

# 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

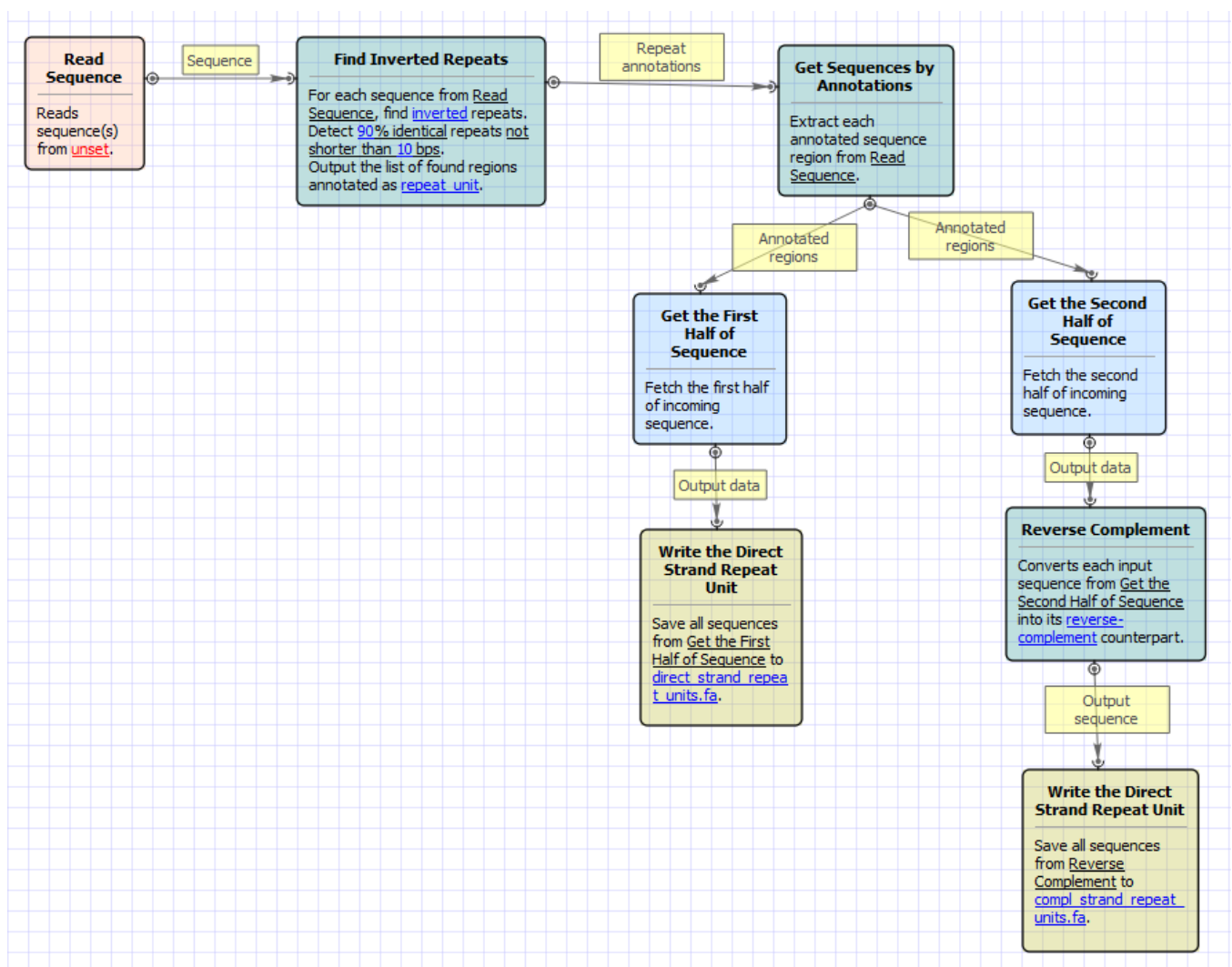
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

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

## Workflow Image

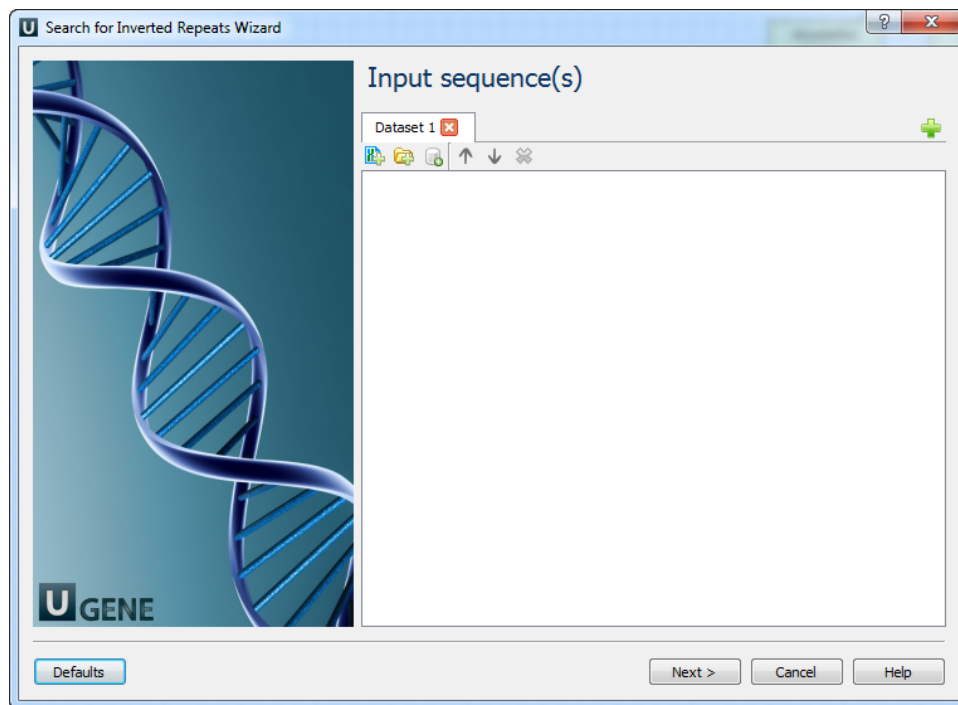
The opened workflow looks as follows:



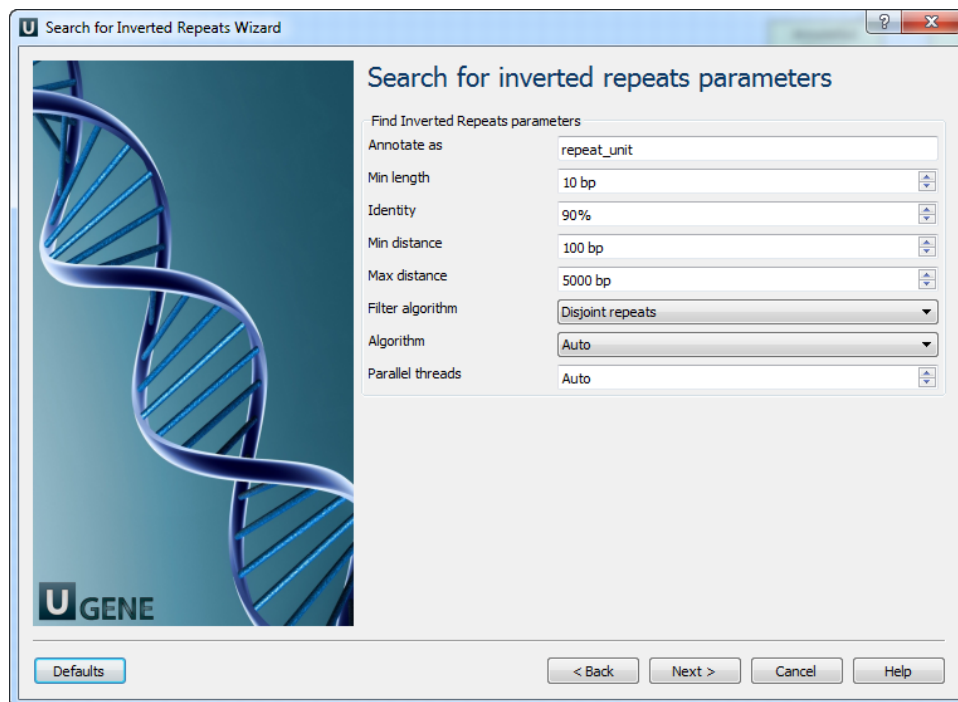
## Workflow Wizard

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.

