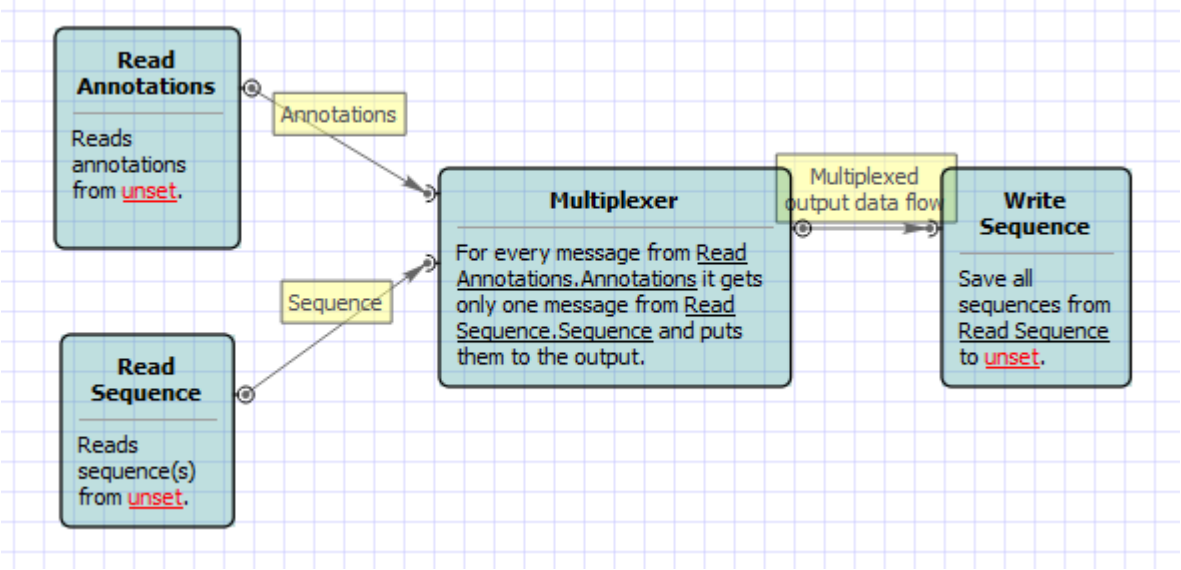
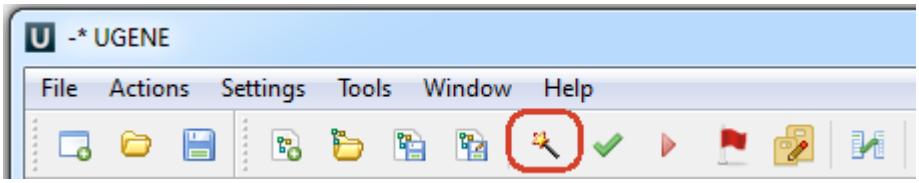
Merge sequences and annotations

If you have a list of files with sequences and separate files with annotation and you want to merge sequences and annotation, this workflow might help you. For instance, you have sequence in FASTA format and separate annotation in GFF. You want to merge them and write annotated sequences into Genbank files. Be default, multiplexer takes sequences and annotation one by one, sticks one annotation to one sequence and passes it to the output. But you may change that behavior in parameters of Multiplexer.



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: