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Crypto-tomography: the data assembly challenge in single-molecule diffraction[1]

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In the absence of a molecular alignment mechanism, the diffraction patterns collected in single-molecule XFEL experiments will sample randomly oriented, 2D slices of a 3D data set. The signal to noise ratio in the individual slices will be so low that the relative orientations of any two will be poorly determined. This talk describes a new strategy for data assembly, where the relationships among multiple slices are determined collectively.

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