

SUNBIM evolution: new tools for a reliable (GI)SAXS/ (GI)WAXS data reduction

Francesco Scattarella^{1,*}, Dritan Siliqi¹, Liberato De Caro¹, Massimo Ladisa¹,
Alberta Terzi¹, Davide Altamura¹, Teresa Sibillano¹, and Cinzia Giannini¹

¹ Istituto di Cristallografia, Consiglio Nazionale delle Ricerche (IC-CNR), via G.
Amendola, 122/O, 70126 Bari, Italy

Abstract: SUNBIM (Supramolecular and sUBmolecular Nano- and Biomaterials X-ray IMaging) is a scientific package for X-ray imaging of nano- and biomaterials using SAXS, WAXS, GISAXS and GIWAXS techniques. With SUNBIM it is possible to perform a number of functions for data analysis such as: centering, q-scale calibration, two-dimensional to one-dimensional folding of small- and wide-angle X-ray scattering (SAXS/WAXS) data, also in grazing-incidence (GISAXS/GIWAXS); indexing of two-dimensional GISAXS frames and extraction of one-dimensional GISAXS profiles along specific cuts; quantitative scanning microscopy in absorption and SAXS/WAXS (SWAXS) contrast. New tools have been developed to enrich SUNBIM suite. The main novelty is the possibility to perform a deeper data reduction including dark current subtraction, background evaluation and subtraction and absorption normalization of the SAXS/WAXS map. The previous release of the software has already been used successfully to analyse several nano-structured samples. We are confident that the new features will allow a more correct and extensive analysis of the (GI)SAXS/(GI)WAXS data.

Keywords: computer programs; tools for crystal and crystallographic issues; SAXS/WAXS; imaging; microscopy



SUNBIM is entirely developed at the Institute of Crystallography of Bari and more specifically at XMI-L@b. Those are all the people involved directly and indirectly with SUNBIM. Most of the codes are written by Dritan Siliqi and me, but the whole group cures the theoretical and the experimental aspects as they are the first testers of the program.

 <https://www.facebook.com/xmilab>

 <http://www.ic.cnr.it/ic4/en/x-ray-microimaging-laboratory-xmi-lb-ic-bari/>

 JOURNAL OF
APPLIED
CRYSTALLOGRAPHY
ISSN 1600-5767

SUNBIM: a package for X-ray imaging of nano- and biomaterials using SAXS, WAXS, GISAXS and GIWAXS techniques

**Dritan Siliqi,^{a*} Liberato De Caro,^a Massimo Ladisa,^a Francesco Scattarella,^b
Annamaria Mazzone,^a Davide Altamura,^a Teresa Sibillano^a and Cinzia Giannini^{a*}**

Received 9 November 2015
Accepted 24 April 2016

^aIstituto di Cristallografia (IC-CNR), Via G. Amendola 122/O, Bari, 70126, Italy, and ^bIOM CNR Laboratorio TASC, Area Science Park, Basovizza, Building MM 55 14, Trieste, 34149, Italy. *Correspondence e-mail: dritan.siliqi@ic.cnr.it, cinzia.giannini@ic.cnr.it

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Case Study

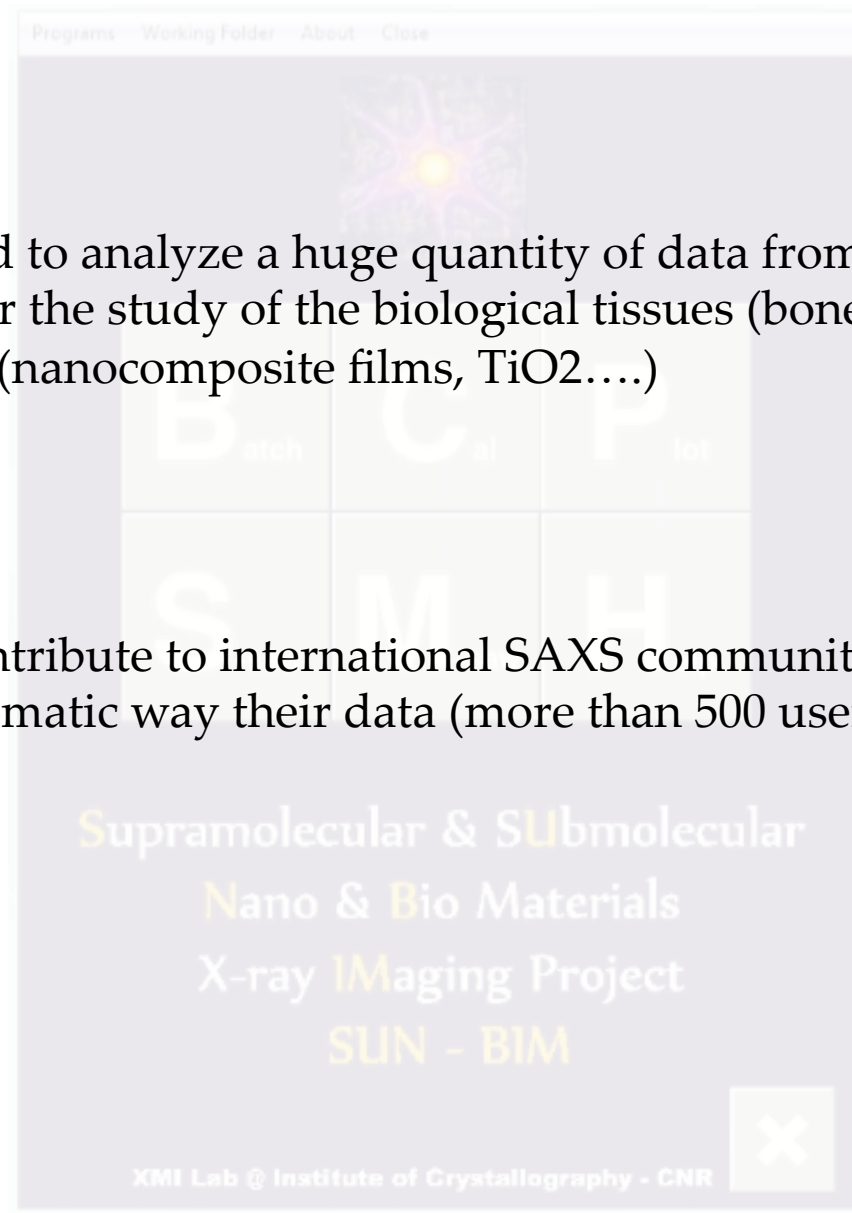
- Nanomaterials
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Obtaining & Installation

Acknowledgements

Why SUNBIM?

- To perform and to analyze a huge quantity of data from SWAXS experiments for the study of the biological tissues (bones, cornea, ...) and nanomaterials (nanocomposite films, TiO₂....)
- To give our contribute to international SAXS community an useful tool to process in automatic way their data (more than 500 users up to now)



Why SUNBIM?

Programs Working Folder About Close

Batch **C**al **P**lot

S-saw **M**-saw **H**elp

Supramolecular & SUBmolecular
Nano & Bio Materials
X-ray IMaging Project
SUN - BIM

XMI Lab @ Institute of Crystallography - CNR

Why SUNBIM?

SUNBIM is a computer suite of 5 integrated main programs:

① Calibration package

- centering patterns
- q-scale calibration

② S-SAWANA

- from 2D to 1D folding on data
- indexing of 2D GISAXS frames
- extraction of 1D GISAXS profiles along cuts
- **geometric aberration correction for WAXS folded data (NEW!)**

③ M-SAWANA

- **data reduction (NEW!)**
- manage with collections of data
- scanning microscopy in absorption and SWAXS contrast

④ Batch Script

- prepare batch script files (ASCII files) to run a sequential acquisition of two-dimensional frames (in scanning mode)

⑤ One-D Data Analysis Manager (Plot)

- quick plot of 1D profiles
- 1D background evaluation and subtraction
- denoising and deconvolution of the primary beam angular divergence on SAXS/GISAXS profiles

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FOCUS

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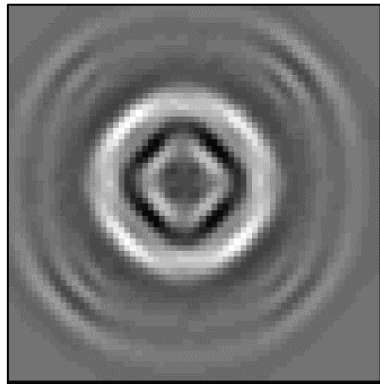
Crystals
2020

① Calibration: Main Features

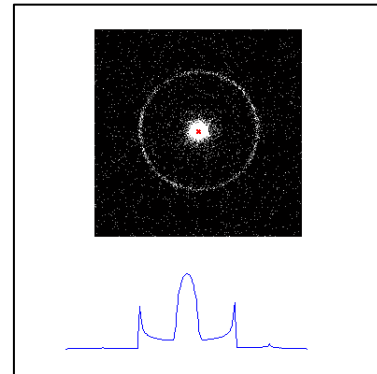
Users can calibrate their data using a number of function able to convert diffraction pattern from pixels space into q-space:

➤ Beam centering calculation

- manually (click one point directly on the center)
- selecting three points along a specific diffraction ring
- automatically (by using two different approaches)



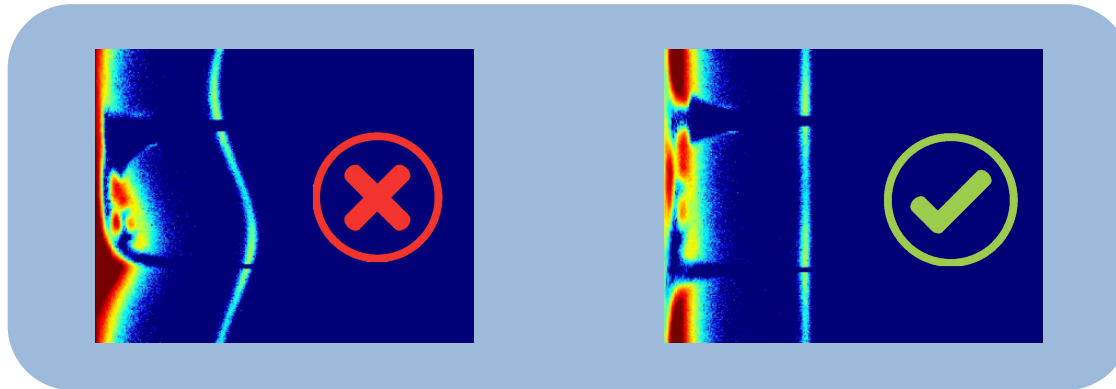
Based on a set of fluid dynamics equations (Landau & Lifshitz, 1987), known as **Shallow Water Equations (SWE)**



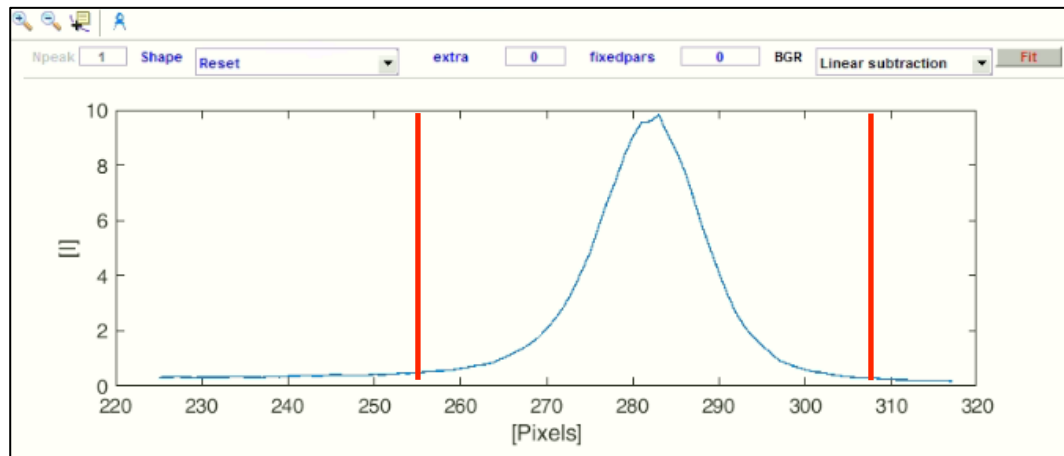
Based on the **Integral Radon Transform** (Radon, 1986; Barbano et al., 2009),

① Calibration

- Representation in polar coordinates of the diffraction pattern to check the correctness of the center



- Tool for Sample-to-Detector distance calculation



① Calibration Window

File Calibration Help

Working Folder: C:\Users\Francesco\Desktop\examples\calibration

IMG Filename: AgBehenate_saxs_gisaxs.mpa

IMG size: 1024 x 1024

Energy (keV): 8.04

Detector size (mm): 200

#pixels: 1024

Pixel size (mm): 0.195313

Window: Min Max Reset

Center marked at (499,489)

Y [pixel]: 1024, 768, 512, 256

X [pixel]: 256, 512, 768, 1024

Experiment Type: SAXS/GISAXS

Standard used: Silver Behenate

d(A): 58.38

q: 1.0763 nm⁻¹

Image Center (x,y): 499, 489

SD Distance (mm): 2307.44

Experimental
Settings

Diffraction Pattern
of
the standard sample

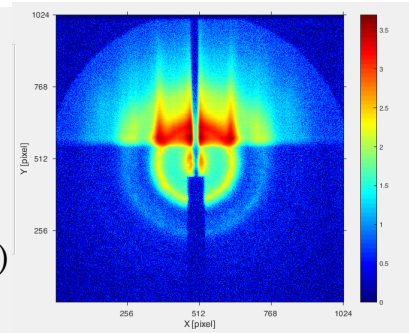
Calibration
Results

② S-SAWANA (Single scan SWAXS and Data Analysis): Main Features

➤ Load and visualize a single two-dimensional frame

Relevant tools

- change the colour map or colour scale
- shift, rotate and transpose the pattern
- import calibration data
- extract one or more cross sections and plot them (vertical, horizontal, radial) and more.....



➤ Fold the two-dimensional data (radial integration)

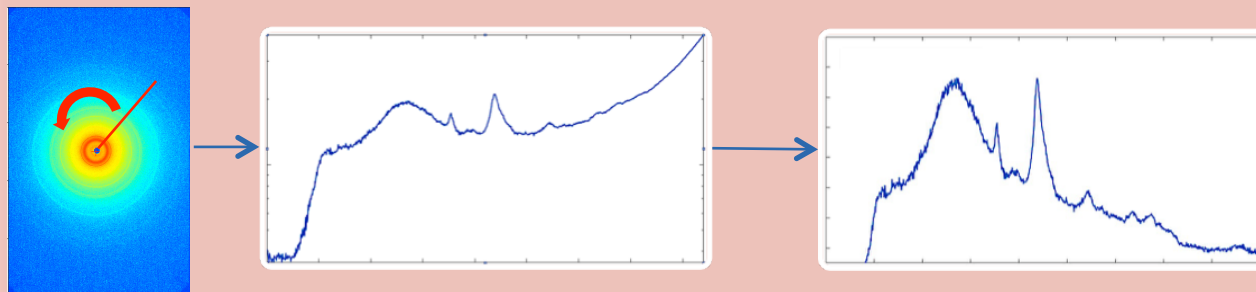
Relevant tools

- Radial Integration (full circle or angular sectors)
- Automatic Background Subtraction for WAXS data

Geometric aberration for small sample-to-detector distance could affect WAXS data.

For this reason, we developed an automatic evaluation (directly from the 2D pattern) and subtraction (if necessary) of the background from the 1D profile of the radial integration to enhance peak visibility at large scattering angles.

NEW
FEATURE

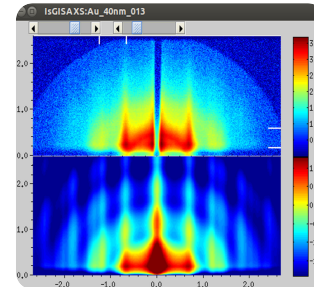


② S-SAWANA (Single scan SWAXS and Data Analysis): Main Features

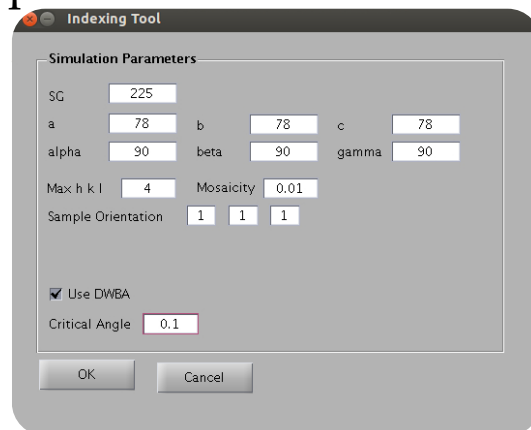
➤ Export data for simulation into:

- IsGISAXS program format¹
- ASCII text file (free format)

The simulated (IsGISAXS) image can be uploaded and compared with the experimental one²

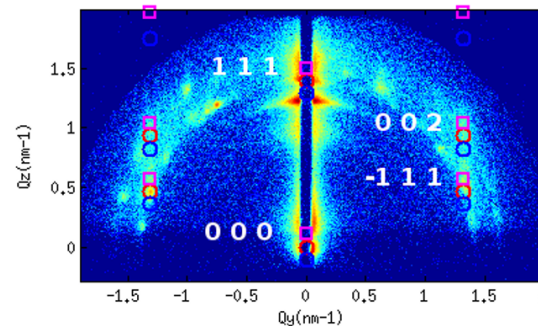


➤ Indexing GISAXS/GIWAXS data: simulate the pattern produced by a collection of nanoparticles assembled on top of a substrate according to the space-group symmetry, the unit-cell size, the orientation and the disorder in the sample³



The screenshot shows the 'Indexing Tool' window with the following parameters:

Simulation Parameters					
SG	225				
a	78	b	78	c	78
alpha	90	beta	90	gamma	90
Max h k l	4	Mosaicity	0.01		
Sample Orientation	1	1	1		
<input checked="" type="checkbox"/> Use DWBA					
Critical Angle	0.1				
OK	Cancel				



¹ Lazzari, R. (2002). J. Appl. Cryst. 35, 406–421

² Corricelli M et al. J. Phys. Chem. C, 2014, 118, 7579-7590.

³ Tate M. P. et al. (2006). J. Phys. Chem. B, 110, 9882–9892.

② S-SAWANA Window

The screenshot displays the S-SAWANA software interface. At the top, there is a menu bar with 'File Status', 'Axis Option', 'Cuts', and 'Indexing'. Below the menu is a toolbar with various icons for file operations and image manipulation. The main window area is divided into several sections:

- Working Folder:** C:\Users\Francesco\Desktop\examples\s-sawana\gisaxs
- IMG Filename:** gisaxs.mat
- IMG size:** 1024 x 1024

The central part of the interface is a large plot showing a diffraction pattern. The X-axis is labeled 'X [pixel]' and ranges from 0 to 1024, with major ticks at 256, 512, 768, and 1024. The Y-axis is labeled 'Y [pixel]' and also ranges from 0 to 1024, with major ticks at 256, 512, 768, and 1024. The plot shows a central vertical beam stop and a horizontal equator, with a four-lobed diffraction pattern in the quadrants.

On the left side, there is a 'Loaded Calibration Info' panel with the following parameters:

- Image:** AgBehenate_saxs_gisaxs.mpa
- SD Distance (mm):** 2289.34
- Energy (keV):** 8.04
- Pixel size (mm):** 0.195313

Below these parameters is a green checkmark icon and a 'Load Calibration File' button. An arrow points from this panel to a box labeled 'Calibration Parameters'.

On the right side, there is an 'Experiment Type' panel set to 'GISAXS' and an 'Angle of Incidence (deg)' panel set to '0.00'. Below these is a 'Simulated Image' panel with a 'Compare O/S' button. An arrow points from this panel to a box labeled 'IsGISAXS Simulation'.

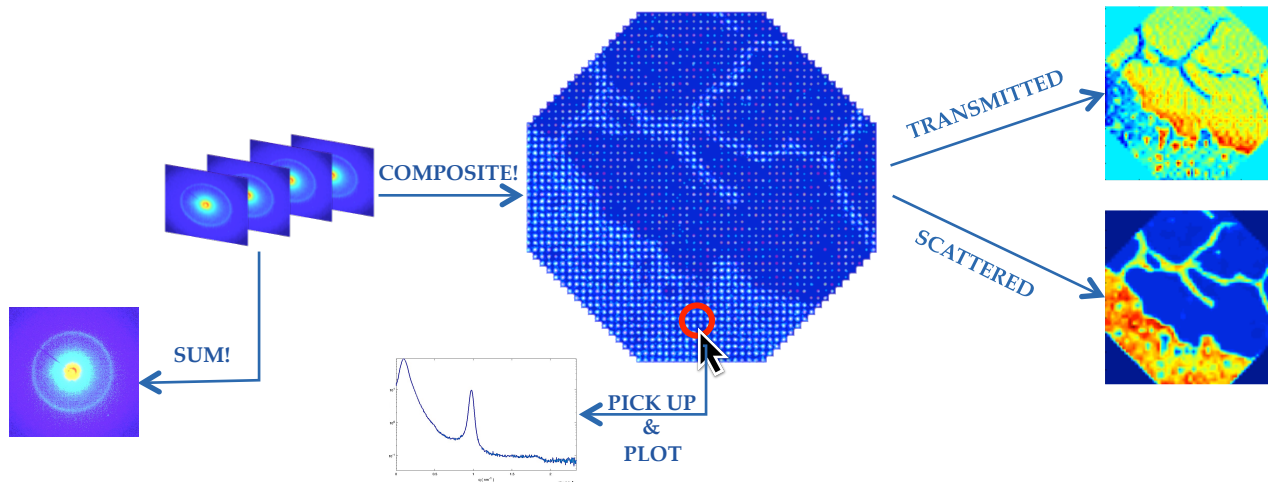
③ M-SAWANA (Multi scan SWAXS and Data Analysis): Main Features

This tool is useful when scanning SWAXS has been performed. Multi scan SWAXS gives point by point a 2D signal that can be arranged in colour maps by SUNBIM.

➤ Composite

Relevant tools

- composite of the as-collected two-dimensional SAXS frames into a single image
- transmitted and/or scattered single mesh image of intensities in the whole q range
- average pattern calculated over the whole set of the data or over a particular ROI to increase SNR



Interactive Composite

- pick up and plot one or more specific one-dimensional profile (and the corresponding 2D image) corresponding to a scan
- find a scan position into the mesh
- free-hand draw area (ROI) and calculating comparative parameters (vertex coordinates, area size, Δq and integrated intensity)

③ M-SAWANA (Multi scan SWAXS and Data Analysis): Main Features

➤ Analysis Section (1/2)

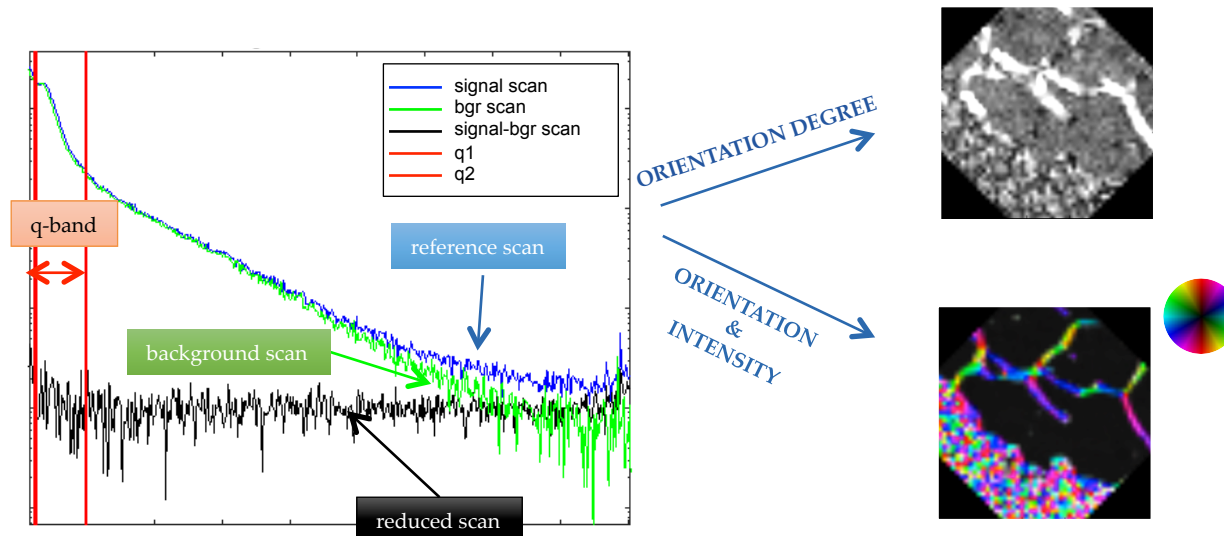
Multi-modal imaging approach: transform a mesh of two-dimensional SAXS frames into microscopy images*

Relevant tools

- each 2D frame of the mesh is folded into a one-dimensional profile
- from a specific 1D profile, properly selected from the composite map, the user has to choose one or more diffraction peaks (a q range)

Orientation & Intensity

- Intensity distribution along the azimuth of the selected rings is analysed for each 2D frame and transformed into microscopy images.
- For each monitored peak, the subtracted background can be evaluated by polynomial interpolation or using an experimental background scan



③ M-SAWANA (Multi scan SWAXS and Data Analysis): Main Features

➤ Analysis Section (2/2)

CCA (Canonical Correlation Analysis) map

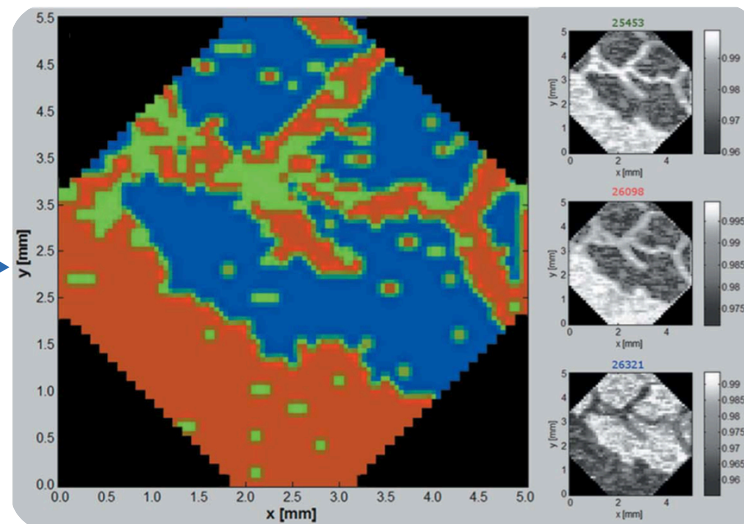
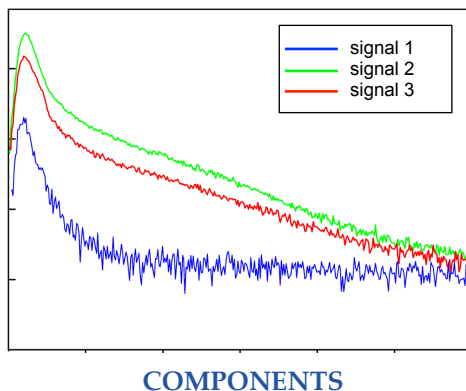
Extract from 1D mesh profiles a few data which can characterize the investigated sample.

CCA is a statistical technique (Hotelling, 1936) to assess the relationship between two sets of variables.

CCA quantifies the relationship between two random variables, x and y , by means of the so-called correlation coefficient.

Exploit the spatial information characterizing the composite SAXS/WAXS data set:

- the variable x is a multivariate vector with components representing the set of acquired diffraction profiles of the composite map
- the variable y also consists of a multivariate vector having few components; these are (usually three) models extracted from the composite map by means of different methods (i.e. adaptive binning), which represent the less correlated SWAXS profiles among the entire set of data



③ M-SAWANA Window

Composite Tool

Analysis Section

Radial Integration
& Plot

CCA

Scanning

The screenshot displays the M-SAWANA software interface, organized into several functional sections:

- Status Calibration Reduction**: A top navigation bar.
- COMPOSITE & VISUALIZATION Section**: Contains fields for Scans Folder (C:\Users\Francesco\Desktop\examples\m-sawana\multiscans_41740\), Scan Number (From 2629, To 3180), Part of scan IMG into composite (%: 50), Root name for created IMGs (test), and RUN Options (Composite selected).
- ANALYSIS Section**: Includes Analysis Folder (C:\Users\Francesco\Desktop\examples\m-sawana\multiscans_41740\analysis), Rigaku Ins dropdown, Scan Number (From 2629, To 3180), and a 2D IMGs Tool button.
- Radial Integration**: Features a RUN button, checkboxes for Reduction, Denoising, and Export to .dat, Axis Options (X: Pixels, Y: log(Int.) x Q^A), Select from options (Composite selected), and Plots Options (Same plot selected).
- CCA**: Includes checkboxes for On denoised data and On reduced data, Prepare, RUN, and View buttons, and Models selection options (Automatic selected).
- Scanning**: Contains checkboxes for On denoised data and On reduced data, Subtract Background From Scan, Interval in size(nm) (0 to 0), Scan (0), Preview Selected Scan, and RUN buttons, along with Figure options like Root name for Titles, Flip Up/Down, Flip Left/Right, Permute, and Flip Color Wheel.

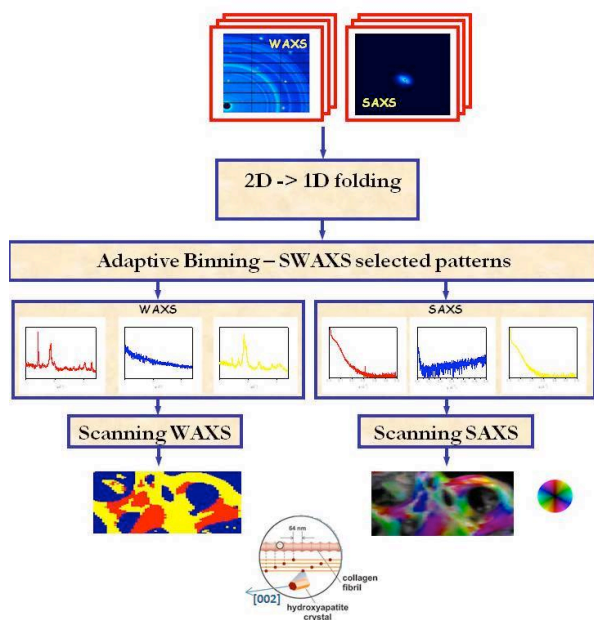
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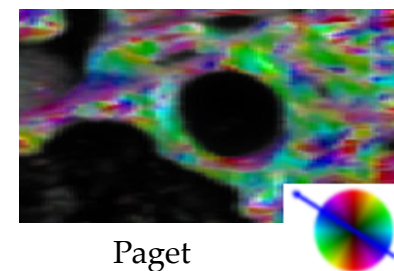
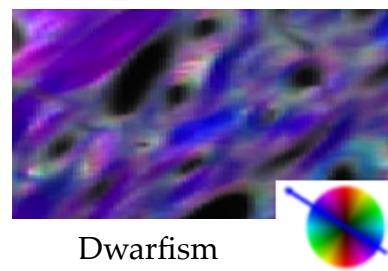
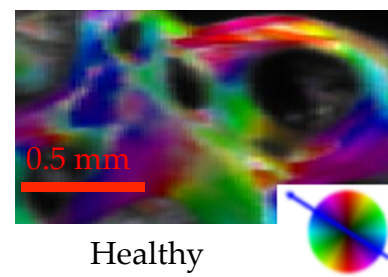
Biological Tissues (1/2)

- Scanning small and wide angle X-ray scattering (scanning SWAXS) experiments were performed on healthy and pathologic human bone sections (Paget's disease and dwarfism).

Methods: M-SAWANA Flow Chart



Results: Intensity & Orientation Maps

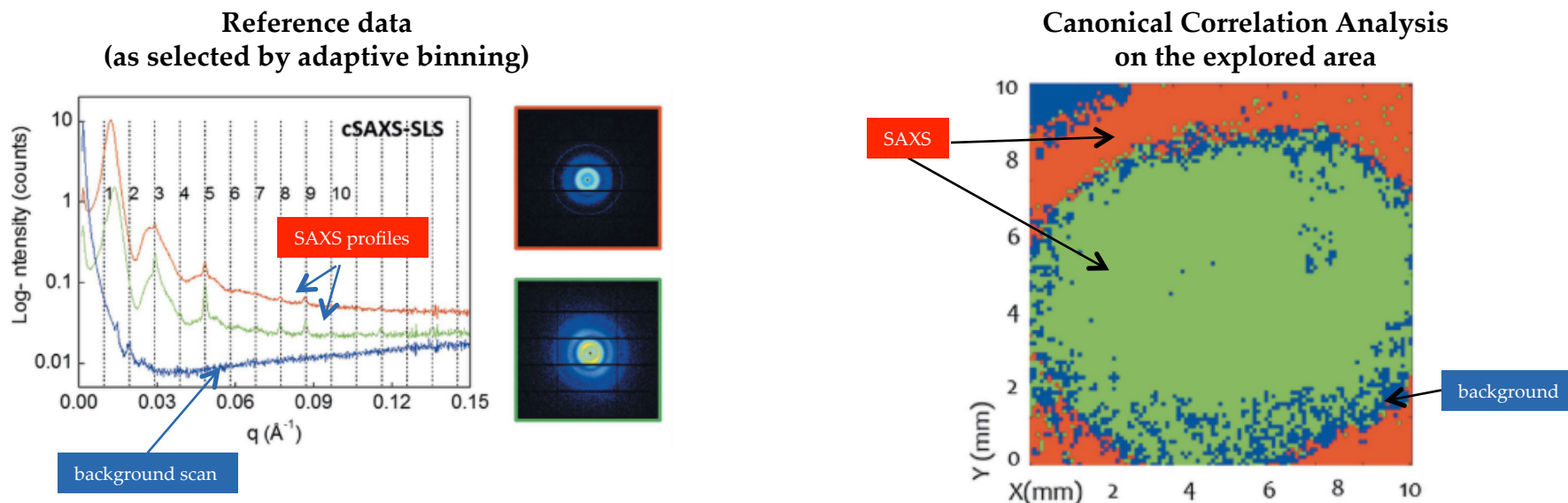


RESULT

SWAXS images and analysis allowed extracting information of the mineral nanocrystalline phase embedded (hydroxyapatite), with and without preferred orientation, in the collagen fibrils, mapping local changes at sub-osteon resolution.

Biological Tissues (2/2)

- Bovine cornea was studied with scanning small-angle X-ray scattering (SAXS) microscopy, by using both synchrotron radiation and a microfocus laboratory source
- A combination of statistical (adaptive binning and canonical correlation analysis) and crystallographic (pair distribution function analysis) approaches allowed inspection of the collagen lateral packing of the supramolecular structure.



RESULT

Decrease in the interfibrillar distance and in the shell thickness around the fibrils from the periphery to the center of the cornea; the central area coincides with the region (approx. 10 mm) where the epithelium has been removed.

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Data Reduction Panel

An accurate data reduction is mandatory on SAXS/WAXS to obtain readable, reliable and quantitative data (even more so if they are acquired by laboratory sources).

STEPS

- ① The Dark Current (DC) signal (beam off) is subtracted from the SAXS signal to reduce the instrumental noise of the detector
- ② The resulting signal is normalized to the transmission coefficient T , so as to make it independent of the different degree of absorption of the sample
- ③ A background signal is subtracted from the normalized signal, taken as an average of the SAXS signal in an area outside the sample.

$$SAXS_{redu} = \frac{SAXS - DC}{T} - BG$$

$$BG = \frac{\sum_{i=1}^M (SAXS_i - DC)}{M}$$

DC = Dark-current signal

BG = Background measured outside the sample area

M = number of selected BG patterns

A number of new functions have been implemented in SUNBIM.

A personalized Data Reduction is now possible!

Main Options

- Four options to calculate T map and BG using:
 - max intensity of the map
 - max of each row
 - area (to increase SNR)
 - external file (if measured)
- Post processing functions (to improve maps quality):
 - Background Compensation*
 - Gaussian Filter
 - SAXS signal normalization row by row



What's new?

Data Reduction Panel

Apply Reduction

SAXS Dark Current
Integration Time (s): 900
File: C:\Users\Francesco\Desktop\examples\DarkCurrent
Browse...

Transmission Dark Current
Integration Time (s): 900
Value: -7.39045e-15

Transmission & Background
File: Browse...
from max
 Background Compensation Gaussian Filter
 SAXS Normalization By Row

SAXS DARK
CURRENT SUBTRACTION

TRANSMISSION DARK CURRENT
SUBTRACTION

TRANSMISSION COEFFICIENT
CALCULATION AND
BACKGROUND SUBTRACTION

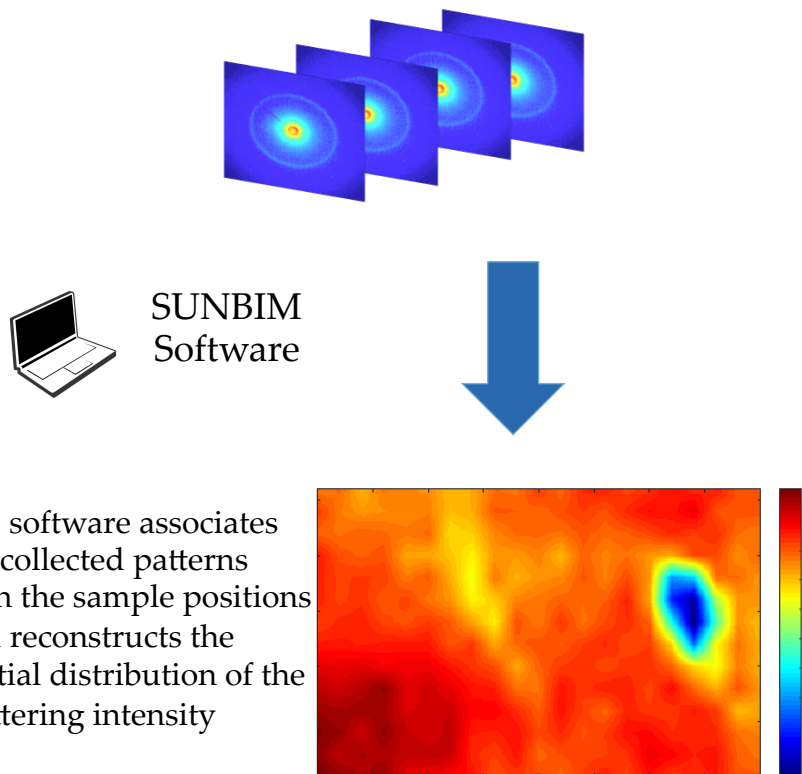
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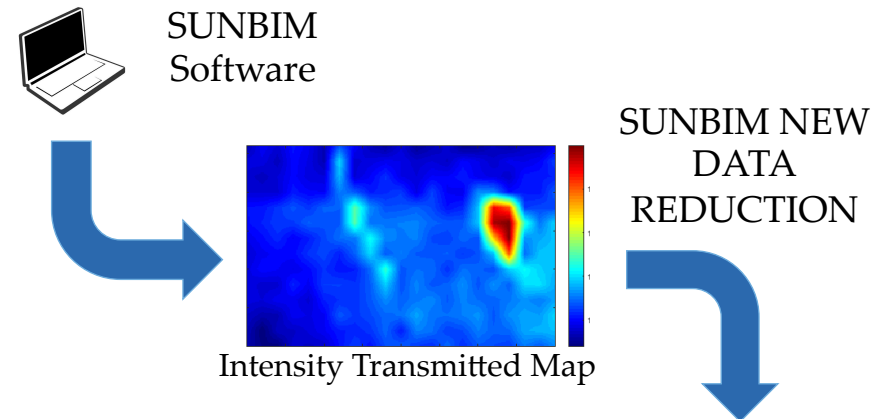
Nanomaterials: Whey Protein Concentrate (WPC) Films + TiO₂

Scanning SAXS at XMI-L@b

1. The sample is moved in steps (~ 200 μm) along the two xy directions and for each step a 2D diffraction pattern is acquired by the SAXS detector.



2. The instrument also collects data on the absorption of the sample point by point (pin diode).



It is possible to retrieve a map of the **Transmission Coefficient T** of the sample

$$T = e^{-\mu t}$$

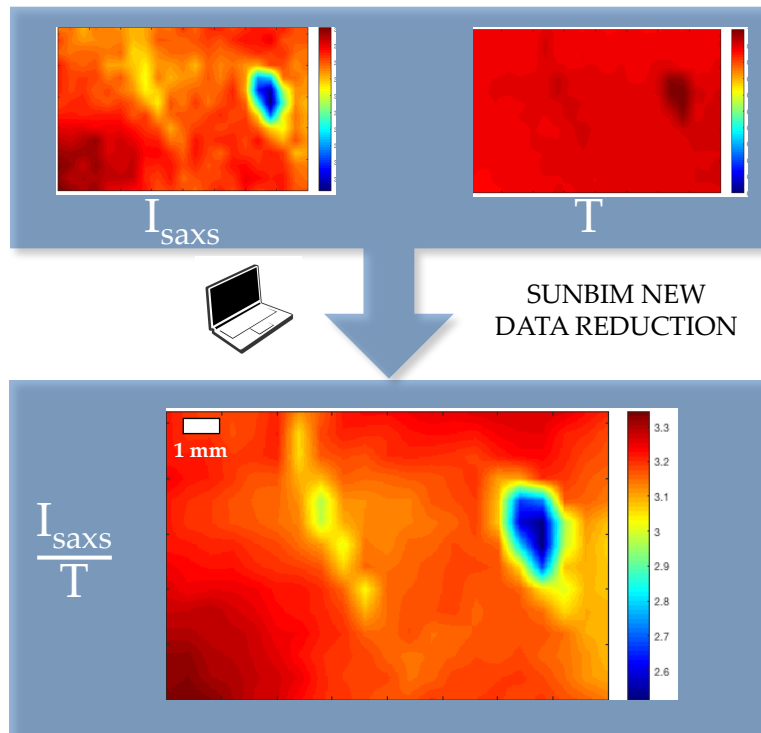
Lambert-Beer Law

Possible estimation of local sample thickness

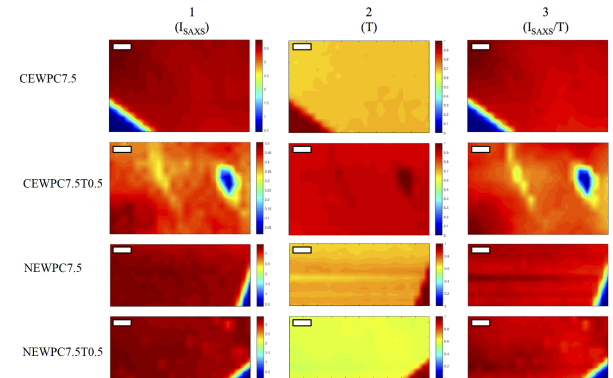


Case Study

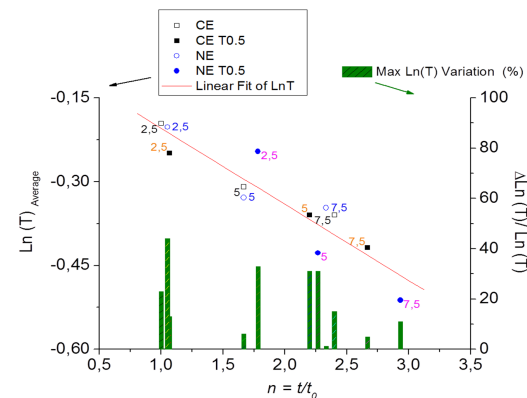
Nanomaterials: Whey Protein Concentrate (WPC) Films + TiO₂



Scattering/Absorption contrast of films CEWPC7.5 with TiO₂ loading. SAXS/T maps lead to an **enhancement of contrast and resolution** related to thickness/density and structure variations, or a flattening of the inhomogeneities when these are due to bare density/thickness variations*.



- SAXS
- T
- SAXS/T maps of different films



From Lambert-Beer Law we derived the logarithmic plot of T (average) as a function of the normalized sample thickness $n=t/t_0$ and extrapolated the unknown thickness value for very thin samples

*J. M. Montes-de-Oca-Ávalos, D. Altamura, M. L. Herrera, C. Huck-Iriart, F. Scattarella, D. Siliqi, C. Giannini, R. J. Candal, *Physical and structural properties of whey protein concentrate - corn oil - TiO₂ nanocomposite films for edible food-packaging*, Food Packaging and Shelf Life (2020), **in press**

List of Selected papers

- J. M. Montes-de-Oca-Ávalos, D. Altamura, M. L. Herrera, C. Huck-Iriart, F. Scattarella, D. Siliqi, C. Giannini, R. J. Candal, *Physical and structural properties of whey protein concentrate - corn oil - TiO₂ nanocomposite films for edible food-packaging*, Food Packaging and Shelf Life (2020), in press
- T. Sibillano, A. Terzi, L. De Caro, M. Ladisa, D. Altamura, A. Moliterni, R. Lassandro, F. Scattarella, D. Siliqi and C. Giannini, Crystals, 10(4), 274, (2020)
- Terzi A., Gallo N., Bettini S., Sibillano T., Altamura D., Campa L., Natali M. L., Salvatore L., Madaghiele M., De Caro L., Valli L., Sannino A., Giannini C., Front. Bioeng. Biotechnol., 7, 203 (2019)
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Obtaining & Installation

- Only for Windows (64 bit)
- Download from: <http://www.ba.ic.cnr.it/softwareic/sunbim/> (after a valid registration)
- Run the installation file (SUNBIMInstaller.exe) accepting the “license agreement”

SUNBIM is developed on MATLAB and deployed **with MATLAB Runtime Compiler R2020a** (included in setup file and automatically installed)

- Find the executable run file under “Programs” or as a link on the “Desktop”
- Useful info at:
<http://www.ba.ic.cnr.it/softwareic/sunbim/tutorials/> (video tutorials)
<http://www.ba.ic.cnr.it/content/sunbim-examples> (zip file with few examples)

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Acknowledgements

Acknowledgements

This work was partially supported by the Italian PON MIUR “Energy for TARANTO - Tecnologie e processi per l'Abbattimento di inquinanti e la bonifica di siti contaminati con Recupero di materie prime e produzione di energia Totally green” project (Proposal Code: ARS01_00637)

Thanks to:

- Bilateral agreement Italy-UK (CNR/Royal Society-UK London) on the project entitled “Label-free multi-scale X-ray imaging for the study of cell differentiation and colonization of scaffolds in regenerative medicine”;
- Bilateral agreement Italy-Argentina (CNR/CONICET) on the project entitled “TiO₂ casein polymeric composite films for food preservation”;
- Rocco Lassandro is acknowledged for technical support in the XMI-LAB.



THANK YOU FOR YOUR ATTENTION.....