



Synchrotron X-ray computed microtomography: procedures for image reconstruction and analysis

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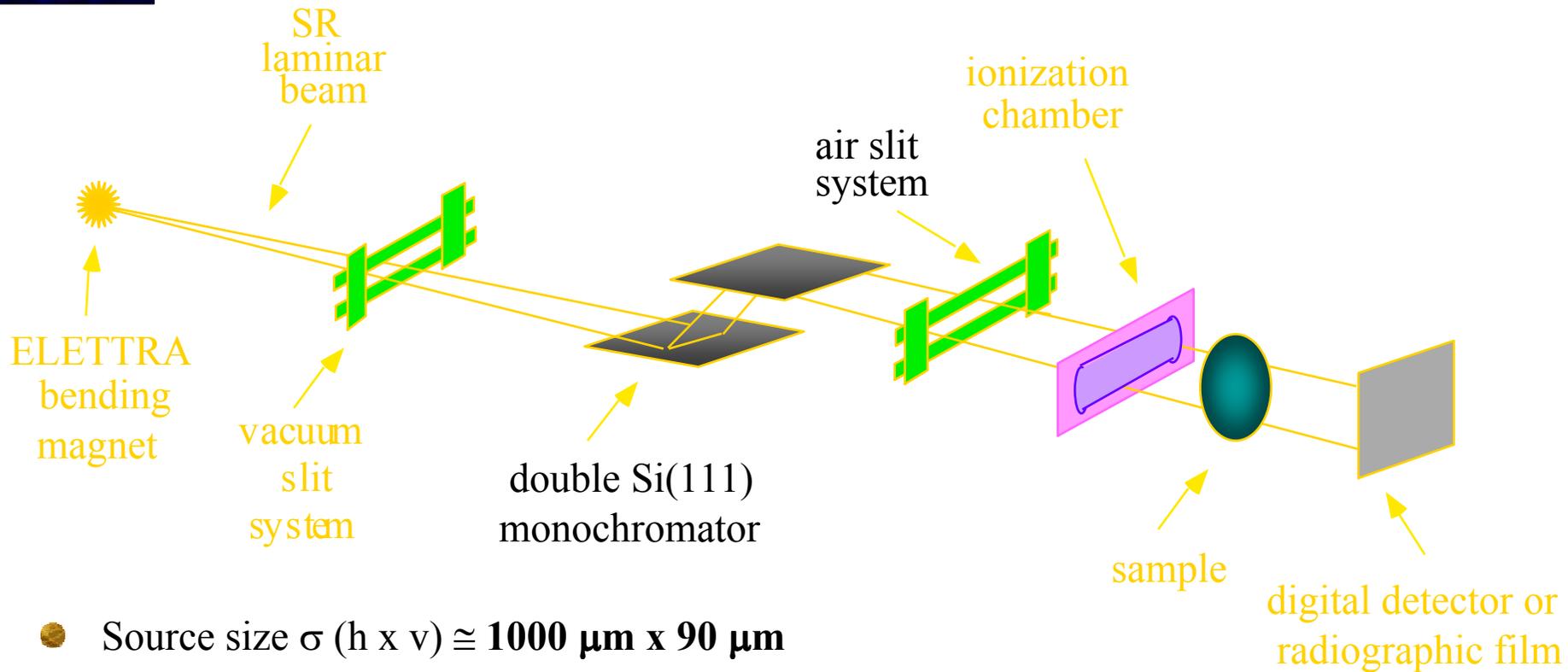
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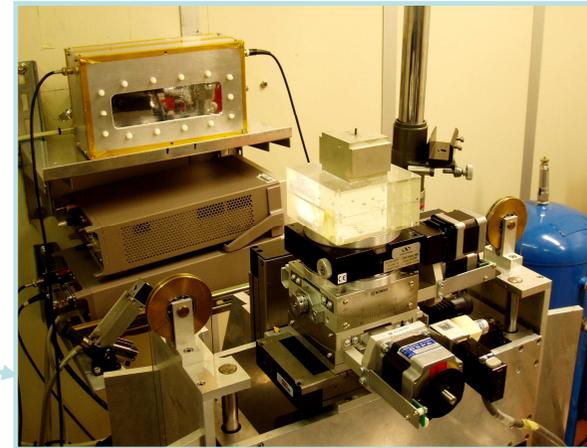
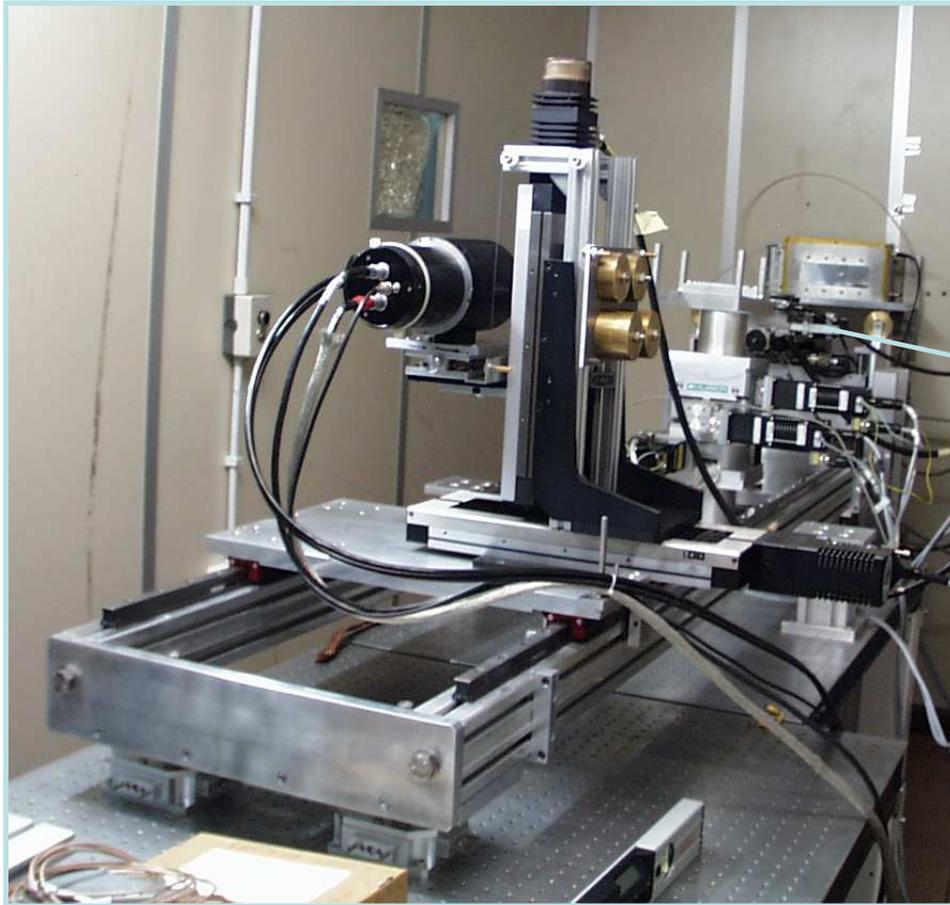
The SYRMEP beamline



- Source size σ (h x v) \cong **1000 μm x 90 μm**
- Source-to-sample distance: **D \cong 24 m**
- Beam size at sample (h x v) \cong **150 mm x 6 mm**
- Energy range: **8.3 \div 35 keV**, Bandwidth $\Delta\lambda/\lambda \cong 2 \times 10^{-3}$
- Typical fluxes at 15 keV \cong **$2 * 10^8$ phot./mm² s** (@ 2 GeV, 300 mA)
 $7 * 10^8$ phot./mm² s (@ 2.4 GeV, 180 mA)



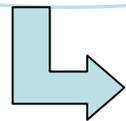
The experimental hutch at SYRMEP





X-ray imaging at a 3rd generation SR facility

- high energy photons and high flux
 - **heavy** and/or **bulky samples** in transmission geometry
 - **tunability** in a large energy range
 - **short** exposure times
- small angular source size and big source-to-sample distance
 - **high spatial resolution** ($< \approx 1 \mu\text{m}$ at SYRMEP)
 - possibility of **big sample-to-detector distances** ($< \approx 1 \text{ m}$ at SYRMEP)
 - **high spatial coherence** of the X-ray beam ($L_c \cong 10 \mu\text{m}$ @ 15 keV)



Phase-sensitive techniques



SR X-ray imaging studies



Medical imaging:

- bones, dental implants
- mammography
- tissues

Material science imaging:

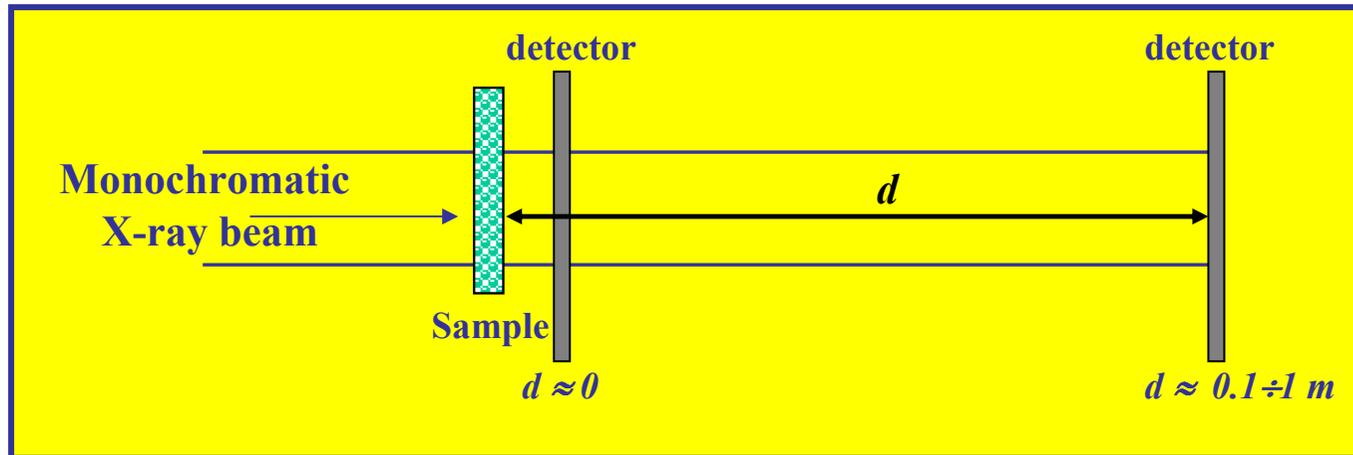
- crystals
- rocks and minerals
- food science
- archeological samples
- engineering science



The X-ray imaging techniques



Absorption and Phase Contrast (PC) Radiography



$$(\Delta I/I)_{\text{abs}} = e^{-c \Delta \mu} - 1$$

$$\Delta \phi = 2\pi c \Delta \delta / \lambda$$

$r \ll a \Rightarrow$ edge detection regime

$r \cong a \Rightarrow$ holographic regime

$r \gg a \Rightarrow$ Fraunhofer diffraction

$\mathbf{n} = 1 - \delta - i\beta$: refraction index

$\mu = 4\pi \beta / \lambda$: linear absorption coeff.

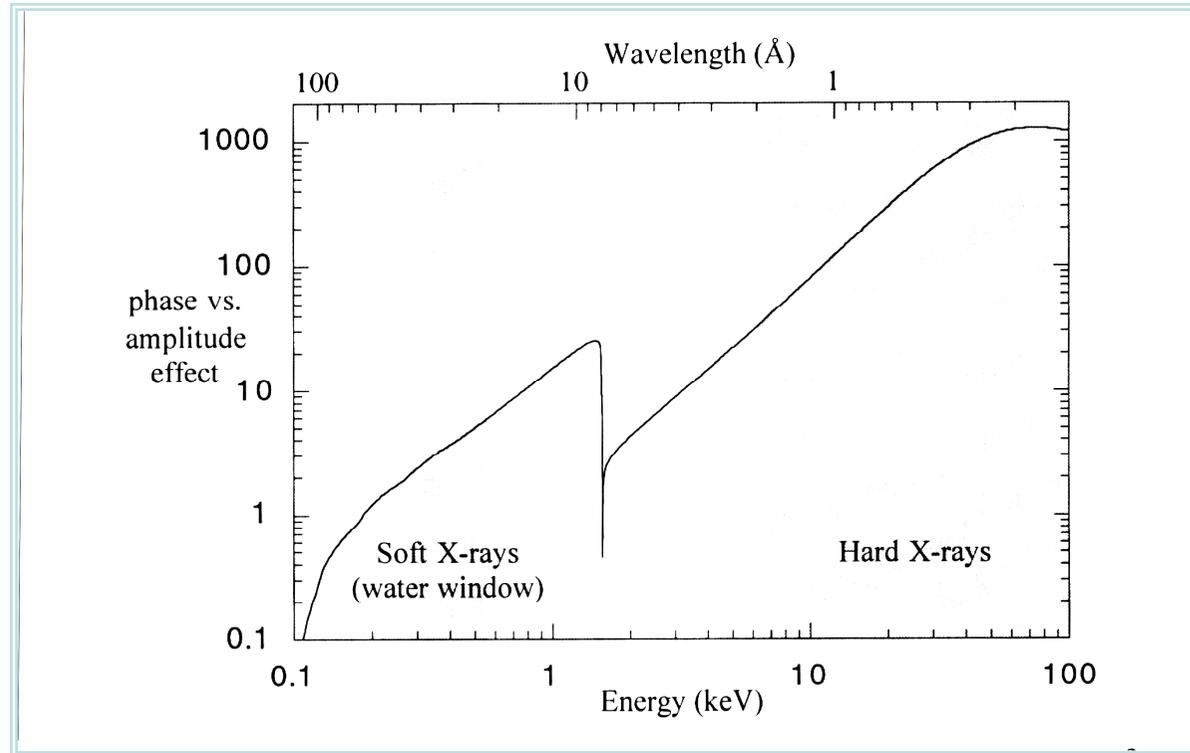
c : object size // to beam direction

a : object size \perp to beam direction

$r = (\lambda d)^{1/2}$: first Fresnel zone radius



Absorption vs. Phase Contrast

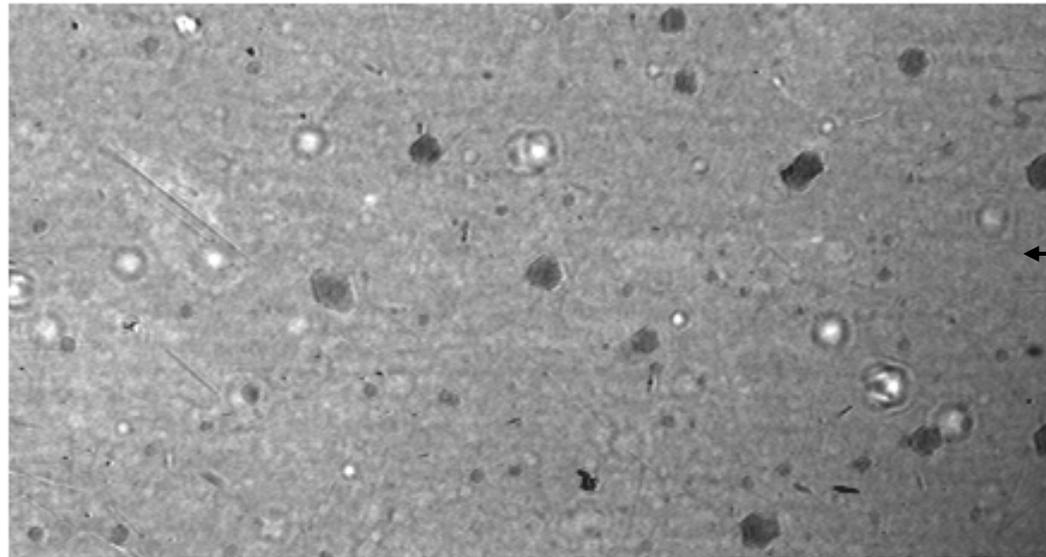


- Analysis of **materials**
 - with **weak absorption** with respect to **hard X-rays**
 - producing **significant variations** of X-rays **optical path**

Radiographs of an AlPdMn grain recorded at the ESRF (France)

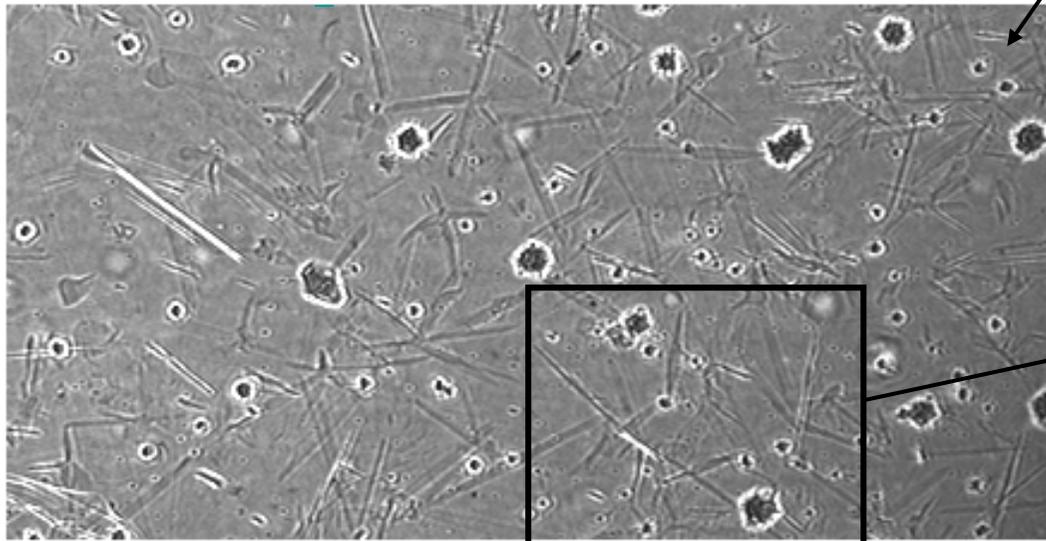


L. Mancini, PhD Thesis, 1998



Absorption radiograph

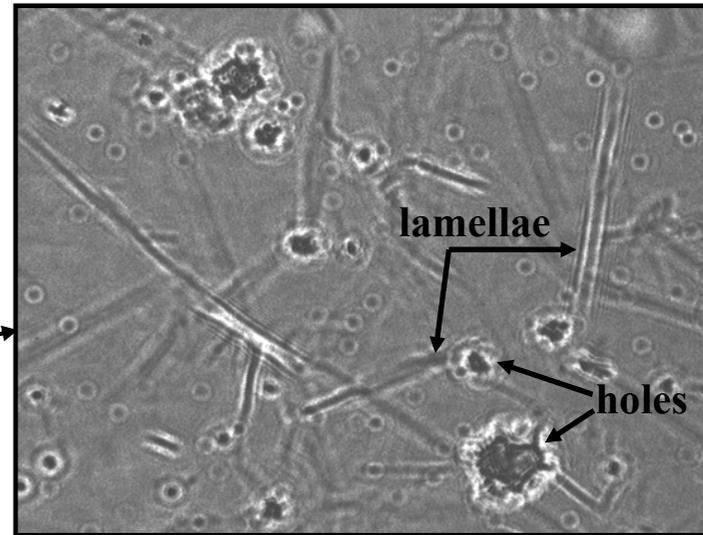
$d = 2 \text{ cm}$



Phase radiograph

$d = 50 \text{ cm}$

400 μm



lamellae

holes

200 μm



Vertical source size σ estimation from PCR of a nylon wire



Sample: Nylon wire (120 μm \varnothing)

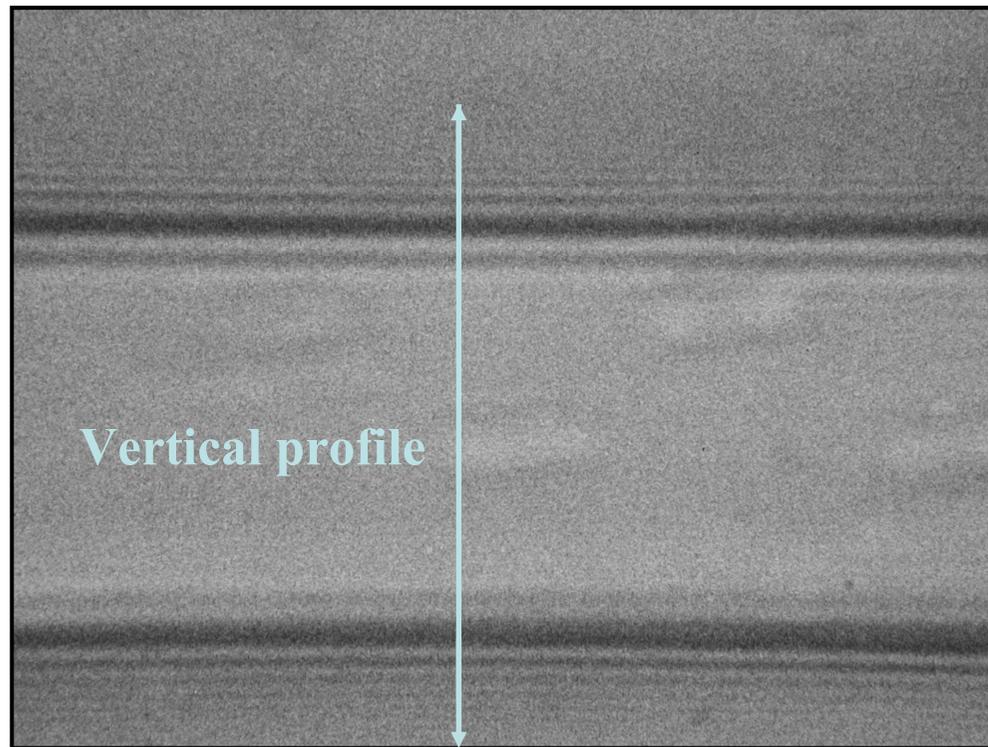
E = 10 keV

Refraction index: $\delta = 2.55 \times 10^{-6}$, $\beta = 2.72 \times 10^{-9}$

d = 1 m

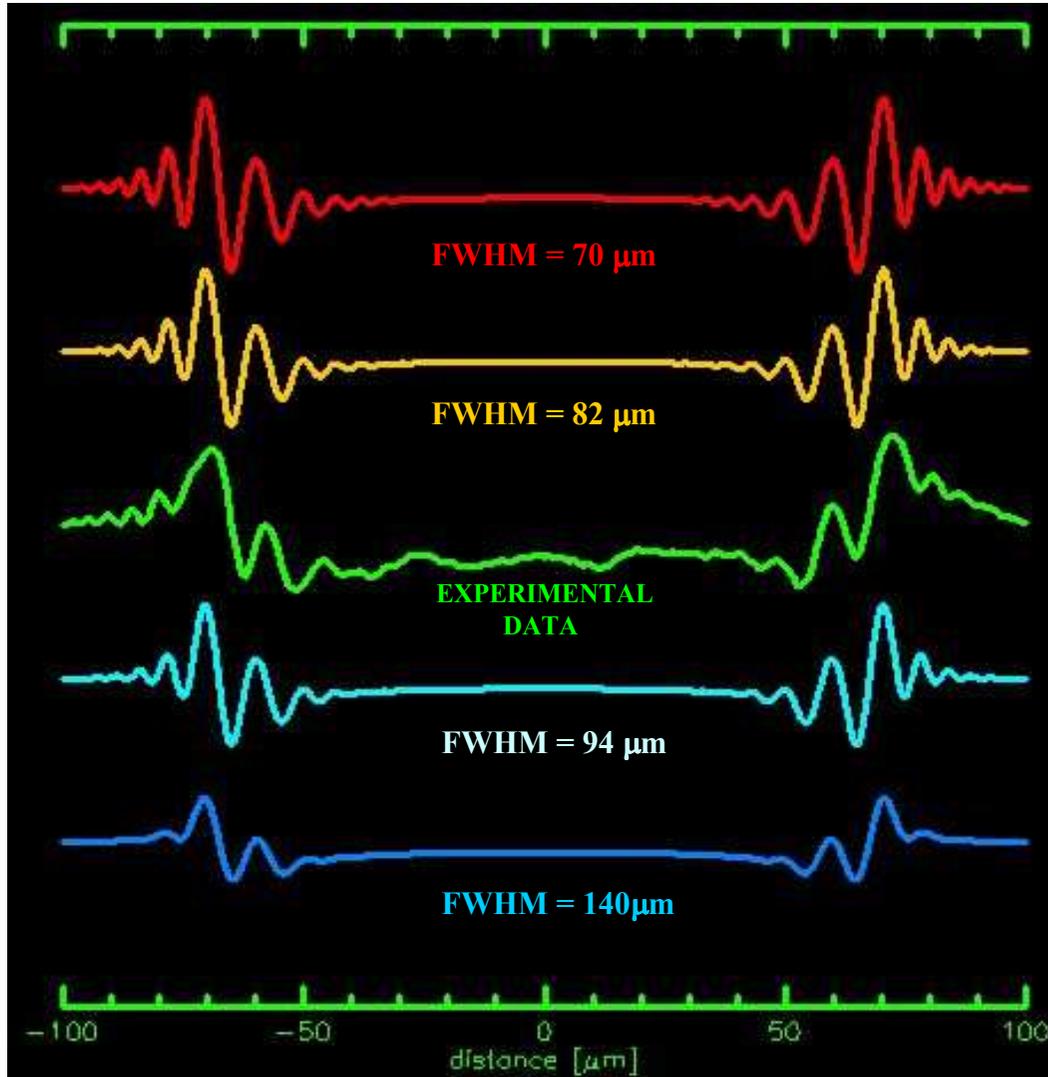
D = 24 m

Detector: 1 μm resolution film





Experimental and simulated profiles for different σ values



Nylon wire (120 μm \emptyset)
E = 10 keV
d = 1 m



$\sigma < \cong 90\text{-}100 \mu\text{m}$

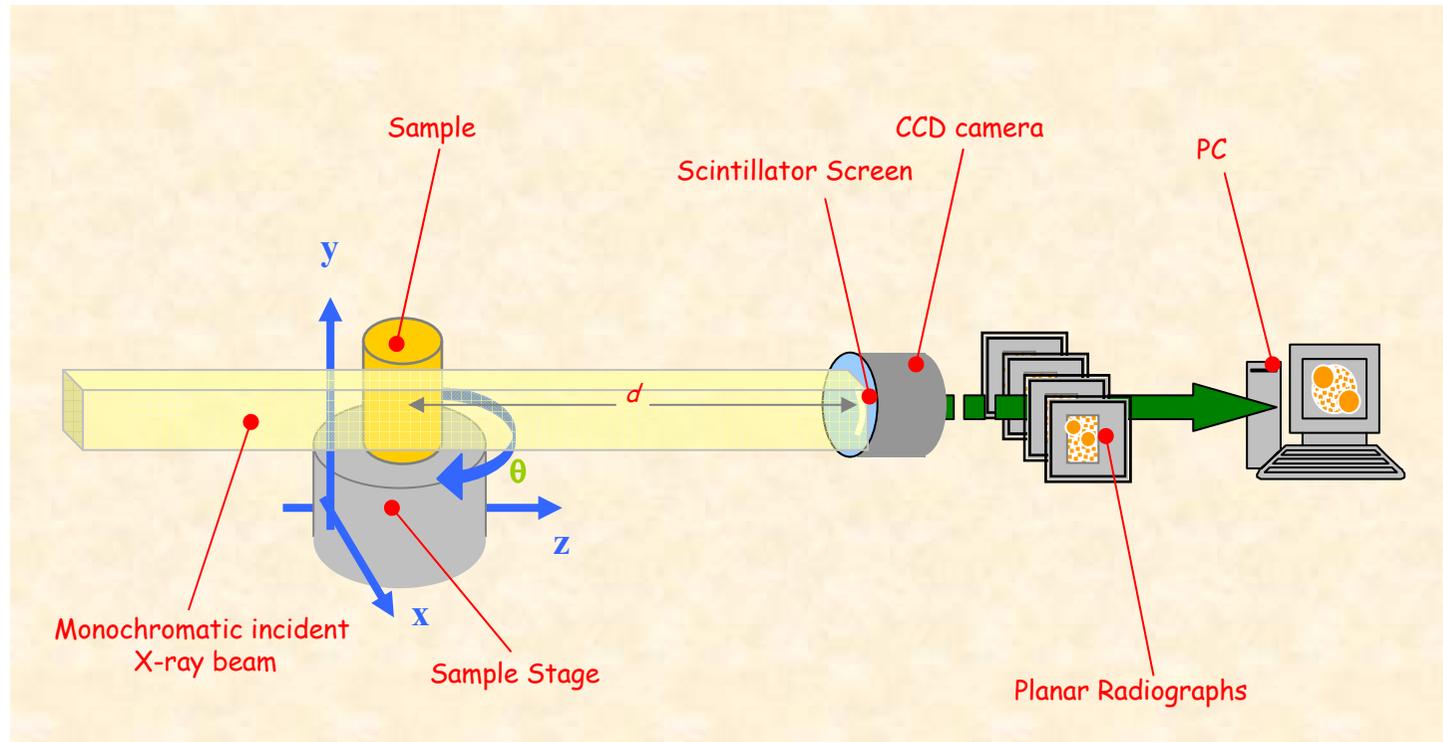


Results

- **Spatial resolution $\rho = \sigma d / D < \cong 1 \mu\text{m}$ up to $d = 0.3 \text{ m}$
 $\cong 4 \mu\text{m}$ at $d = 1 \text{ m}$**
- Possibility to work at **big sample-to-detector distances: $D > \approx 1 \text{ m}$**
- **High transverse coherence of the beam: $L_c = \lambda D / (2 \sigma) \cong 10 \mu\text{m}$**



The principle of computed microtomography



CCD camera: 2048x2048 pixels², pixel size: 14 μm , FOV: 28x28 mm²

- **Precious** for investigation of **internal features without sample sectioning**:
 - in many cases the **sectioning procedure** modifies the structures under analysis
 - the sample can be after **studied by other experimental techniques**,
 - or submitted to several **treatments** (mechanical, thermal, etc...)



SR X-ray imaging

***In-situ* and *ex-situ* experiments in a large range of materials:**

- growth processes
- mechanical and thermal treatments
- phase transitions

The aim

**to investigate the relationship between microstructural
and physical properties**

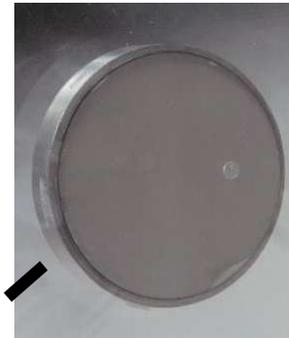


CCD Detector & Optics



● Photonic science

- 2048 x 2048 pixel
- each pixel 14 x 14 μm^2



- 1:1 Optics
 - 20 (40) μm thick IS
 - effective pixel size: 14 μm
 - PSF \sim 30 (50) μm



- 11:40 (Magnifying) Optics
 - \sim 5 μm thick IS
 - effective pixel size: 3.85 μm
 - PSF \sim 13 μm



New VHR detector

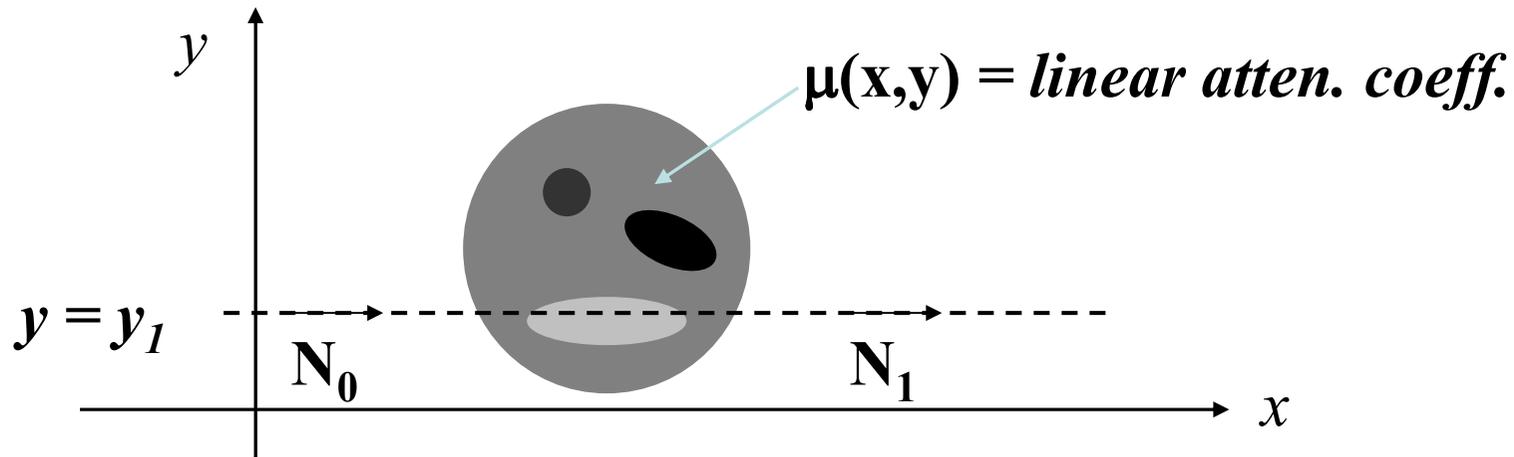
- Water cooled **12/16 bit** camera
 - **4008 x 2672** pixels²
 - each pixel $9 \times 9 \mu\text{m}^2$
- **1:2 (Magnifying) optics**
 - $\sim 9 \mu\text{m}$ thick GdOS scintillator
 - effective pixel size: $4.5 \mu\text{m}$
 - PSF $\sim 13 \mu\text{m}$
 - 1.8 full frames/sec at bin = 1×1





Principles of transmission X-ray μ -CT

Kak A.C., Slaney M., IEEE Press, 1987



$$N_1 = N_0 \exp[- \int_{\text{path}} \mu(x,y_1) dx] \quad (\text{Beer-Lambert law})$$

$$\ln (N_0 / N_1) = \int_{\text{path}} \mu(x,y_1) dx = P_{\theta}(t) \quad ((\theta, t) \text{ polar coordin.})$$

Repeating such a measurement along a sufficient number of straight lines within the same slice delivers the **Radon transform** of the object. The inverse of the Radon transform **allows to reconstruct** the $\mu(x,y)$ map of the slice.



The Fourier Slice Theorem

Kak A.C., Slaney M., IEEE Press, 1987

A **line integral** $P_{\theta}(t)$ represents the integral of the $\mu(x,y)$ of the object along a line. $P_{\theta}(t)$ is known as the **Radon transform** of the function $\mu(x,y)$.

A **projection** is formed by combining a set of line integrals. The simplest projection is a collection of parallel ray integrals **at a given angle (θ)**.

The **Fourier Slice Theorem** demonstrates that the 1D Fourier transform of a parallel projection of an image $\mu(x,y)$, taken at an angle θ , gives a slice of the 2D transform of the object function.

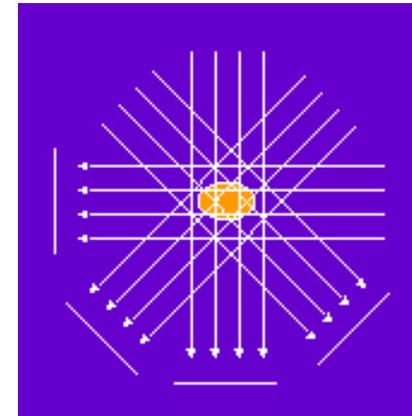
Then, **given the projection data**, it should be possible to **estimate the object** by simply performing a **2D inverse Fourier transform**.



Elaboration of tomographic images

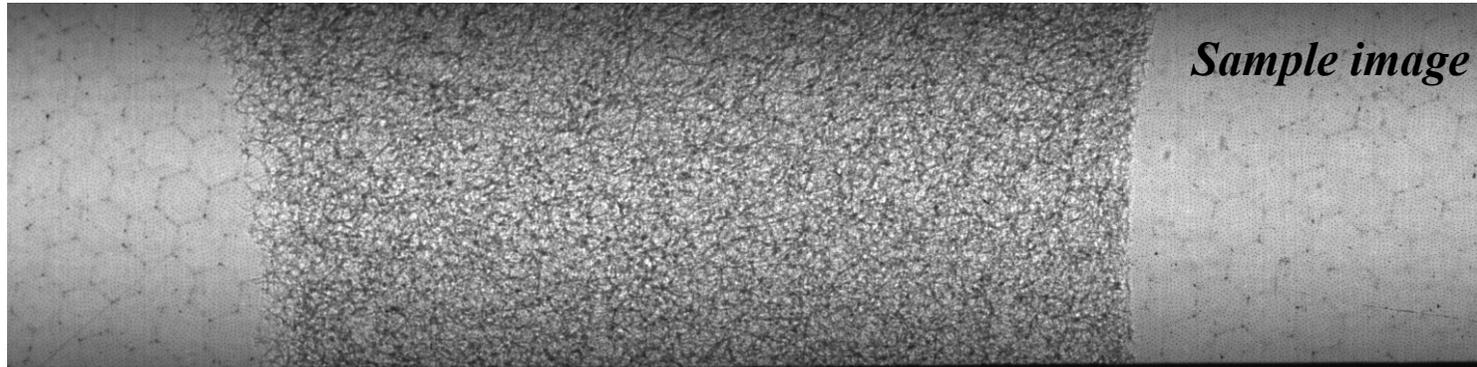


- Planar radiographs are elaborated by a **reconstruction procedure**:
 - **filtered backprojection** algorithm [*Herman, 1980*]
 - for each projection an **intensity map** is recorded in the xy detector plane
 - projections are submitted to **filtering procedures**
 - each intensity map is **back projected** along the normal to the projection itself
 - finally, the intensities are added for all the projections
- Reconstructed slices are then treated by a **rendering procedure**:
 - 2D slices visualized as **Stack**
 - 3D views of the sample can be obtained (**Volume rendering**)
- Rendered images can be elaborated applying filters, false colors, **segmentation tools** to extract quantitative information.

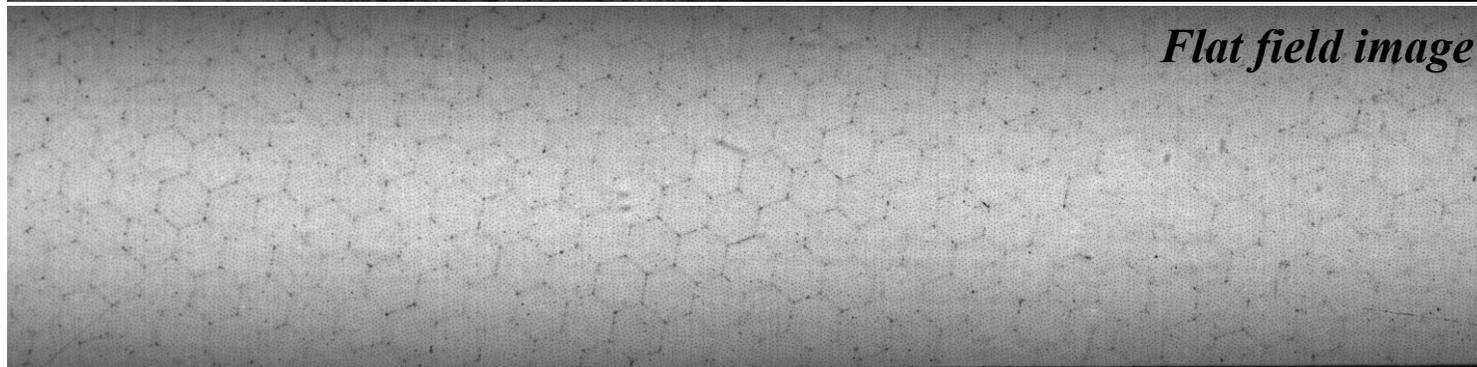




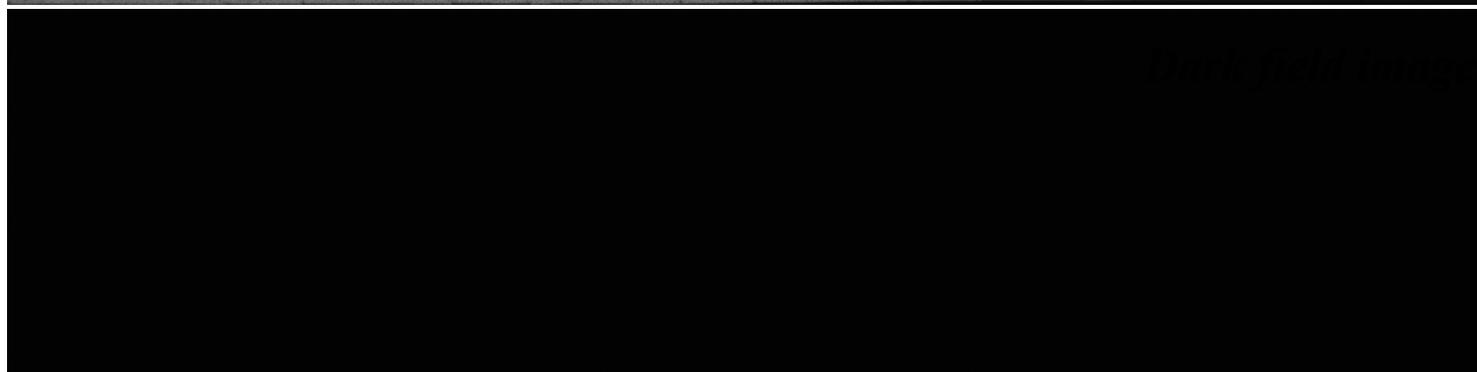
Recording of tomographic images



Sample image

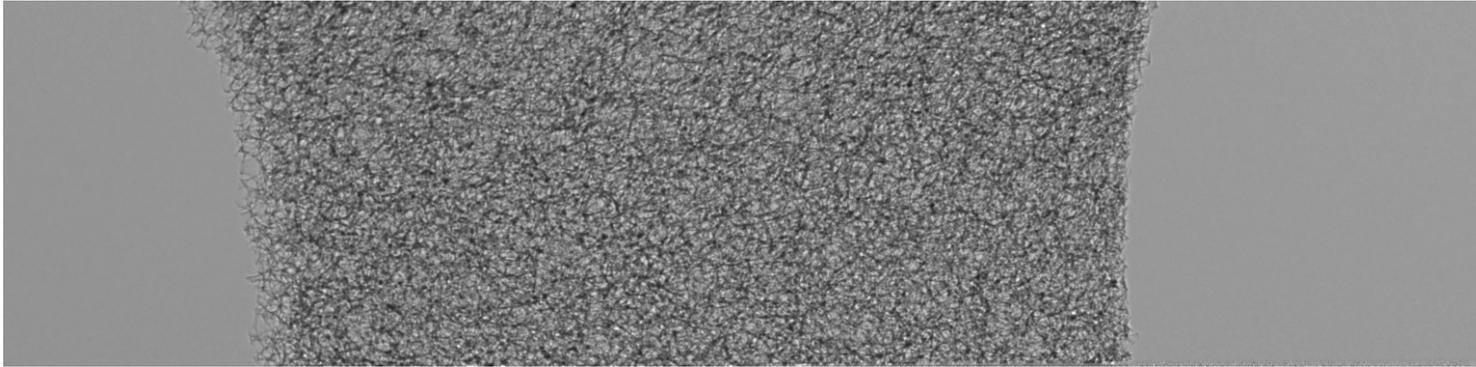


Flat field image





Flat procedure for the tomographic images



$$I_{flatted} = (I_{sample} - I_{dark}) / (I_{flat} - I_{dark})$$



Starting of the reconstruction procedure



The screenshot displays the SYRMEP TOMO PROJECT software interface, which is used for tomographic reconstruction. The main window is titled "SYRMEP TOMO PROJECT" and contains several panels and controls:

- File Panel:** Contains a "Filter" dropdown set to "GEN_HAMMING", an "Interpolation" dropdown set to "BILINEAR", and several input fields: "Interp. parameter" (-0.5), "Kernel Width" (250), "Rem Ring Width" (3), and "Rem Zinger Width" (3). Below these are buttons for "LOAD COLOR TABLE", "PROFILES SIND", "RECONSTRUCT VOLUME", "Volume 8bit Convert", "Stack 8bit Convert", and "Stack 16bit Convert".
- SINOGRAM BASE---** Panel: Includes input fields for "Sinogram from Slice" (0), "Crop Left-Right" (0, 0), and "Normalization Widths" (0, 0).
- PROJECTION_BASE Panel:** Features a path input field showing "c:/", and buttons for "Image Number: 0", "Slice Number: 0", "CREATE SINOGRAM", "PROFILES IMA", and "CREATE VOLUME FOLDER". A large black rectangular area is visible below these controls.
- VOLUME RENDERING Panel:** Located in the bottom right, it includes a "--VOLUME FILE--" section with "X size:", "Y size:", and "Z size:" labels, each followed by an input field containing "0". Below these are buttons for "3D RENDERING" and "CREATE MOVIE".



Choice of the slice to reconstruct



PROJECTION_BASE

--FRAME BASE--

Image Number: Slice Number: CREATE SINOGRAM PROFILES IMA CREATE VOLUME FOLDER

Slice number 200

The image shows a grayscale tomographic slice of a porous material. A horizontal cyan line is drawn across the slice, with an arrow pointing to it from the text "Slice number 200". A vertical red line is also present, with numerical labels 50, 100, 150, and 200 along its length.

PROJECTION_BASE

--FRAME BASE--

F:\ATOMO_RESULTS\PU_SORRENTINO\PU_NERO_DEFOMISURA TOMO\

Image Number: Slice Number: CREATE SINOGRAM PROFILES IMA CREATE VOLUME FOLDER

The image shows the same tomographic slice as above. A blue arrow points from the "CREATE SINOGRAM" button to the slice. A horizontal red line is drawn across the slice, and a vertical red line with numerical labels 50, 100, 150, and 200 is also present.



Creation of the sinogram



SYRMEP TOMO PROJECT

File

Filter: SHEPP LOGAN

Interpolation: BILINEAR

Interp. parameter: -0.5

Kernel Width: 250

Rem Ring Width: 3

Rem Zinger Width: 3

LOAD COLOR TABLE

PROFILES SINO

RECONSTRUCT VOLUME

8bit CONVERT

---SINOGRAM BASE---

Sinogram from Slice: 200 F:\TOMO_RESULTS\PU_SORRENTINO\PU_NERO_DEF0\MISURA TC

Crop Left-Right: 300 1800

Normalization Widths: 200 1900

RECONSTRUCT SLICE

A sinogram plot showing a dense collection of curved lines representing projections. The plot has a vertical axis with tick marks at 200, 400, 600, 800, 1000, 1200, 1400, and 1600. A horizontal red line is drawn across the plot at the 500 mark on the vertical axis. A blue arrow points from the 'RECONSTRUCT SLICE' button to this red line. Another blue arrow points from the 'Crop Left-Right' input fields to the plot area. A third blue arrow points from the 'Normalization Widths' input fields to the plot area.



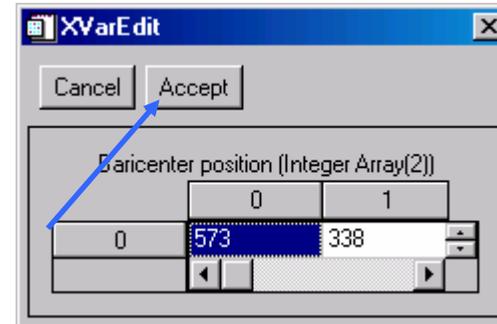
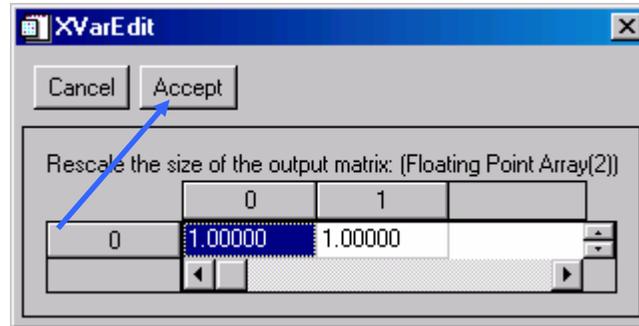
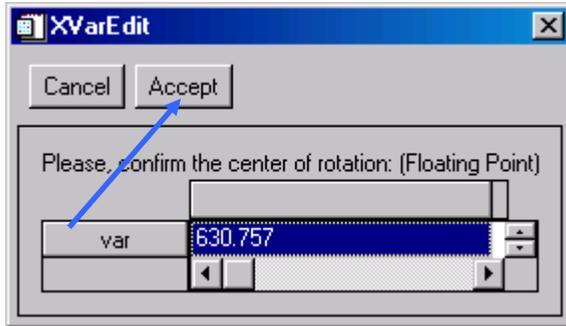
Filtering procedure

The screenshot displays the SYRMEP TOMO PROJECT software interface. The top window, titled "SYRMEP TOMO PROJECT", shows the "SINOGRAM BASE" configuration. The "Filter" is set to "SHEPP LOGAN", and the "Interpolation" is set to "BILINEAR". The "Sinogram from Slice" is 200, and the "Crop Left-Right" is 300 1800. The "Normalization Widths" are 200 1900. The bottom window, also titled "SYRMEP TOMO PROJECT", shows the "RECONSTRUCT SLICE" configuration. The "Filter" is set to "GEN_HAMMING", and the "Interpolation" is set to "RAMLAK". The "Sinogram from Slice" is 200, and the "Crop Left-Right" is 1000 1500. The "Normalization Widths" are 200 1900. A blue arrow points to the "SHEPP LOGAN" filter selection in the top window.

If in the reconstruction the backprojection is done without filtering the sinogram first, the resulting image is very blurry. In practice **one always filters the sinogram before the backprojection**. In this example the sinogram will be filtered using a **Shepp-Logan filter**, which is an edge-sharpening filter.

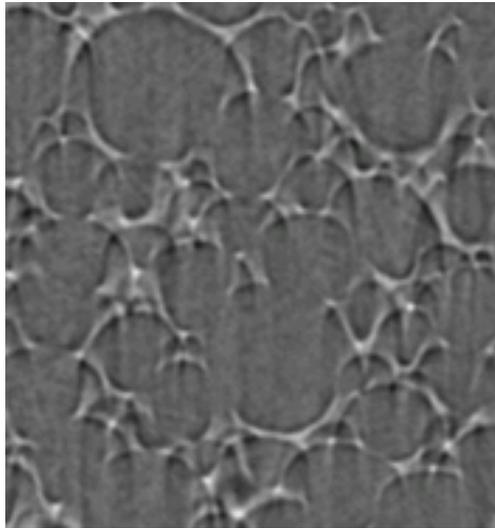


Choice of the reconstruction parameters

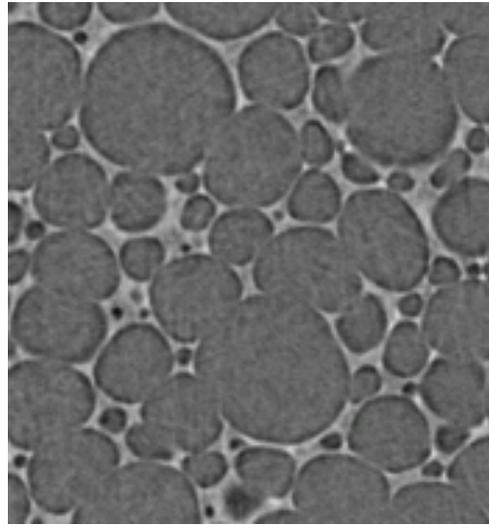




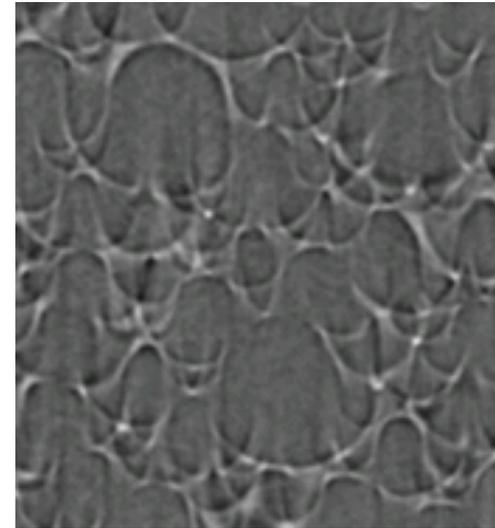
Slice reconstruction: optimization of the rotation center



$C = 624.750$



$C = 630.750$



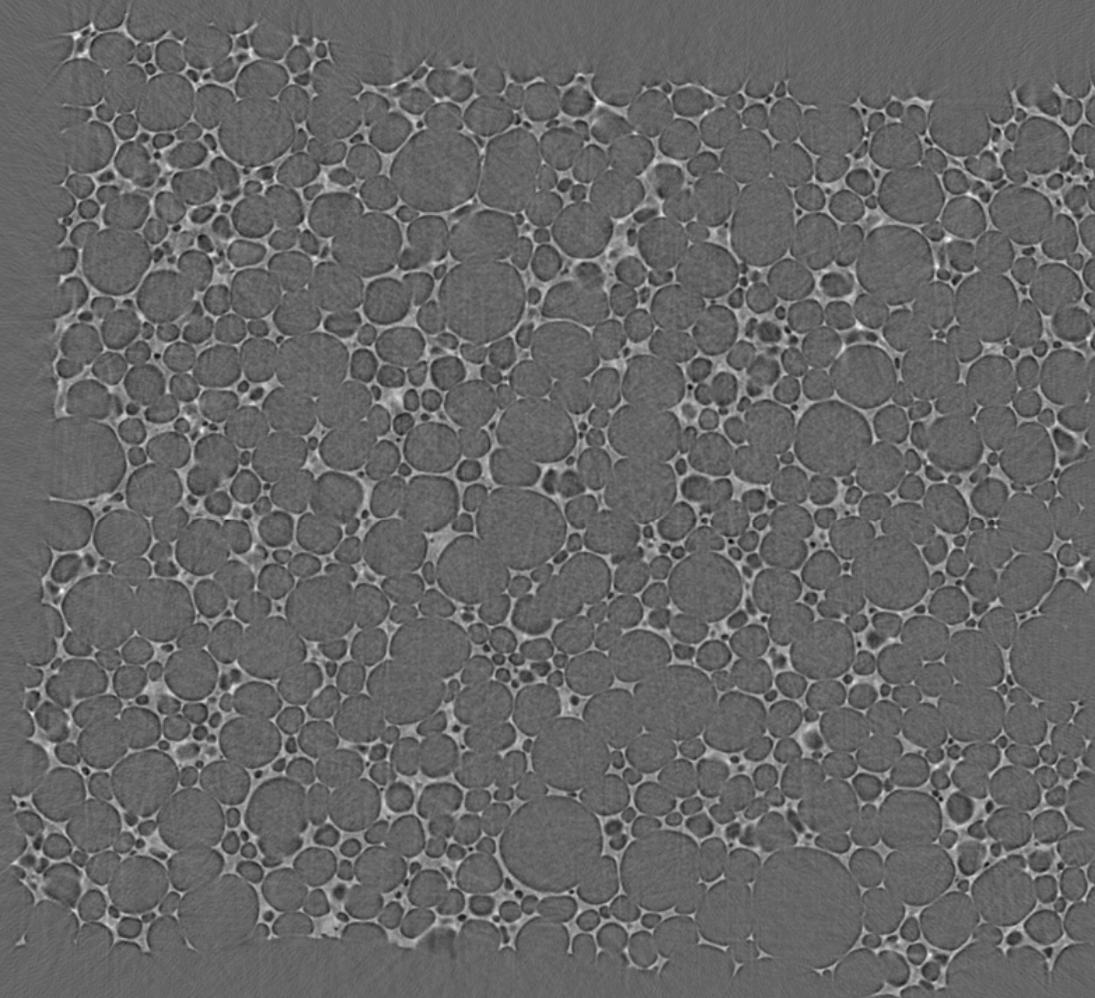
$C = 638.750$

A poor centering causes **arc artifacts**. An automated centering procedure gives a sinogram which is better centered on the rotation axis by determining the center-of-gravity of each row in the sinogram, and fitting this center-of-gravity array to a sin wave. The symmetry axis of the fitted sin wave is the rotation axis. The sinogram is then shifted left or right so that the rotation axis is exactly on the center column of the sinogram array.

SLICE_BASE

Save

Slice reconstruction: good rotation center



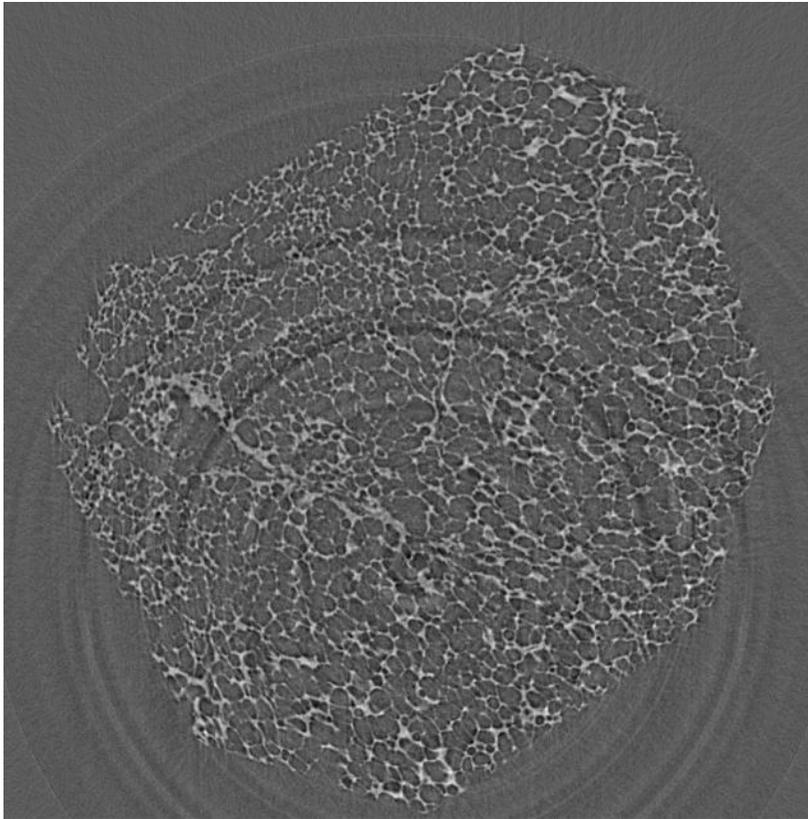
No more artifacts visible on this image

Created: Tue Jun 10 09:33:07 2003
Directory: F:\TOMO_RESULTS\PU_SORRENTINO\PU
Row Number: 200
Center of Rotation: 630.757
Interpolation: bilinear
Rem_Zinger Width: 3
Rem_Ring Width: 3
Kernel Width: 250
Filter: SHEPP_LOGAN





Ring artifacts reduction



The ring artifacts are due to drifts or non-linearities in the detector response.

A bad detector element will show up as a vertical stripe in the sinogram.

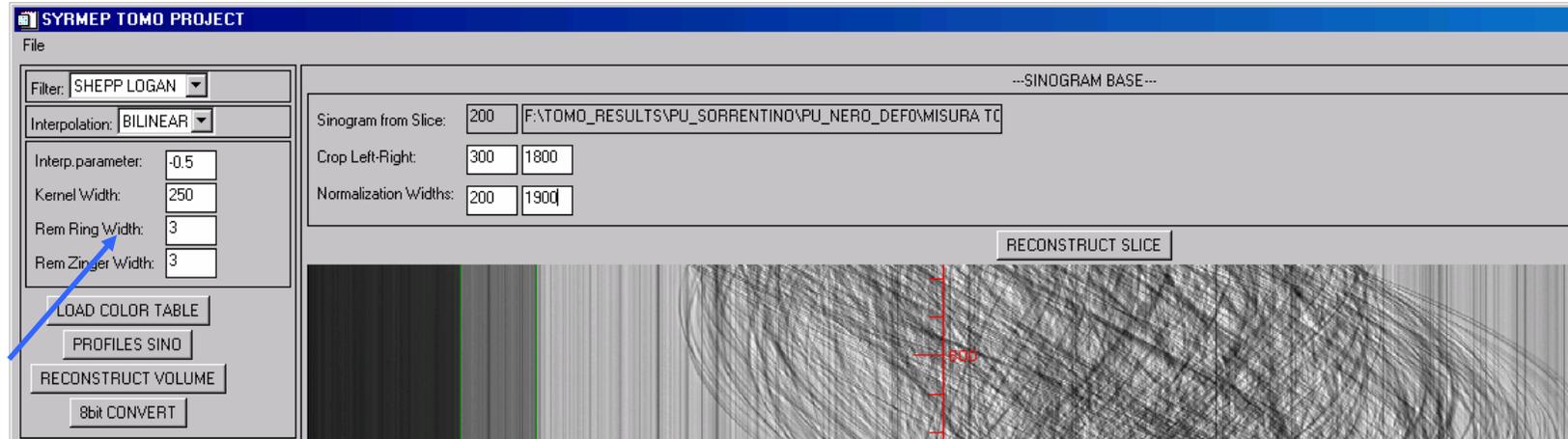
Two vertical lines in the sinogram would appear as a thin cylinder centered on the rotation axis in the real object.

The causes of these vertical stripes in the sinogram can include the following:

- Drifts in the detector element sensitivity in between white-field calibrations
- Non-linear detector element response
- Higher energy harmonics in the incident beam



How to reduce the ring artifacts?



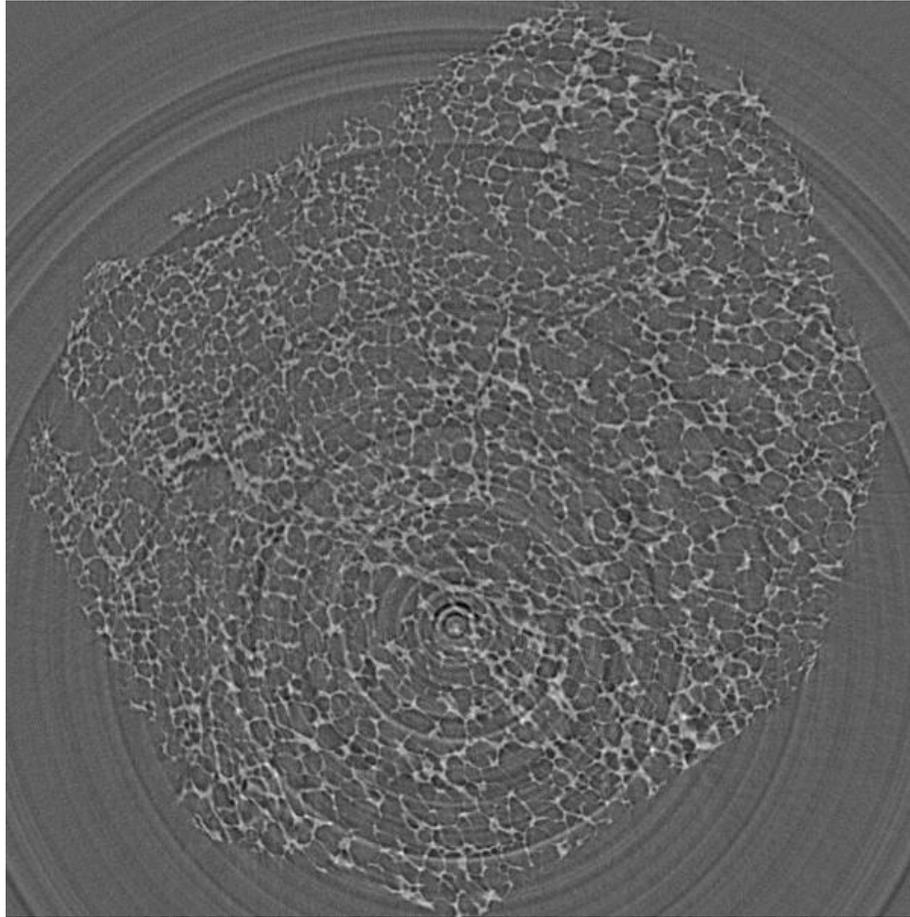
→ Compute the **average row of the sinogram** by summing down each column and dividing by the number of rows. This **average row** should have very little high-frequency content, since real objects will be moving in the sinogram, and will be blurred out when computing the average row.

→ Compute the magnitude of these detector anomalies by **subtracting a smoothed version of the average row** from the average row.

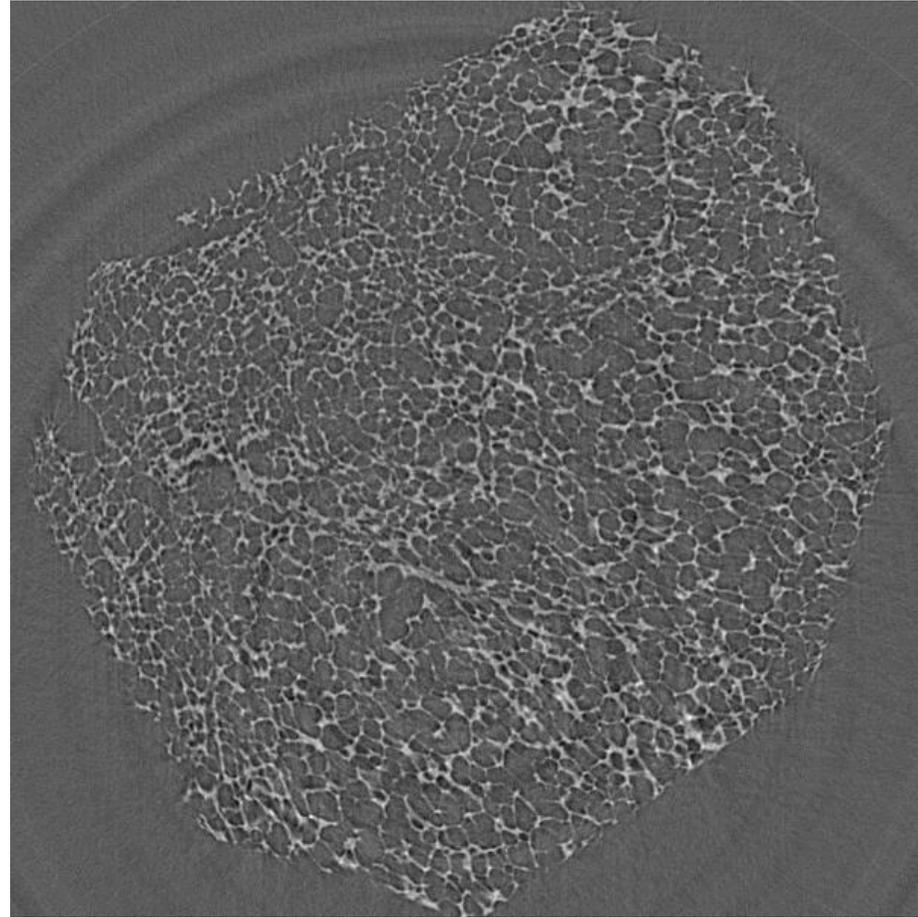
→ **Subtract the result** of previous step, the detector anomalies, **from each row in the sinogram**. This results in a sinogram with much less vertical striping.



Result of the ring artifacts reduction



Before



After (rem ring = 7)



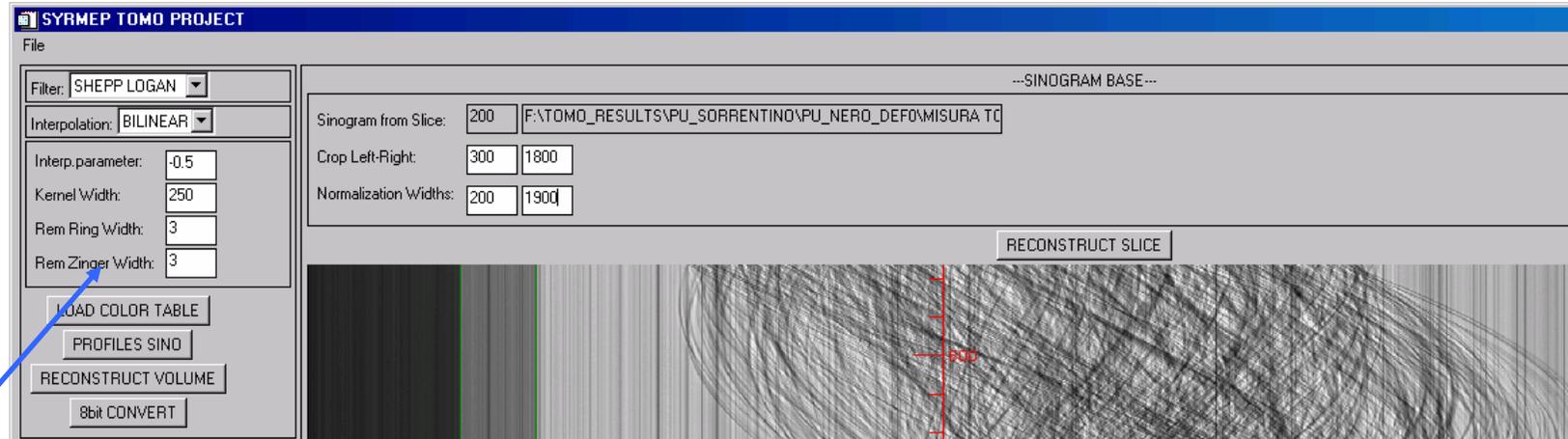
Zinger removal

A close look to the reconstructed slice can also reveal perfectly straight, bright lines at random orientations in the image. These bright lines, which look like scratches, are due to **zingers**, or anomalously bright pixels, in the raw images. These zingers are caused by cosmic rays or scattered X-rays hitting the CCD chip directly, causing large energy deposition relative to the visible light photons from the scintillator crystal.

Eliminating these zingers is best done when the raw data and white field images are first read in.



How to remove zingers?



- Smooth the raw image with a low-pass filter
- Subtract the raw image from the smoothed image
- Divide the difference image from step 2 by the smoothed image to produce an image of anomalous pixels on a relative scale
- Any pixels in the image from step 3 which are greater than a threshold value (typically 1.2) are defined to be zingers. The intensity of zinger pixel at location N is replaced by the average intensity of the pixels at location $N-2$ and $N+2$. Pixels $N-1$ and $N+1$ are not used because some zingers affect 2 adjacent pixels.



Volume reconstruction

PROJECTION_BASE

--FRAME BASE--

F:\TOMO_RESULTS\PU_SORRENTINO\PU_NERO_DEF0\MISURA TOMO\

Image Number: 200 Slice Number: 200 CREATE SINOGRAM PROFILES IMA CREATE VOLUME FOLDER

XVarEdit

Cancel Accept

Vertical Volume Limits: (Floating Point Array(2))

	0	1
0	0.000000	99.0000

dir con sinogrammi:

Current:
c:\rsi\idl55

Directories:

- c:\
- RSI
- IDL55
- bin
- Diego_temp
- docs
- examples
- external

Drives:
c:

OK Cancel



SYRMEP TOMO PROJECT

File

Filter: SHEPP LOGAN

Interpolation: BILINEAR

Interp.parameter: -0.5

Kernel Width: 250

Rem Ring Width: 3

Rem Zinger Width: 3

LOAD COLOR TABLE

PROFILES SINO

RECONSTRUCT VOLUME

8bit CONVERT

...SINOGRAM BASE...

Sinogram from Slice: 200 F:\TOMO_RESULTS\PU_SORRENTINO\PU_NERO_DEF\MISURA TC

Crop Left-Right: 300 1800

Normalization Widths: 200 1900

RECONSTRUCT SLICE

XVarEdit

Cancel Accept

Slices to be reconstructed: (Floating Point Array(2))

	0	1	
0	0.000000	99.000000	

Navigation arrows: left, right, up, down



VOLUME RENDERING

--VOLUME FILE--

X size: Y size: Z size:

0 0 0

3D RENDERING

CREATE MOVIE

Browse For Folder

Dir containing the slices:

- Desktop
- My Documents
- Lusi's Computer
- My Network Places
- Recycle Bin

Make New Folder

XInterAnimate

Animation Speed:
Frames/Sec: 0.0

Animation Frame:
8

Active Slider

End Animation

Colors...

Write MPEG

Help



8bit .raw volume creation



SYRMEP TOMO PROJECT

File

Filter: SHEPP LOGAN

Interpolation: BILINEAR

Interp. parameter: -0.5

Kernel Width: 250

Rem Ring Width: 3

Rem Zinger Width: 3

LOAD COLOR TABLE

PROFILES SINO

RECONSTRUCT VOLUME

8bit CONVERT

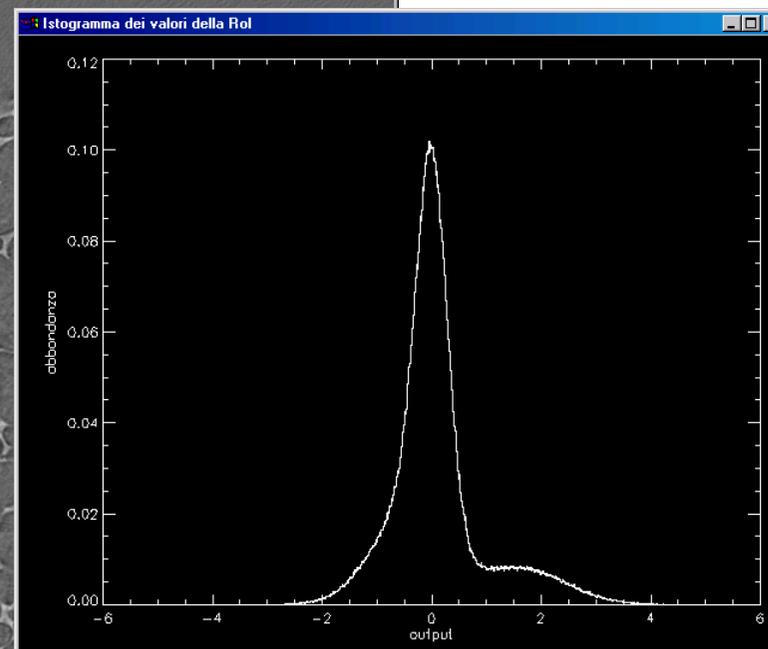
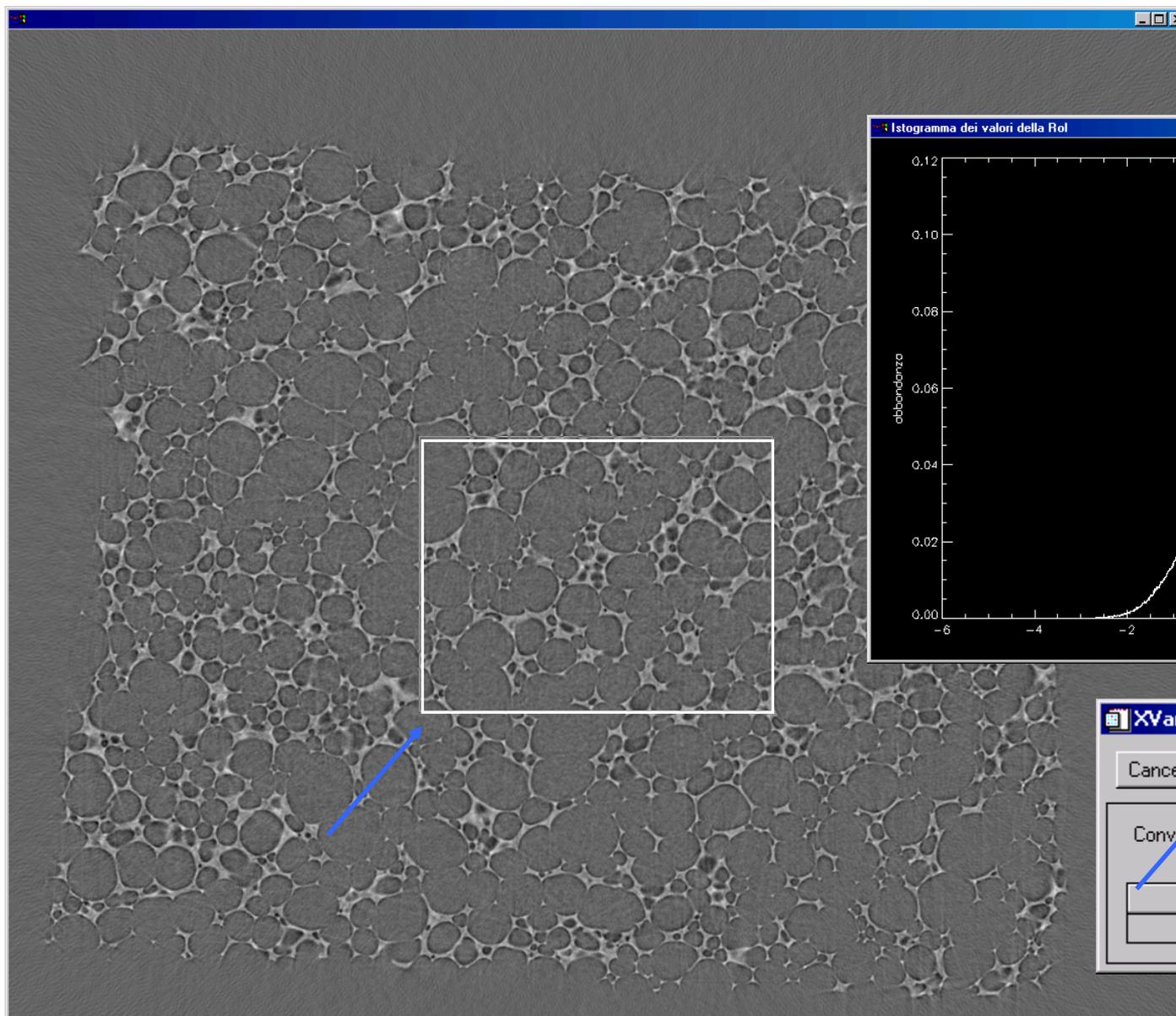
---SINOGRAM BASE---

Sinogram from Slice: 200 F:\TOMO_RESULTS\PU_SORRENTINO\PU_NERO_DEF\MISURA TC

Crop Left-Right: 300 1800

Normalization Widths: 200 1900

RECONSTRUCT SLICE



XVarEdit

Cancel Accept

Conversion interval: (Floating Point Array(2))

	0	1
0	-4.19280	5.71597



Data visualization: volume rendering



SYRMEP TOMO PROJECT

File

- Open Data Folder
- Open Sinogram
- Open RAW Info

Interp.parameter: -0.5

Kernel Width: 250

Rem Ring Width: 3

Rem Zinger Width: 3

LOAD COLOR TABLE

PROFILES SIND

RECONSTRUCT VOLUME

8bit CONVERT

---SINOGRAM BASE---

Sinogram from Slice: 0

Crop Left-Right: 0 0

Normalization Widths: 0 0

RECONSTRUCT SLICE



Volume rendering procedure



volume.raw_info - Notepad

```
File Edit Format View Help
|Thu May 18 04:55:08 2006
Created from: H:\Bettuzzi_D\H36_nt_LR\slices\slice_0002.tif
to: H:\Bettuzzi_D\H36_nt_LR\slices\slice_0000.tif
x cut: 0.000000 469 Dx: 470
y cut: 0.000000 402 Dy: 403
n slices: 8
Range: -0.772907 4.46046
```

VOLUME RENDERING

--VOLUME FILE--

X size: Y size: Z size:

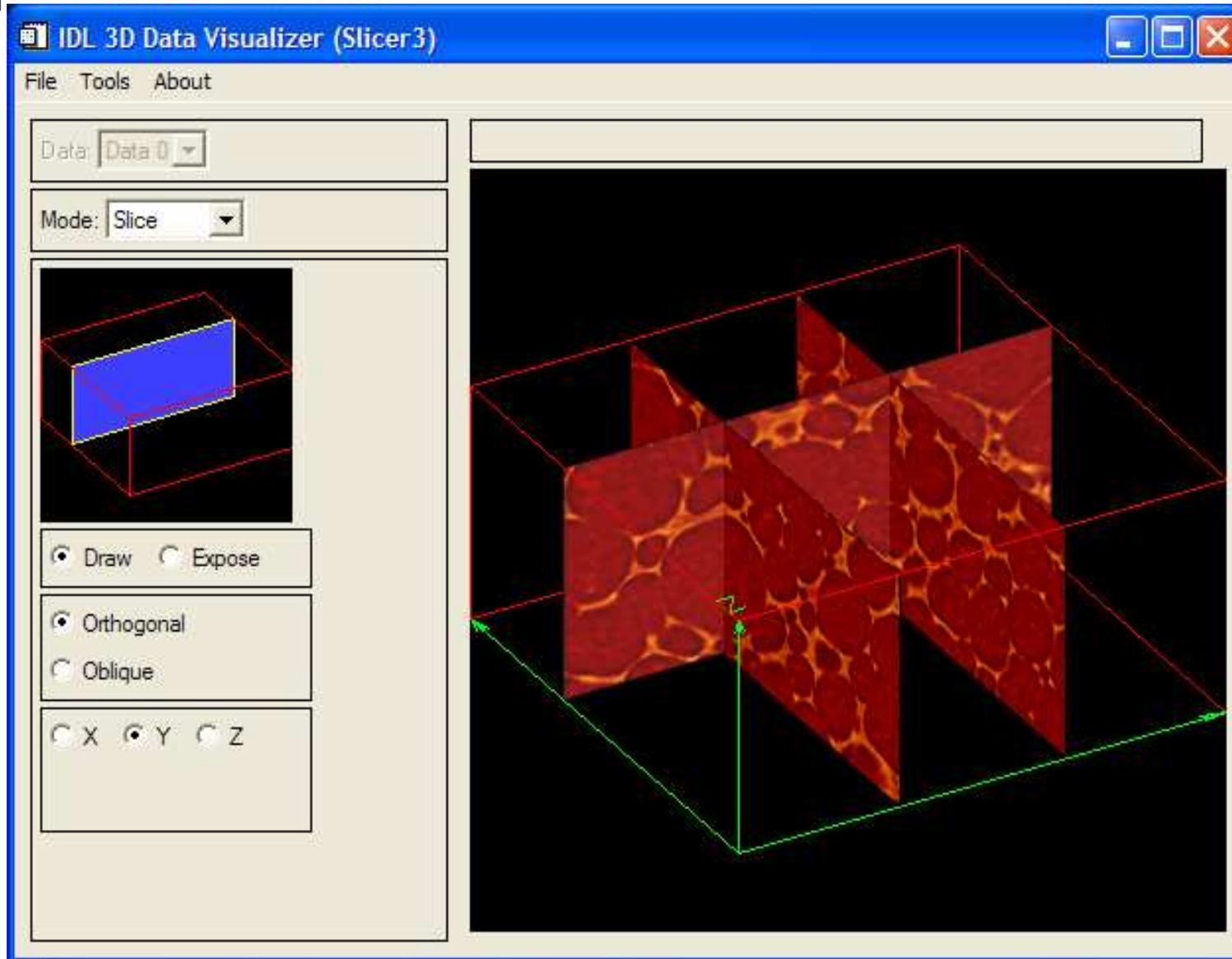
0 0 0

3D RENDERING

CREATE MOVIE

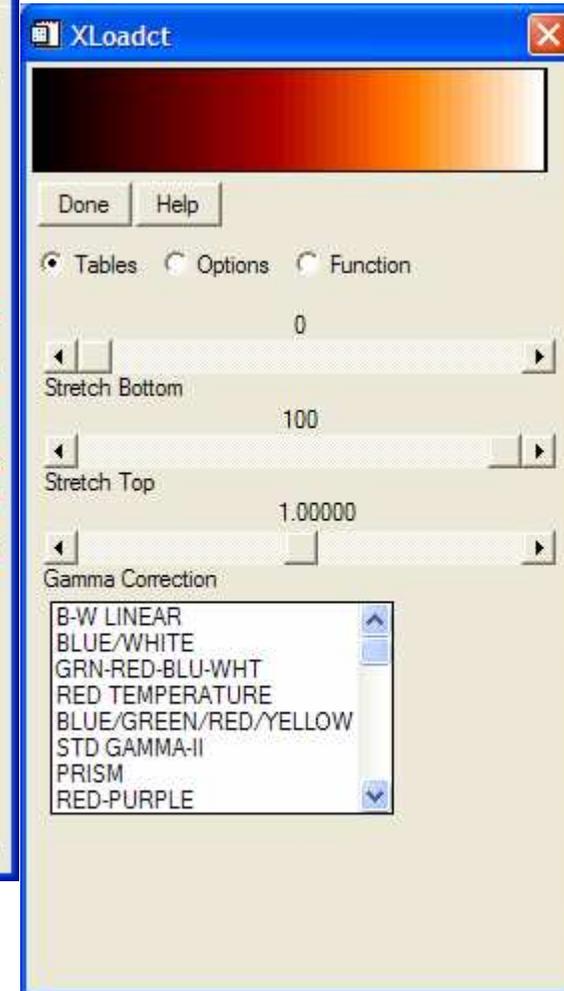
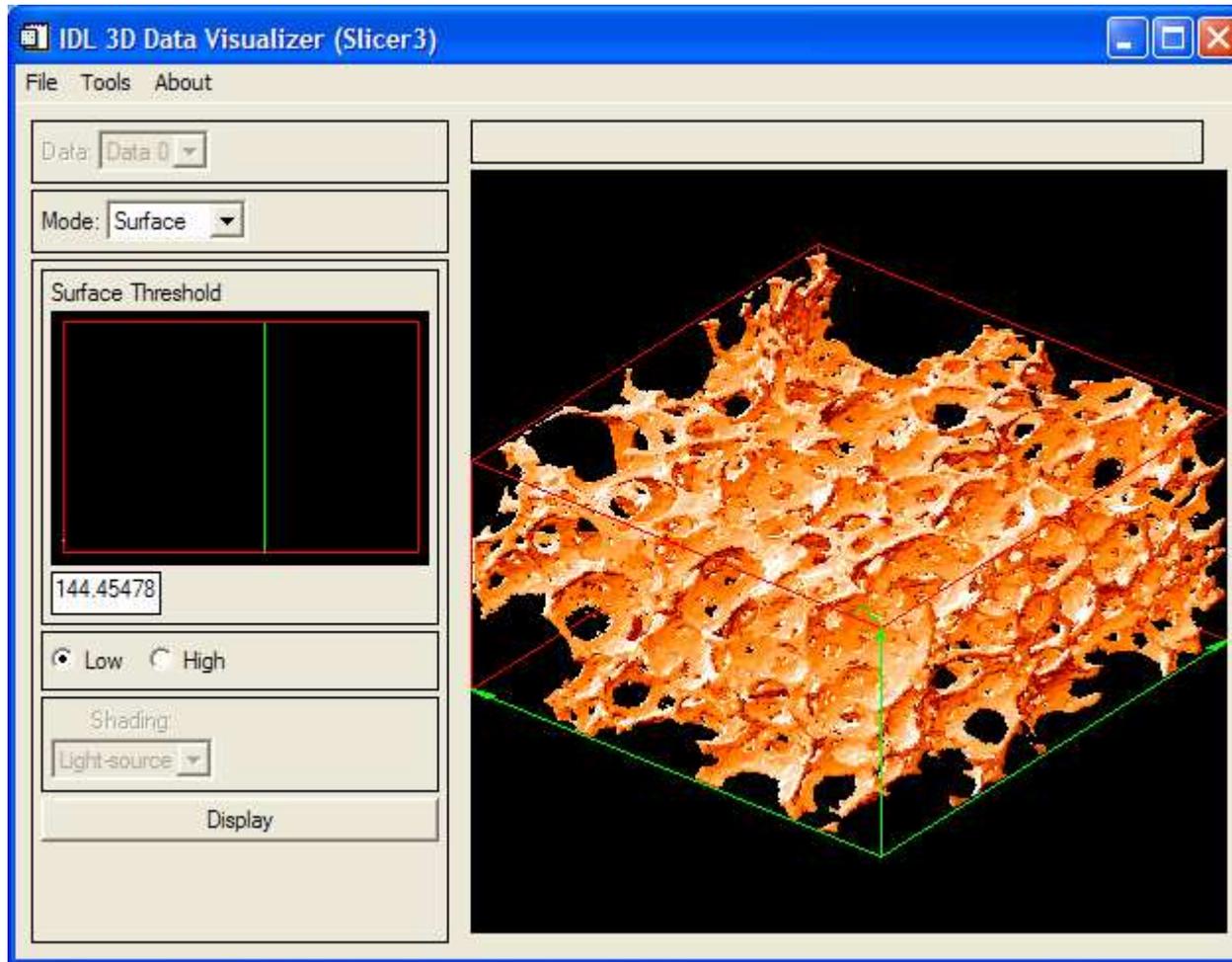


Slice visualizer





Isosurface rendering



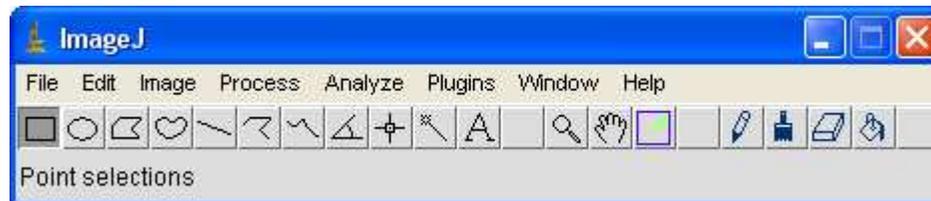


The ImageJ software



A public domain, Java-based image processing program developed at the National Institutes of Health.

<http://rsb.info.nih.gov/ij/index.html>



Rasband, W.S., ImageJ, U. S. National Institutes of Health, Bethesda, Maryland, USA, <http://rsb.info.nih.gov/ij/>, 1997-2007.

Abramoff, M.D., Magelhaes, P.J., Ram, S.J., *Image Processing with ImageJ. Biophotonics International, volume 11, issue 7, pp. 36-42, 2004.*