

Outcomes from EMDataResource Model Challenges

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Electron cryo-microscopy (cryo-EM) is rapidly becoming a mainstream area of structural biology and medicine, enabling visualization and modelling of a wide variety of biologically important complexes. This recent explosion of new cryo-EM structures raises several important questions. How accurate are these maps and their model interpretations? What criteria are currently being used and are they good enough? This paper describes the outcomes of the 2019 Model Metrics Challenge sponsored by EMDataResource (<https://challenges.emdataresource.org>). The goals of this challenge were two-fold: (1) to evaluate the quality of models that can be produced using current modelling software, and (2) to assess the performance of metrics currently in use to evaluate cryo-EM models. In both instances the focus was on map targets selected the near-atomic resolution regime (1.8-3.1 Å), with an innovative twist: three of four maps formed a resolution series from the same specimen/imaging experiment. The results permit several specific recommendations to be made about validating near-atomic cryo-EM structures, both in the context of an individual laboratory experiment and for in the context of a structure data archive. We will also touch on preliminary results from our ongoing 2021 Ligand Model Challenge.