# Recent advances in serial electron crystallography

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Electron crystallography of three-dimensional nanocrystals (3D ED), also called MicroED, has known many successes in the last decade or so, with the development of new acquisition protocols. The introduction of these methods created new opportunities for structure determination, notably in the study of materials that do not form large well-ordered crystals. While 3D ED is conceptually similar to single-crystal x-ray diffraction (SCXRD), another hallmark of XRD techniques, serial crystallography, found little echo in the field of electron crystallography until recently. We proposed an implementation of serial electron crystallography in a scanning transmission electron microscope [1]. The method consist in collecting still diffraction patterns from randomly-oriented nanocrystals dispersed on a TEM grid by shifting a parallel nanobeam. We present recent progress and ongoing work in making serial electron crystallography more robust and accessible. A data analysis pipeline optimized with parallel processing was developed based on the CrystFEL suite, which is complemented by our python package diffractem. The framework of the Instamatic library was extended toward a portable implementation of the method. Supervised machine learning, in combination with vector analysis, was applied to serial crystallography datasets to extract structural information about the crystalline lattice, in order to decrease the amount of a priori knowledge required by experiments. Finally, recent attempts at structure solution on a wide variety of molecules (e.g. macromolecules, nanoporous materials, etc.) will be discussed. [1] Bücker, R, et al, "Serial protein crystallography in an electron microscope", Nature Communications 11, (2020).