Practical guidelines for the features described in the talk
“Low resolution model building and refinement tools in COOT and REFMAC5.”
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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: Choose the Calculate > Map Sharpening menu item.
DNA/RNA support: In the latest 0.8 pre build: Use the Refmac Extra Restraints menu item

ProSMART
Via CCP4:
(A) ProSMART interface in CCP4
(B) By using the ProSMART button in the REFMAC interface

In manual mode: bla
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: The library libg will be distributed with the next REFMAC release. It will assign base pair and stacking restraints if residue names are appropriate and residues are approximately parallel.
Map sharpening: Via the CCP4 interface (Monitoring and Output Options > Perform Map Sharpening)

TUTORIALS
www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/tutorials/refmac_tutorial/
www2.mrc-lmb.cam.ac.uk/groups/murshudov/content/tutorials/prosmart_tutorial/