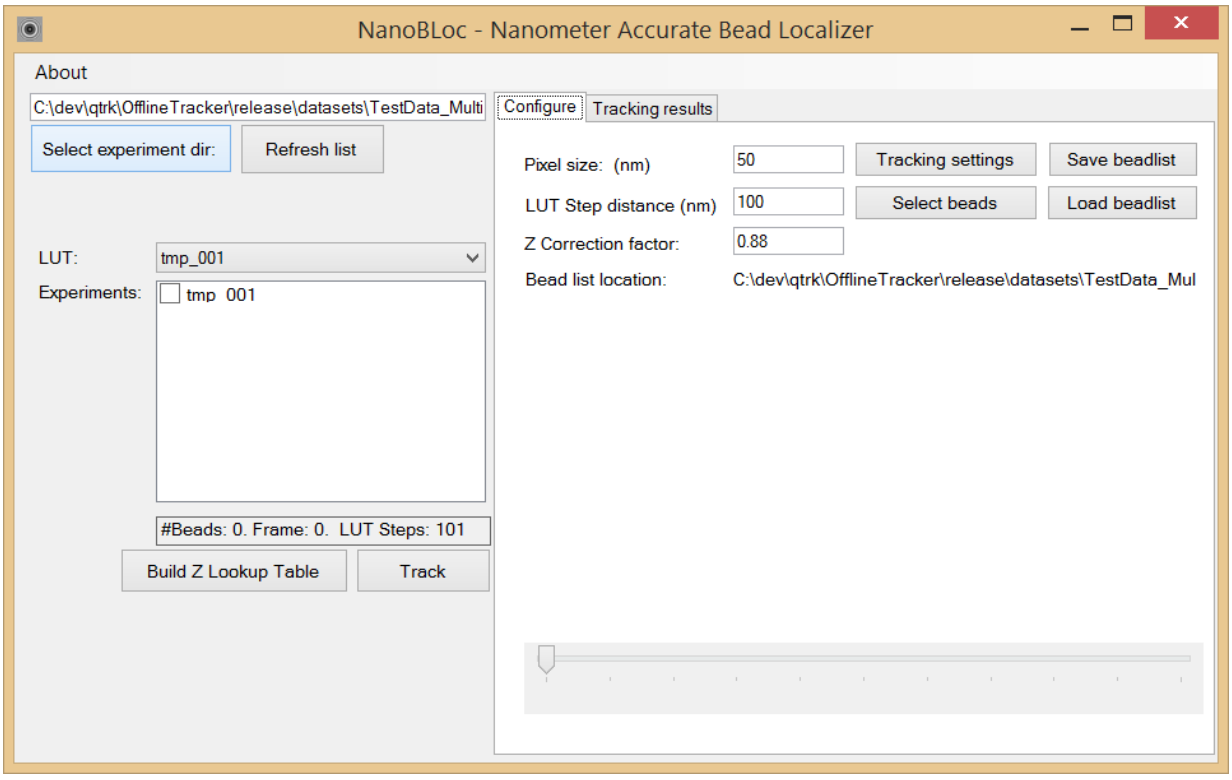
NanoBLOC Example workflow

This quick guide assumes that you can already generate a dataset with images and a set of images for the Z lookup table.

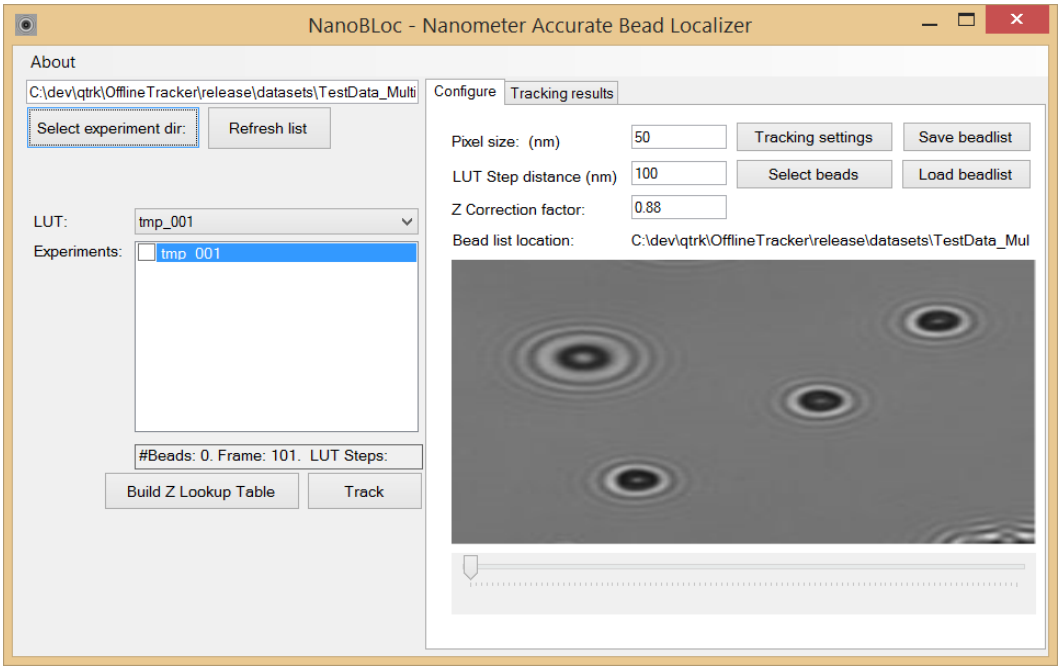
1. “Select experiment dir”

   This selects the base directory in which different folders with image files can be found. The idea is that in a typical workflow, you have a flowcell with a number of beads which you select, and with that set of beads you do different kinds of experiments (ex: rotating the magnet or flushing in different substrates into the flowcell) . Each of those experiments gets its own image folder, and the set of bead locations is the same for each image folder (in the example this is tmp_001, tmp_002).

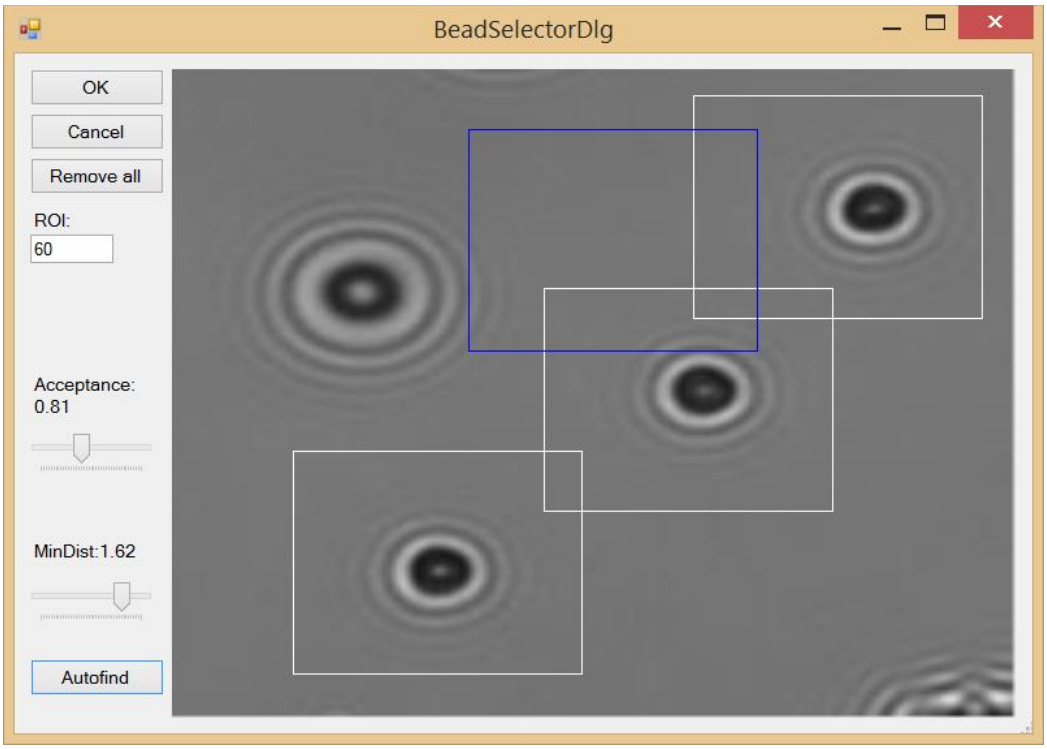
   The directory “datasets” contains an example set of images that show how they should be organized.



2. Select one of the folders to show the image:

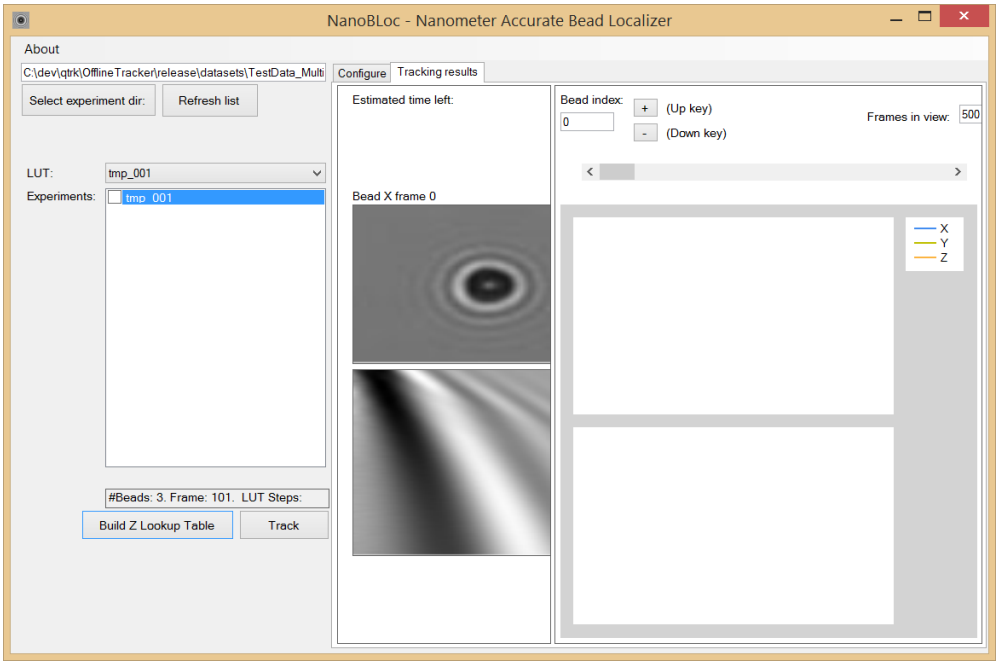


3. Click “Select beads”, and select a few beads to track. Middle mouse button, or control+left mouse button will remove bead again. Autofind can be used to automatically locate beads based on selecting one sample bead.



4. Make sure that pixel size and LUT Step distance are set up correctly in nm. The Z correction factor can be kept at 0.88 typically, for details see this paper.

5. Select the right image folder for the LUT (in this case we only have tmp_001), and click “Build Z Lookup Table”. The result will be displayed in the tracking results tab.



6. Check all the experiments you want to have processed and “Track”. Results are displayed and also stored in the base directory, in this case as “tmp_001-xyz.txt”. This is a tab separated file, where the first column is FrameNumber, second is FrameTime (always zero currently), and remaining columns are bead coordinates (Bead1X, Bead1Y, Bead1Z, Bead2X, …)

   Every time the trace view is opened the data is loaded again from the text file, so you can also quit and reopen the program to view back the traces.