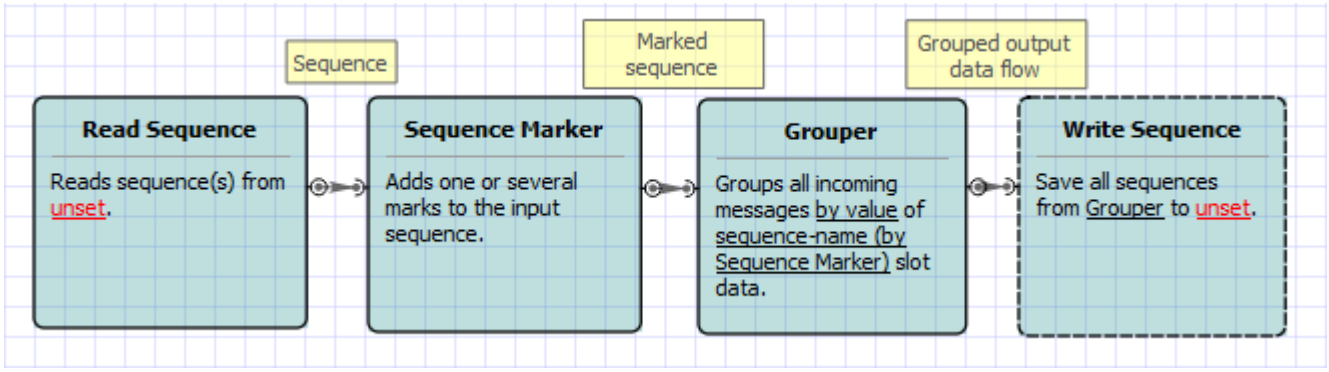
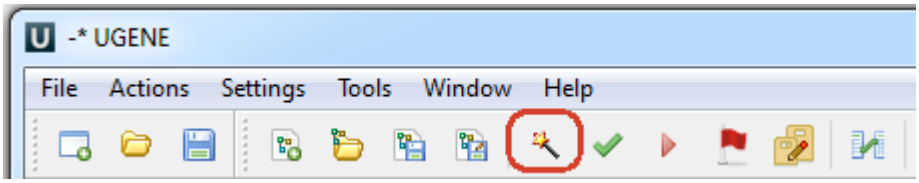
Merge Sequences and Shift Corresponding Annotations

This scheme describes how to merge sequences and manipulate with its annotations.

First, the workflow reads sequence(s) from file(s). Then, marks the input sequences with the sequence name marker. After marking the sequences are grouped by the marker. Sequences with equal markers are merged into one sequence. Annotations are shifted using the position of the corresponding sequence at the merged sequence. And finally, the grouped data are written into file, specified by a user.

By default, sequence is marked using the sequence name marker. You can configure this value in the *Marker* element parameters. Also, you can configure the *Grouper* element parameters.

To try out this sample, add the input files to the *Read Sequence*, select the name and location of the output files in the *Write Sequence* element and run the workflow.



Also, if required, you can change parameters. Use the workflow wizard to guide you through the parameters setup process. The first wizard page will appear when you click on the Show wizard button on the Workflow Designer toolbar: