for increasing resolution, since output memory would have to be bigger than input memory.

```
ipl> noipscale
-input_output         [in] > a
-down_scale          [2.000 2.000 2.000] >
-up_scale            [1.000 1.000 1.000] >
-average              [true] >
```

set_value

With this command you can set the value of all non-zero voxels of a segmented object to a given value and all zero voxels to another. Useful for inverting foreground/background of the object and for producing a negative image (`value_object -127`).

```
ipl> set_val
-input                [in] >
-value_object         [127] >
-value_background     [0] >
```

concat

Concatenates two objects. `Common_region_only`: if two objects with unequal dimensions or unequal positions are chosen, this flag controls whether the region common to both objects is taken; or whether the box region surrounding both objects is produced. `Add_not_over` lay: Controls whether voxel values of second object are added to the first object - with overflow taken care of, i.e. $60+90=127+50=127$ for *char* images; or whether non-zero values are laid over the first object, useful for mapping the segmented image onto the original

gray-scale data. Make_edge: controls whether edges are made of second object (or first, if second is gray scale and first is char). The second object can be shifted with shift_ofin2 and turned in the x-y plane with turnangle. Turnpoint_global is tried to be set to the original rotation center of the scanner, i.e. for 512x512 images to 256,256 etc. The turned image2 is mapped into the same box as image2, thus for larger angles the image may be cut at the boundary if there is not enough free space left around the object to contain the turned image2. Subtraction of two binary images can be performed by a combination of /set_value of input2 to -127 and then concat it with input1, flag add true.

```
ipl> concat
-input1          [in] > a
-input2          [in1] > b
-output         [out] > c
-common_region_only [true] >
-add_not_overlay [true] >
-make_edge       [false] >
-shift_ofin2     [0 0 0] >
-turnangle       [0.000000] >
-turnpoint_global [-1-1] >
```

join_uncompress

This operation joins two segmented volumes directly while reading and uncompressing from the disk, thus only needs the memory of the output volume once. It may be useful if concat does not work because of too small virtual memory. The compressed files are read from disk and the uncompressing is done directly into the correct memory location in the output. The volumes may be overlapping, but then the respective part of file2 is overwritten (including zeros) onto file1.



Notice

Join_uncompress only works for compressed files on disk and only works for volumes with the same dimensions in x and y direction!

```
ipl> /join
-file1          [file1] > rat_seg_part1.aim
-file2          [file2] > rat_seg_part2.aim
-output         [out] >
-shift_ofin2_z   [0] >
```

bounding_box_cut

This operation determines the smallest box around the object of non-zero voxels. An additional boundary can be chosen with border. z_only controls if only the bounding box in z direction is determined and cut out with a given border.

```
ipl> /bounding_box_cut
-input1          [in] >
-output         [out] >
-z_only         [false] >
-border         [0 0 0] >
```

flip_aim

Flips an object to a side, i.e. x, y and z direction are switched according to new_xydir (NB: it is not necessarily a proper rotation of the object in 3D space!). The new x direction is the first letter given in new_xydir, the new y direction is the second letter, the new z direction is the remaining direction.

```
iplt> flip_aim
-input          [in] > a
-output         [out] > f
-new_xydir      [yz] > xz
```

offset_add

Changes the offset around the object. The offset is the same for the beginning and the end for one direction (voxels run from +off.x to dim.xoff. x), but may be different for the different directions x, y and z. The offset is then disregarded in subsequent image processing or statistical examinations.

```
iplt> offset_add
-input          [in] > a
-add_offset     [0 0 0] > 0 0 4
```

offset_set

Changes the offset around the object, independent of what it was before.

```
iplt> offset_set
-input          [in] > b
-new_offset     [0 0 0] > 2 2 1
```

clear_offset

Sets all voxels in the (optionally new) offset to zero.

```
iplt> clear_offset
-input          [in] > b
-new_offset     [-1-1-1] > 2 2 1
```

fill_offset_mirror

Fills the offset of an object with the mirrored values just to the inside of the offset. May be used after operations that 'steal' from the image, e.g. gauss-filter. Be aware that voxel information is just duplicated and that values calculated afterwards can be biased.

```
iplt> fill_offset_mirror
-input          [in] > in
```

convert_to_type

This converts objects from one input type to another, e.g. a 'char' image to a 'short' image. The output type is given by out_type.

```
iplt> convert_to_type
-input          [in] >
-output         [out] >
-out_type       [short] >
```

xray

Produces a virtual (linear) X-ray image of the object along the z-axis (flip the object with 'flip_aim' first for other desired orientations). The output is a 'char' image. The voxel values (for every x and y) are added along the z-axis from startslice for number_of_slices, and the sum is either normalized with the largest occurring voxelsum (fixed_norm_char false) or to a fixed norm for binary input volumes (fixed_norm_char true).

```
ipl> xray
-input                [in] >
-output              [out] >
-startslice          [0] >
-number_of_slices    [16] >
-fixed_norm_char     [true] >
```

msq_from_aim

Write an object in memory to disk in the .MSQ format, e.g. to view it with the 3D-Display program.

```
ipl> msq
-aim_name             [out] >
-msq_filename         [default_file_name] >
```

from_aim_to_isq

Write an object in memory to disk in the .ISQ format, e.g. to produce a GOBJ with the Evaluation program again. The object will be at its original (global) position.

```
ipl> from_aim_to_isq
-aim_name             [out] >
-isq_filename         [default_file_name] >
```

For an extensive discussion of the obtained structural indices see Appendix see "Explanation of Structural Indices" p. 81.

UCT_THREEDEE_BATCH

Use this program to recreate a 3D-result-sheet including the 3D-image and the histomorphometry-values calculated by IPL.

Filename

Enter the correct filename of the sample/measurement you want. It **MUST** have a filename of *_**SEG.AIM**. The file is usually located in the following directory: DK0:[MICROCT.DATA.ssssssss.mmmmmmm], where s is the 8-digit sample number and m is the 8-digit measurement number.

PrintFilename

You can enter any valid filename for the intermediate storage of the resulting PostScript-File. We recommend a filename like SYS\$SCRATCH:filename.PS.

Ambient

This value corresponds to the scaler of Ambient Light in the interactive 3D-Display-Program. The value can be from 0 to 100%, here to be entered as a value between 0.0 and 1.0.

Shading

A value of 1 will lead to shadows, a value of 0 not.

Size

This value determines the quality of the 3D-image but also affects the calculation time.

Elevation/Rotation

These two numbers define the position of the observer relative to the object in degrees.

Copies

Enter a value between 0 and 9, and the corresponding number of copies will be printed. At the end of printing, the result file (printfilename) will be deleted. If you enter a value of 0, the file will neither be printed nor be deleted afterwards, but is kept on the hard-disk. This option can be used to print it on a different printer later.

UCT_LIST

Once you have measured many biopsies, you might want to have all your results in table form to include them into a spreadsheet program.

You can delimit the range of your samples being listed by entering the measurement number range.

```
$> uct_list
Template-File [UCT_3D_LIST_SHEET]:
Output-File [SYS$SCRATCH:UCT_EVAL.TXT]:
From Meas. # [0]:300
To Meas. # [0]:400
```

The resulting data is written to the file given in Output-File. The template file input- field can be used for different types of report. You can modify the files using a text editor. If you start the program by entering a measurement number as parameter, you will get the information of that specific measurement on the screen:

```
$ uct_list 43
Processing measurement 43
Measurement-Nr      :43
Measurement-Date    :15AUG1994 09:01
Filename            :C0000007
Sample-Name         :Koller Bruno
Sample-Nr           :1
Date of Birth       :06-SEP-1994
MIL
-----
-BV                  : 1.7211
TV                   : 5.0782
BS                   : 35.4409
BV/TV                : 0.3389
BS/BV                : 20.5926
Tb.Th               : 0.0971
...
```

WRITE_INFO

Once you have measured many biopsies, you might want to have all information about filenames, archiving data (directories, tape labels etc.) in table form. You can delimit the range of your samples being listed by entering the sample numbers and/or the sample names.

```
$> write_info
```

```
Sample Index from [ 0]: 13
```

```
Sample Index to [ 0]: 64
```

```
Sample Name from [           ]: S
```

```
Sample Name to [           ]: T
```

The logical UCT_DB_INFO usually points to the resultant text file which is usually in sys\$scratch.

11 Error Messages

The most common error messages (caused by insufficient or incorrect information for a measurement) are self-explaining.

Unforeseen system error messages are explained in the alphabetic list below. All error messages must be acknowledged with MBI. If the error is only a "WARNING", you can continue working. If the error is "FATAL" however, the program will then be terminated, as a continuation is impossible (can also occur by "ERROR").

Italic text shows what you can do yourself against the error. If there is no *italic text* after the error message, contact SCANCO Medical.

Creating directory

Write error on the hard disk.

Creating operator logical

Operating personnel cannot be registered. *Try starting the program again.*

Decoding Measurement Nr.

Measurement number invalid.

Decoding Sample or Patient Nr.

Sample or Patient number invalid.

Decoding Site

Measurement site invalid.

Decoding Slice Number

Image number invalid.

Deleting indexed Record

An entry in the database cannot be deleted.

Disk must have a name

Diskette was not initialized (formatted). *Initialize the diskette.*

Encoding Slice Number

Image number invalid.

End of file. No more records available

There are no further entries to be read in the database, as you have reached the end.

File Read Error

A tomogram cannot be read. *Usually appears only when a measurement was interrupted or if the images belonging to a measurement have been deleted.*

Freeing logical unit number ...

General database error.

Getting Binary Time

The time cannot be determined.

Getting current date/time

The time cannot be determined.

Getting free logical unit number

General database error.

Getting number of free blocks

Free space on a storage device cannot be determined

Getting volume name

The label of a storage device cannot be determined.

Keyword not found

An entry in the database cannot be found, for example, when looking for a sample or patient who has not yet been registered, or whose name has been spelt incorrectly.

Name contains a wrong character

Names of data media can only use the letters A - Z or the numbers 0 - 9, but no spaces or special characters.

No Controlfile selected

You have not yet selected a controlfile (Measurement site and cast)

No Sample- or Patientname

You have not yet entered a sample's or patient's name

No Sample- Patientnumber

You have not yet selected a sample or patient

No images available

The pictures for the measurements cannot be read. Have you selected a valid measurement? Have you possibly deleted its images?

No logical unit number free

General database error.

No operator selected

For measurement and evaluation, the field OPERATOR must be filled in with a valid name. Check in the *sample* or *patient* registration program whether the operator has been accidentally entered as a patient or as a physician (operator must be a member of the staff).

No scout-scans performed

Number of slices = 0 is not allowed

Not enough disk space left

Hard disk is full. *First delete or archive other measurements.*

Not enough space on disk

Optical disk is full. *Use new optical disk.*

Not more than 15 characters

The label of a diskette or an optical disk may not be longer than 15 characters. In addition, no special characters or spaces may be used.

Opening database file

General database error.

Opening filename

General database error.

Opening scanner datafile

Scanner calibration data cannot be opened.

Opening slicename file

Slicename-file cannot be opened.

Reading Slice Number

General database error.

Reading filename

General database error.

Reading indexed record

An entry in the database is not found, for example when looking for a sample or patient who has not been entered or has been spelt incorrectly.

UM:FULL_BACKUP.COM

General error by weekly backup.

Selected operator is not an operator

You have attempted to enter an invalid person as the operator (for example a patient or doctor). If this is not the case, check with the sample or patient recording program whether the STAFF button is pressed.

Unable to translate logical

General program error

Unknown error

Error for unknown reason

Unlocking indexed record

General database error.

Updating indexed record

General database error.

Error Messages 83

Writing Slice Number

General database error.

Writing data

General database error.

Writing filename

General database error.

Writing indexed record

General database error.

Wrong Volume (label)

Wrong diskette or optical disk has been loaded.

copying files

General database error.

deleting filename

General database error.

dismounting device

Error while dismounting a diskette or optical disk. *End the program and start again from new. Possibly check with the archiving program whether the storage device is still "mounted". Normally, both optical disks and diskettes are "dismounted".*

freeing context of lib\$find_file

General database error.

get device information

The specifications of a storage device could not be determined

getting free lun0

General database error.

initializing device (label)

Diskette or optical disk could not be initialized. *Check whether the "Write-Protect" switch is correctly set. Diskettes must be of the HIGH DENSITY (HD) format, DD or ED diskettes are not allowed.*

mounting device (label)

Diskette or optical disk could not be "mounted". *Check with the archiving program. (see dismount)*

PC formatted diskettes are not readable on your computer without formatting.

opening file

General database error.

reading Scanner data

General database error.

starting init command

Initialization / formatting error.

writing scanner data

General database error.

Appendix A: Additional Information

Mouse Operation

MB1 means left mouse button. MB2 is the middle mouse button. Usually, all actions are performed using MB1, except for scaling a ROI or VOI in the evaluation program.

Elements of the Graphical User Interface

Window / Dialog Box

All windows have a frame. The active window (in which your switch commands are carried out) has a dark frame, and the inactive windows have light frames.

You can move the windows around the screen by clicking on the top bar using MB1 and dragging it to the desired position. To iconize a window, click on the small rectangle on the top right. To restore the window from the icon, double click on the icon using MB1.

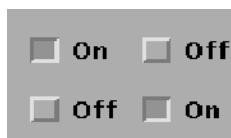
All error messages must first be acknowledged with OK or CANCEL before you can make other entries.

This is also the case with most of the other input windows (for example, finding a patient, Scout-View, measurements, etc.).



Push-Button

Click with MB1 on the button. The function which describes the button will be carried out.



Toggle-Button

Selection: The button can either be pressed or not. (with MB1)



Radio-Button

Selection: Only one button can be pressed (with MB1)



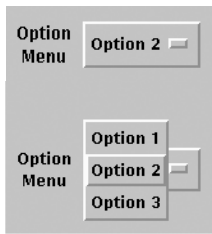
Text-Field

Click on the field with MB1 and then enter the text.



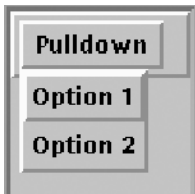
Scroll-Bar

Click on the bar in the middle with MB1. Hold MB1 pressed and move the mouse. The field next to the scroll bar moves. The length of the scroll-bar corresponds to the whole field, the length of the bar corresponds to the displayed area.



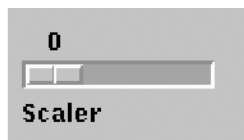
Option-Menu

Selection: Click on the menu with MB1 and all the possibilities then appear. You can now make your choice with MB1.



Pull-down-Menu

Selection: Click on the menu with MB1 and all the possibilities appear. You can now make your choice with MB1.



Scaler

Click on the scaler with MB1. Hold the key pressed and move the mouse. The input values change. If the scaler is surrounded by a rectangle click on it to make it active) you also can use the LEFT and RIGHT ARROW keys to change the value. By using CTRL/ARROW, you can change the values in larger steps.

General Information Regarding CT Measurements

Using the MicroCT you can determine 2- and 3-dimensional histomorphometric bone parameters based on the principle of computed tomography.

In this process, many slices (images, tomograms) are taken for every measurement, from which the individual bone parameters are calculated.

The individual slice thicknesses is between 6 and 36 μm . The scan diameter can be chosen, and the distance between the different slices should always be selected close to the resulting pixel size. This means, that if you choose a diameter of 10.5 mm, the slice distance should be 10 μm (10500 μm /1024). To obtain accurate histomorphometric values, you should obtain more than 100 to 150 slices.



Caution

The machine works with X-rays. You should therefore be careful. Although the X-ray tube is shielded in all directions, the machine may only be operated by personnel with a special training. While the door is opened or while the machine is not measuring (either scout or scan), the tube is put to stand-by mode, thus removing/inserting samples is safe.

Positioning of the sample

Put the sample into the sample holder. Choose the sample holder with the smallest diameter that fits. You have to fix the sample in a way that it does not move (rotate in the sample holder) while it is being measured. To achieve this, use e.g. rubber foam to fix it. If you want to compare the parameters regarding isotropy, you should carefully position the biopsies into the sample holder. Rotate the biopsies so a specific marker or part of the biopsy is aligned to the groove of the sample holder. Also make sure that the sample holder is always put in the same way, e.g. always with the groove to the left side.

Scout-View

Measurement Area

For the Scout-View, the program will propose the length of the overview image.

The start position is on the top of the sample holder, while the end position is at the bottom. The inputs are in mm from 0 to 80, corresponding to the measurement area of the scanner of 80 mm. (After starting the measurement program, the scanner is in the uppermost position so you can exchange the sample holders)

If the sample has been measured before, the Scout-View of the first measurement will be displayed on the screen. You can now limit the area on both sides, which will improve the measurement quality of the Scout (Improved resolution in longitudinal direction).

Radiation Display



Radiation display: If the yellow lamp is illuminated, X-ray radiation is present in the measurement area (scanner opening).

Stop

You can interrupt both the Scout-View and the measurement of an individual slice by clicking on the CANCEL button.

Input / Change of the Header and Footer of the Print-Out

On the result sheets the name of the physician or hospital appears at the top and bottom of the sheet.

You may have either the default output sheets or customized ones.

If you have the standard sheets, you can change the header and footer. Choose the operator registration program and find the **number 1**.

At the top of the sheet appear the fields **Name** and **Address 1**, at the bottom of the sheet the fields **Address 2**, **Zip-Code** and **City**.

Appendix B: Files used by MicroCT

Directory Structure

The directory structure is as follows:

```
MICROCT|--DATA----|--00000001--|--00000048
      |      |      |      |--00000049
      |      |      |      |--00000050
      |      |      |      |--00000051
      |      |      |
      |      |      |--00000005--|--00000065
      |      |      |--00000066
      |      |      |--00000067
      |      |
      |      |--00000007--|--00000129
      |      |--00000130
      |
      |--SCOUTS
      |
      |--DATABASE
      |--MAIN
      |--RESULTS
      |--SCRATCH
      |--TIPS
      |--UIL
      |--UTIL
      |--XDEFAULTS
```

The directories [MICROCT.DATA...] reside on DISK2, all other directories are located on DISK1.

(MICROCT)

- LOGIN.COM User definitions
- MICROCTXXXX.COM MicroCT definitions
- MICROCT_DATABASE.COM Database logicals

(MICROCT.DATA.SSSSSSSS.MMMMMMMMMM)

Main measurement directory, where SSSSSSSS (8 digits) is the sample number and MMMMMMMM (8 digits) is a consecutive measurement number (unique for one database).

In these directories, the following files can be found:

Cxxxxxxx.RSQ Raw Data (Sinogram sequence)

Cxxxxxxx.ISQ Image Data (Slice sequence)

Cxxxxxxx.AIM VOI of Image data

Cxxxxxxx_SEG.AIM Binarized VOI

Cxxxxxxx.MSQ Animated 3D-Sequence (not always present)

where xxxxxxx is a consecutive 7-digit number (unique number for scanner)

(MICROCT.DATA.SCOOTS)

ssssssssccc.SCV compressed Scout-Views

where ssssssss is the 8-digit sample number and ccc is the 3-digit controlfile number.

(MICROCT.DATABASE)

UCT_CONTROLFILES_nnn.DAT	Controlfile-DB
UCT_EVALUATIONS_nnn.DAT	Evaluation-DB
UCT_MEASUREMENTS_nnn.DAT	Measurement-DB
UCT_OPERATORS_nnn.DAT	Operator-DB
UCT_SAMPLES_nnn.DAT	Sample-DB
UCT_SCANNER_xxxx.DAT	Scanner calibration
UCT_SLICENAME_xxxx.DAT	Slicenumber
UCT_ZIP_CODES_nnn.DAT	Zip-Codes (operator)

where nnn is the name of the customer and xxxx is the scanner SN.

(MICROCT.MAIN)

contains all programs and command-procedures needed for operating the system.

(MICROCT.RESULTS)

Contains the summary-files of 2D-Histomorphometric evaluations. The file names are HISTO_2D_xxx.DAT, where xxx is the measurement number.

(MICROCT.SCRATCH)

All temporary files for evaluation and printing are stored to this directory. Content can be deleted at any time.

(MICROCT.TIPS)

Sample documents describing OpenVMS-tasks as well as actions to perform interactive segmentation etc.

(MICROCT.UIL)

User Interface Description Directory. Files define the look of the programs. If available, subdirectories for different language variants. The template files for printing (*.PS) also are located in this directory.

(MICROCT.UTIL)

This directory contains Utility-Programs mainly used by Service Personnel.

(MICROCT.XDEFAULTS)

Directory containing settings for X-Windows-Environment.

Appendix C: Logicals and Symbols

Definition of Logicals and Symbols

The logicals and symbols used by MICROCT are defined in the following files:

- SYS\$STARTUP:SCANCO_SYLOGICALS.COM (Systemwide)
- DISK1:[MICROCT]LOGIN.COM (Process/Job)
- DISK1:[MICROCT]MICROCTXXXX.COM (Process/Job)
- DISK1:[MICROCT]MICROCT_DATABASE.COM (Process/Job)
- DISK1:[MICROCT]MICROCT_RECON.COM (Process/Job)

Logicals

Logical	Meaning	Default Value	Type
MICROCT_SCSI	SCSI-Controller	DKB100	S
UCT_ACQ_LINE	SCSI-Controller	MICROCT_SCSI	P
DISK0	System-Disk	DKA0	S
DISK1	User-Disk	DKA0	S
DISK2	Data-Disk	DKA100	S
DK0	Data-Disk	DKA100	P
MO0	Magneto-optical drive	WDB200	S
FD0	Floppy-Drive	DVA0	S
TP0	Streamer Tape	MKC500	S
SYS\$LOGIN	Login Directory	DISK1: [MICROCT]	P
SYS\$SCRATCH	Scratch Directory	DISK1: [MICROCT.SCRATCH]	P
UM/SCM	Directory for Programs	DISK1: [MICROCT.MAIN]	P
UU/SCU	Directory for Interface and Printing-	DISK1: [MICROCT.UIL]	J
UCTD/SCD	Directory for Database-Files	DISK1: [MICROCT.DATABASE]	P
UCT_MEASUREMENT_DATA	Measurement Main Directory	DK0: [MICROCT.DATA.]	P
SCANCO_SCOUT_DATA	Scout-View-Directory	DISK1: [MICROCT.DATA.SCOUTS]	P
UCT_HISTO_RESULTS	Directory for 2D_Hist. Results	DISK1: [MICROCT.RESULTS]	P
UCT_BATCH_MEASUREMENT	Batch-Measurement-Script	UM: UCT_BATCH_MEASUREMENT.COM	P
UCT_MEASUREMENT_QUEUE	Measurement Batch Queue	SYS\$BATCH	P
UCT_RECONSTRUCTION	Slice Reconstruction Image	UM: FAN_RECONSTRUCTION.EXE	P
UCT_RECONSTRUCTION_QUEUE	Reconstruction Batch Queue	SYS\$SLOW	P
UCT_RECONSTRUCTION_FILE	Reconstruction Command Proce-	UM: UCT_RECONSTRUCTION.COM	P
UCT_RECONSTRUCTION_SCALING	Reconstruction scaling factor	4096	P
UCT_BEAMHARD_FACTOR	Beamhardening Correction	system dependent	P
UCT_BEAMHARD_POWER	Beamhardening Correction	system dependent	P
UCT_EVALUATION	3D-Evaluation Batch-Template	UM: UCT_EVALUATION_V4.COM	P
UCT_RAY_VOLUME_SIZE	Min. Volume-Size in MB for linear	500000000 (=500 MB)	P
SCANCO_DEF_PRINTER	Default Printer Queue	DL3500_PS	P
SCANCO_BW_PRINTER	B/W Printer Queue	DL3500_PS	P
SCANCO_COL_PRINTER	Color Printer Queue	TEK_PS	P
SCANCO_PS_PRINTER	PostScript-Printer Queue	SCANCO_DEF_PRINTER	P
UCT_EVALUATION_SHEET	Template for 3D-Histomorph. Eval-	UU: UCT_EVALUATION_EN.PS	P
UCT_HISTO_2D_SHEET	Template for 2D-Histomorph. Eval-	UU: UCT_HISTO_2D_EN.PS	P
UCT_RAY_SHEET	Template for Ray-Tracing	UU: UCT_RAY_EN.PS	P
UCT_SINGLE_IMAGE_SHEET	Template for Main-Image	UU: UCT_SINGLE_IMAGE_EN.PS	P
UCT_ONE_IMAGE_SHEET	Template for image printing (1)	UU: UCT_ONE_IMAGE_EN.PS	P
UCT_FOUR_IMAGES_SHEET	Template for image printing (4)	UU: UCT_FOUR_IMAGES_EN.PS	P
UCT_SIXTEEN_IMAGES_SHEET	Template for image printing (16)	UU: UCT_SIXTEEN_IMAGES_EN.PS	P
UCT_3D_LIST_SHEET	Template for Listing of 3D-param-	UU: UCT_3D_LIST.TXT	P
UCT_3D_SINGLE_SHEET	Template for Display of 3D-param-	UU: UCT_3D_SINGLE.TXT	P
UCT_CONTROLFILES_DATABASE	Controlfiles-DB	UCTD: UCT_CONTROLFILES_cust.DAT	P
UCT_MEASUREMENT_DATABASE	Measurement-DB	UCTD: UCT_MEASUREMENTS_cust.DAT	P
UCT_EVALUATION_DATABASE	3D-Evaluation-DB	UCTD: UCT_EVALUATIONS_cust.DAT	P
UCT_SAMPLE_DATABASE	Samples-DB	UCTD: UCT_SAMPLES_cust.DAT	P
UCT_SCANNER_DATA	Scanner Calibration Data	UCTD: UCT_SCANNER_xxxx.DAT	P
UCT_SLICE_NAME_FILE	Current Slice number	UCTD: UCT_SLICENAME_xxxx.DAT	P
SCANCO_PATIENT_DATABASE	OperatorDB	UCTD: UCT_OPERATORS_cust.DAT	P
SCANCO_ZIP_CODE_DATABASE	Zip-Codes-DB (operators)	UCTD: UCT_ZIP_CODES_cust.DAT	P
UCT_DB_RESULTS	Result-File of DB 3D-histo-query	SYS\$SCRATCH: RESULTS.TXT	P
UCT_DB_INFO	Result-File of DB Infor-query	SYS\$SCRATCH: INFO.TXT	P
UCT_BACKUP_COMMANDFILE	Command-Procedure for offline	SYS\$SCRATCH: ARCHIVE.COM	P

Symbols

Symbol	Meaning	Default Value
ANIMATION	Command for calculating an Animation	\$UM:ANIMATION.COM
UCT	Foreign command for Main Program	\$UM:UCT_MAIN.EXE
UCT_BACKUP	Foreign command for Backup Program	\$UM:UCT_B.EXE
UCT_EVALUATION	Foreign command for 3D-Evaluation Program	\$UM:UCT_K.EXE
UCT_LIST	Foreign command for DB-QueryProgram	\$UM:UCT_LIST.EXE
UCT_MEASUREMENT	Foreign command for Measurement Program	@UM:UCT_MEASUREMENT.COM
UCT_MOVIE	Foreign command for AnimationProgram	\$UM:UCT_MOVIE.EXE
UCT_SAMPLE	Foreign command for Sample Edit Program	\$UM:UCT_A.EXE
UCT_THREEDEE	Foreign command for Interactive 3D-Display	\$UM:UCT_RAY.EXE
UCT_THREEDEE_BATCH	Foreign command for Batch 3D-Display	\$UM:UCT_RAY_BATCH.EXE
UCT_UTILITIES	Foreign command for Tools Program	\$UM:UCT_M.EXE
IPL	Foreign command for Segmentation Program	\$UM:IPL_SCANCO_M.EXE /INTER
SCANCO_ADDRESS	Foreign command for Operator Edit Program	\$SCM:A.EXE
SCANCO_DECWRITE	Foreign command for Word Processor	\$DECWRITE
SCANCO_SUBMIT_COMMAND	How to submit batch jobs	SUBMIT/NOPRINT/QUE=SYS\$FAST / LOG=SYS\$SCRATCH
SCANCO_UTILITIES	Foreign command for Tools Program	\$SCM:U.EXE
SCANCO_ANSI_PRINT_COMMAND	How to print text files	PRINT/QUE=DL3500/DELETE
SCANCO_PS_PRINT_COMMAND	How to print PostScript files	PRINT/QUE=SCANCO_PS_PRINTER/DELETE
WRITE_INFO	Create Informational Report	\$UM:UCT_WRITE_INFO.EXE

Appendix D: 3D-Batch Evaluation

Batch Procedure

As soon as you click START EVALUATION... in the Evaluation Program, the command procedure UCT_EVALUATION (logical name, see above for current file specification) is submitted using the symbol SCANCO_SUBMIT_COMMAND.

This command procedure writes another command procedure to SYS\$SCRATCH: with the following name:

image_sequence_name.COM

e.g. SYS\$SCRATCH:C0000123.COM. You can modify UCT_EVALUATION, but be sure to keep an original version of this file.

Checking Status and Progress of batch jobs

To check whether batch jobs are running, enter one of the following commands:

1. \$ SHOW ENTRY
2. \$ SHOW ENTRY/FULL
3. \$ SHOW SYSTEM/BATCH

To check the progress or status of a batch job, you have to take a look at the batch log file SYS\$SCRATCH:UCT_EVALUATION_V4.LOG. Use the following command:

\$ TYPE/PAGE SYS\$SCRATCH:UCT_EVALUATION_V4.LOG

You also can omit the /PAGE qualifier and use F1 (toggle for Hold Screen) to check the file.

Modifying UCT_EVALUATION



Caution

Do not try to modify this command procedure until you know how to edit a file on OpenVMS! Check Documentation, ask your system manager or call SCANCO Medical!

Content

The content of the original UCT_EVALUATION is as follows:

```

$      FILENAME = F$PARSE("P2'",,,"NAME") ..... a
$      DEV = F$PARSE("P2'",,,"DEVICE")
$      DIR = F$PARSE("P2'",,,"DIRECTORY")
$      COMMANDFILE := SYS$SCRATCH:'FILENAME'.COM ..... b
$      PRINTFILE := SYS$SCRATCH:'FILENAME'.EPS
$      AIMFILE := 'DEV'DIR'FILENAME'.AIM
$      SEGFILE := 'DEV'DIR'FILENAME'_SEG.AIM
$!
$      SHOW SYMBOL COMMANDFILE
$      SHOW SYMBOL PRINTFILE
$      SHOW SYMBOL AIMFILE
$      SHOW SYMBOL SEGFILE
$!
$      OPEN/WRITE OUTFILE 'COMMANDFILE'
$      COMMANDFILE = F$SEARCH("COMMANDFILE") ! GET VERSION NR
$!
$!      First create AIM-File
$!
$      WRITE OUTFILE "$ RUN UM:ISQ_TO_AIM.EXE" ..... c
$      WRITE OUTFILE "P2'"
$      WRITE OUTFILE "P3'"
$      WRITE OUTFILE "P4'"
$      WRITE OUTFILE "P5'"
$      WRITE OUTFILE "P6'"
$      WRITE OUTFILE "P7'"
$      WRITE OUTFILE "P8'"
$!
$!      Histomorphometric Evaluation
$!
$      WRITE OUTFILE "$@UM:IPL_FIXED_BATCH_V4.COM ''AIMFILE' ''SEGFILE'" ... d
$!
$!      Now create 3D-Image
$!
$      WRITE OUTFILE "$ RUN UM:UCT_RAY_BATCH.EXE" ..... e
$      WRITE OUTFILE "SEGFILE'"
$      WRITE OUTFILE "PRINTFILE'"
$      WRITE OUTFILE "0.2" ..... f
$      WRITE OUTFILE "1" ..... g
$      WRITE OUTFILE "1024" ..... h
$      WRITE OUTFILE "30" ..... i
$      WRITE OUTFILE "35" ..... j
$      WRITE OUTFILE "P1'" ..... k
$!
$      CLOSE OUTFILE
$!
$      @'COMMANDFILE'
$      DELETE/NOLOG/NOCONFIRM 'COMMANDFILE'
$      EXIT

```

- a. FILENAME is the name of the Image Sequence, e.g. C0000125
- b. COMMANDFILE is executed in the Batch-Job, contains all steps leading to the final result sheet
- c. Program which extracts VOI out of ImageSequence
- d. Command procedure which calls the segmentation of the VOI and calculation of the histomorphometric parameters. Usually this file is called IPL_FIXED_BATCH_V4.COM for fixed threshold.
- e. Program which calculates 3D-Display and prints result sheet
- f. Parameter for 3D-Display (% of Ambient Light [0.0..1.0])
- g. Parameter for 3D-Display (0 = no shades, 1 = shades)
- h. Parameter for 3D-Display (Resolution [1..1024])
- i. Parameter for 3D-Display (Elevation [-90..+ 90])
- j. Parameter for 3D-Display (number of copies, P1 of UCT_EVALUATION)
- k. Parameter for 3D-Display (Rotation [-180..180])

Modifying IPL_FIXED_BATCH_V4.COM

To customize the evaluation to your needs (human/rat etc.), edit the file which is called from UCT_EVALUATION (see footnote 4 on p. 78) and change only the indicated parameters



Caution

Do not try to modify this command procedure until you know how to edit a file on OpenVMS!

Check Documentation, ask your system manager or call SCANCO Medical AG!



Caution

The two dots (..) in the last IPL line are very important. DO NOT DELETE OR FORGET THEM! At the IPL startup in 'batch mode', the whole string is read up to the two dots, and then commands in the string are executed one by one.

Content

The content of IPL_FIXED_BATCH_V4.COM is as follows:

```
$! IPL Batch Scanco
$
$ sigma_gauss      := 0.8 ..... a
$ support_gauss    := 1 ..... b
$ threshold_seg    := 145 ..... c
$ peel_iter_gobj   := 0
$!
$! Segmentation with gauss filter and thresholding.
$!
$ define org_file 'p1'
$ define gobj_file 'p2'
$ define seg_file 'p3'
$
$ thick_histo = "'p1'" - F$PARSE(P1,,, "VERSION") - ".AIM" + "_TH.TXT"
$ separ_histo = "'p1'" - F$PARSE(P1,,, "VERSION") - ".AIM" + "_SP.TXT"
$ inv_n_histo = "'p1'" - F$PARSE(P1,,, "VERSION") - ".AIM" + "_1-OVER-N.TXT"
$!
$ ipl_scanco_prog := $um:ipl_scanco_m.exe
$!
$ ON ERROR THEN EXIT
$ ipl_scanco_prog

/db_scanco_activate true
/read org org_file
/sup org
  -supdim_numbers      4 4 1
  -testoff_pixels      "support_gauss
  -suppos_pixels_local -1 -1 -1
  -subdim_pixels       -1 -1 -1

/seg_gauss org seg
  -sigma      "sigma_gauss
  -support    "support_gauss
  -low        "threshold_seg
  -upp        1000 ..... d
  -value      127

/gobj
  -input_output      seg
  -gobj_filename     gobj_file
  -peel_iter         "peel_iter_gobj

/write seg seg_file
  -compress bin

/etc
/etc
.. (ATTENTION! The two dots (..) in the last IPL line are very important!) ..... e
$ exit
```

- a. This parameter describes the sigma (width) of the Gaussian low-pass filtering, in units of pixels.
- b. This parameter describes the support on each side of the Gauss filter, i.e. total support is $2 \times \text{support} + 1$ for each dimension. Usually, choose support to be the next biggest integer of sigma.
- c. This parameter describes the lower threshold level in percent x 10 (e.g. 275 means 27.5%)
- d. This parameter describes the upper threshold level in percent x 10 (e.g. 1000 means 100.0%). Usually you do not have to modify this value.
- e. ATTENTION! The two dots (..) in the last IPL line are very important. DO NOT DELETE OR FORGET THEM! At the IPL startup in 'batch mode', the whole string is read up to the two dots, and then commands in the string are executed one by one.

Appendix E: Explanation of Structural Indices

MIL method

With the original MIL method, test lines are traced through the segmented volume and the intercepts are counted. The test-line length is then divided to give the mean intercept length. The MIL method as implemented in the IPL module works only for a sphere within the volume of interest. MIL is used to determine the surface to volume ratio (**BS/BV**), and then assuming a plate-model of bone, trabecular number **Tb.N**, thickness **Tb.Th** and separation **Tb.Sp** can be derived. The distribution of the MILs is taken to determine the principal directions of the MIL ellipsoid and the **Degree of Anisotropy**.

Further literature:

H.J.G. Gundersen, T.B. Jensen, R. Østerby. Distribution of membrane thickness determined by lineal analysis. *J Microsc* 1978;113:2743.

TRI method

TRI is used to triangulate the surface of the segmented object, and calculate the volume of the enclosed tetrahedrons and the surface of the triangles. It is a more direct way to get to the surface to volume ratio (BS/BV) than with the MIL method. Still assuming a plate-model of bone, **Tb.N**, **Tb.Th** and **Tb.Sp** can be calculated. To calculate the principal directions of the MIL ellipsoid and the Degree of Anisotropy, the area of the surface triangles are projected onto a directional surface distribution (skalar product of areaweighted normal vector with the directions of the direction distribution), which is the inverse of the directional MILs.

Artificial boundaries at the edge of cubic or conforming (GOBJ produced) volumes of interest are not counted in the calculation, i.e. boundary problems are taken care of.

Further literature:

T. Hildebrand, A. Laib, R. Müller, J. Dequecker, P. Rüeggsegger. Direct 3-D morphometric analysis of human cancellous bone: microstructural data from spine, femur, iliac crest and calcaneus. *J Bone Miner Res* 1999;14(7):1167-74.

Structure Model Index

With this index the structural appearance of trabecular bone is quantified. The triangulated surface is dilated in normal direction by an infinitesimal amount, and the new bone surface and volume is calculated. By this, the derivative of the bone surface (dBS/dr) can be determined. The SMI is then

$$SMI = 6 \bullet \frac{BV \bullet \frac{dBS}{dr}}{BS^2}$$

and relates the convexity of the structure to a model type. Ideal (flat) plates have an SMI of 0 (no surface change with dilation of the plates), whereas ideal cylindrical rods have an SMI of 3 (linear increase in surface with dilation of rods). Round spheres have an SMI of 4. Values below 0 can come from 'air bubbles' within the bone ($\Rightarrow$ concave structure gives negative dBS/dr).

Artificial boundaries at the edge of the volume of interest are not included in the calculation and thus suppressed

Further literature:

T. Hildebrand, P. Rüegsegger. Quantification of bone microarchitecture with the structure model index. *Comp Meth Biomech Biomed Eng* 1997;1:15-23.

Distance Transformation Methods

By distance transformation, the calculation of the metric distance of every bone (object) voxel to the nearest bone-air (background) surface is understood. These distances can be imagined as the radius of a sphere with centre in this voxel that fits inside the structure. Then redundant spheres are removed - 'big sphere eats small encompassed spheres'. The result is the mid axes transformed structure with the centres of maximal spheres filling the structure completely.

To calculate **Tb.Th***, each voxel then gets the value of the radius of the maximal sphere it sits in, and twice the mean value of all structure voxels then is the mean thickness.

To calculate **Tb.Sp***, the same procedure is performed for the background of the structure, i.e. object (bone) and background (air) are switched.

To calculate **Tb.N***, the spacing of the mid axes is calculated as for Tb.Sp*. Then the inverse of the mean spacing is Tb.N*.

Further literature:

T. Hildebrand, P. Rüegsegger. A new method for the model independent assessment of thickness in threedimensional images. *J Microsc* 1997;185:67-75.

T. Hildebrand, A. Laib, R. Müller, J. Dequecker, P. Rüegsegger. Direct 3-D morphometric analysis of human cancellous bone: microstructural data from spine, femur, iliac crest and calcaneus. *J Bone Miner Res* 1999;14(7):1167-74.

Connectivity Density

Connectivity density Conn.D. is calculated with the Conn-Euler method of Odgaard et al. Their boundary/edge problem suppression is applied on the surfaces of cubic AIMs, but not on the possibly artificial surface of contoured (GOBJ) determined volumes. Usually, conforming volume of interests are much larger than cubic ones, so the boundary problem has a much smaller effect. For measurements of intact bones, we propose to calculate the connectivity of the complete bone (incl. cortex), or to put an artificial cortex around the spongiosa again with the help of the GOBJ. (create mask.aim from GOBJ with /gobj_to_aim, concat with segmented object with /concat -input1 seg -input2 mask -output shelled_seg -common true -add true -make_edge **true**, /cl shelled_seg, then /gobj_maskaimpeel_ow shelled_seg again to calculate relative masked volume, then calculate connectivity with /conn_nocl shelled_seg).

Further literature:

A. Odgaard, H.J.G. Gundersen. Quantification of connectivity in cancellous bone, with special emphasis on 3-D reconstruction. *Bone* 1993;14:173-182.

Appendix F: Checklists

Checklist for Measurements

- Switch on Equipment (30 Minutes before first measurement)
- Start main program
- Enter sample's data
- Start measurement program
- Insert sample/sample holder
- Choose/Define/Modify measurement protocol (controlfile)
- Perform Scout-View
 - define Scout-View region
 - perform Scout-View measurement
 - if OK, set reference line
- Perform Measurement (batch or interactive mode)
- Remove sample

Checklist for Evaluation

- Switch on equipment (printer, optical disk and computer)
- Start the main program
- Select evaluation program
- Select sample and measurement
- Click on EVALUATION
- Click on DEFINE VOI
- Draw volume of interest
- Position VOI using MB1 (move) or MB2 (scale) or enter values directly with keyboard.
- Check Dimensions of VOI (should be equal)
- Rectangles indicate VOI for 3D-Display
- Circles indicate VOI for 3D-Histomorphometric Evaluation
- Click on START EVALUATION
- Exit program

Checklist for Shutdown

- Exit from the main program (click on EXIT button) (optional)
- End Session using Session Manager
- Enter "Shutdown" as Username, press RETURN twice
- Wait for the message SYSTEM SHUTDOWN COMPLETE -...
- Switch off equipment

Appendix G: Specifications

Operational conditions

Ambient conditions:	+20 to +25° C, 20%-80% humidity for operation +5 to +40° C, 20%-80% humidity for storage
Temperature variations:	maximum 5° C / h



Caution

Measurements outside these temperature ranges can cause inaccuracies!

Dust, smoke:	Operate the system in a clean environment. Accumulations of dust or other particles can damage sensitive parts. SCANCO Medical AG recommends a smoking prohibition in the area of the MicroCT.
Vibrations:	Vibrations can have negative influence on results. Place the instrument on a flat and stable surface free from vibrations.

Measurement Method

Measurement type:	Computed tomography, small-angle-cone-beam
Measurement area:	Ø max. 38 mm longitudinal max. -140 mm

Accuracy

Slice Thickness:	3.5 - 70 µm
Image-Matrix:	512 x 512, 1024 x 1024 or 2048 x 2048 pixels
Resolution:	3.5 - 70 µm nominal (pixel size)

Archiving

Tomograms:	to tape (Streamer)
------------	--------------------

Dimensions

Scanner:	830 x 1150 x 490 mm (HxWxD)
Computer:	750 x 580 x 390 mm (HxWxD), approximately value (depending on individual configuration)

Weights

Scanner:	approx. 203 kg
Computer:	25 kg, approximately value (depending on individual configuration)

Mains Connection MicroCT 35

100-230 V ~ (AC) / 50-60 Hz / 345 W 1.5 A
(230V)

Mains Fuses MicroCT 35

2 x T 6.3 A

Power requirement

MicroCT 35	345 W
Tape Drive	about 300 W
Monitor	about 300 W
Disk Tower	about 370 W / Supply (2 supplies possible)
HP Integrity Server rx2620	max. 1350 W

Hardware

Source:	X-Ray-Tube with a current of 0.1/0.18 mA and a peak energy of 50/60/70 kVp
Radiation Dose	Equipment is fully shielded, i.e. radiation in 5 cm distance of housing is less than 5 μ Sv/h.
Computer:	HP Integrity Server, 64bit rx2620 or rx4640 Memory 4 to 128GB TFT Color Monitor 300 GB to multiple TB internal 3½"-Harddisk 40/80 GB DLT, 160/320 GB SDLT or 300/600 GB SDLT II external Tape (Streamer)



Printers:	Network PostScript printer via TCP/IP (raw or lpd/lpr protocol)
-----------	---

8 Glossary

Artifact

Error in the exposure, caused by, for example, a sample holder being too large, movement of the sample during the measurement, malfunction of the equipment etc. Visible in the form of lines, light or dark areas or stripes in the image.

Backup

Safety copy of the databases and programs from internal hard disk to optical disk. It is recommended that a backup is made once a week.

CT

Abbreviation for Computed Tomography.

Diskette

See Floppy-Disk.

File

Collection of related data in a computer, for example, letters, a tomogram etc.

Floppy-Disk

Diskette. Removable storage device of low capacity, similar to a tape recorder cassette. All the data of one patient is stored on this, with the exception of the images. For every patient, one individual diskette will be used.

Harddisk

Fixed internal storage device of high capacity. Here are stored all the programs, all patient data, all Scoutviews and all images which have not been archived. Cannot be exchanged by the user!

LUT (Look-Up-Table)

Color scale, normally adjusted to the gray tone scale.

Optical Disk

Removable storage device with large capacity. The images are archived on this device. A separate optical disk is kept as a safety copy of the complete system. (see Backup)

ROI

Region Of Interest

Scanner

Measuring unit, in this case a tomograph.

Scout, Scout-View

Overview image, comparable to a radiograph.

Shutdown

Program for ending the operating system. Ensures that all data and programs in the computer can be read again without problem at the next operation.

VOI

Volume Of Interest

Zoom

Magnify

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