# Search for Inverted Repeats

For each input sequence the workflow performs a search of inverted repeats.

Then it saves the repeats found on the direct strand to the "direct_strand_repeat_units.fa" file and the complement ones to the "compl_strand_repeat_units.fa" file.

**How to Use This Sample**

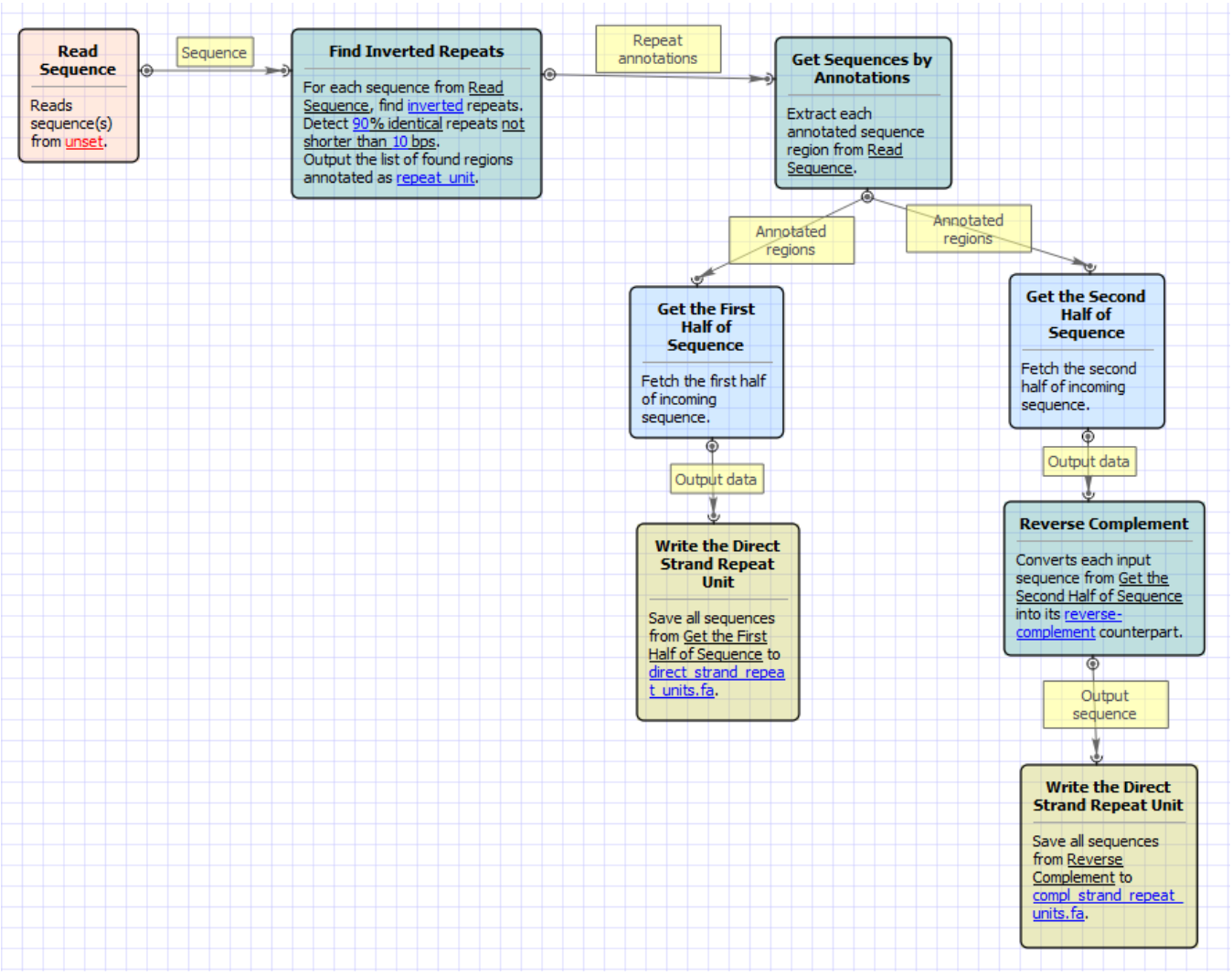
If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

## Workflow Sample Location

The workflow sample "Search for Inverted Repeats" can be found in the "Scwnarios" section of the Workflow Designer samples.

## Workflow Image

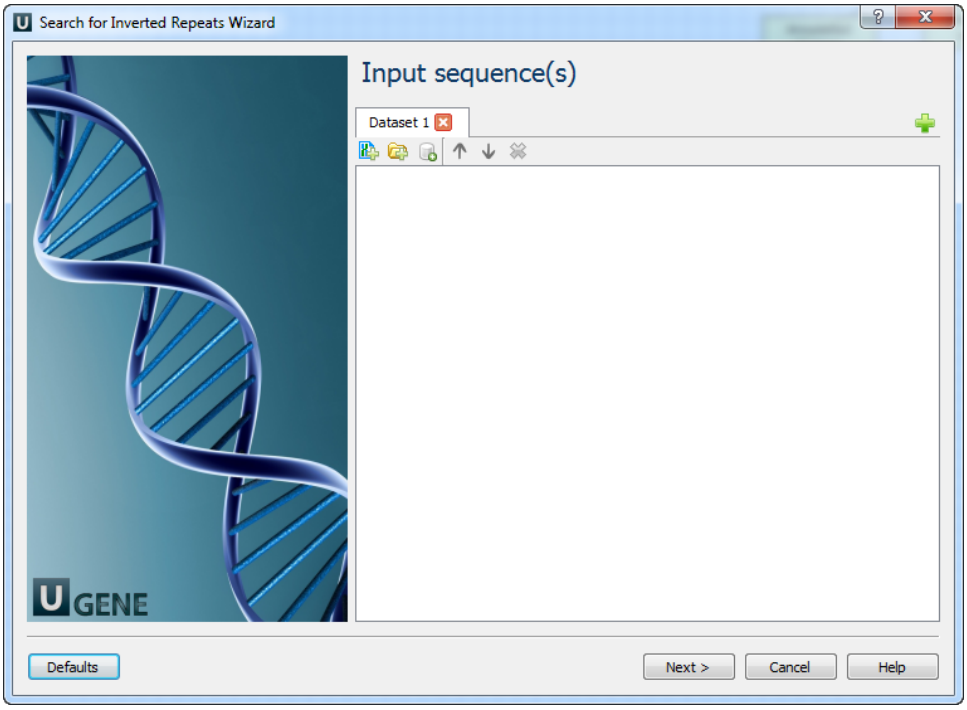
The opened workflow looks as follows:



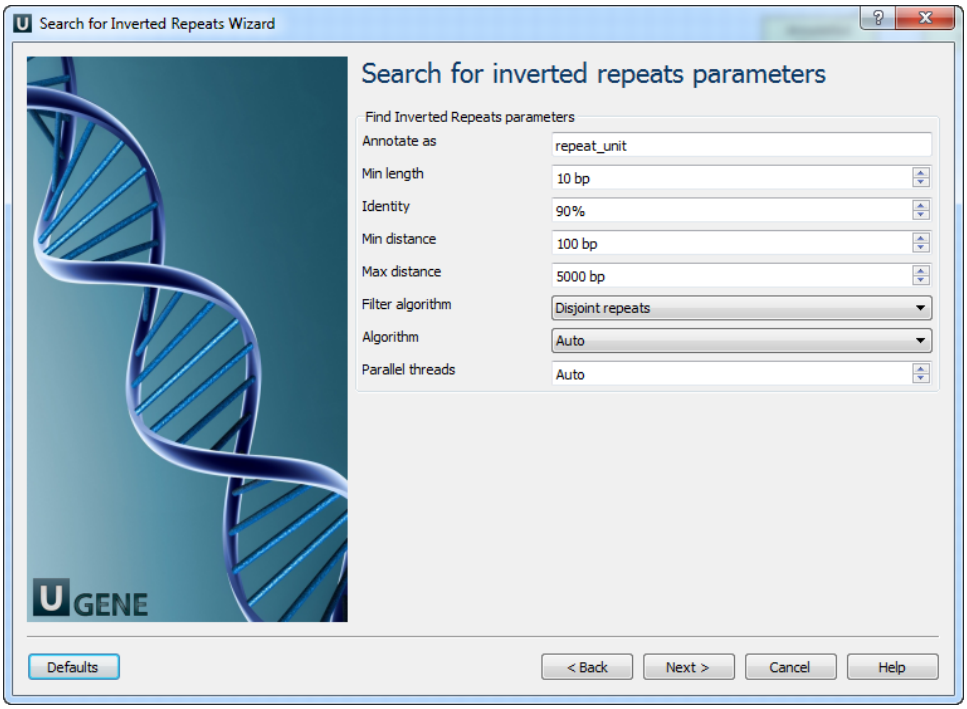

## Workflow Wizard

The wizard has 3 pages.

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

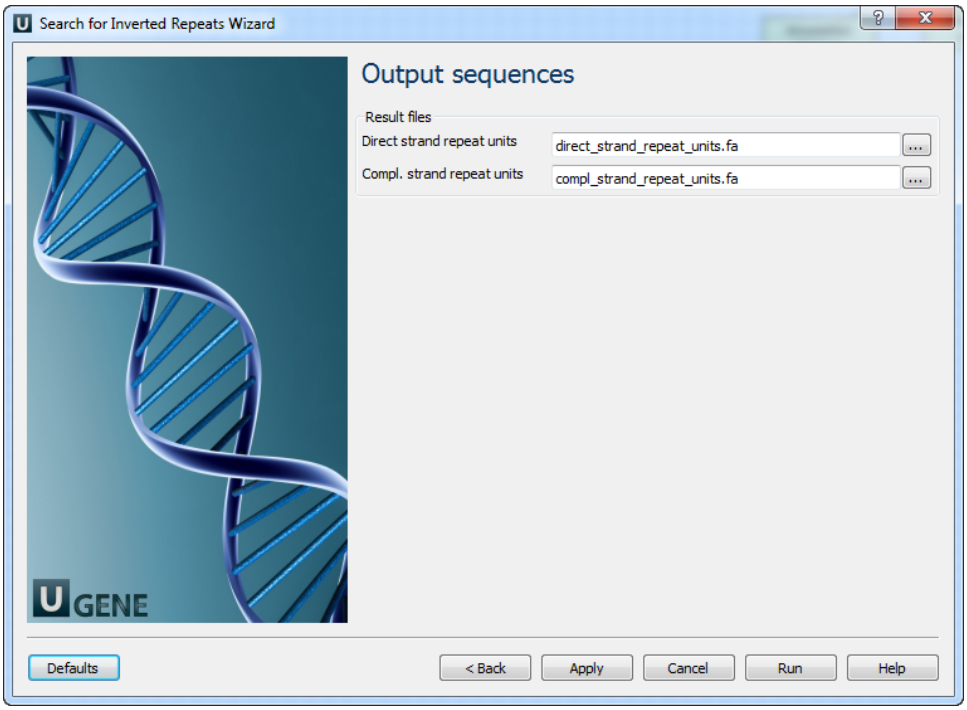



2. Search for inverted repeats parameters: On this page you can modify inverted repeats parameters.




The following parameters are available:

| | |
|---|---|
| Annotate as | Name of the result annotations marking found repeats. |
| Min length | Minimum length of repeats. |
| Identity | Repeats identity. |
| Min distance | Minimum distance between repeats. |
| Max distance | Maximum distance between repeats. |
| Filter algorithm | Filter repeats algorithm. |
| Algorithm | Control over variations of algorithm. |

| | |
|---|---|
| Parallel threads | Number of parallel threads used for the task. |

3. Output Sequences: On this page you can modify result file(s) settings.