3D structures of biological matter: from model systems to cells and tissues

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X-rays are famous as a unique tool to unravel the 3D structure of biological macromolecules, as we are well aware of in the centennial of crystallography. Here we address the 3D structure analysis in the non-crystallographic state, in a setting without long range order and hierarchical length scales. We show how -with the advent of highly brilliant radiation, coherent focusing, and lens-less diffractive imaging - these challenges can now be met.

Starting with biomolecular model systems in liquid crystalline states studied by diffraction, followed by small-angle diffraction carried out on the single cell level to study cytoskeleton structures or compactified DNA, up to the scale of tissues, we present approaches to quantitative reconstruction of the 3D density distribution underlying biological function.

We illustrate how nano-focused coherent x-ray synchrotron beams can be used for scanning coherent diffractive imaging with the sample in the focal plane, as well as for full field holographic x-ray imaging when the sample is in a defocus position. In both cases, the central challenge is to invert the intensity data by phase retrieval algorithms. With a generalized ptychographic approach, both the object and the probing beam can be reconstructed, overcoming idealizing assumptions on the wave front. Along with the experimental and conceptual aspects of image formation, object reconstruction in a combined setting of phase retrieval and tomography will be discussed. Examples of biological imaging are presented, ranging from bacterial and eukaryotic cells, to nerve tissue, up to the level of organs or small organisms.