Find Substrings in Sequences

This sample workflow shows how to find substrings in input sequences, annotate them, and merge the found substring annotations with the original sequence annotations.

The steps of the workflow are these:

1. The workflow reads sequences from the input sequence files (e.g. GenBank). The input data may also contain the annotations, associated with the sequences.
2. The workflow reads text strings (patterns) from the input text files.
3. The data are multiplexed using the Multiplexer element. Multiplexing rule "1 to many" is used, so each input sequence is concatenated with each pattern. The concatenating results are sent to the *Find Substrings* element.
4. The *Find Substrings* element searches for the specified patterns in each sequence.
5. The next element Grouper merges annotations, read for the sequence in the *Read Sequence* element, with annotations, found for the sequence by the *Find Substrings* element. A sequence ID is used to group the appropriate sets of annotations.
6. And finally, the data are written to the output file ("substrings.gb" , by default).

How to Use This Sample

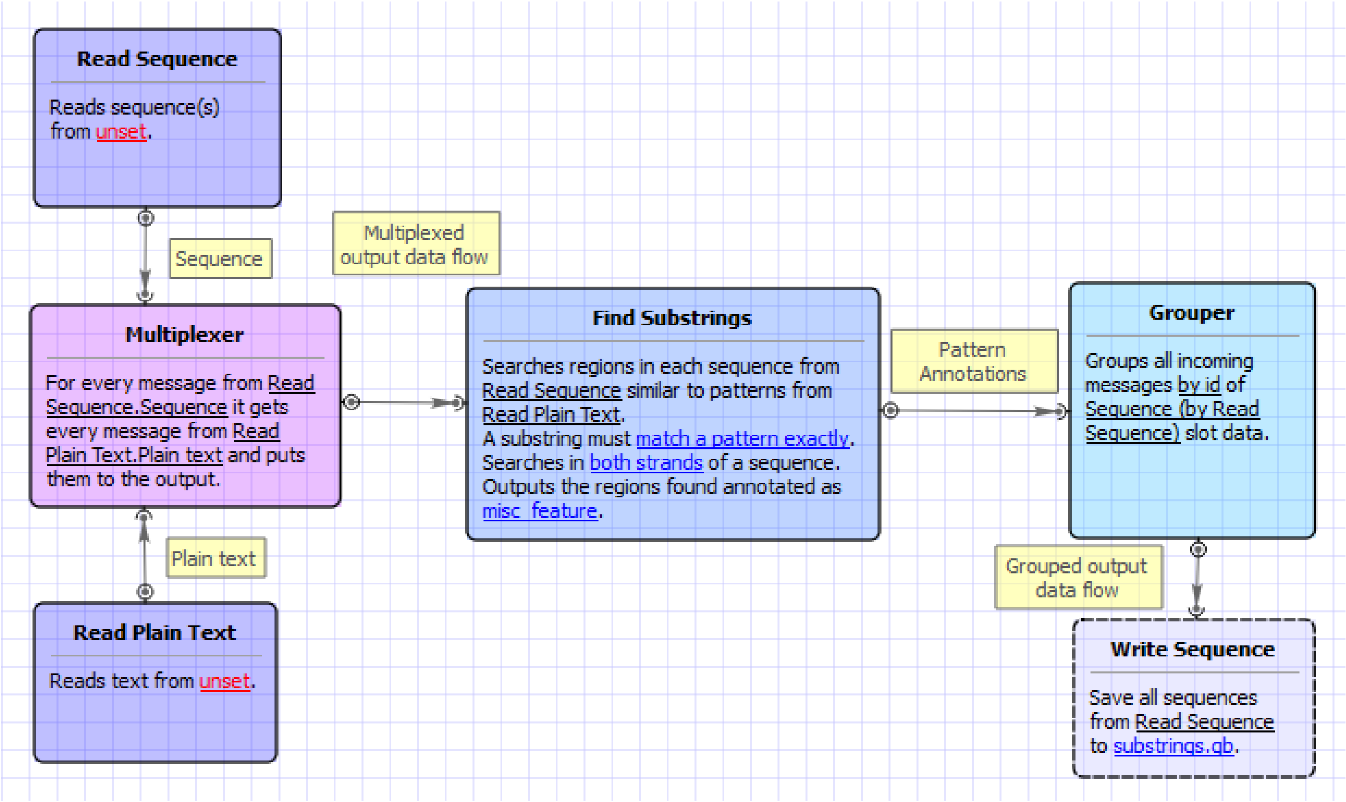
If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

The workflow sample "Find Substrings at Sequences" can be found in the "Data Merging" section of the Workflow Designer samples.

Workflow Image

The workflow looks as follows:



Read Sequence

Reads sequence(s) from unset.

Multiplexer

For every message from Read Sequence.Sequence it gets every message from Read Plain Text.Plain text and puts them to the output.

Read Plain Text

Reads text from unset.

Find Substrings

Searches regions in each sequence from Read Sequence similar to patterns from Read Plain Text. A substring must match a pattern exactly. Searches in both strands of a sequence. Outputs the regions found annotated as misc_feature.

Grouper

Groups all incoming messages by id of Sequence (by Read Sequence) slot data.

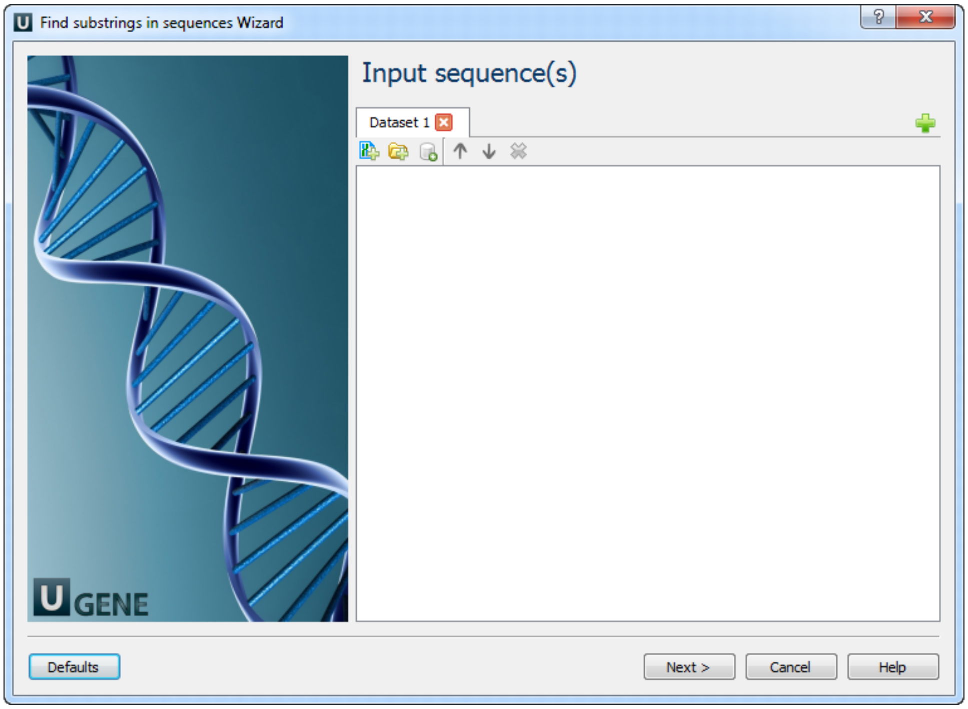
Write Sequence

Save all sequences from Read Sequence to substrings.gb.

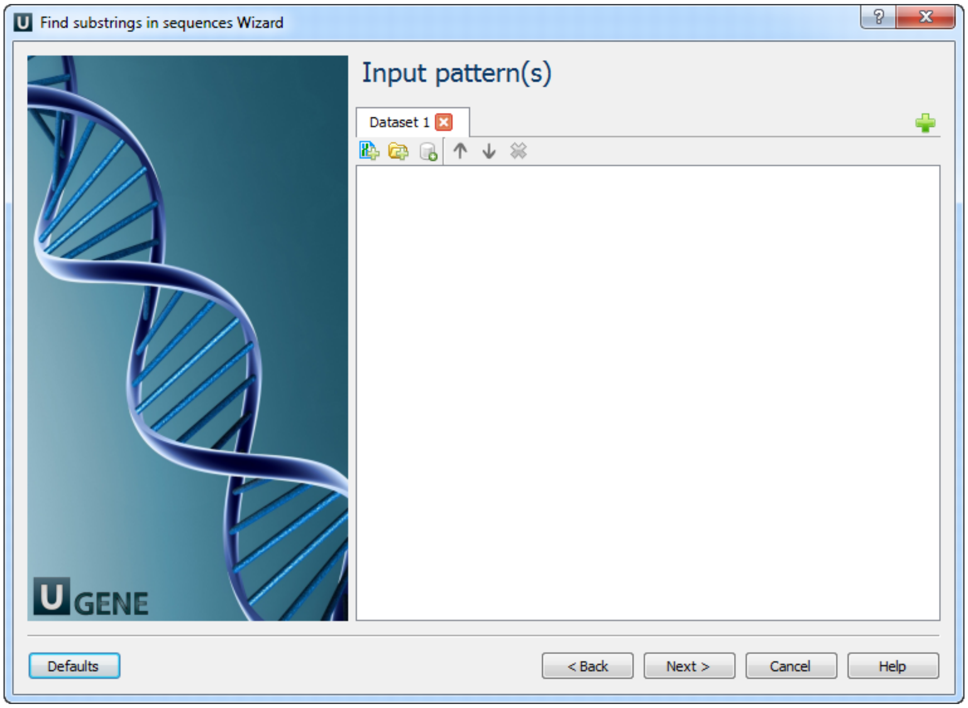
Workflow Wizard

The wizard has 3 pages.

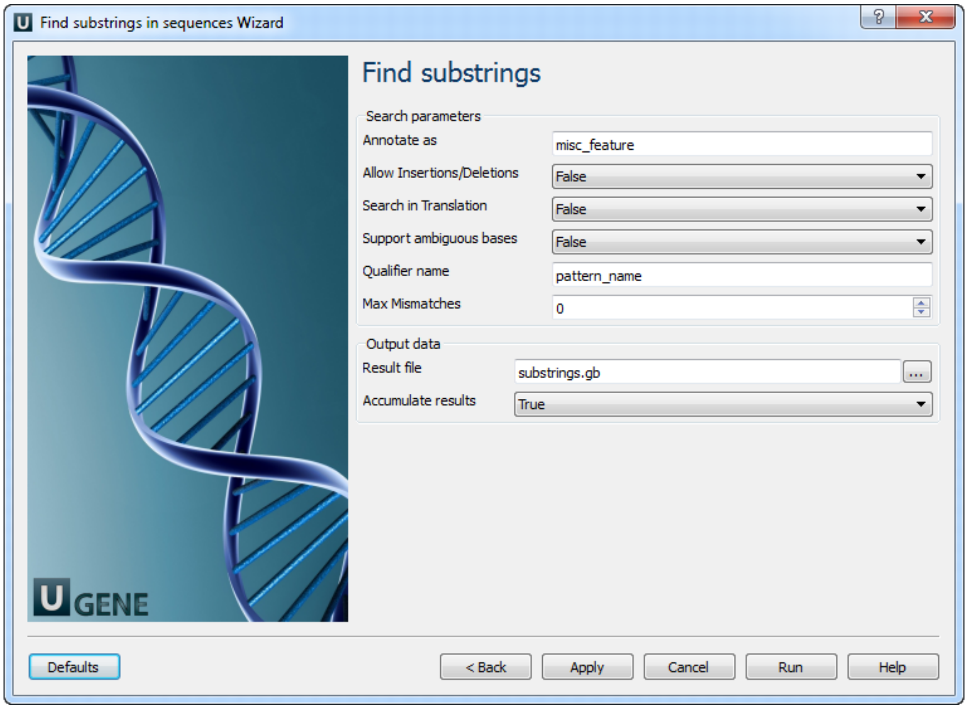
1. Input sequence(s): On this page you must input sequence(s).



2. Input pattern(s): On this page you must input pattern(s).



3. Find substrings: On this page you can modify search and output parameters.



Find substrings in sequences Wizard

Find substrings

Search parameters

Annotate as: misc_feature

Allow Insertions/Deletions: False

Search in Translation: False

Support ambiguous bases: False

Qualifier name: pattern_name

Max Mismatches: 0

Output data

Result file: substrings.gb

Accumulate results: True

The following parameters are available:

Annotate as	Name of the result annotations.
Allow Insertions /Deletions	Takes into account possibility of insertions/deletions when searching. By default substitutions are only considered.
Search in Translation	Translates a supplied nucleotide sequence to protein and searches in the translated sequence.
Support ambiguous bases	Performs correct handling of ambiguous bases. When this option is activated insertions and deletions are not considered.
Qualifier name	Name of qualifier in result annotations which is containing a pattern name.
Max Mismatches	Maximum number of mismatches between a substring and a pattern.
Result file	Location of output data file. If this attribute is set, slot "Location" in port will not be used.
Accumulate results	Accumulate all incoming data in one file or create separate files for each input.In the latter case, an incremental numerical suffix is added to the file name.