Find Patterns

This simple workflow finds patterns in you sequences and save them as annotations. You can use the workflow to map primers, regulatory signals, genes, etc. It loads any set of sequences from your files or folders and finds patterns in them.

How to Use This Sample

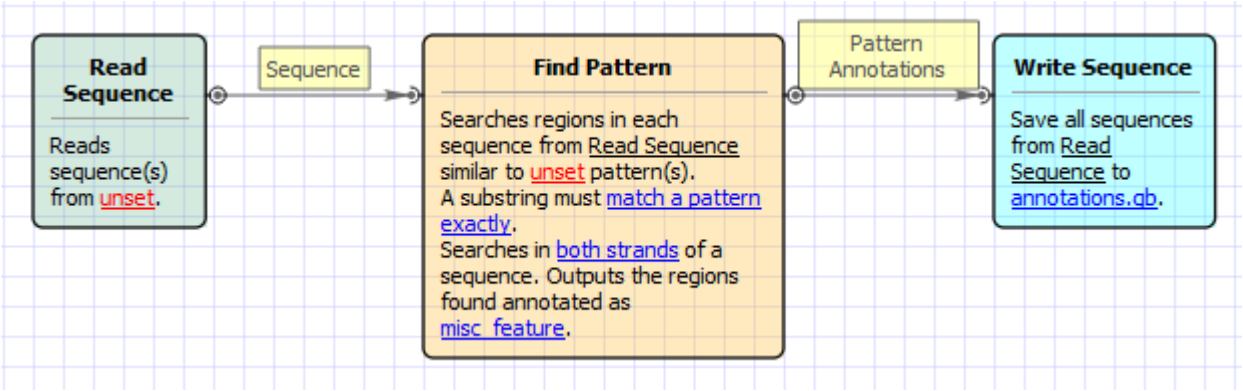
If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

The workflow sample "Find Patterns" can be found in the "Scenarios" section of the Workflow Designer samples.

Workflow Image

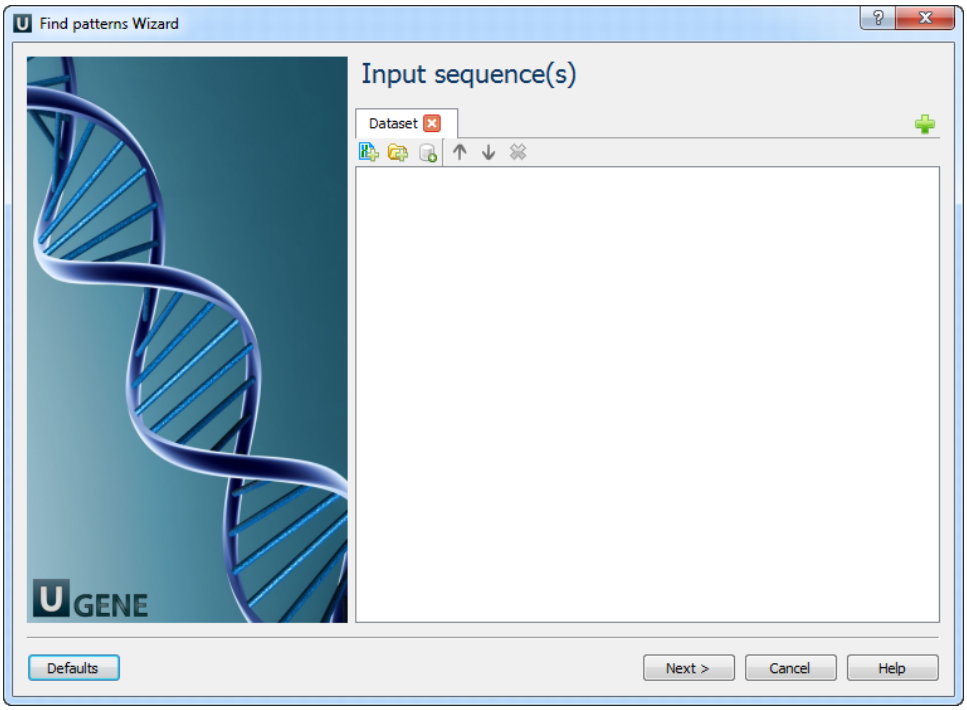
The workflow looks as follows:



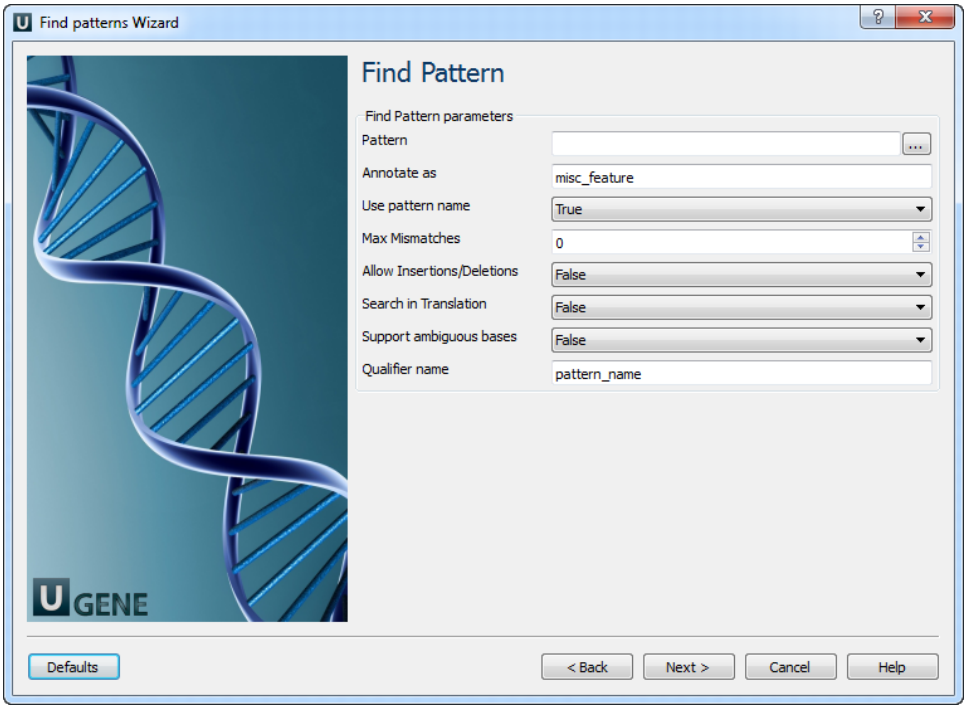
Workflow Wizard

The wizard has 3 pages.

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



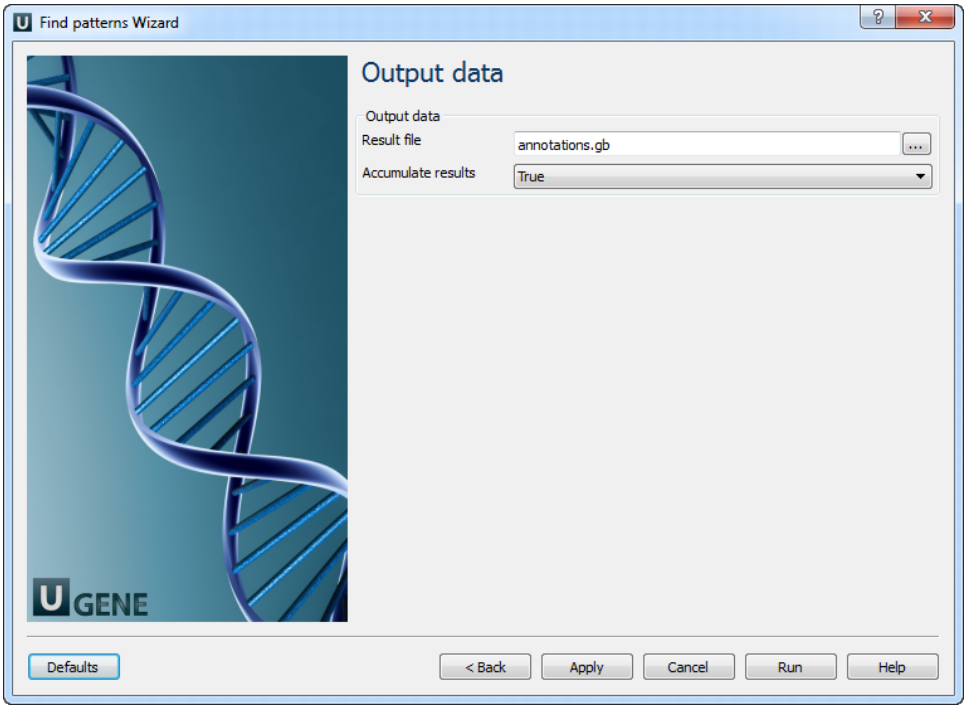
2. Find pattern: On this page you must input pattern(s) and you can modify searching parameters.



The following parameters are available:

Pattern	Semicolon-separated list of patterns to search for.
Annotate as	Name of the result annotations.
Use pattern name	If patterns are loaded from a file, use names of pattern sequences as annotation names. The name from the parameters is used by default.
Max Mismatches	Maximum number of mismatches between a substring and a pattern.
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.

3. Output data: On this page you can modify output parameters.


Find patterns Wizard
Output data
Output data
Result file
annotations.gb
Accumulate results
True
UGENE
Defaults
< Back
Apply
Cancel
Run
Help