# *From Crystallography to Imaging*


### *Cinzia Giannini*

### *Institute of Crystallography National Research Council Bari – Italy*


From the discovery of X-ray diffraction in 1912 by M. Laue, W. Friedrich, P Knipping, and from the first crystal structure determination in 1913 by W.H. and W.L. Bragg (father and son) more than 30 nobel pizes were awarded for works related to X-ray Crystallography in chemistry, physics, medicine and biology. Crystallography allowed and still allows to discover the most invisible secrets of the world around us, which can been explored down to atomic resolution. One limit only: the need for a crystal, namely a regular 1D or 2D or 3D arrays of atoms/molecules extended for few nanometers (nanocrystals), micrometers (microcrystals) or even millimeters. Crystals are familiar to us (salt, aspirin, precious stones etc) and many of their structures have been determined so far with X-ray Crystallography. However, biologic matter is largely non crystalline or only partially crystalline. For example, the mineral component of our bones is made of hydroxyapatite nanocrystals, or collagen in several human tissues forms fibers, which can be considered as 1D crystals. In these cases, X-ray diffraction patterns contain characteristic structural or morphological features which can be measured and transformed into quantitative microscopies, making this technique an effective tool for i) the engineering of a smart tissue, ii) the design of a novel drug or iii) the diagnosis of a specific pathology.

Nowadays, matter can be imaged with X-rays at different length scales and with several imaging techniques, the more and more efficiently thanks to the recent advent of high-brilliance X-ray sources, the fabrication of X-ray focusing optics and the appearance of novel high-performances detectors. When relying on the presence of distinctive structural properties in the X-ray diffraction pattern, incoherent X-ray beams are sufficient. If dealing with completely disordered specimens (such as recalcitrant proteins not readily crystallizable) coherent X-ray beams are today available. In this latter case, a revolution is going on with the novel third and fourth generation X-ray sources. Through them, the complex and costly methods of crystallization, studied so far to achieve reasonably pure and defect free protein crystals, with the dimensions and quality required for a diffraction study at atomic resolution, are destined to become just an obsolete need.

**In this lesson an introduction to some X-ray Imaging techniques will be given with applications taken from the world of engineered smart materials and natural biomaterials.**