

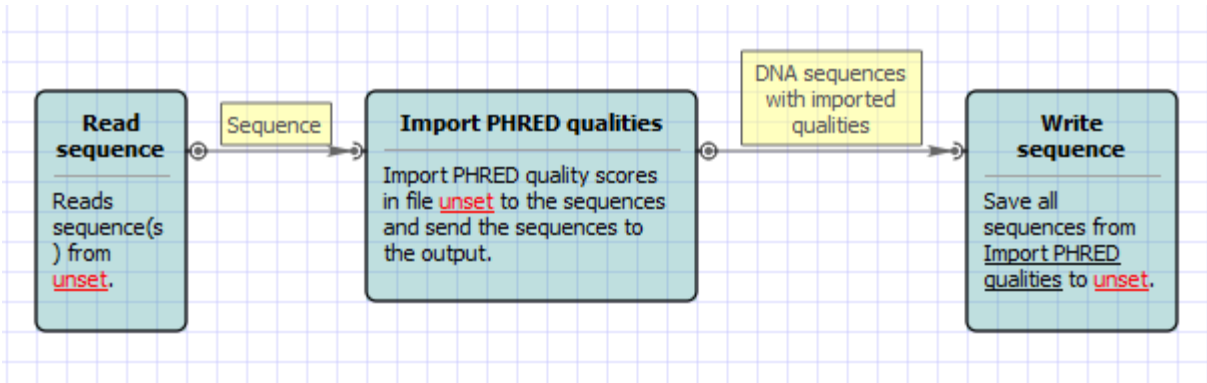
Convert "seq/qual" Pair to FASTQ

This workflow allows to add PHRED quality scores to the sequence and save output to Fastq. For example, one can read a Fasta file, import PHRED quality values from corresponding qualities file and export the result to Fastq.

To execute the workflow do the following:

1. Select "Sequence Reader" task and specify source file(s) at "URL" field in the Property Editor.
2. Select "Import PHRED qualities" task and specify URL to the quality file. Usually such files have .qual extension.
3. Launch the schema with pressing Ctrl+R shortcut.

After running the workflow, target fastq file will appear in the same folder as the source file, with the same name but different extension.



How to Use This Sample

If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.