Cone Beam Reconstruction Software Package
COBRA Version 5

User Manual

Type of Document

Specifications
Operation Description
Work Instructions
S/W Version Documentation
Test Plan
Test Report
βsite Report
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References:

[1]: L.A. Feldkamp, L.C. Davis, and J.W. Kress, “Practical cone-beam algorithm”, *J.Opt.Soc.Amer.*, vol. A1, pp. 612-619, 1984.

[2]: D.L. Parker, “Optimal short scan convolution reconstruction for fan beam CT” *Med.Phys*. **9**, 254-257 (1982).

Table of Contents

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1 Introduction

1.1 Scope of this User's Manual

This document describes Exxim's *Cone Beam Reconstruction Software Package, COBRA Version 5*, from a user's point of view. The package includes a guide to:

- *Co*ne *B*eam *R*econstruction *A*pparatus (*COBRA)*
- Viewer (*COBRAViewer*)

The full version of COBRA additionally includes an **SDK (software development kit)** with:

- Programmer's Guide containing the complete information necessary for development of Windows® applications using COBRA's functionality. It explains how to arrange the reconstruction process in-line with ongoing data acquisition.
- Three C++ projects (*Microsoft Visual Studio Version 6* workspaces convertible to *C++.NET* solutions) with code examples.

1.2 COBRA Functionality – Overview

Exxim's COBRA software provides the following functionality:

1. Full 3-dimensional image reconstruction from a set of 2-dimensional projection images and associated geometry information. Either input projection or output slice files can be viewed within the COBRA application, or by using an additional MPR volumetric viewer (COBRA Viewer).
2. Geometric information as well as control of the reconstruction process, which happens through a text file parameter.xxm, and can be edited by the user through Windows® Notepad.
3. Input projections to COBRA are read from a hard disk location. Multiple formats are accepted.
4. Output images from COBRA are stored as one file per slice in a user designated location.
5. Numerous options influencing image quality, including interpolation method, convolution kernel, artifact reduction, post-processing and data formats (density, Hounsfield Units, DICOM) are supported
6. A geometry calibration tool called GeoWizard supports the measurement of variable scanner misalignment parameters which can then be used in geometry correction files. This greatly enhanced spatial resolution.

COBRA can be easily adapted to all scanner configurations as long as the source trajectory is approximately circular, or a turn-table design is used. This flexibility of use, however, forces the user to study the following User Manual to fully utilize the product.

2 Summary of Changes in Version 5

2.1 New Features

Extended View mode

COBRA Version 5 supports image reconstruction from projections with off-set detector. The diameter of the reconstructed field of view can be almost doubled over the conventional size if the detector is moved sideways by up to one half of its width. Please contact Exxim for more details how to get bigger objects accurately reconstructed with the same detector size.

Automatic and faster MAR (metal artifact reduction)

In COBRA Version 5, metal artifact reduction does not require any parameter tuning. It also works 25% faster than in previous versions.

Advanced de-noising post-processing

COBRA Version 5 incorporates an advanced 3D post-processing component providing significant noise reduction while preserving object edges.

DICOM and HU

COBRA Version 5 provides DICOM format and/or Hounsfield units. Earlier versions had only flat files of density data.

Cluster Solutions (full version only)

The setup process for COBRA's cluster solutions is completely automatic in Version 5. Cluster-specific restrictions in output volume dimensions have been removed.

Scanner Geometry Calibration

COBRA Version 5 contains a geometry calibration component for cone-beam CT scanners named COBRA *Geo Wizard*. It extracts a set of geometry parameters for every projection from data taken with the optional Exxim Calibration Phantom.

More flexible cube size setting

COBRA Version 5 allows more flexibility in size settings of the reconstructed cube.

2.2 Not Supported in Version 5

Non-equal cluster distribution

In version 5 all cluster nodes are set to reconstruct equal parts of the volume; in version 4 one could apply non-equal distribution (with restrictions).

Solid volume output

Output to the solid volume is not supported (all slices in a single file).

Periphery smoothing (post-processing)

Operation has been replaced by de-noising filter.

2.3 Current Improvements.

Version 5.3.x vs. 5.2.x

A new protrusion correction algorithm is introduced, along with a new tag OPTTAG_PROTRUSIONCMODE to activate the correction procedure.

A "volume cropper" is added to clean up the space outside of the field of view.

Supports projection sizes larger than 8 megapixels.

Version 5.2.x vs. 5.1.x

The calibration of static geometrical parameters has been enhanced and developed into a standalone tool.

Version 5.1.x vs. 5.0.x

Starting version 5.1.0 Geo component also supports a special mode, in which all parameters are constants. See chapter 14 for details.

Starting version 5.1.0 COBRA can reconstruct datasets with non-uniform header length of projections.

Version 5.0.4x vs. 5.0.37

Two new tags are introduced: OPTTAG_DEADPIXDETECT (detector dead pixel auto-detction procedure) and PARTAG_NEGATIVE_DENIED (negative densities are converted to 0)

Starting version 5.0.44 Geo component also outputs the parameter file Geo_Out.xxm. See chapter 14 for details.

3 COBRA Installation and brief Tutorial

COBRA is available as a free download for limited demonstration use only. Full use of all COBRA features requires installation of a USB HASP key, which enables licensed use. If the USB HASP key is not installed, the software will run in a demonstration mode.

3.1 Installation

3.1.1 Installing the USB HASP key

The COBRA package contains a USB HASP key (see Figure 1).

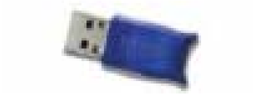


Figure 1 : USB HASP key

To install this key:

- Connect the HASP key into a PC USB port.
- Please install USB HASP driver. It is available on the COBRA installation package in the folder \hasp\drivers\install or on the HASP key vendor website: www.aladdin.com. The current link is ftp://ftp.aladdin.com/pub/hasp/new_releases/driver/HASP4_driver_setup.zip

  If the link above does not exist, please search Aladdin's website for the end user driver for HASP4. Please note that the conventional driver setup process (via .inf files or plug&play) may not work in certain configurations, and the user has to explicitly run the setup process mentioned above.

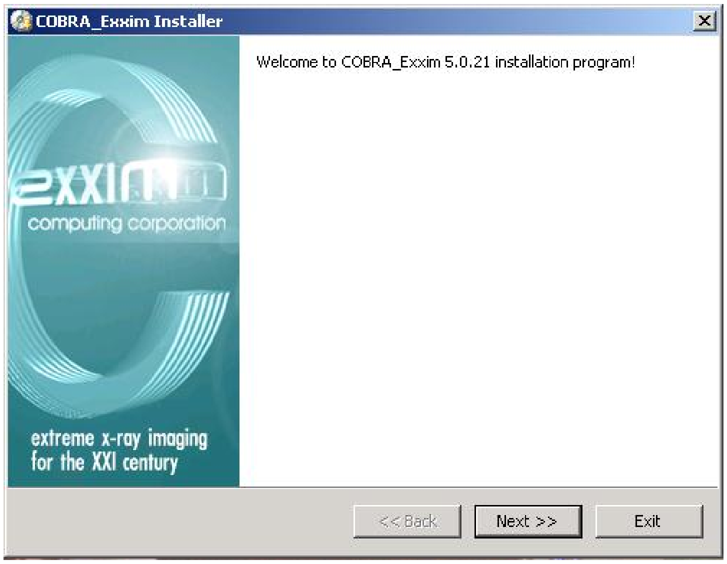
3.1.2 Installing the COBRA software

- Please manually un-install any existing installation of COBRA (via the start button or Add/Remove Programs) every time before you install a new version.

- Download the latest version of the COBRA installation executable. This executable is downloadable at http://www.exxim-cc.com/download.htm

- Start setup process by running COBRA_Exxim_v5XXX_Setup.exe (5XXX stands for the particular version).

Successfully executing the set-up file will prompt the user with the screen shown in Figure 2.



Welcome to COBRA_Exxim 5.0.21 installation program!

Figure 2: set-up program

Complete the installation as prompted by agreeing to the standard terms and conditions. The set-up application will inform you when installation is completed. The COBRA program components are located in the Windows® start menu in the program group entitled "COBRA_Exxim" as shown in Figure 3.

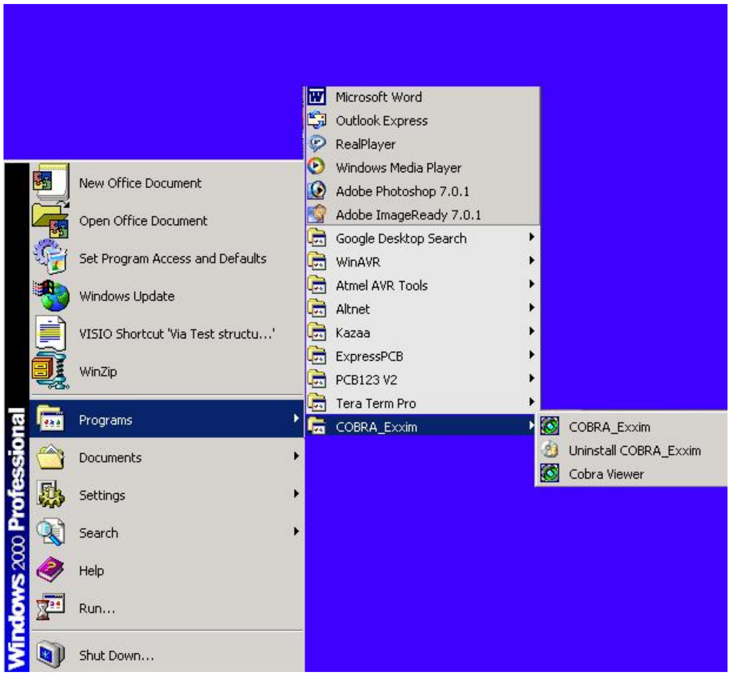
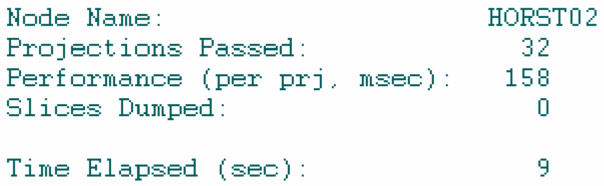


Figure 3 : COBRA_Exxim program group

3.2 Brief Tutorial

3.2.1 Steps to Run COBRA with Exxim's "Three SpheresPhantom"

- Download "Artifical Phantom" data (located at http://www.exxim-cc.com/download.htm). This dataset is a pure math model imitating x-ray absorption by idealized line integrals. The phantom comprises three balls (DC value = const) in vacuum (DC value = 0). The dataset contains 95 projections at 512x512 each.
- Extract archive into any desired directory.
- Run COBRA_Exxim.exe.
- Click "Parameters-> Open File" and select the Three Spheres Phantom data "parameter_512_std.xxm" (for reconstruction into a 512^3 cube) or "parameter_256_std.xxm" (256^3 cube).
- Click "Operations → Start Reconstruction" to reconstruct the data.
  To observe the reconstruction progress (under "View → Progress" tab) a table similar to Figure 4 will display the completion progress.

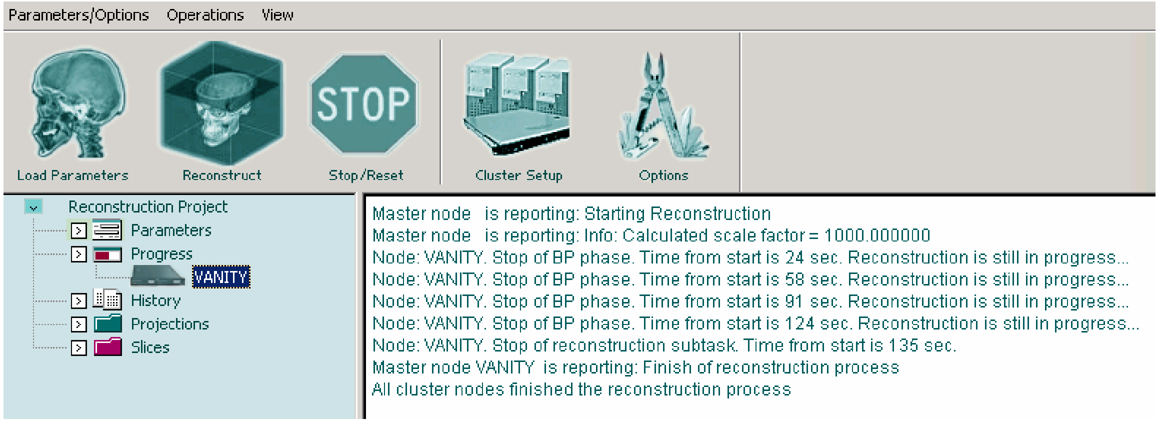


```
Node Name:                        HORST02
Projections Passed:                 32
Performance (per prj, msec):       158
Slices Dumped:                       0

Time Elapsed (sec):                  9
```

Figure 4 : View Progress table example

- After reconstruction is complete, COBRA will display a screen indicating this as shown below.



```
Master node  is reporting: Starting Reconstruction
Master node  is reporting: Info: Calculated scale factor = 1000.000000
Node: VANITY. Stop of BP phase. Time from start is 24 sec. Reconstruction is still in progress...
Node: VANITY. Stop of BP phase. Time from start is 58 sec. Reconstruction is still in progress...
Node: VANITY. Stop of BP phase. Time from start is 91 sec. Reconstruction is still in progress...
Node: VANITY. Stop of BP phase. Time from start is 124 sec. Reconstruction is still in progress...
Node: VANITY. Stop of reconstruction subtask. Time from start is 135 sec.
Master node VANITY  is reporting: Finish of reconstruction process
All cluster nodes finished the reconstruction process
```

Figure 5 : Reconstruction Complete

- To display output slices, click “View → Slices" using COBRAviewer.exe (remember that the volume contains three spheres in air, so some slices are blank). Slice 300 is a good starting point.

- To adjust the slice view/window level select “View → Window/Level” and a window/level bar appears on the screen.

- To display projections, similarly select “View → Projections”.

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4 System Requirements and Performance

4.1.1 Minimal and typical hardware requirements.

The software can be installed on any PC with Windows 2000/XP. 3D reconstruction is a computationally intensive task. The minimum hardware requirements are:

PIII / 500MHz / 512 MB

However, this minimal configuration limits the performance of COBRA. To take full advantage of COBRA performance, the following configuration or better, is strongly recommended:

dual CPU / 2 GHz / 1-2 GB RAM .

PC configuration	Input projections	Output volume	Reconstruction time
PIII / 500 MHz / 512 MB	360 projections 512x512	512x512x512	Reconstruction: 1250 sec Total (including slice dumping): 1300 sec
Dual Athlon 2000 / 1.6 GHz / 2 GB	360 projections 512x512	512x512x512	Reconstruction: 132 sec Total (including slice dumping): 175 sec
Dual Athlon 2000 / 1.6 GHz / 2 GB	320 projections 1024x1024	1024x1024x1024	Reconstruction: 950 sec Total (including slice dumping): 1250 sec

Table 1. Benchmarks of COBRA performance

4.1.2 Main factors affecting reconstruction performance and our recommendation regarding optimal hardware

Reconstruction time depends on scanner parameters (detector size in pixels, number of projections) and on reconstructed volume (number of voxels). All values shown above have been obtained under conditions where projection size, volume size, and resolution fit together. Cases where projection/volume resolutions are significantly different (e.g. a projection size of 1024^2 being reconstructed to a volume of 256^3), can affect performance up to a factor 2: slower or faster, depending on the exact configuration.

A recommended PC configuration for COBRA has 2 GB memory on board and maximum cache (512 –1024 kB). One can instantly gain speed using dual-CPU's or/and dual-core CPU's. At the same time please be aware that hyper-threading units can slow down the process.

5 Input and Output Data

5.1 Input and output format

Input projections and output slices are represented by files (one file per projection and one file per slice) using arrays of 16-bit integers (short data type in C). The files may have a header or may be header-less. In any case, COBRA cannot extract any parameters from the headers. All reconstruction parameters have to be described in a parameter file (see next Chapter). The input and output file naming conventions can be set in "Options" or through the parameter file, as will be described later. In certain case, COBRA also can take 32-bit floating point data as input (see section 6.5).

5.2 DICOM compliance

Besides the header-less plain array of 16-bit integers, COBRA also provides output into "subset" of standard DICOM format, with the following restrictions:

1) One file contains one slice (the whole volume thus is represented by a series of files)
2) Files are non-compressed
3) File names are provided without Exxim ID and study ID embedded into file names, since Exxim does not have assigned DICOM ID. Rather, they are specified by a name template string through a parameter file (see section 6.4)

The resultant DICOM files contain a minimal set of DICOM tags that can be handled by most viewers and workstations. The geometric tags are obtained from the input .xxm parameter files; the demographic tags, however, are created using default dummy values. After the first reconstruction, a file named “research.xxm” file will be generated (if it did not exist) in the source data folder, and it contains the demographic tags and their corresponding values applied. To change the value of a tag, the user can just modify the value assigned to that tag in the file research.xxm using any text editor. The file then can be used for subsequent reconstructions to generate images with the desired tag values, by placing it in the input projection directory.

The default tags included in the COBRA-generated research.xxm file are listed in the following example:

```
//ROOT ID
DCM_ROOT_UID=1.2.826.0.1.3680043.2.855.

//PATIENT NAME
DCM_TAG_0010_0010=CT_data

//PATIENT ID
DCM_TAG_0010_0020=CT_data_20061012_124532
```

```
//ID Institution Name
DCM_TAG_0008_0080=Here_Is_Inst_Name

//ID Station Name
DCM_TAG_0008_1010=Station_name_HERE

//PATIENT BIRTHDAY
DCM_TAG_0010_0030=19500101

//MANUFACTURER
DCM_TAG_0008_0070=MANUFACTURER

//ACCESSION_NUMBER
DCM_TAG_0008_0050=123456

//MODALITY
DCM_TAG_0008_0060=CT

//REFERRING MD
DCM_TAG_0008_0090=REFERRING_MD

//STUDY_DESCRIPTION
DCM_TAG_0008_1030=DESCRIPTION

//OPERATOR
DCM_TAG_0008_1070=OPERATOR

//DCM_RELSERIESNUMBER
DCM_TAG_0020_0011=1

//ORIENTATION
DCM_TAG_0020_0037=1.000000\0.000000\0.000000\0.000000\1.000000\0.000000

//PIXEL REPRESENTATION
DCM_TAG_0028_0103=1

//STUDY ID
DCM_TAG_0020_0010=STUDY_ID
```

To change the patient name, for example, the user will just have to edit the value after the corresponding tag "DCM_TAG_0010_0010" and assign the right name to it in this syntax: DCM_TAG_0010_0010=Indiana Jones

This file can be precreated and/or edited. For example, you may add tag: DCM_TAG_MMMM_NNNN = VALUE, where MMMM and NNNN are the corresponding DICOM codes for that applied tag. The change will take effect in subsequent reconstructions.

5.3 Coordinate system

The calculations on the input projections and the output reconstruction volume are based on the following coordinate systems:

The object is placed in a coordinate system x,y,z (as shown in Figure 6) which is a fixed 'world coordinate system' in a rotating gantry scanner, or a rotating coordinate system in a turn-table design. The axis of rotation is the z-axis.

The source is at a radius SOD in the mid-plane. The central ray runs from the source through the origin at an angle theta measured from the x-axis. The detector is perpendicular to the central ray at distance SDD from the source. It has detector coordinates u and v. Ideally, u is parallel to the x,y-plane and v is anti-parallel to z.

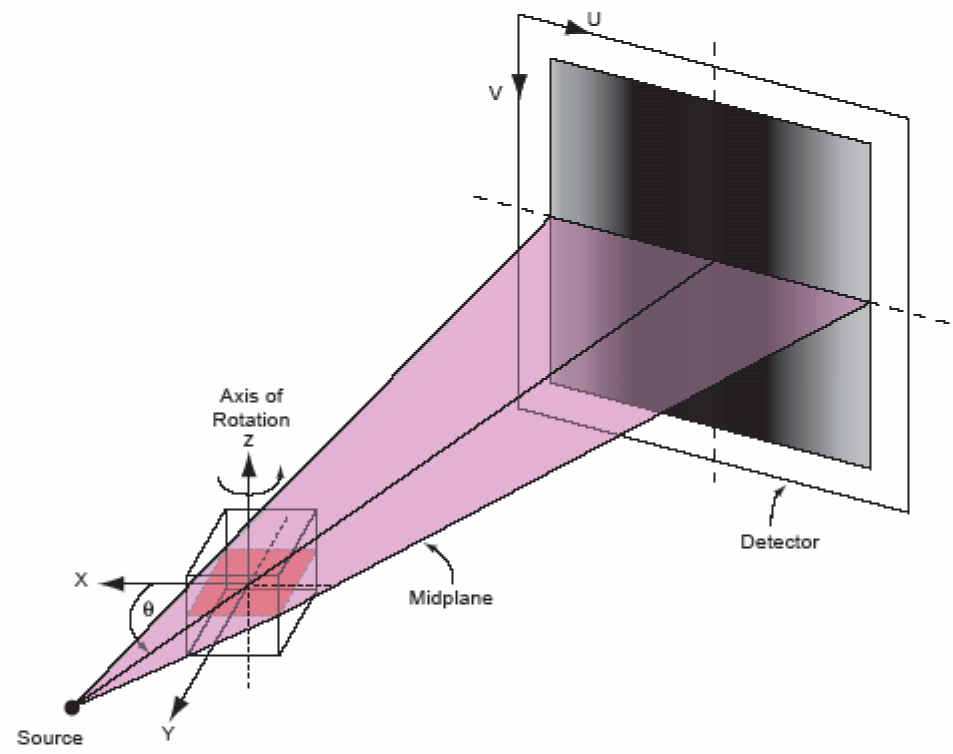

Figure 6 : Detector Coordinate System

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6 Reconstruction parameters

The scanner geometry and other parameters relevant for the reconstruction are defined in parameter files. A description of these files follows.

6.1 Main parameter file

General information is contained in a parameter file (a regular text file with extension .xxm). The parameter file is constructed of an array of strings, one parameter per string, with the following syntax:

TAG = value
or
TAG

An example of the file content:

```
PARTAG_SRCDATAPATH    = C:\CT_DATA\data
PARTAG_DSTDATAPATH     = C:\CT_IMAGES\images
PARTAG_SRCOBJDIST      = 1000.000000
PARTAG_SRCDETDIST      = 1550.000000
PARTAG_SCANANGLE       = 360.000000
PARTAG_STARTANGLE      = 0.000000
PARTAG_PROJACQUIRED    = 321
PARTAG_PROJRECON       = 320
PARTAG_DETSIZEU        = 1024
PARTAG_DETSIZEV        = 1024
PARTAG_DETOFFSETU      = 0.000000
PARTAG_DETOFFSETV      = 0.000000
PARTAG_DETPITCHU       = 0.400000
PARTAG_DETPITCHV       = 0.400000
PARTAG_CUBESIZEX       = 1024
PARTAG_CUBESIZEY       = 1024
PARTAG_CUBESIZEZ       = 1024
PARTAG_CUBEPITCHX      = 0.250000
PARTAG_CUBEPITCHY      = 0.250000
PARTAG_CUBEPITCHZ      = 0.250000
PARTAG_SCALEFACTOR     = -1.000000
PARTAG_INPUTHEADERLEN     = 0
PARTAG_INPUTISUNSIGNED    = 0
PARTAG_INPUTREQSWAP       = 0
BPMODETAG_NRSTNBR
```

Tags can be defined in any order. Missing tags are assigned default values as given in the table below.

6.2 Tags describing scanner geometry

Tag name	Description	Default Value	Remarks
PARTAG_PROJACQUIRED	Number of projections acquired	361	
PARTAG_PROJRECON	Number of projections to reconstruct	360	
PARTAG_SRCOBJDIST	The distance in **mm** between X-ray source and origin (rotation center)	500	Can be angle-dependent. In that case, applicable arrays are represented by files: SrcOrigDist.bin OrigDetDist.bin
PARTAG_SRCDETDIST	The distance in **mm** between X-ray source and detector	1000	
PARTAG_SCANANGLE	Scan angle (**degrees**)	360	Angular positions can be represented by the file angle.bin. If so all information in xxm file is ignored during reconstruction
PARTAG_STARTANGLE	Start angle (**degrees**)	0	
PARTAG_ROTATIONDIR	Rotation direction 1 is CW -1 is CCW	1	
PARTAG_DETSIZEU PARTAG_DETSIZEV	Projection size (pixels). U is horizontal axis V is anti-parallel to the axis of rotation	512x512	
PARTAG_DETOFFSETU PARTAG_DETOFFSETV	Detector offset in pixels (coordinates where central ray hits the detector)	0,0	Can be angle-dependent. In which case applicable arrays are represented by files: uoffset.bin voffset.bin
PARTAG_DETPITCHU PARTAG_DETPITCHV	Detector pitch size, **mm**	1.0, 1.0	

6.3 Tags describing reconstruction volume

Tag name	Description	Default Value	Remarks
PARTAG_CUBESIZEX PARTAG_CUBESIZEY PARTAG_CUBESIZEZ	Reconstruction volume size, **pixels**	512x512x512	
PARTAG_CUBEORIGINX PARTAG_CUBEORIGINY PARTAG_CUBEORIGINZ	Reconstruction volume origin, **pixels**	0,0,0	One can reconstruct a cube with eccentric center
PARTAG_CUBEPITCHX PARTAG_CUBEPITCHY PARTAG_CUBEPITCHZ	Voxel pitch size, **mm**	1,1,1	

6.4 Input/output data naming

Tag name	Description	Default Value	Remarks
OPTTAG_PRJNAMEFORMAT	Format string for source file in C-syntax (projection name convention)	raw.%04i	e.g. raw.325
OPTTAG_SLCNAMEFORMAT	Format string for slice file in C-syntax (slice name convention)	%04i.slice	e.g. 416.slice
PARTAG_PRJSTARTFROM	The projection counter starts from this number	0	Needed if, e,g. , the set of projections to reconstruct is 0010.prj – 0370.prj
PARTAG_SRCDATAPATH	Source data folder	The folder where the current xxm file exists	No need to set this tag if xxm file is in the same folder as data
PARTAG_DSTDATAPATH	Slice data folder	- “ -	No need to set this tag if xxm file is in the same folder as slices

6.5 Input data formats

Tag name	Description	Default Value	Remarks
PARTAG_INPUTHEADERLEN	Projection file has a header. The length of the header (in bytes) is set by this tag	0	Applicable starting v3.0 Starting 5.1.0 the header length may vary (recognized automatically)
PARTAG_INPUTISUNSIGNED	The projection contains unsigned 16-bit integers	0	Applicable starting v3.0 Setting to 0 means No Setting to 1 means Yes
PARTAG_INPUTREQSWAP	The projection contains big-endian 16-bit integers	0	Applicable starting v3.0 Setting to 0 means little endian Setting to 1 means big endian
PARTAG_INPUTLOGGEDFLOAT	Projection contains logged attenuation or filtered data in 4-byte floating point format	0	COBRA does not accept intensity (raw) data in the floating point format

6.6 Output data formats and post-processing

Tag name	Description	Default Value	Remarks
PARTAG_MINUS1000	Converting slice from density values to HU if set to 1	0	Subtracts 1000 from voxel values. Precise HU require scanner calibration with a water tank.
PARTAG_SLICEOFFSETVALUE	Arbitrary offset of reconstructed values	0	Just adding operation.
PARTAG_POSTPROFACTOR	3-dimensional de-noising procedure	0	20 is for low de-noising, 100-200 is for aggressive de-noising
PARTAG_DICOM	DICOM output	0	
PARTAG_NEGATIVE_DENIED	Negative densities are converted to 0	0	Tag is ignored (always =1) if DICOM format or post-pro denoising are active

6.7 Pre-processing

Tag name	Description	Default Value	Remarks
PARTAG_INPUTDOWNSAMPLE_X	Input projection is downsampled (binned) along U (horizontal) axis by defined factor	0	Valid values =0, 1, 2, 4,8
PARTAG_INPUTDOWNSAMPLE_Y	Input projection is downsampled (binned) along V (vertical) axis by defined factor	0	Valid values =0,1,2,4,8
PARTAG_INPUTDOWNSAMPLED	If set the detector is down-sampled (binned) by factor 2x2	0	
OPTTAG_ZFILTERN	Coefficients 0-15 for V (vertical) axis filter (N stands for any number 0-15)	0	Valid value is in the range 0-255
OPTTAG_AIRCAL	Use air calibration step in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_LOG	Use logarithm step in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_OFFSET	Use offset step in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_FFT	Use FFT step in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_PARKER	Use Parker weighting step in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_SLVERTFILT	Use vertical filtering in preprocessing procedure	Defined by “Options” Dialog Box (GUI)	Should be set to 0 or 1
OPTTAG_VRTSMOOTH	Use more vertical filtering in preprocessing procedure	Defined by “Options” Dialog	Should be set to 0 or 1

		Box (GUI)	
OPTTAG_FILTERNUM	Used filter (FFT step) in preprocessing procedure	Defined by "Options" Dialog Box (GUI)	Valid numbers are 1-4
OPTTAG_DEADPIXDETECT	Auto detecting dead pixels on the detector. The auto detection process is applied to AirRaw file (if one exists).	1	Valid numbers are 0 and 1
OPTTAG_PROTRUSIONCMODE	Select which build-in method to use for protrusion correction 0: no correction 1: based on linear functions 2: based on non-linear functions	1	Valid numbers are 0, 1 and 2. Mode 2 should only be used in biomedical applications.

6.8 Reconstruction Modes/Branches

Tag name	Description	Default Value	Remarks
BPMODETAG_NRSTNBR	Using nearest neighbor interpolation during back-projecting	adding this tag to xxm file makes this mode effective	efficient code, but not recommended for medical applications
BPMODETAG_LINITRP	Using bi-linear interpolation during back-projecting	adding this tag to xxm file makes this mode effective	improves image quality
BPMODETAG_CONEBEAM	Conventional cone-beam setup	adding this tag to xxm file makes this mode effective	
BPMODETAG_GENERIC	Cone-beam setup defined by projective transform matrices	adding this tag to xxm file makes this mode effective	Projective transform matrices have to be provided (COBRA_Generic.gxm file)
PARTAG_HBTC	Extended (double) view mode	0	Contact Exxim for details

6.9 Scale factors

Tag name	Description	Default Value	Remarks
PARTAG_SCALEFACTOR	Factor for fitting the dynamic range of the filtered projections into signed word scale	1000	Does not affect final slice values unless there is underflow or overflow
OPTTAG_SLICESCALE	Slice scale factor		Use this factor for calibrating scanner to get correct density values

6.10 SAMARA tags

Tag name	Description	Default Value	Remarks
SAMARATAG_HIGHCONTRASTLEVEL	SAMARA parameter controlling appearance of high contrast details		See paragraph 12
SAMARATAG_LOWCONTRASTLEVEL	SAMARA parameter controlling appearance of low contrast details		See paragraph 12
SAMARATAG_HIDENSLEVEL	SAMARA parameter controlling threshold of high density objects (metal)		See paragraph 12

6.11 Tags applicable only in SDK

Tag name	Description	Default Value	Remarks
MODE_INLINE	Implementing in-line reconstruction	Adding this tag to xxm file makes this mode effective	
MODE_INLINE_PARAMETERS	Implementing in-line parameter control	Adding this tag to xxm file makes this mode effective	
OPTTAG_3DBUFFERSIZE	3D buffer size for making reconstruction	Default value depends on used PC	In megabytes. Note that 4-byte buffer is used for every voxel. May be set via Options (Cobra GUI)
OPTTAG_WORKDIR	Setting the folder for intermediate output (logging , etc.)		May be set via Options (Cobra GUI)
PARTAG_INSTANT_ANGLEPOSITION PARTAG_INSTANT_DETOFFSETU PARTAG_INSTANT_DETOFFSETV PARTAG_INSTANT_SRCOBJDIST PARTAG_INSTANT_SRCDETDIST PARTAG_INSTANT_HORTILTING PARTAG_INSTANT_VRTTILTING PARTAG_INSTANT_PIVOTING PARTAG_INSTANT_UPITCH PARTAG_INSTANT_VPITCH PARTAG_INSTANT_PROJMATRIX	Setting instant scanner geometry parameter inline with the scanner		See Programmer's Guide for details

NB. All tags described above are defined in the file TagDefinitions.h. Please note that there are many other tags with similar syntax defined in this file. Tags that not described above are for internal COBRA use or reserved for future implementations/versions.

6.12 Example Parameter File for Exxim’s web site data set

Please find below the example of the parameter file for the mouse scan available via Exxim’s web site www.exxim-cc.com .

```
PARTAG_SRCOBJDIST    = 395.730011
PARTAG_SRCDETDIST    = 529.590027
PARTAG_SCANANGLE     = 195.000000
PARTAG_STARTANGLE    = 0.000000
PARTAG_PROJACQUIRED  = 196
PARTAG_PROJRECON     = 195
PARTAG_DETSIZEU      = 512
PARTAG_DETSIZEV      = 1022
PARTAG_DETOFFSETU    = 4.000000
PARTAG_DETOFFSETV    = 0.000000
PARTAG_DETPITCHU     = 0.161760
PARTAG_DETPITCHV     = 0.161760
PARTAG_CUBESIZEX     = 512
PARTAG_CUBESIZEY     = 512
PARTAG_CUBESIZEZ     = 128
PARTAG_CUBEPITCHX    = 0.100000
PARTAG_CUBEPITCHY    = 0.100000
PARTAG_CUBEPITCHZ    = 0.100000
PARTAG_CUBEORIGINX   = 0
PARTAG_CUBEORIGINY   = 0
PARTAG_CUBEORIGINZ   = 0
PARTAG_OFFSET        = 0
PARTAG_ROTATIONDIR   = 1
PARTAG_SCALEFACTOR   = 710.289673
OPTTAG_AIRCAL     = 1
OPTTAG_LOG        = 1
OPTTAG_OFFSET     = 1
OPTTAG_FFT        = 1
OPTTAG_PARKER     = 1
OPTTAG_SLVERTFILT = 0
OPTTAG_VRTSMOOTH = 0
OPTTAG_FILTERNUM   = 1
BPMODETAG_NRSTNBR
BPMODETAG_CONEBEAM
OPTTAG_SLICESCALE    = 2.000000
BPMODETAG_DUMP16
OPTTAG_PRJNAMEFORMAT   = raw.%04i
OPTTAG_SLCNAMEFORMAT   = %04i.slice
```

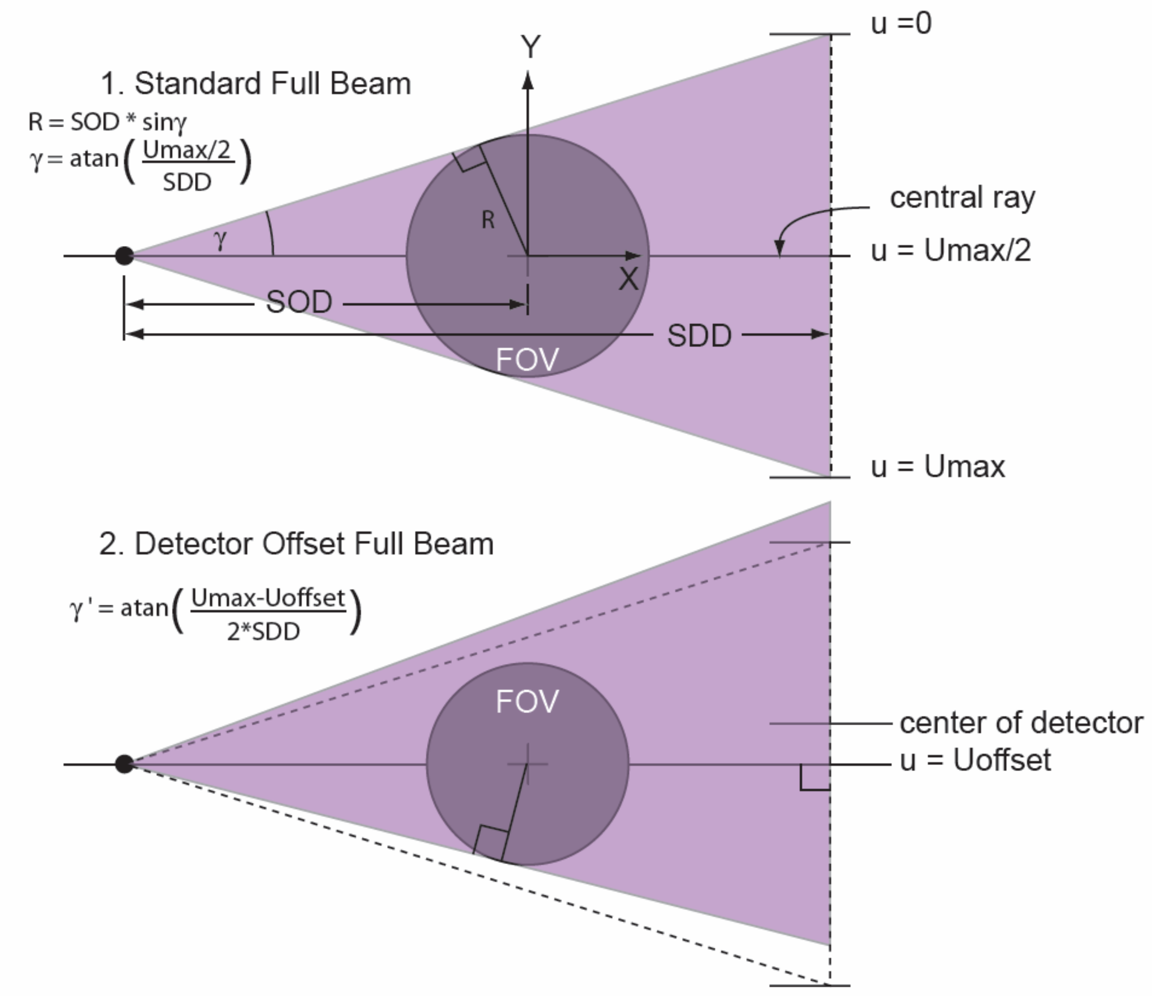

Fig. 7 Detector offset and direction of rotation as seen in the xy-plane.

Figure 7 above demonstrates the effect of a detector displacement in the xy-plane along its u-coordinate:

- The amount DetoffsetU measured in pixels has to be set in the parameter file to preserve good spatial resolution;
- The FOV is a bit reduced as the fan angle γ becomes smaller;
- In certain cases, it may be useful to offset the detector by ¼ pixel to improve sampling over 360 degrees.

Note that the FOV is slightly smaller than half of the detector width divided by the magnification SDD/SOD.

6.13 Files describing angular-dependent geometry

COBRA can reconstruct 3-D images from non-ideal geometries. E.g., the rotation speed may vary slightly during the scan, or the gantry may have some wobble. Under the assumption that these deviations are reproducible, they can be measured and written to correction files. COBRA will then use this geometry information per projection during the back-projection process.

All geometry files should be named as defined in the following table, and should be placed in the input data directory. Any number of these files can be omitted, in which case the default geometry parameters from the parameter file will be used. All files should contain arrays of 4-byte floating point numbers (float data type in MSVC). The length of arrays should be at least PARTAG_PROJACQUIRED elements.

Filename	**Description**
angle.bin	Value of angular stops in **degrees**
uoffset.bin voffset.bin	Value of horizontal and vertical detector offsets in **pixels** (coordinates where the central ray intersects the detector)
SrcOrigDist.bin	Distance in **mm** between the X-ray source and the origin (rotation center)
OrigDetDist.bin	Distance in **mm** between the origin and the detector.
HorTilting.bin	Angle in **degrees** of the detector tilt relative to its horizontal axis (u-axis). Defaults to 0 if this file is omitted.
VrtTilting.bin	Angle in **degrees** of the detector tilt relative to its vertical axis (v-axis). Defaults to 0 if this file is omitted.
Pivoting.bin	Angle in **degrees** of the detector tilt relative central ray. Defaults to 0 if this file is omitted.

7 Optional use of projective transform matrices

COBRA (version 4 and higher) supports scanner geometry description in form of projective transform matrices. For comprehensive definition of the scanner geometry one should use a set of these matrices (one matrix per each angular position)

This mode is turned on by the tag BPMODETAG_GENERIC in the parameter.xxm file or via call of CobraDispatcher_SetReconMode with this tag included (see Programmer's Guide).

Each projective matrix defines the correspondence between a volume voxel and its projection (voxel's "shadow") on the detector.

The size of each matrix is 4x3 (12 elements total). Values of matrix elements have to be set in a file called COBRA_Generic.gxm. The file COBRA_Generic.gxm has to exist in the folder containing input data set (controllable via PARTAG_SRCDATAPATH).

The file COBRA_Generic.gxm is a text file, which can be created/edited by conventional MS DOS compatible text editors (e.g. Notepad) or other relevant programs (e.g. the scanner controlling software).

In the file COBRA_Generic.gxm each line (starting at the very first line) represents one matrix (so please make sure that this file contains enough lines). Matrix elements are separated by space character(s).

Let us consider an example. The first line of COBRA_Generic.gxm might look like that:

0.41184 7.46044 0.03632 505.3131 -0.7434 0.150 -7.468 568.573 -0.00131 0.000186 0.000008568 1.0

It defines the following matrix

A00 = 0.41184	A01 = 7.46044	A02 = 0.03632	A03 = 505.3131
A10 = -0.7434	A11 = 0.150	A12 = -7.468	A13 = 568.573
A20 = -0.00131	A21 = 0.000186	A22 = 0.000008568	A23 = 1.0

The matrix A is defines the correspondence between the voxel coordinates and its projection (shadow) on the detector. The volume coordinates are measured in millimeters, the origin of the volume coordinate system is the center of the volume. The detector coordinates are measured in pixels. The origin is the detector's upper left corner.

The mapping rule is the following. If (X,Y,Z) is some volume voxel (measured in millimeters relative to the volume's center) then its "shadow" coordinates (U,V) on the projection is calculated as follows:

$$\xi = A00 * X + A01 * Y + A02 * Z + A03 * 1.0$$
$$\psi = A10 * X + A11 * Y + A12 * Z + A13 * 1.0$$
$$\zeta = A20 * X + A21 * Y + A22 * Z + A23 * 1.0$$
$$U = \xi / \zeta$$
$$V = \psi / \zeta$$

NB.

- Defining the scanner geometry by providing projective matrices makes some tags in the parameter file (e.g. PARTAG_SRCOBJDIST, PARTAG_SRCDETDIST, etc.) obsolete. However, we still ask to supply approximate values for these tags (10% accuracy).
- Calculating projective matrices for a particular scanner is not a trivial task and it is not covered by the COBRA package. However, Exxim Computing Corporation has know-how and tools (phantoms, software) and is offering the calculations as R&D service. Please contact us for additional information.

8 Preprocessing Procedures

Preprocessing includes three main steps: detector correction, filtering, and post-filtering. Any of these steps may be skipped as described below.

8.1 Detector Correction

Detector correction starts with electronic offset subtraction. It then takes the logarithm of the signal, and applies the air map correction (the projection acquired with no object in the scanner). The logarithm of the attenuation signal, which is used for further filtering, is defined as:

S (u,v) = log (**S_air**(u,v) - **S_offset**(u,v)) - log (**S_prj_in**(u,v) **-** **S_offset**(u,v))

where

S_prj_in is the input projection,
S_offset is the offset calibration file represented by a file named **offset**,
S_air is the air calibration file (the projection acquired with no object) represented by a file named **AirRaw**.

NB: The files **AirRaw** or/and **offset** can be omitted. In these cases default values of 32000 and 0, respectively, are applied.

8.2 Filtering

COBRA performs Feldkamp's filtered back-projection algorithm; hence each acquired projection has to be filtered line by line. This is done in the Fourier domain. The filter coefficients to be applied reside in the file hrz_ctfilter_N_MMM.bin (see below). This file contains the coefficient array represented as 4-byte floats. The n^{th} element is the multiplier for the n^{th} frequency component. The filter file representing pure derivatives (“ramp”) is 0., 1., 2., 3., 4.,… Filtering is a floating point operation; therefore filter coefficients can be scaled in any desired manner (also see "Scaling factor"). The length of the filter should match the horizontal size of the projection; it must be greater or equal to the nearest larger power of 2 plus 1.

Examples:

Horizontal projection size (pixels)	Filter length (elements)
160	257
400	513
512	513
513	1025
1024	1025
1300	2049

The installation package contains filter files with 257, 513, 1025 and 2049 coefficients.

Filter files are put into the same directory as the main COBRA_Exxim program.
Syntax: hrz_ctfilter_1_257.bin, hrz_ctfilter_1_513.bin, …, hrz_ctfilter_2_2049.bin.

suffix 1 means Shepp-Logan

suffix 2 means cosine filter

Suffix 3 means user filter (e.g. hrz_ctfilter_3_513.bin). User filters are not supplied.

Filters contain N frequency domain coefficients. The first element is the zero frequency component.
Representation : array of 4-byte floats, no header.

8.3 Parker Weighting

This compensates for ray redundancy in cases where the scan angle is less than 360 degrees (typically in the case of 180 degrees + fan angle). For an explanation in 2-D CT see [2].

8.4 Smoothing

After filtering, the input projections can be smoothed. Three smoothing masks are provided:

- vertical mask [0.5, 1.0, 0.5] ("Slight vertical smoothing" in Options and Settings),
- vertical mask [0.5, 1.0, 1.0, 1.0, 0.5] ("Vertical smoothing" in Options and Settings).

The default filter is "Slight vertical smoothing". See also "Options and Settings".

8.5 Scaling Procedure

COBRA performs filtering as a floating-point operation, while back-projection is a 32-bit integer operation to increase performance. Because of the diversity of data (biological, industrial, etc.), and the variety of preprocessing algorithms and filter coefficients, the filtered projection should be scaled to obtain a reasonable range of integer values. If the scale factor is too small, information is lost due to underflow, and the resulting image will show poor low contrast. If the scale factor is chosen too high, overflow happens in the accumulation process, and dense objects will have erroneous voxel values.

8.5.1 How to find the correct ScaleFactor

8.5.1.1 Working with the default value

The default value for PARTAG_SCALEFACTOR is 1000. This should give an initial image for most objects; however, it may not be optimal. If the object composition is such that there is not much contrast between adjacent regions, then 1000 may not be enough to preserve the full low-contrast capability of the scanner (underflow). If the object contains regions with high contrast (e.g. metal pieces in plastic), then 1000 may be too high, which results in wrong density values (overflow).

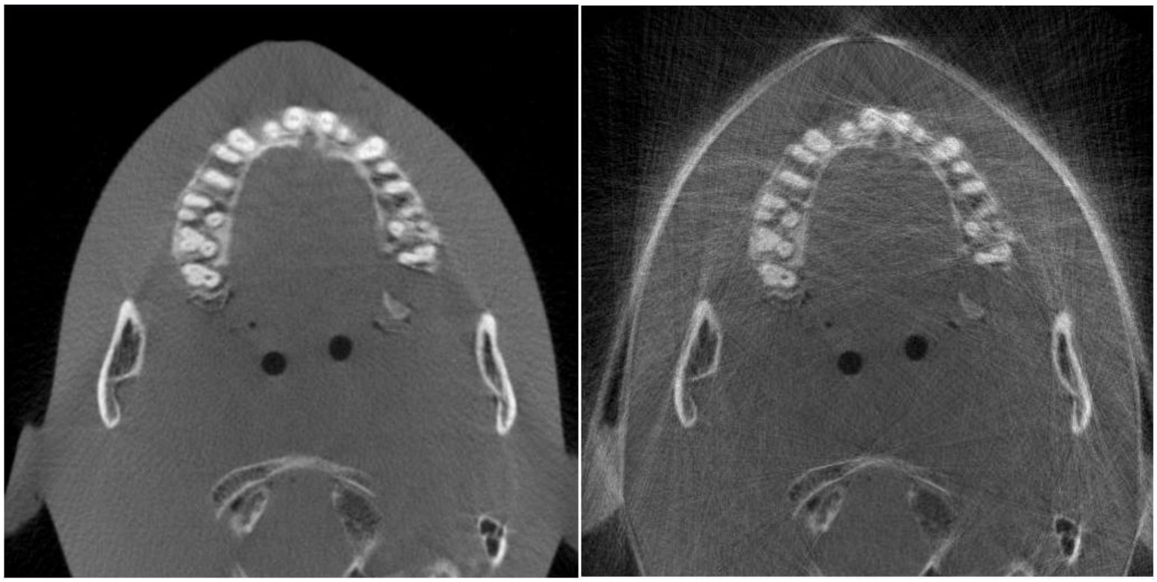

Fig. 8 Correct scaling on the left, overflow on the right.

8.5.1.2 Scanning biological objects

For biological objects, using the full preprocessing procedure and a ramp filter, the recommended scaling factor is 700.

8.5.1.3 Scale Factor Auto-Detection

The scale factor can be auto-detected. Auto-detection is enabled by setting PARTAG_SCALEFACTOR to -1. This setting achieves correct scaling for most cases, by analyzing the first projection. However, in the case of very inhomogeneous objects or non-rectangular detectors (e.g. a circular image intensifier), the auto-selection procedure may fail and cause overflow or underflow.

The following procedure is recommended:
- Select auto-select, PARTAG_SCALEFACTOR to -1.
- 4-5 seconds after start of the reconstruction, check the first preprocessed projection (use COBRA_View_Exxim). This projection will be available as file **preprocd_proj.000** in the working directory (see also "Options and Settings"). The preprocessed projection should have pixel values in the range +/- 24000, and should display as a recognizable edge-enhanced image. Underflow may occur if extreme pixel values are below 3000. Overflow may occur if the pixel values exceed 30,000. If underflow or overflow is suspected, then an appropriate scaling factor (which is available in the "Messages" GUI page) must be applied.

Example: The auto-selected scale factor reported by COBRA_Exxim is 300. **preprocd_proj.000** contains pixels with values in the range of +/- 500 (obvious case of underflow). The recommended value for PARTAG_SCALEFACTOR in this case would be in the range of 3000-5000.

NB: COBRA also allows reconstructing “log-ed” projections (air compensation and logarithm transform already have been done on the client side). Auto-detection also works for those cases. Typical scale factor for biological objects is 0.2.

8.5.2 OPTTAG_SLICESCALE

This is not a pre-processing step, but mentioned here for completeness. After performing the back-projection/accumulation procedure, every voxel value is divided by the number of projections. At this point of the algorithm it is possible to perform additional scaling, for example for calibrating the whole system to HU.

For better understanding all steps of the reconstruction routine and controlling them via post-filtering and slice-scale, please find the accurate description below.

- *Step one: Detector offset calibration*

Signal_1(u,v) = InputPrjSignal (u,v) – Offset(u,v)
Air_1(u,v) = AirSignal (u,v) – Offset(u,v)
where
InputPrjSignal(u,v) is the input projection (raw intensity signal),
AirSignal(u,v) is the intensity without absorber (nothing inside FOV), presented by file **airraw** (value of 32767 is applied in every pixel if **airraw** is missing)
Offset(u,v) is the electronic signal offset value, presented by file **offset** (value of 0 is applied to every pixel if **offset** is missing).
All data are 16 bit signed integers.
This step is not obligatory for all detectors and is automatically skipped if the file **offset** is missing.

- *Step two: Taking the logarithm*

Signal_2(u,v) = log{ Signal_1(u,v) }
Air_2(u,v) = log{ Air_1(u,v) }
Signal_1 and Air_1 are 16 bit signed integers. Signal_2 and Air_2 are 32 bit floats.

- Step three: Air calibration

Signal_3(u,v) = Air_2(u,v) - Signal_2(u,v)
All are 32 bit floats. Signal_3 is also called "log attenuation". It is equal to $\mu \cdot d$ (attenuation coefficient x path length).

- *Step four: filtering or convolution*

Signal_4(u,v) = ForwardFourierTransform{Signal_3(u,v)}
Signal_5(u,v) = Filter_Coefficients(u,v) * Signal_4(u,v)
Signal_6(u,v) = InverseFourierTransform{Signal_5(u,v)}
Signal_7(u,v) = Scale1* 0.25 * Filter{Signal_6(u,v)}.

Signal_3 is 32 bit floats. Signal_4, Signal_5, and Signal_6 are 64 bit floats. Signal_7 is 16 bits signed integer.
Scale1 is the value defined by PARTAG_SCALEFACTOR (see 7.5.1 above). The additional factor 0.25 has some "historic" nature and results in approximate units of [mg/cm^3] for the default PARTAG_SCALEFACTOR of 1000 (unless steps 1-3 are already done outside COBRA).
Please note

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- The main purpose of the factor Scale1 is to push the filtered signal to the range of plus/minus 32767. We do not recommend using this factor for calibrating the whole system to HU (also see below).
- The factor Scale1 (defined by PARTAG_SCALEFACTOR) obviously depends on the scale of filter coefficients applied. We use 0,1,2, etc. (for example) for the ramp filter, which corresponds approx. 1000 as Scale1. If to use 0,2,4, etc. but 500 as Scale1 instead the result of this step will be the same

- *Step five: Back-projection (accumulation)*

Cube32 (x,y,z) = Cube32 (x,y,z) + Mapped{ Signal_7(u,v) }
Signal_7 is a 16 bit signed integer. Cube32 is a 32 bit signed integer.

- *Step six: Final scaling*

CubeRes (x,y,z) = Cube32 (x,y,z)/NOP * Scale2
where CubeRes(x,y,z) is resulting cube voxel, NOP is number of projections (views), Scale2 is the slice scale factor. The factor Scale2 is defined by OPTTAG_SLICESCALE and can be used for entire system calibration to [mg/cm^3]. Hounsfield Unite [HU] can be obtained by subtracting 1000 from the density values (see PARTAG_MINUS10000. Cube32 is a 32 bit signed integer. Scale2 is a 32 bit float. CubeRes is a 16 bit signed integer.

8.6 Options and Settings

The GUI page "Options and Settings" provides general control over the program operation and modes. It contains the following GUI controls. Note that the program must be restarted for option changes to take effect.

8.6.1 Selection "Preprocessing Procedure"

Provides on/off control for preprocessing steps.

8.6.2 Selection "Slice Scaling"

(default value =1)
This provides for additional scaling of slice values (they are scaled from 32-bit integers to 16-bit integers). If "auto-select" mode was used in the preprocessing procedure, slice values have some arbitrary range (usually approximately –200 - 5000). If this range is not suitable for conversion into DICOM format then appropriate Slice Scaling factor can be applied.

8.6.3 Selection "Work Directory"

This directory is used by the COBRA program for temporary files. The most important files are the log-file (COBRA_Protocol.log) and the preprocessed projection preprocd_proj.000 (used in scale factor autodetection). This directory contains the "history" of the program execution.

8.6.4 Selection "Name Templates"

This establishes the rules for naming projection and slice files. The templates use the regular C format syntax. Default templates are "**raw.%04i**" for projections and "**%04i.slice**" for slices.

Use of "raw.%04i" means that input projection files are named as follows:
raw.0000, raw.0001, raw.0002, raw.0003, ...

Use of "prj_num_%03i.prj" means that input projection files are named as follows:
prj_num_000.prj, prj_num_001.prj, prj_num_002.prj, ...

Use of "%04i.slice" means that output slice files are named as follows:
0000.slice, 0001.slice, 0002.slice, 0003.slice, ...

Use of "animal_%03i.slc" means that output slice files are named as follows:
animal_000.slc, animal_001.slc, animal_002.slc, ...

NB: Projection and Slice file name indices must start with zero.
(i.e. Raw.0000, prj_num_000.prj, 0000.slice, animal_000.slc)

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8.7 3D Buffer Size and output volume

8.7.1 Buffer size

This controls how much RAM is allocated for the reconstruction buffer. COBRA automatically enters multi-pass mode if the whole reconstructed cube cannot be created in the PC's RAM. It is strongly recommended that the buffer size be set to half of the PC's RAM or less.

PC's RAM	Recommended "3D Buffer Size" option
256 MB	128 MB
512 MB	256 MB
1 GB	512 MB
2 GB or more	1536 MB

8.7.2 Restrictions on output volume dimensions

COBRA can reconstruct output volumes of arbitrary size, as long as the following restrictions are obeyed:

Standard case: Any dimension (x, y or z) must be divisible by 32, e.g. 544x544x320 is allowed if the buffer size is 512 MB.
Multi-pass case: if a multi-pass reconstruction is necessary, the dimensions should be divisible by 256. A multi-pass reconstruction is entered by COBRA automatically in the case that the output volume does not fit into the 3D Buffer.

9 Other GUI elements

9.1 "Progress" Page

This contains timers and a window showing progress in five slices. This window should only be considered a progress indicator. Actual output slices are better than shown in this window (a simplified reconstruction procedure is used for this display). However, it is a convenient tool providing preliminary information how the reconstruction is proceeding, and for early detection of obvious reconstruction issues.

9.2 "Parameters" Page

This is the main control tool for COBRA. It allows opening the desired parameter file (text file with xxm extension), controls the reconstruction process (start/stop), and permits checking the applied parameters and options. Selecting the "Perform Reconstruction" button, without opening any .xxm-parameter file, will cause a reconstruction to be performed using the previously selected parameter set.

9.3 "History" Page

Reports the progress of COBRA execution in "Message" format. The user receives information about auto-selected scale factors, reconstruction durations, and possible errors.

10 Distributed (Cluster) Solutions

10.1 Getting Started with the Exxim PC's.

Exxim Computing supplies the computer system(s) with COBRA_Exxim software fully installed and configured for the distributed mode of operation.

Before starting the user must ensure that the PC's have the proper network connection. The PC's are configured as WORKGROUP nodes.

Any of the PC's can be used as a Master. "Master" means that the computer is executing the main COBRA program (see below). The other PC(s) will be remotely controlled without any additional interaction.

Exxim supplies both the "Mouse" and the "Head" examples. These can be used for system check and for evaluation.

Important! Do not start the main COBRA program on more than one of the node computers at the same time. Doing so will prevent them to work in parallel as a cluster.

Important! If the main COBRA program cannot communicate with the remote PC(s) error messages will appear. In this case refer to Troubleshooting described in 9.4 (Distributed Solution Specific Troubleshooting**).**

10.2 COBRA_Exxim Distributed Master/Slave Model

The Distributed Version of COBRA_Exxim is based on a Master/Slave model. This is described as follows.

- Once installed on any network connected computer, COBRA can perform either as Master node or as Slave node.
- Starting the COBRA_Exxim main program on one computer automatically selects that computer as the Master node.
- All other computers with COBRA (distributed version) installed, which are connected to the network, are automatically available as Slaves (see Restrictions below).
- Slaves are completely controlled by the Master node, so no user interaction (other than the initial installation) is required on the Slave computers.
- A network can have any number of Masters and Slaves.

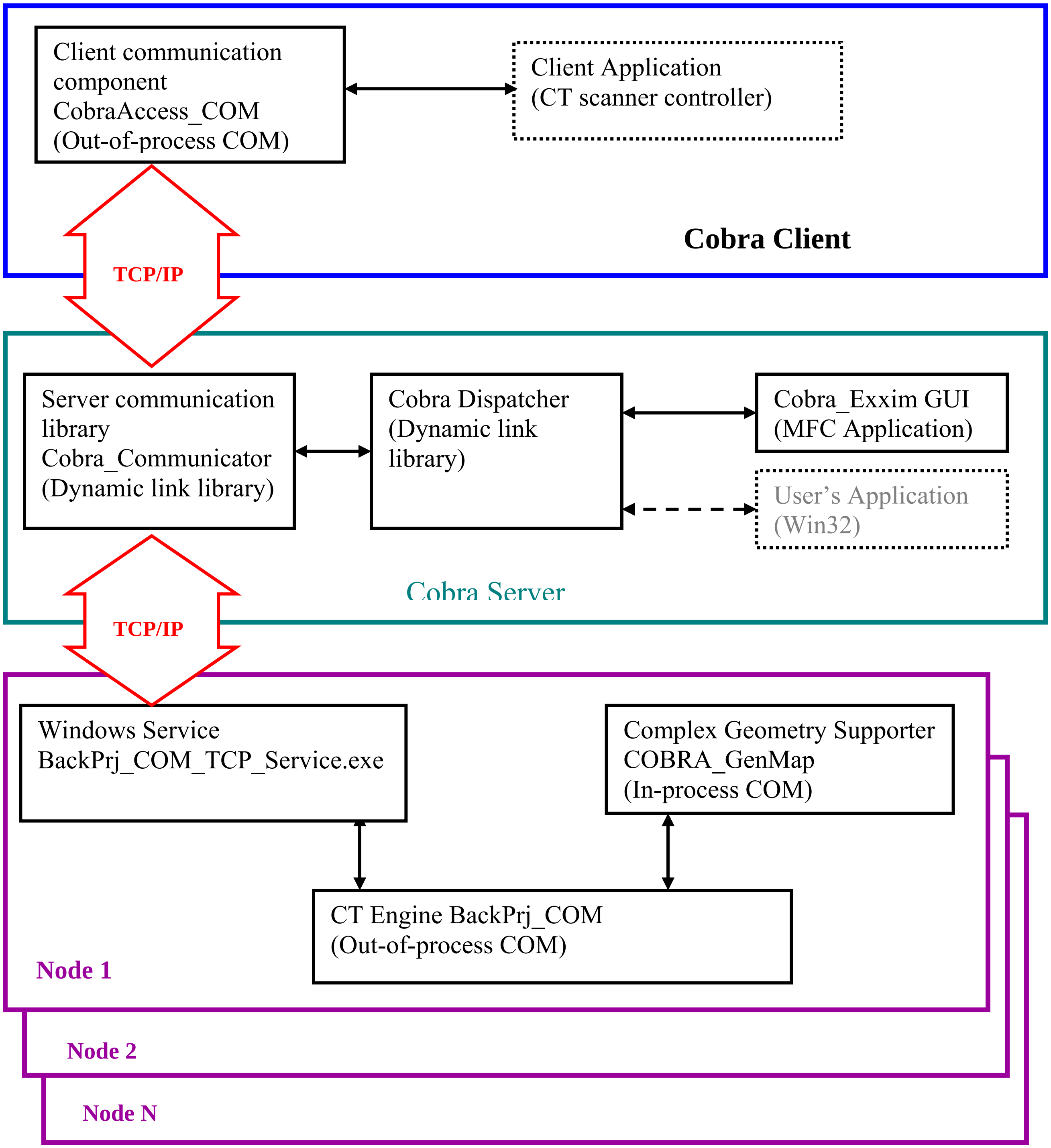
The software architecture uses a DCOM- and Winsock-based design. It allows the program to be built from independent executable components. They are represented as files on the hard drive and as processes during execution.

NB

Restrictions of the model:

- Any computer which is already running in Master mode cannot simultaneously be a Slave (the same computer can not be Master and Slave at the same time).
- Masters cannot share Slaves.
- Up to 4 Slaves are supported.

The model is illustrated in the diagram below.



10.3 Using Distributed Mode

If the COBRA_Exxim package (version 2.0 and higher) is correctly installed on two or more computers (see 10.5 for installation details), COBRA_Exxim can be used in distributed mode.

The first step to be done is selecting the Slave computer(s) and the participation parameters. To accomplish this, open the Distribution tab and to enter the Slave names in the textboxes (the Master's name is already present and is not available for editing). All nodes should be dedicated to participate in the CT reconstruction process. All nodes will contribute evenly to the process; therefore, a network of equally performing nodes will give best results.

During the reconstruction process each designated node completes the work for an appropriate part of the cube. When sharing reconstruction between nodes, the whole cube is divided in slabs along the Z axis (sub-volumes).

Sub-volumes must obey the same rules as the whole volume. The participation parameters have the following restrictions: any sub-volume must have the Z-size divisible by 32. In practice it means that volumes with a Z-size such as 256, 512, 768, 1024, 1536, etc. can be shared easily among 4 nodes. A cube with a Z-size of 480 cannot be shared at all. If the opened parameter file does not comply with this rule, an appropriate message will appear and execution of the reconstruction process will be blocked.

An additional complication appears if it is necessary to use a multi-pass process for sub-cube reconstruction (the sub-cube is larger than the designated 3D buffer). In such a case there is no simple and straightforward recommendation about the cube metrics. If some unusual size is needed, then the basic recommendation is to load a 'best guess' parameter file and check the History tab. If an error message appears then try another distribution, or another cube size, or both. e.g. consider using 512 or 1024 instead.

Once the Master and Slave parameters are selected, all other interactions between the COBRA_Exxim GUI and the User, or between COBRA_Exxim and a Client program (see Programmers Guide for details about in-line mode), are almost identical to the non-distributed version. Easily overlooked is the possibility to switch the progress screen (five slices on the Progress tab) between the different sub-cubes (nodes). The "Show Progress" radio buttons (Distribution tab) provide immediate status and control of the reconstruction progress in any node. The selected choice is effective immediately after the selection is made.

NB.

The Master computer is allowed to get zero as the participation parameter.

The COBRA_Exxim engine pipelines the reconstruction process. This "masks" any network/hard drive operations "behind " the reconstruction process. For this to work as designed, the distributed version of COBRA_Exxim must be installed correctly on a

network. The required sections from the input projections are then acquired by the Slave computer(s) without interrupting or delaying the reconstruction process.
To change a PC from Master mode to Slave mode, reboot the PC.

10.4 **Troubleshooting**

Typical problems, specific to the clustered implementation, are addressed as follows: **COBRA Master does not remotely activate or communicate correctly with BackPrj_COM_Server**. The usual cause of this is network issues. Either a connection problem exists or excessive traffic is slowing down the network. Interruption of network communications during the active phase of COBRA can lock out remote operation of BackPrj_COM_Server. As a last resort, **re-booting all COBRA nodes should help** but the network issues must be resolved.

It is more convenient and easier to do the following:
- Close the main COBRA program on the Master node.
- Start the Task Manager (use Ctrl-Alt-Del) on all nodes and select the Processes tab.
- For every node in the cluster ensure that the process BackPrj_COM_Server is not listed. Close the process if required to remove it from the list. Note that the process may be listed as BACKPR~1.EXE
- Restart the COBRA program on the Master node.

NB
It is recommended that the Task Manager be displayed on all nodes. Use it to monitor CPU, memory and network usage.

10.5 COBRA Installation for Distributed Mode

The installation process for cluster solutions is the same for all nodes. The user has to install COBRA on every node of the cluster. Please note that the HASP dongle has to be set only on the Master PC.

11 Nearest Neighbor vs. Bi-Linear Interpolation

COBRA v3.0.x (and higher) allows user to make a choice between nearest neighbor and bi-linear interpolation during back-projecting process. Note:

1. Reconstruction process based on bi-linear interpolation is approximately 2.5 times longer
2. Bi-linear interpolation achieves better S/N ratio; nearest neighbor interpolation requires post-processing to remove some of the frequency noise (see picture below).

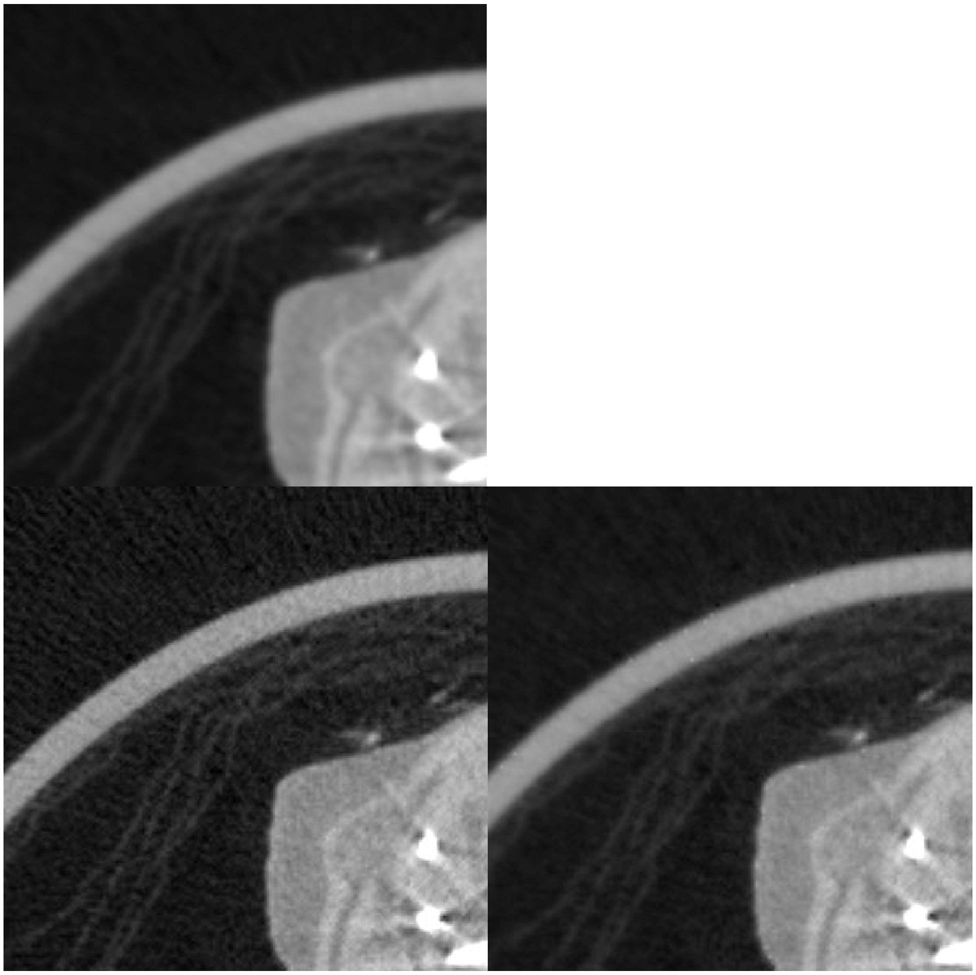


Fig. 9 Upper Left: Bi-Linear interpolation. Lower Left: Nearest neighbor interpolation. Lower Right: Nearest neighbor interpolation plus COBRA's post-processing filtering.

12 Streak and Metal Artifact Reduction Algorithm (SAMARA)

12.1 What is SAMARA?

SAMARA stands for Streak Artifact and Metal Artifact reduction algorithm. It is an iterative algorithm for 3D reconstruction, which is more tolerant against input data imperfections than the standard Feldkamp method. Such data imperfections can be caused by;
- absorption non-linearity,
- scanner geometry misalignment,
- non-equidistant angular stepping or
- insufficient number of projections (e.g. less than 200).

The technique is designed to reconstruct better images than a standard Feldkamp procedure.

For performing SAMARA- reconstruction of volumetric data it is necessary (and enough) to define relevant SAMARA parameters in the actual parameter.xxm file (see below). After reconstruction the slices will appear in the destination slice folder (controllable by the tag PARTAG_DSTDATAPATH) and in subfolders (created automatically) /SAR (streak artifacts are reduced) and /MAR (metal artifacts are reduced)

SAMARA reconstruction can be performed in two different modes: streak artifact reduction (SAR) and metal artifact reduction (MAR). SAR is performed if the tags SAMARATAG_HIGHCONTRASTLEVEL and SAMARATAG_LOWCONTRASTLEVEL are defined in parameter.xxm file. The reconstruction procedure is automatically turned into MAR if the tag SAMARATAG_HIDENSLEVEL is also defined. The best way to find optimal tag values is using SAMARA Tuning dialog (see below). The duration of SAR is approximately 2.5-3 times longer than conventional Feldkamp reconstruction. MAR is approx. 3.5-4.5 longer than Feldkamp.

12.2 SAMARA parameters

The implementation both of Feldkamp and SAMARA algorithms require the same parameters for scanner and target volume description. However, SAMARA should be supplied with some additional parameters as follows:

- The parameter called “High Contrast Details Appearance”, which usually is one third of the difference between average values for air and water (so = 300 if the system is calibrated to HU). In parameter.xxm this value is controlled by the tag SAMARATAG_HIGHCONTRASTLEVEL
- The parameter called “Low Contrast Details Appearance”, which does not have a straightforward physical equivalent. In parameter.xxm this value is controlled by the tag SAMARATAG_LOWCONTRASTLEVEL
- For metal artifact reduction, additionally the average density value of metal (obligatory). In parameter.xxm this value is controlled by the tag SAMARATAG_HIDENSLEVEL

SAMARA requires a substantial amount of additional parameters, but the reconstruction routine is not very sensitive to particular values. In other words, the parameters have to be set "just about right". In most cases, changes in the range of ± 20% are not noticeable. Also, once SAMARA parameters have been tuned (optimized), they do not need to be re-optimized for the same equipment and similar scanned objects.
Please find below an example of the parameter file for the mouse scan available on Exxim's web site www.exxim-cc.com (including streak artifact reduction).

```
PARTAG_SRCOBJDIST    = 395.730011
PARTAG_SRCDETDIST    = 529.590027
PARTAG_SCANANGLE     = 195.000000
PARTAG_STARTANGLE    = 0.000000
PARTAG_PROJACQUIRED  = 196
PARTAG_PROJRECON     = 195
PARTAG_DETSIZEU      = 512
PARTAG_DETSIZEV      = 1022
PARTAG_DETOFFSETU    = 4.000000
PARTAG_DETOFFSETV    = 0.000000
PARTAG_DETPITCHU     = 0.161760
PARTAG_DETPITCHV     = 0.161760
PARTAG_CUBESIZEX     = 512
PARTAG_CUBESIZEY     = 512
PARTAG_CUBESIZEZ     = 128
PARTAG_CUBEPITCHX    = 0.100000
PARTAG_CUBEPITCHY    = 0.100000
PARTAG_CUBEPITCHZ    = 0.100000
PARTAG_CUBEORIGINX   = 0
PARTAG_CUBEORIGINY   = 0
PARTAG_CUBEORIGINZ   = 0
PARTAG_OFFSET        = 0
PARTAG_ROTATIONDIR   = 1
PARTAG_SCALEFACTOR   = 710.289673
OPTTAG_AIRCAL     = 1
OPTTAG_LOG        = 1
OPTTAG_OFFSET     = 1
OPTTAG_FFT        = 1
OPTTAG_PARKER     = 1
OPTTAG_SLVERTFILT = 0
OPTTAG_VRTSMOOTH = 0
OPTTAG_FILTERNUM   = 1
BPMODETAG_NRSTNBR
BPMODETAG_CONEBEAM
OPTTAG_SLICESCALE    = 2.000000
BPMODETAG_DUMP16
OPTTAG_PRJNAMEFORMAT   = raw.%04i
OPTTAG_SLCNAMEFORMAT   = %04i.slice
SAMARATAG_HIGHCONTRASTLEVEL   = 200
SAMARATAG_LOWCONTRASTLEVEL  = 160
```

<u>Restriction:</u> SAMARA and 3-D filtering will not work in cluster configurations where the master node is also acting as computing node (back-projector).

13 Post-Processing

COBRA provides 3-dimensional smoothing as a post-processing feature, controlled by PARTAG_POSTPROFACTOR. This is a boundary-preserving de-noising procedure.

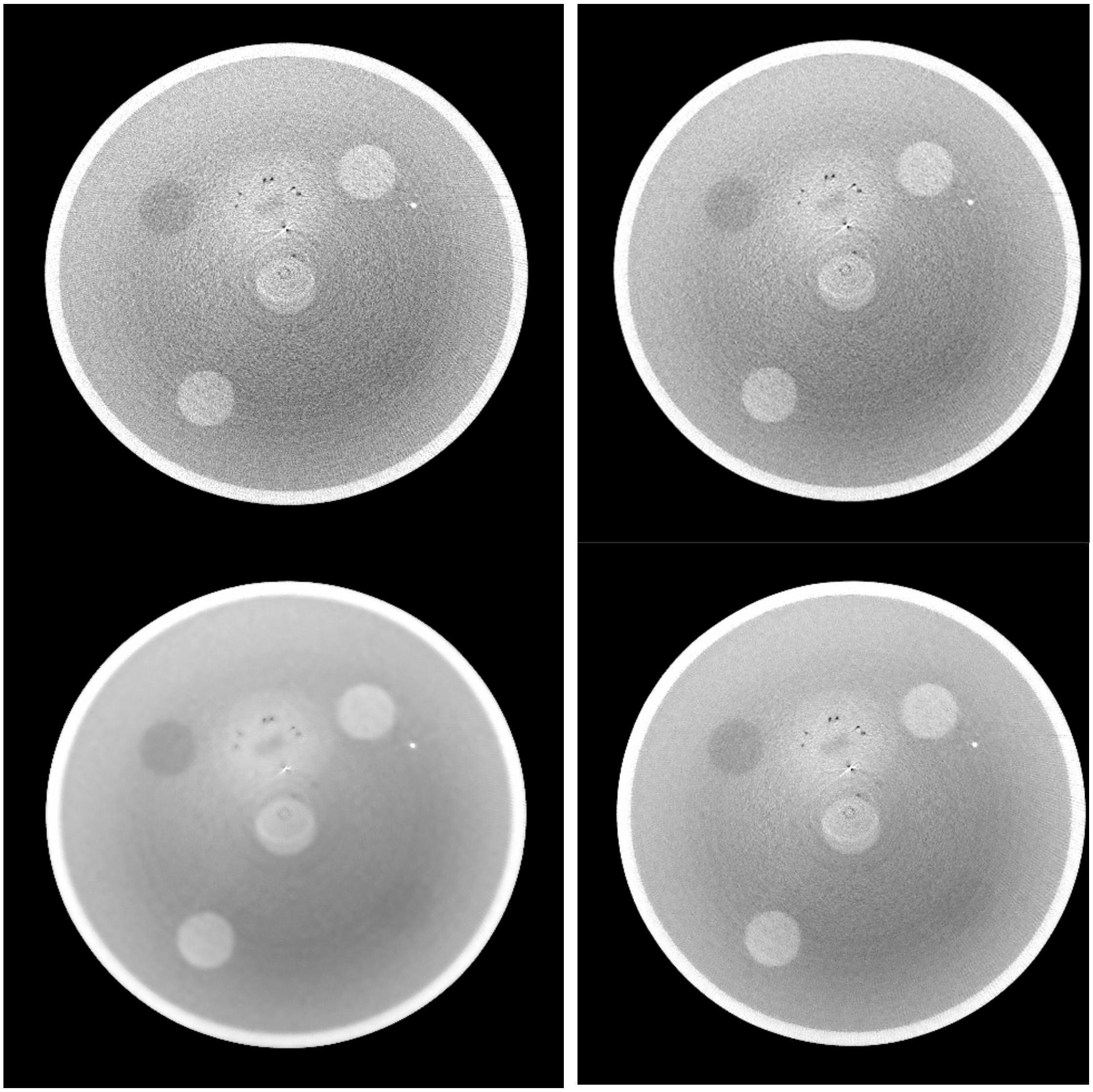


Fig. 10 PARTAG_POSTPROFACTOR 0, 30, 120, 200 in clockwise order.

Note that random noise is gradually smoothed out without sacrificing spatial resolution. At very high values of the control parameter >100 in this case), contrast loss occurs.

Restriction: SAMARA and 3-D filtering will not work in cluster configurations where the master node is also acting as computing node (back-projector).

14 COBRA_Geo User Manual

14.1 Introduction

Image quality is strongly dependent on correct description of the scan geometry. Static deviations from idealized parameters (misalignment), can be handled through PARTAGS (see above), or through precise scanner alignment, if possible. Dynamic geometry parameters, which change from projection to projection due to gravity, centrifugal force or lack of balancing, can also be handled by COBRA. The geometrical calibration is provided at two levels, for static and dynamic parameters, respectively. The static parameter calibration is done by a stand-alone program “CobraGeoCalibration”. It also can be done through SDK function calls. Please refer to COBRA Programming Guide for the use of the calibration SDK, and the general work procedure will be demonstrated based on the stand-alone GUI based CobraGeoCalibration program The dynamic parameters are given by COBRA_Geo, which will extract the most important of these dynamically changing parameters from the scan of a phantom:

- u-offset;
- v-offset;
- angular position (azimuth of the gantry position)
- magnification ratio (detector-object distance).

COBRA_Geo generates the following files: uoffset.bin, voffset.bin, angle.bin, SrcOrigDist.bin, OrigDetDist.bin.
Please note the following.

COBRA Geo provides geometry data on a per projection basis, and it can calibrate rather instable scanner mechanics as well as scanners configured for half-beam mode. u-offset.bin is a field of offset data indexed by the projection number, containing u-offset values for each projection..

Please also be aware that the scanner mechanics instability may not be covered by the selected parameters mentioned above in all cases. For example, detector pivoting is assumed to be a static parameter, which does not vary with projection direction. Also, the deviations may not be reproducible due to loose mechanics etc. In this case, the calibration procedure may not improve image quality.

Also, the geometry parameters may depend on scan speed. Therefore, COBRA_Geo calibration should be done for each scan mode.

In the next sections, the static parameter calibration will be described first. It then is followed by a detailed explanation of the procedure of performing the dynamic parameter calibration.

14.2 Static Parameter Calibration Procedure

14.2.1 Step 1: Scanning of bead phantom

Exxim provides an optional calibration phantom which is specially designed for scanners with a FOV of about 10cm diameter, to be used with the COBRA calibration tool. The phantom is a 100 (70 or 32) mm diameter cylinder with four sets of metal beads. Each set of beads lies in a plane perpendicular to the cylinder's axis and contains 8 beads (d = 1.6 mm or 1.0 mm) at 45 degree angles.

The user can consider scanning his/her own phantom, in which case Exxim should be contacted regarding additional details.

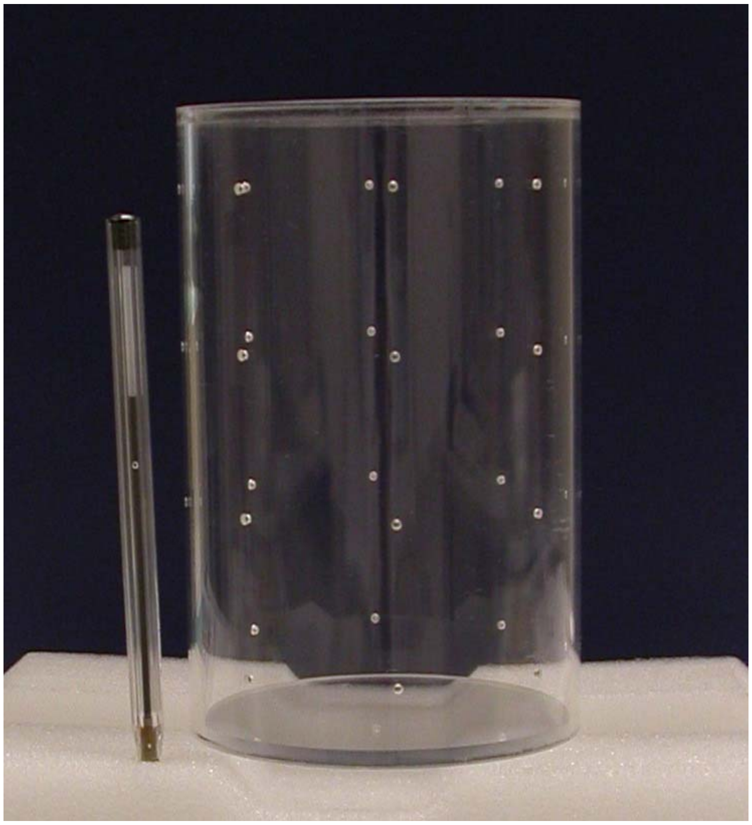


Fig. 11 Exxim's 100mm plastic phantom with metal beads.

The calibration phantom should be placed at the center of the field of view, with its axis as parallel to the axis of rotation as possible. It must be made sure that at least two layers of beads should be projected onto the detector, with one above the equatorial plane the other below the equatorial plane.

After the projections of the calibration phantom are acquired, the user should first examine the projections to verify that the phantom was position correctly and did not wobble throughout the scan. At the top and bottom of each projection, depending on the phantom size and the size of the field of view, the end surfaces of the cylindrical calibration phantom may produce ellipses or partial ellipses that appear darker than other region of each projection, and should be excluded during the process of calibration in order to ensure the accuracy of automatic bead detection. A typical projection of the phantom will look like what shown in the figure below, with full-beam and half-beam scan configuration, respectively.

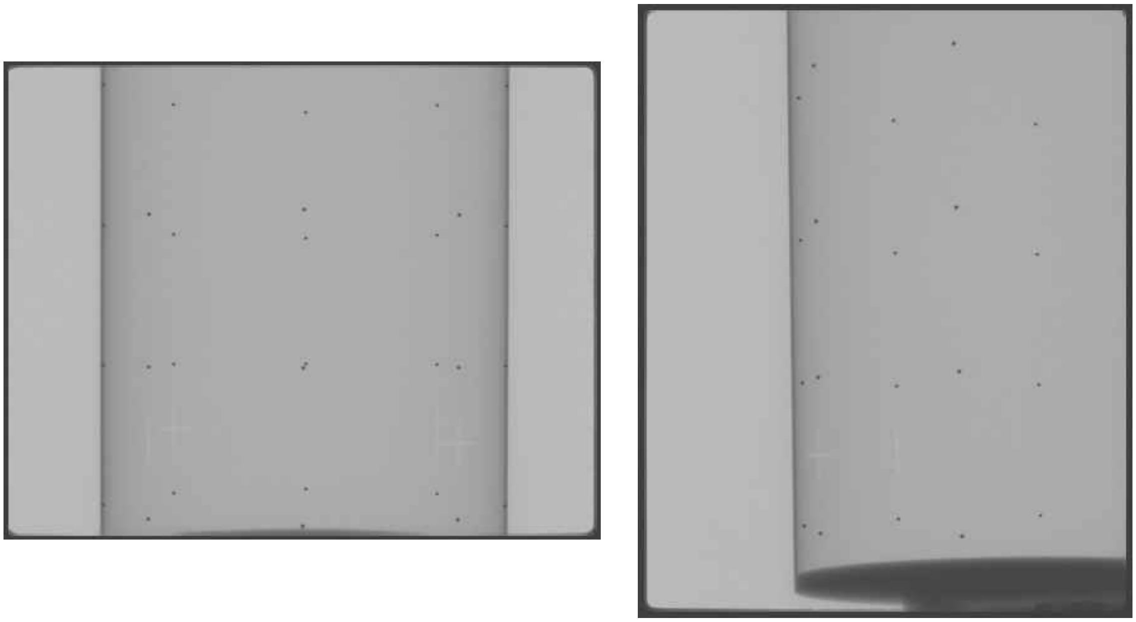


Fig. 12 Typical projection images of the calibration phantom, under full-beam and half-beam scan modes.

14.2.2 Step 2: Start CobraGeoCalibration and input phantom information

a) Input phantom geometry

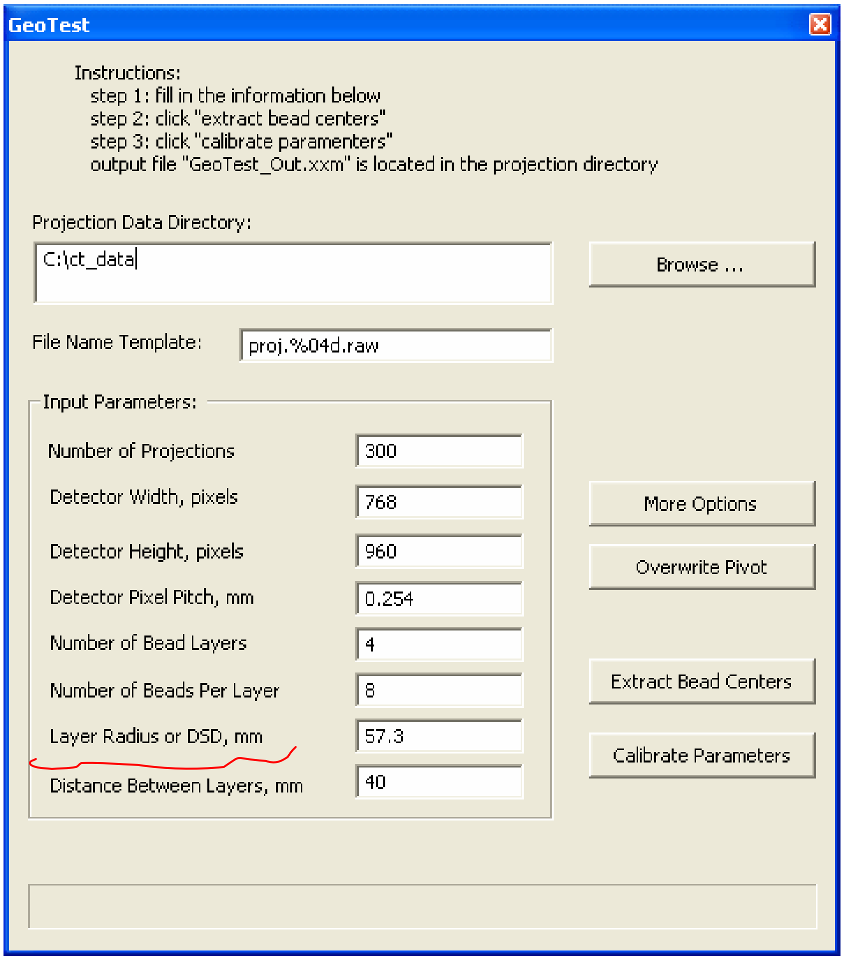
When the program starts, it provides with the default values for the detector and the phantom. The user has to set up the correct values for both the detector and the phantom. The values of the detector include the number of pixels and the pixel pitch in millimeters. Those of the phantom include the phantom diameter, the number of bead layers, the number of beads in each layer, and the distances between two neighboring layers.

The other information needed at this step is the path where the projection files are stored, the name template of those files, and the number of projections will be used in calibration. A screen shot of the program is shown in Fig. 13.

Besides the standard cylindrical calibration phantoms shown in Fig. 11, the CobraGeoCalibration program also can take a much simplified “straw” phantom, which is a line phantom with small metal beads embedded at equal distances. This functionality is designed to offer flexibility and serves as an alternative to calibrating systems with

FOV diameter and length not suitable to the standard calibration phantoms. A straw phantom can virtually fit into any sizes of FOVs. However, because of the lack of depth information in a straw phantom, it requires some prior information about the system geometry. The user should provide, to the best knowledge, the value of the x-ray source - isocenter distance in addition to the aforementioned input parameters. The program also assumes the scan angle to be 360°.

When a straw phantom is used, the box of "Layer Radius or DSD, mm" in Fig. 13 as marked out by red, should be entered with the source-isocenter distance. The rest of the boxes, as well as the rest calibration steps, remain the same as that for a standard calibration phantom.



Instructions:
step 1: fill in the information below
step 2: click "extract bead centers"
step 3: click "calibrate paramenters"
output file "GeoTest_Out.xzm" is located in the projection directory

Projection Data Directory: C:\ct_data

File Name Template: proj.%04d.raw

Input Parameters:

Number of Projections	300
Detector Width, pixels	768
Detector Height, pixels	960
Detector Pixel Pitch, mm	0.254
Number of Bead Layers	4
Number of Beads Per Layer	8
Layer Radius or DSD, mm	57.3
Distance Between Layers, mm	40

Fig. 13 Start the CobraGeoCalibration program and input values relating to the calibration phantom and the detector

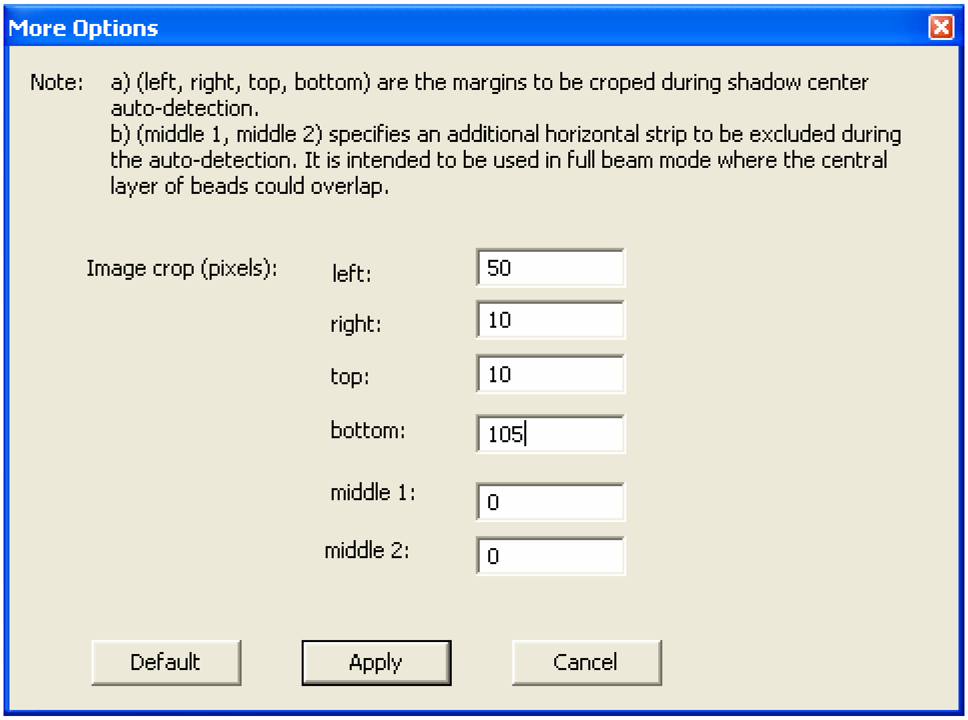
b) Setup the image margins

The dark partial ellipse in the half-beam scan in Fig. 12 can influence the bead detection process and should be excluded. This is done by setting up the image margins before starting calibration. In some cases, the beads on a certain layer can overlap with each other depending the phantom positioning and projection angle. For the reason of calibration accuracy, that entire layer of beads should be masked out in calibration as well.

To do this, please click the button “More Options”. This will bring up a dialog box, as shown in Fig 14. In this dialog box, there are 6 parameters to be set up: 4 parameters for the margins; and 2 for masking out of the overlapped bead layer (referred as strip for convenience). The margins are measured in pixels from their corresponding edges, while the strip is always specified in pixels from the top of the projection image. When there is no overlap in all the visible bead layers, the two parameters for the strip is ignored and should be set to zero’s.

Note: In full-beam mode, the values of the left and the right margins should be set to be the same, while in half-beam mode they must not be the same. In half-beam mode, the side where the phantom is truncated should be set to have a smaller margin than the other side.

Note: When one bead layer is excluded by setting up the values for strip due to bead overlapping, the distance between two neighboring layers should be adjusted accordingly. When this happens, please make sure that only two layers are included in the images after the margin and the strip being excluded, and the layer distance is set twice bigger as the physical value.



Note: a) (left, right, top, bottom) are the margins to be croped during shadow center auto-detection.
b) (middle 1, middle 2) specifies an additional horizontal strip to be excluded during the auto-detection. It is intended to be used in full beam mode where the central layer of beads could overlap.

Image crop (pixels):
left: 50
right: 10
top: 10
bottom: 105
middle 1: 0
middle 2: 0

Fig. 14 The dialog box to setup the image margins to be excluded during calibration.

14.2.3 Step 3: Extract bead centers

After all aforementioned values have been set up correctly, one can proceed to the next step which is to extract the bead centers from each projections, by clicking the button “Extract Bead Centers”. This is done automatically by the program and, depending on the size of each projection and the number of projections, it can roughly take from 1 minute to 5 minutes. The progress bar at the bottom of the program (see Fig. 13) indicates the progress of the extraction process. When it is done, the time it used will be displayed. If the process stops prematurely, the user should check if the phantom is positioned in the center of the field of view and parallel to the axis of rotation. The user also should verify that the input parameter values in step 1 and 2 are correct.

14.2.4 Step 4: Calibrate the geometry

This is the last step of the static parameter calibration procedure. When the bead extraction is finished, the user can then click the button “Calibrate Parameters”. This is a rather fast step and takes less than a second. At this step the program generates a parameter file, named as “GeoTest_output.xxm” and located under the same directory as the projection files, that can be directly used for reconstruction. The key output parameters are: the source-object distance, the source-detector distance, the detector U offset, the detector V offset (refer to 6.2, Tags Describing Scanner Geometry). The detector pivot also is outputted but at a separate file named “pivoting.bin”.

Besides the two main files containing geometrical information, three other files also are saved from intermediate steps. One contains the bead centers extracted from each projection, one contains the values of the input parameters, and the third one contains debug information. The user may ignore these files, but should send them to Exxim for diagnosis if any unexpected geometrical value appears with the calibration.

These four steps describe the procedure of calibrating a scanner with static parameters. In certain cases, a set of dynamic parameter are much desired, especially when a scanner has a gantry not rigid or precise enough but with trajectory reproducible, and needs to be treated differently. This is to be described in detail in the next section.

14.3 Dynamic Parameter Calibration Procedure

14.3.1 Step 1: Scanning of bead phantom and initial reconstruction

For the dynamic parameter calibration, a bead calibration phantom also is first scanned. As mentioned in the last section, Exxim provides optional, standard calibration phantoms which consist of precisely positioned small metal beads at known coordinates. Please refer to Fig. 11 for a typical phantom used for a FOV of about 10cm diameter. For using custom designed phantoms, Exxim should be contacted regarding additional details.

After scanning, one has to reconstruct the volume with a first estimate for the parameters. All beads should be clearly visible in the corresponding slices. We recommend reconstructing into 512x512x512 cube (416x416x416 is good enough in most cases).

NB. Since the purpose of COBRA Geo is geometry calibration, the first reconstruction most likely will contain distorted beads (“doughnuts”, “comets”, etc.) This is a consequence of small errors in the initial estimate of the geometry parameters. It is acceptable as long as the bead images are not distorted too much, meaning one can still make a reasonable guess of the center of the bead image.

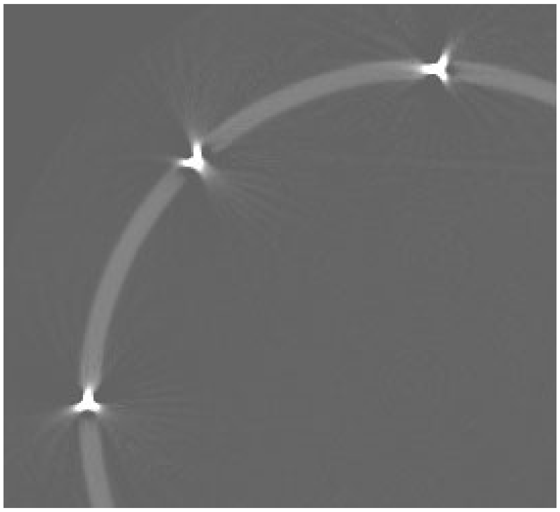


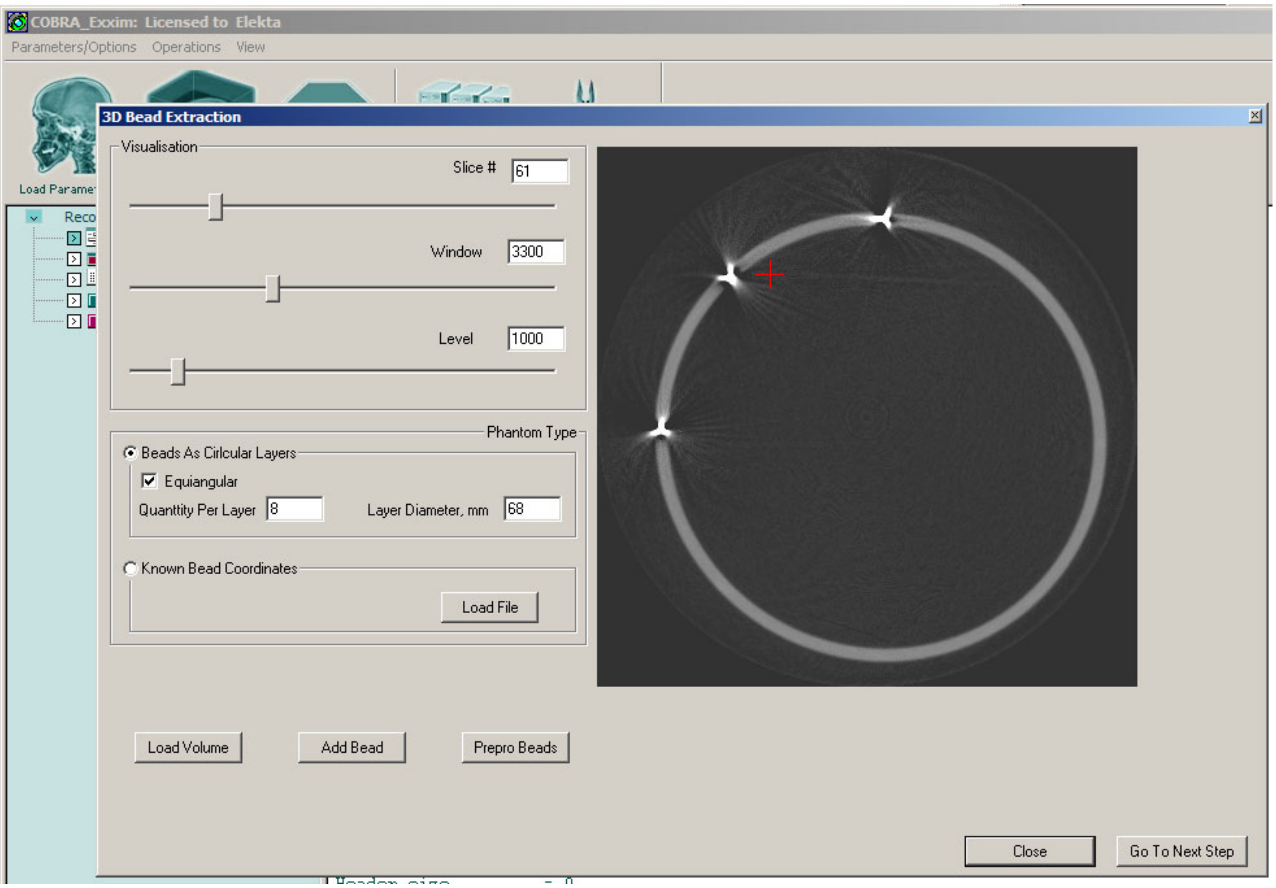
Fig. 12 Initial distortion of bead images is acceptable for COBRA_GEO are acceptable as long as the centers of the beads can be estimated.

14.3.2 Step 2: Verifying bead cluster centers.

The purpose of this step is to find the factual centers of beads in the reconstructed volume. In the case of a perfect reconstruction, this is obviously the center of mass of reconstructed balls. Since we cannot rely upon perfect reconstruction there are two pieces of information are involved:

a) centers of mass of observed clusters;
b) *a priori* knowledge about phantom geometry.

To start this operation, one has to choose the command **Operations/Geo Wizard Step 1** (Extracting Bead Centers) from COBRA GUI and then press the button **Load Volume**.



Slice # 61

Window 3300

Level 1000

● Beads As Cirlcular Layers

☑ Equiangular

Quantity Per Layer 8

Layer Diameter, mm 68

○ Known Bead Coordinates

Fig. 13 Dialog box for verifying bead cluster centers.

NB. Please make sure that this dialog box is started with the same parameter file that was used for the reconstruction. It is a good idea to avoid any xxm-file open operations until the calibration cycle is completed.

After loading the reconstructed volume, the user may need to tune Window and Level to see the (distorted) beads clearly. Please use the Slice# slider to “surf” through volume.

Then please take care about *a priori* information. This version of the tool is designed to work only with one kind of phantom: the beads are located in a plane on a accurate circle and have accurate equiangular distances. So the check box “Equiangular” has to be checked and the edit box “Layer Diameter” has to contain the corresponding information. Please also verify “Beads per Layer” edit box. The original Exxim phantom contains 8 beads.

NB. Please be aware: “Layer Diameter” is the distance measured between opposite bead centers. Example: If the external diameter of the phantom is 70 mm, the thickness of the phantom wall is 2 mm, and beads (d = 2 mm) are inserted into the drilled holes to make the surface even, then the edit box should contain 68 mm.

After that please input bead centers estimates. For that, please slide through the volume and for every reconstructed bead (again, it might have rather complicated form):

- move the red cross cursor to the bead cluster center
- press "**Add Bead**" button.

Please make sure that all beads are added; please also avoid adding the same bead twice.

Since such a manual estimation is a labor-intensive operation, the tool can provide some help to do it. If one makes a mouse double click in some place in the vicinity of the bead then the red cross jumps to the cluster center calculated automatically.

After processing all beads, the user has to press the "**Prepro Beads**" button. This initiates the procedure evaluating the bead centers on the basis of all available information including the reconstructed image and *a priori* knowledge about the bead geometry configuration.

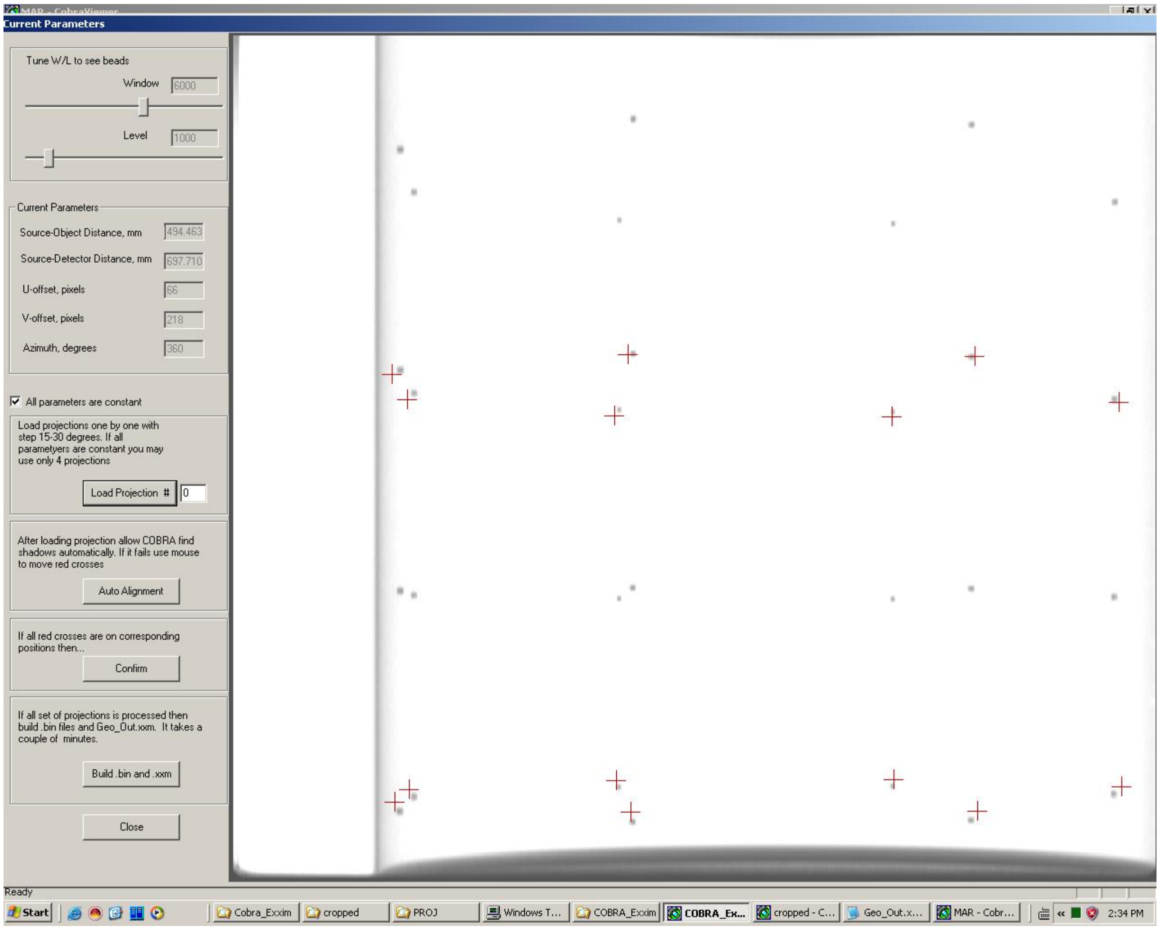
In summary:

1. Start the dialog by Geo Wizard Step 1 (Extracting Bead Centers) command
2. Press "Load Volume"
3. Take care about edit boxes: layer diameter and bead quantity per layer
4. Surf through the volume, double click on every bead, and press "Add Bead"
5. After all beads added, press "Prepro Beads".

NB. You can observe the result of this step in two files (created in the input CT projection folder): beads_raw.prm and beads.prm.

14.3.3 Step 3: Performing “per-projection” calibration

The purpose of this step is to evaluate scanner geometry parameters on a “per-projection” basis. To start this operation, one has to choose the command Operations/Geo Wizard Step 2 (Adjusting Scanner Parameters) from the COBRA GUI.



Tune W/L to see beads

Window 6000

Level 1000

Current Parameters

Source-Object Distance, mm 494.463

Source-Detector Distance, mm 697.710

U-offset, pixels 66

V-offset, pixels 218

Azimuth, degrees 360

☑ All parameters are constant

Load projections one by one with step 15-30 degrees. If all parametyers are constant you may use only 4 projections

Load Projection # 0

After loading projection allow COBRA find shadows automatically. If it fails use mouse to move red crosses

If all red crosses are on corresponding positions then...

If all set of projections is processed then build .bin files and Geo_Out.xxm. It takes a couple of minutes.

Fig. 14 Dialog box for verifying bead shadow centers. Please be aware that this dialog box transforms the projection to fit the screen.

The dialog box contains the following controls:

- The picture of the current projection (see below also) with additional markers (red crosses). The markers correspond to “ideal” shadows defined by the scanner geometry and “ideal” bead centers extracted/calculated on the previous step of the process.
- **Load Projection #** button allows to work with any projection in the dataset.
- **Window/Level** are conventional visualization controls.
- **Current Parameters** shows the scanner geometry parameters.

- **Auto Alignment**. The user is supposed to align the markers with bead shadows. If the crosses are close enough (+/- 11 pixels) to the corresponding shadows, then auto alignment will work. Please do not blindly rely upon this feature as it may not find the right match every time.
- **Confirm**. This button starts the process of geometry parameter alignment for the current projection.

1. *Summary for Step 3:*
   Load the projection to be used in the current step (the projection # 0 is loaded automatically after opening this dialog window).
2. Align all red crosses with shadow centers.
3. Press Confirm button to record the information..
4. The calibration process has to be performed for a reasonable set of projections.

4.1. In the **mode "All parameters are constant"** we recommend doing calibration for the first one, for the last one and then 2-3 other projections. **This is the main mode, which has to be applied**.

4.2. If the mode "All parameters are constant" is off then we recommend doing calibration for the first one, for the last one and then every 30-60 degrees. It is a good idea to choose smaller step size between projections in the start and in the end phase of a rotation because these are the critical regions. Example: If the amount of projections is 600, then suggested projections to calibrate are ## 0, 50, 100, 200, 300, 400, 500, 550, and 599.

5. To finalize calibration one has to press the button **Build .bin & .xxm .** It takes 1-2 minutes to finalize the process.

Important notes.

Please be aware that starting version 5.0.44 Geo component also outputs the parameter file Geo_Out.xxm. To make all calibration results effective one must use values from the following tags:

```
PARTAG_DETOFFSETU
PARTAG_DETOFFSETV
PARTAG_DETPITCHU
PARTAG_DETPITCHV
PARTAG_SRCOBJDIST
PARTAG_SRCDETDIST
PARTAG_SCANANGLE
PARTAG_STARTANGLE
```

Please be aware that for some projections it is hard to understand the right correspondence between the shadow and a cross (see the picture below): shadows can overlap each other in some angular positions. Such projections have to be avoided.

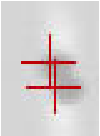


Fig. 15 Bead shadows are overlapped. Please do not use such projections to calibrate your scanner.

In the same time usually it is very important to get the first and last frames calibrated. Please always try to do that in spite of the fact that these projections might contain overlap like shown above. If a couple of red crosses cannot be placed properly, please leave them as-is. The calibration process is based on the average error over the entire set of beads; so 2 wrong settings out of 16 will not disturb the parameters very much. However, the best solution here is to scan the phantom in such a way that you can easily calibrate the first and last frames.

15 Troubleshooting hints

3D reconstruction procedures in general and the COBRA program in particular, require large amounts of accurate data and associated parameter files to provide correct results. From time to time it will be necessary to determine parameters empirically (in particular some of the parameter signs). If the reconstructed image seems erroneous, double check file names, try “+” and “-“ values for parameters, and make sure that the preprocessing procedure sequence is correct.

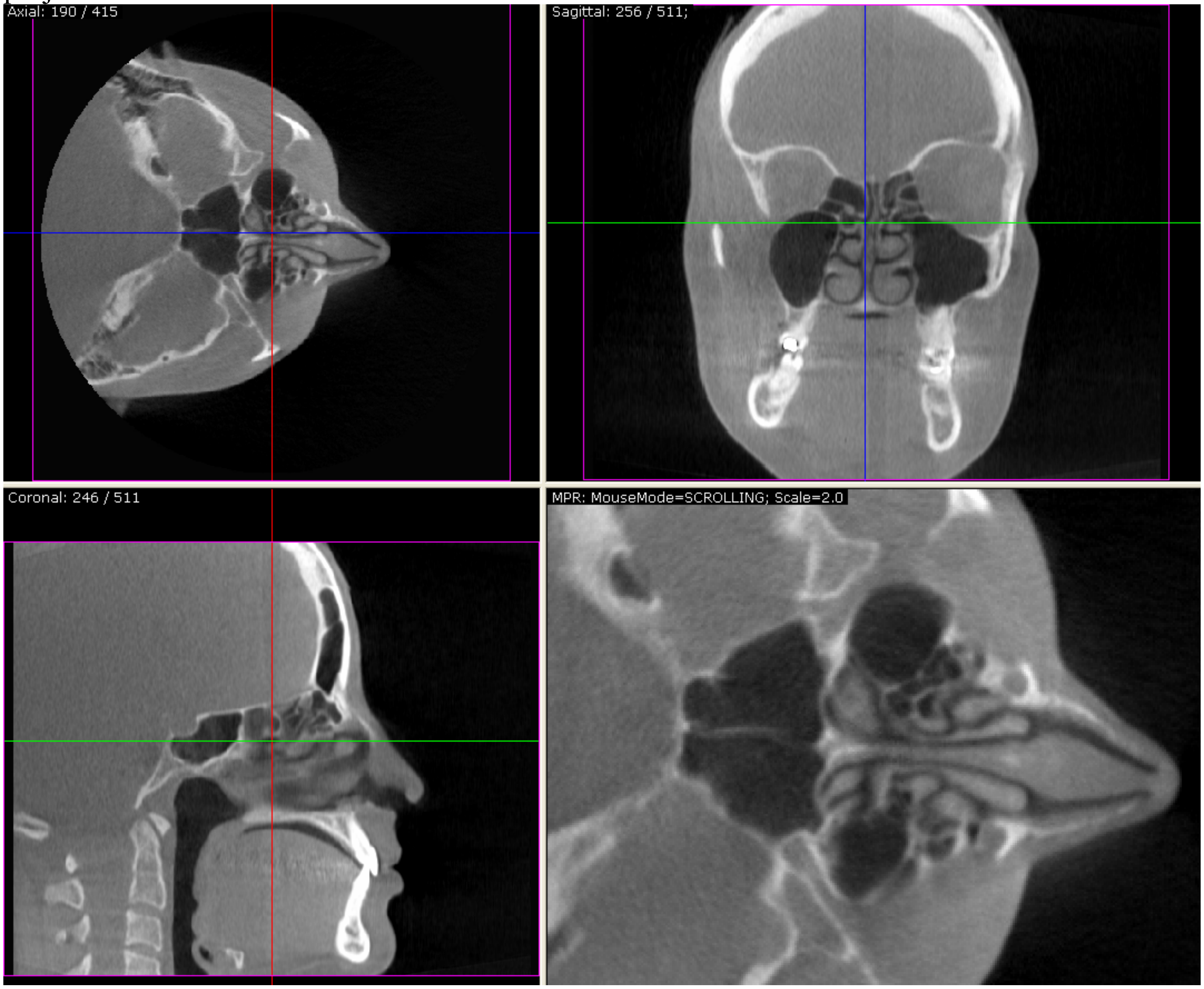
Refer to the table below to resolve some common problems:

Problem	**Possible cause**	**Solution**
The program won't start	COM component BackPrj_COM_Server.exe is not installed correctly	Check whether it is put into the system directory. Try to register it again by executing it from MS DOS window with /RegServer key.
Reconstruction process can be started but it runs very slowly	Allocated memory is bigger than physical RAM	Check used memory using the Windows Task Manager. Close other active applications. Consider changing the option "3D buffer size"
"Performance" tab remains blank after processing 32 projections	Wrong input data folder in .xxm parameter file Wrong input file name template	Check and correct
Output slices have obvious "tails".	Scanner geometry is confused (DSO/DDO/rotation direction)	Check the following parameters: PARTAG_DETOFFSETU PARTAG_DETOFFSETV PARTAG_ROTATIONDIR also these files SrcOrigDist.bin OrigDetDist.bin Try other signs.
Output slices are blurred and/or double-contoured	Inaccurate u/v offset values (possibly just the sign)	Check these parameters: PARTAG_DETOFFSETU PARTAG_DETOFFSETV and these files uoffset.bin voffset.bin Try other signs.

Some reconstructed regions look reasonable, others look confused	Bad scaling with integer overflow can produce complex reconstruction errors like "shadowed" regions	Try setting the PARTAG_SCALEFACTOR value to -1 (minus one). Take a look at preprocd_proj.000 and auto-calculated scale factor. Change the PARTAG_SCALEFACTOR value
Slices are produced but output voxel values look totally confused	Incorrect preprocessing	Make sure that suitable preprocessing steps are used. For example both the air calibration and the logging steps must be excluded if the scanner's controlling PC does them.

16 Viewer - COBRAViewer

This utility is a standard Windows® application providing a simple service for viewing projections and slices.



Notes:

1. Since projections and slices lack header information, it is necessary to define the image proportions when opening files. The program tries to do

this automatically, in which case the width and height dialog does not appear. Sometimes the user needs to define width/height as the proportion auto-detection is defeated (example: image very noisy image). The GUI command/button ***Reformat Image*** can be used at any time.

2. If projections and/or slices use the default names (raw.0000, raw.0001, ... and 0000.slice, 0001.slice, ...) then COBRA_View provides a slide show (a Windows slider is used to select the displayed slice). This is invoked by the GUI command/button ***Show Folder.*** Once the slide-show dialog box is displayed, ensure that ***Template*** and ***Range*** are correct, press ***Apply*** and select the desired images with the slider.

17 Three Spheres Phantom

This is a sample data set to be used in a first test of the available hardware. It is available in the file *ThreeSphPhantom.zip* containing;

- 95 simulated projections of three spheres in 3-D space. The spheres are solid and have a constant density.
- Files ***offset, AirRaw, parameter_512_std.xxm.*** These are necessary for COBRA_Exxim to perform the reconstruction.
- Pre-calculated slices for comparison purposes.

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