Practical guidelines for the features described in the poster
“Improving Low Resolution Refinement with ProSMART, COOT and REFMACS”
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The homepage of the Computational Crystallography Group is:
https://www2.mrc-lmb.cam.ac.uk/groups/murshudov/

Coot is available from: https://www2.mrc-lmb.cam.ac.uk/Personal/pemsley/coot/

The other programs distributed as part of CCP4:
http://www.ccp4.ac.uk/

My homepage is: shelx.uni-ac.gwdg.de/~athorn/

**COOT**

**Model Morphing:** A COOT script is available from Paul Emsley, pemsley@mrc-lmb.cam.ac.uk

**Backrub Rotamers:** A button for backrub rotamers can be found on the top menu. It should be activated to take backrub motions into account when rotamers are fitted.

**Map sharpening/blurring:** Choose the Calculate > Map Sharpening menu item.

**DNA/RNA support:** In the latest 0.8 pre build: Use the Refmac Extra Restraints menu item. LIBBG restraints need to be generated beforehand via REFMAC. External Restraints can be read in the same way, but need to be generated via ProSMART.

**ProSMART**

Via CCP4:

(A) ProSMART interface in CCP4

(B) By using the ProSMART button in the REFMAC interface

Or in manual mode by typing “prosmart” on the command line.

All features discussed in the talk are supported in the current version, including DNA/RNA support.

**REFMAC**

**Jelly Body restraints:** Via the CCP4 interface (Refinement Parameters > use jelly-body refinement)

**DNA/RNA:** LIBG is distributed with REFMAC.

**Map sharpening:** Via the CCP4 interface (Monitoring and Output Options > Perform Map Sharpening)

**TUTORIALS**

https://www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/tutorials/refmac_tutorial/

https://www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/tutorials/prosmart_tutorial/