Reusing phenix.refine for powder data ?

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phenix.refine is an actively developed macromolecular refinement program supporting refinement against x-ray and neutron single-crystal data. Multiple target functions are implemented, incl. standard maximum-likelihood and least-squares targets, and a least-squares twin target. In addition, phenix.refine uses the Python interface of the Phaser program to integrate the Phaser SAD target. This flexibility is achieved via a modular, library-based design implemented in the Python scripting language. A moderate amount of refactoring may enable the inclusion of target functions for x-ray or neutron powder data.