Methods Development and Software Engineering for 2D Electron Crystallography

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Electron crystallography of 2D crystals (2D-EX) of membrane proteins has allowed atomic models of these proteins to be build (1,2). Several advantages of this method over 3D x-ray crystallography can be identified, such as preserving the protein in a more native state or imaging of the crystal with direct amplitude and phase retrieval. Nevertheless, this method has not yet matured to the point of routine use. We pursue the goal to establish 2D-EX membrane protein crystals as a complementary method (next to x-ray crystallography and structural NMR) for resolving atomic resolution structures of biological macromolecules. To this end, we are in the process of implementing and refining the methods utilized by the pioneers of the field (1,2), as well as following novel methodological and algorithmic approaches. In parallel, we are developing an image processing library and toolkit (3), taylored to the specific requirements of these methods.

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