Refining helical structures using Frealix

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Frealix is software designed to refine helical structures calculated from images of frozen-hydrated protein filaments. It can process filament images following the single-particle paradigm or incorporate a number of *a priori* restraints derived from mechanical considerations, which allow it to use arbitrarily short segments for alignment and thereby out-perform single-particle algorithms in cases of high curvature and low signal-to-noise ratios.

In addition to the macromolecular structure of the helical subunit, Frealix refines a 3D representation of each filament in the dataset. In aggregate, these "metadata" describing filament shape, deformations etc. make it possible to test the predictions of models (such as the worm-like chain model) against in vitro observables.

We present an overview of the program, some recently implemented features, and 3D reconstructions in the 3.5-to-5.5-Å range recently obtained with Frealix.