

Reconstruct and label movement trials

After you have calibrated a labeling skeleton for your subject (see [Prepare a subject](#)) and captured the required movement of the subject in a trial or series of trials (see [Capture movement trials](#)), you must reconstruct and label the raw camera data to create 3D markers. You can do this as a separate step, as described below, or you can specify a pipeline that includes **Reconstruct** and **Label** in the **Post-Capture Pipeline Setup** (see [Capture the required movement](#)), so that these operations run straight after capture.

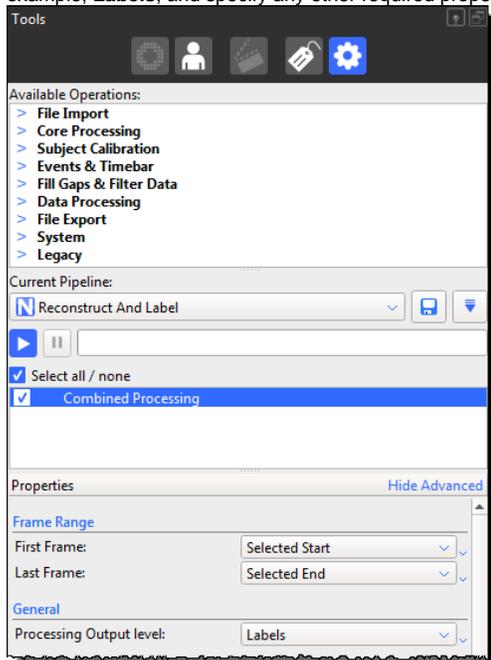


Note

You can choose to reconstruct and then label separately, or run both operations together, by clicking either the **Reconstruct** button  or the **Reconstruct and Label** button  on the Nexus toolbar, or by configuring and running the equivalent pipeline operations. Normally, you would use **Reconstruct** alone if you are working on a labeling skeleton template (VST), but **Reconstruct and Label** if you are processing movement trials.

To reconstruct and label trial data:

1. Display the subject whose data is to be reconstructed in either of the following ways:
 - If you have just captured a trial, ensure that the raw marker data for the subject in the capture volume is still visible in a **Camera** view and in the **Resources** pane, ensure Nexus is in **Offline** or **Pause** mode; or
 - On the **Data Management** tab, open the desired trial file containing raw trial data for the subject.
2. Do one of the following, depending on whether you need to adjust the reconstruct and labeling settings:
 - To run the operations without viewing and changing their settings, on the Nexus toolbar, click the **Reconstruct and Label** button. This runs the **Reconstruct and Label** operation defined in the **Pipeline Tools** pane.
 - Or
 - To view and/or change the operations, on the **Pipeline Tools** pane, from the **Current Pipeline** list, select **Reconstruct And Label**. In the list of current operations, click on **Combined Processing** to select it. set the **Processing Output level** to the required level, for example, **Labels**, and specify any other required properties.



The pipeline progress bar indicates when the operation is complete.

You can now review the results and fill any gaps in the trial data. For information, see [Review trials and fill gaps](#).