As developers in the Phenix project [1], we are confronted with mmCIF in two ways. Firstly, our algorithms produce results that need to be archived. Secondly, access to information stored in databases, such as the PDB [2], is often invaluable in the development and testing of new methods. In contrast to most traditional, static file formats, mmCIF is highly flexible. Therefore we have the opportunity to export parameters and results of ever more complex algorithms in a uniform framework. However, it is non-trivial to import information from mmCIF files since their processing requires very sophisticated tools. Unfortunately, in many contexts adequate practical tools are not available. The limitations of traditional software development technology are probably the most important factors giving rise to this situation. Fortunately, many in the crystallographic methods development community have begun a transition to modern software technology. Database developers, most notably at the PDB, have already published comprehensive mmCIF libraries. Further development of such libraries in a collaborative effort with an open two-way exchange between the communities has the potential to stimulate a much wider use of mmCIF in the future.


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