Lesson 3:
Reconstructing Difficult Cryo Data using BRT

In this exercise, you will use BatchRunTomo (BRT) to build 3 cryo tomograms that have typical issues found in cryo data. Normally, BRT would be used to run many datasets of the same sample type and imaging conditions. Most people will run up one dataset to find appropriate parameters and then process the remaining data in BRT using those parameters. This practice lab is intended to introduce issues that may crop up now and then and is not realistic to how BRT is used on a day-to-day basis.

1) `cd $WORKSHOP_HOME/IMOD_Labs/cryo-practice`

2) `etomo`

3) Press **Batch Tomograms** on the **Front Page**. These data are all within this single directory, so we need to change to **Move stacks to dataset directories under their current location**.

   Select the file chooser for **Starting directive file** and use *Cryo-Practice-Tutorial.adoc*. This file contains information about the data being collected in two directions about zero degrees, which can affect alignment. Select *cryoSample.adoc* as the **System Template**.

4) Switch to the **Stacks** tab. Press **Add Stack(s)**. Highlight all 3 stacks (*Series4.mrc*, *Series5.mrc*, and *Series6.mrc*) and press **Open**.

   For *Series4.mrc*, press the **3D** icon under **Open Stack A**. Many people choose not to use gold fiducials found on the carbon. To exclude these fiducials, check **Boundary Model** in the **Datasets**