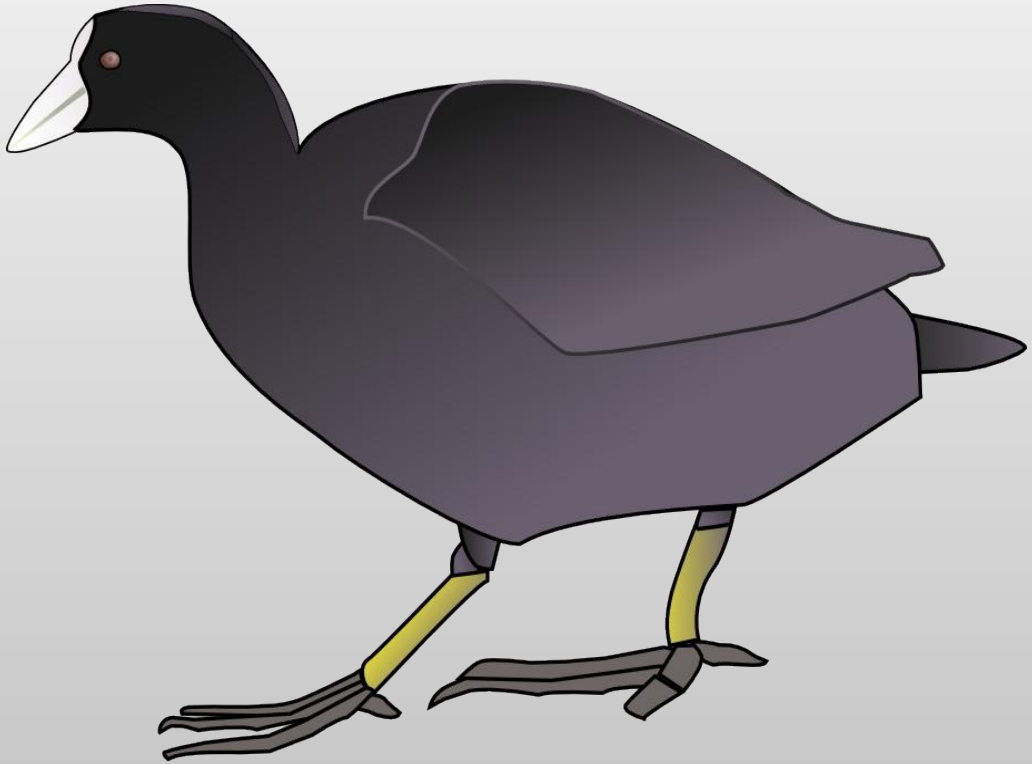
Coot: The Basics



Coot

- Molecular Graphics application
  - Protein Crystallographic model-building tools
  - Designed to “fill the gap” where automatic methods fail
    - (generally, we don't use molecular graphics programs to do what automatic methods can do)
- Interface to (other) programs
  - Refmac, Libcheck,
  - Probe&Reduce (Molprobity),
  - EBI, EDS,
  - Povray… and others

Mouse clicks and motion

- Left-mouse click and drag
  - -> rotate the view
- Right-mouse click and drag
  - -> zoom in
- Middle-mouse click
  - -> label atom
- Middle-mouse scroll
  - -> change map contour level

More mousing

- Left-mouse double click
  - -> label atom
- Ctrl left-mouse drag
  - -> drag view/translate

  Ctrl Shift scroll middle-mouse
  - -> change representation style

  Ctrl Right-mouse drag
  - change depth cue (up/down)
  - translate in screen z (left/right)

Button presses...

- a: auto-zone refinement
- c: toggle cross-hairs
- d & f: depth cueing
- i: toggle spin/rock
- <Shift> l: label atom
- m & n: zoom
- o and <Shift> O: Other NCS chain
- p: (intelligent) nearest atom
- v: undo symmetry view

Ctrl Button presses

- Ctrl s: quick save-as
- Ctrl z: undo model modification
- Ctrl g: go to residue
- Ctrl i: residue info

standard extra button presses

- e: flip residue
- g: go to blob
- h, <shift> h, r, <shift r>, t, x: forms of refine and regularize
- j: auto-fit rotamer
- k and <shift> k: kill and fill side-chain
- q: flip peptide
- y: add peptide
- w: add water under cursor
- <shift> w: add water under blob

Extra accelerators

- Get from the Coot Wiki
  - 2.2.12 for Unix/Mac
  - 2.3.1 for Python version (using in WinCoot)
- Look for extensions in:
  - Extensions → Settings... → Keybindings...