Extract Transcript Sequences

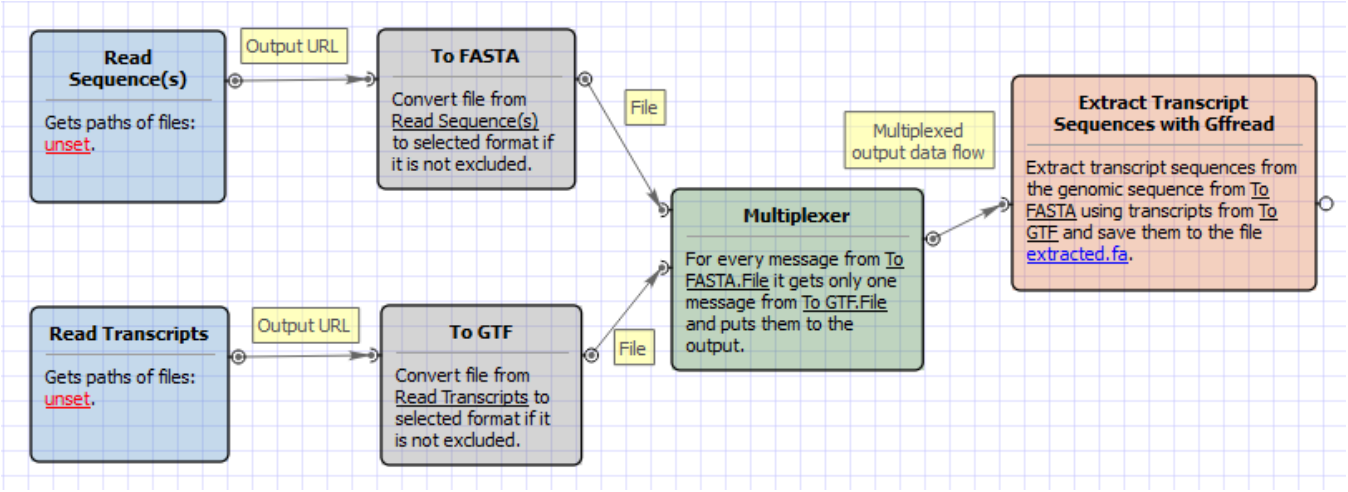
This workflow uses input transcripts and genomic sequences to generate a FASTA file with the DNA sequences for the transcripts. Please make sure that contig or chromosome names in the transcript file(s) have corresponding entries in the input sequence(s).

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.

Workflow Sample Location

The workflow sample "Extract Transcript Sequences" can be found in the "NGS" section of the Workflow Designer samples.

Workflow Image

The workflow looks as follows: