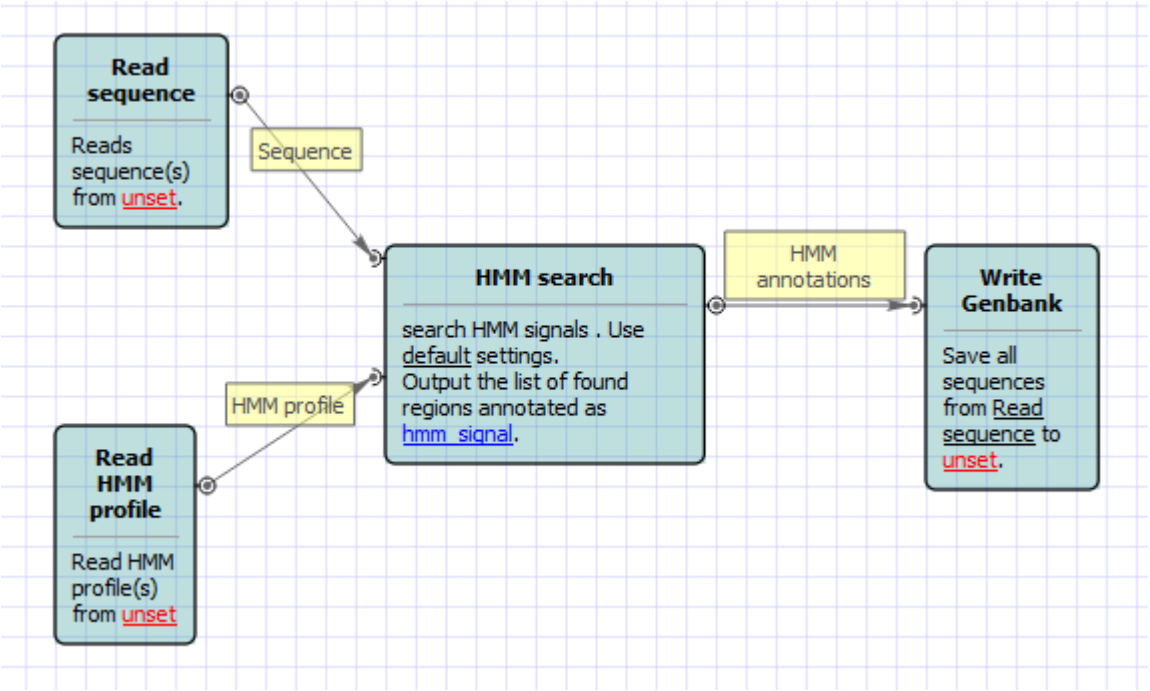
Search Sequences with Profile HMM

This workflow reads an HMM from a file and searches input sequences for significantly similar matches, saves found signals to a file. You can specify several input files for both HMM and sequences, the workflow will process Cartesian product of inputs. That is, each sequence will be searched with all specified HMMs in turn. To specify task parameters, select it and edit interesting fields in table "Parameters" of Property Inspector panel. Schedule the workflow for execution by pressing CTRL+R shortcut. You can watch its" progress in Task View of UGENE.



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.