Enabling Automated Cryo-EM Data Acquisition with Smart EPU

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Cryo-EM has revolutionized the field of structural biology due to its capabilities resolving the three-dimensional structure of proteins, protein complexes, and other biological macromolecules at high or even atomic resolutions. However, acquiring high-quality data for single particle analysis still largely depends on the expertise of the microscope operator emphasizing the need for more robust automation and real-time feedback throughout the data acquisition process. Here we will present the latest developments in Thermo Scientific Smart EPU software, which frees operators from tedious and repetitive tasks and makes Cryo-EM accessible to a wider audience.

The Smart EPU platform provides an open interface that enables algorithms ("Smart Plug- ins") to connect to an ongoing acquisition and optimize it in terms of efficiency and quality by leveraging, in real time, the vast amounts of data and metadata produced by the microscope. This platform will also ensure that the decisions made by the algorithm don't conflict between themselves or compromise the stability of the microscope. Three algorithms have been released to date which digest the results of processing routines such as motion correction and CTF determination to adjust and optimize the ongoing data acquisition session in real time. A fourth algorithm utilizes AI to automatically recognize and discard bad foil holes that would lead to inferior micrographs. Lastly, we will present our open API, which enables development of custom algorithms by member of the Cryo-EM community.