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.

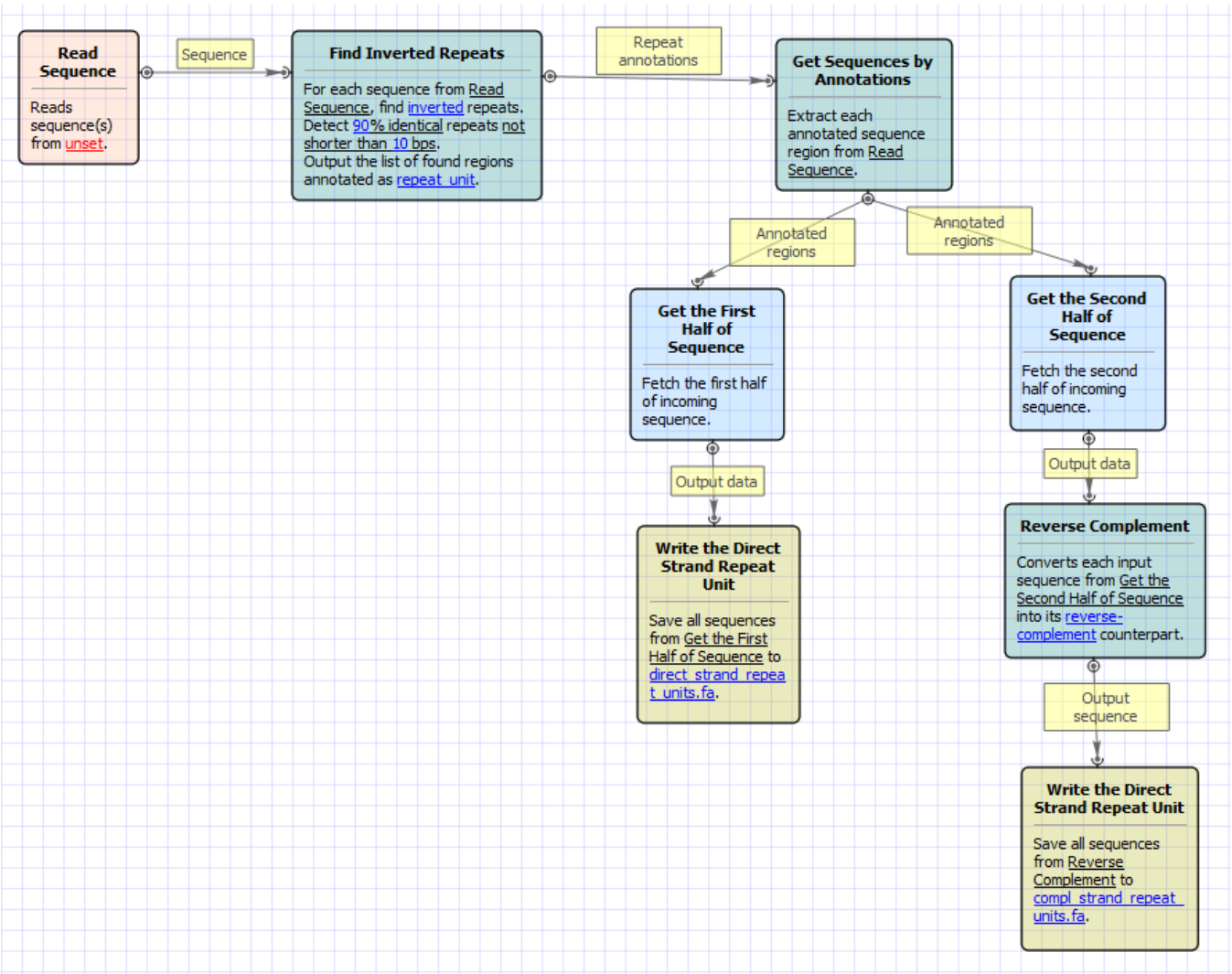
> **How to Use This Sample**
>
> If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

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

Workflow Image

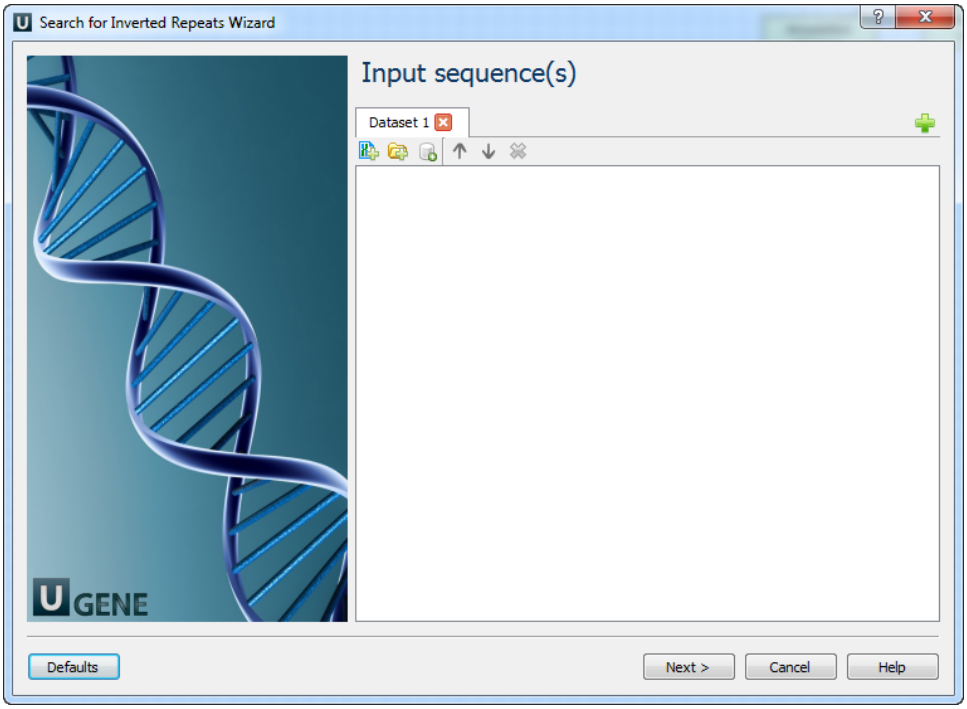
The opened workflow looks as follows:



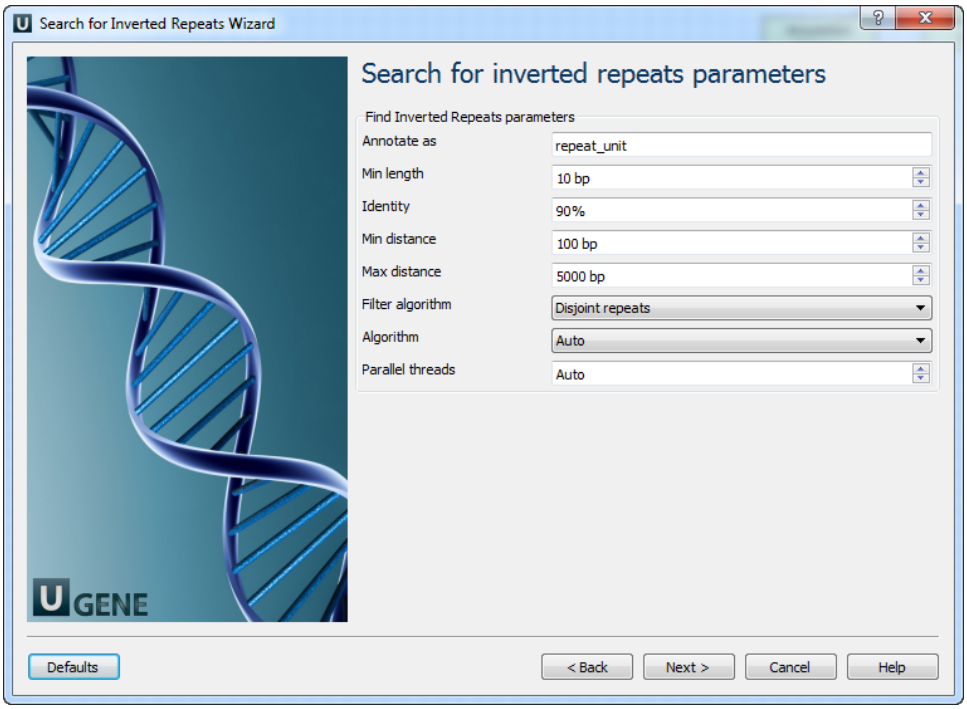
Workflow Wizard

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.