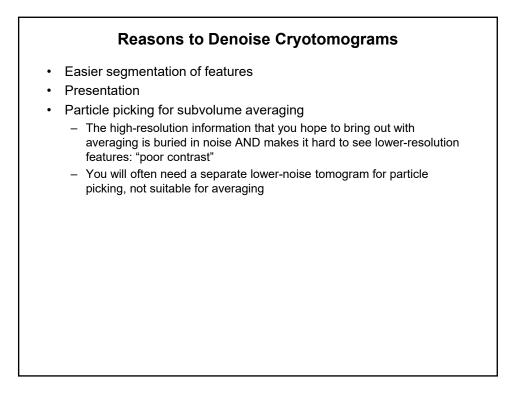
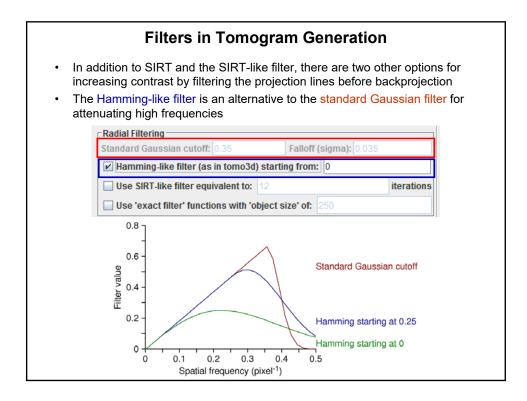
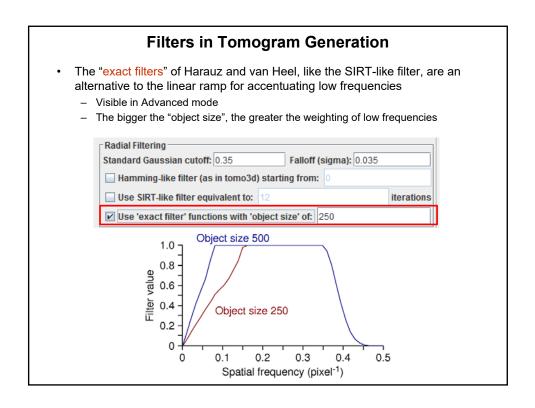
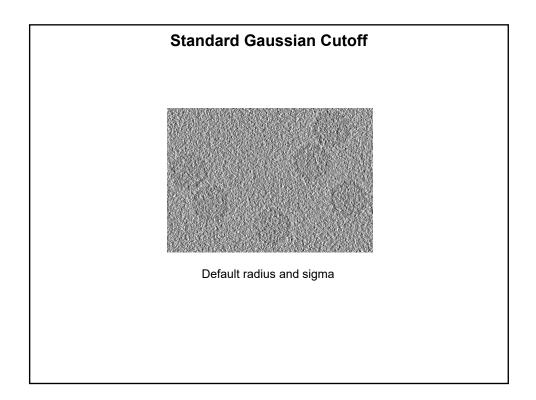
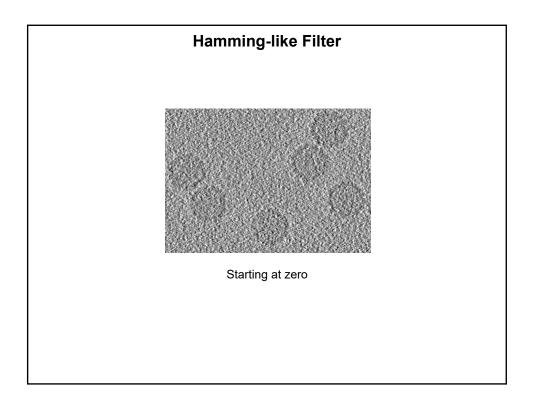
Denoising Cryotomograms with IMOD

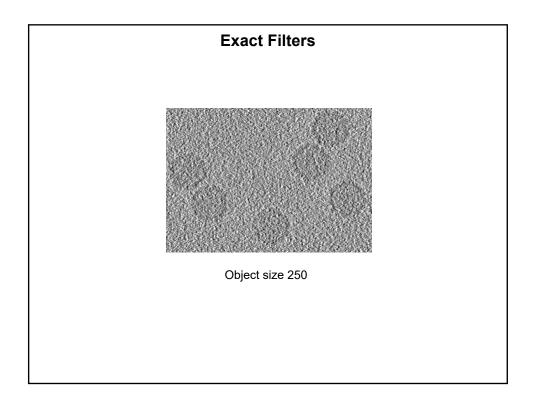


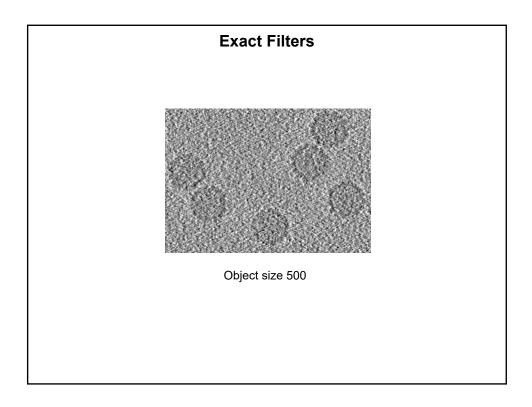


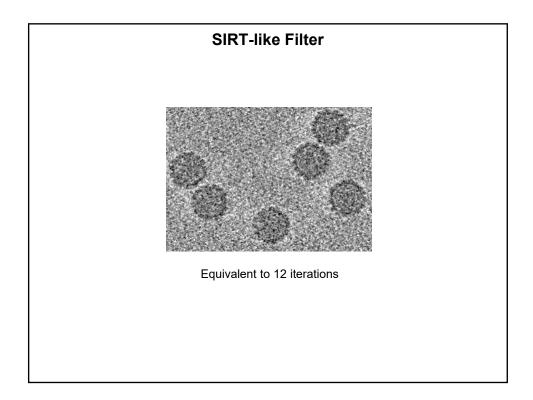


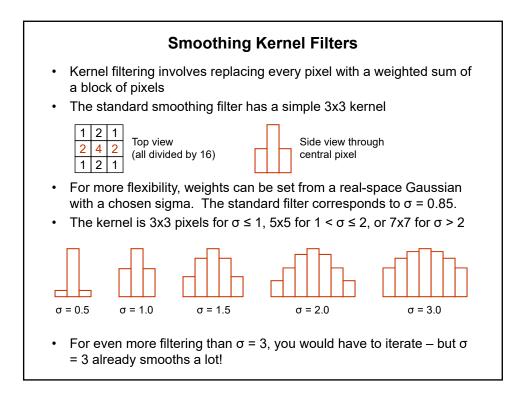


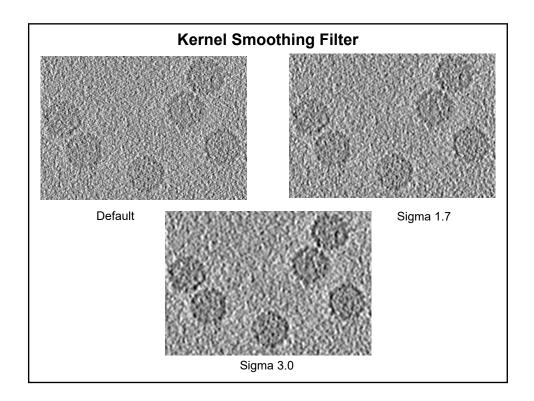


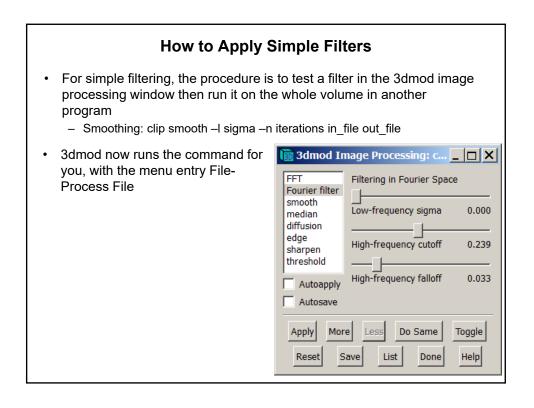


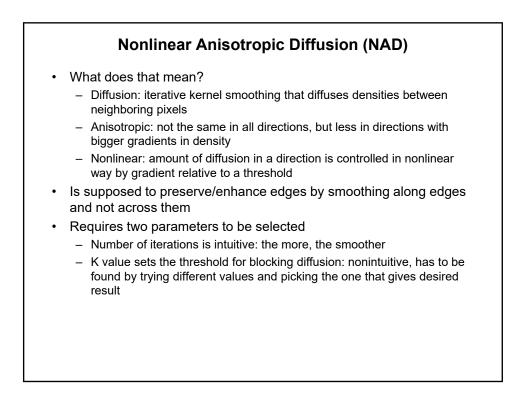


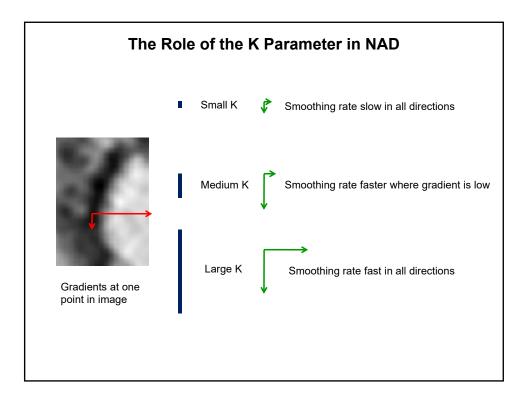


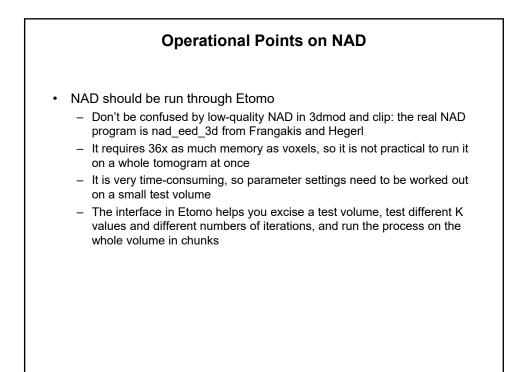












| Running NAD | |
|-------------|---|
| • | In Etomo, select it from the Front Page, or select File – New Nonlinear Anisotropic Diffusion |
| • | A test volume of 200 x 200 x 24 pixels will run reasonably quickly; it can be thinner (down to 16 pixels) if you need to see larger area |
| • | Start with wide range of K values |
| | K is relative to the gradients (thus intensities) in the file; this means integer data will need higher K values than byte data for same effect |
| | For byte data, try 0.4, 1.6, 6.4, 26, 102 or 0.4, 1.0, 2.5, 6.4, 16, 40, 100 |
| | K tests are run in parallel to the extent possible |
| • | Pick a K range that gives the kind of filtering desired and rerun at finer intervals in the range |
| | You will see K values where intensities "plateau" over many pixels |
| | Lower K values preserve edges while reducing this effect, but may not allow much smoothing |
| | Higher K values give essentially isotropic smoothing |
| • | Vary the iterations to pick the amount of smoothing |
| • | When running on whole volume, memory = 36 x voxels in chunk so default chunk is 14 M voxels. |