Using Coot to Model N-linked Carbohydrates

Coot [1] is molecular graphics application initially designed for model-building and validation of protein models using X-ray data. Since its release, the focus of development has shifted to include building and validation tools for ligands and protein-ligand complexes. A particular specialization included recently is the task of building models of glycosylation. Recently the start of the art for glycosylation structures and model-building has been reviewed [2] in which Coot's building has been analysed. This presentation will discuss monomer, link, torsion and reference distance restraints and demonstrate how Coot has been updated and can be used for rapid model-building and refinement of N-linked glycosylation.
