

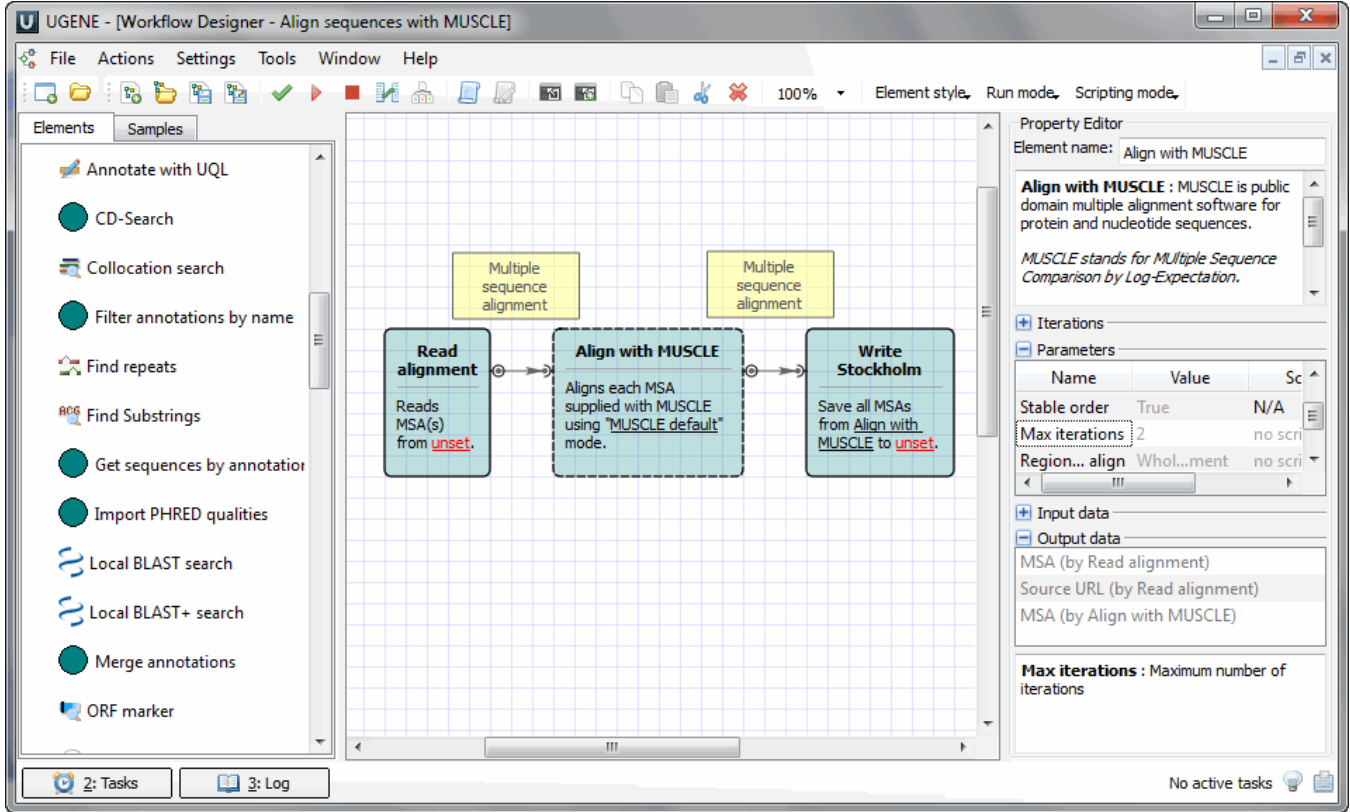
# Running Workflow from the Command Line

UGENE provides command line interface (CLI). To learn more about UGENE CLI and commands available read [main UGENE User Manual](#).

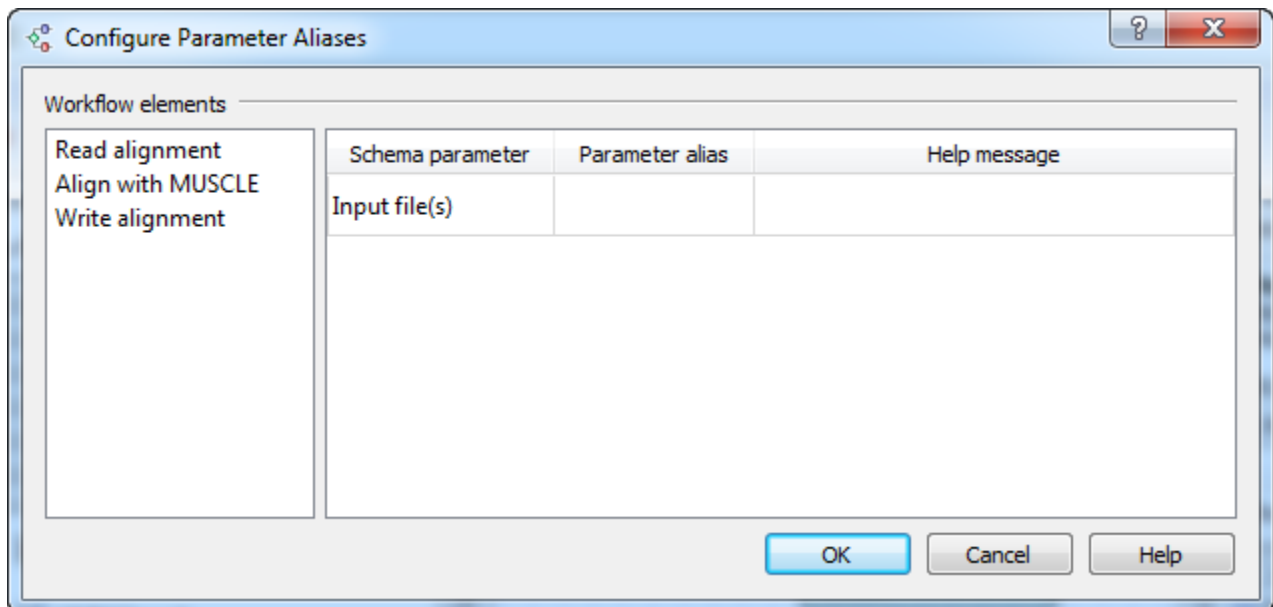
This chapter describes how you can create a new command using a *workflow*.

To run a workflow from the command line do the following:

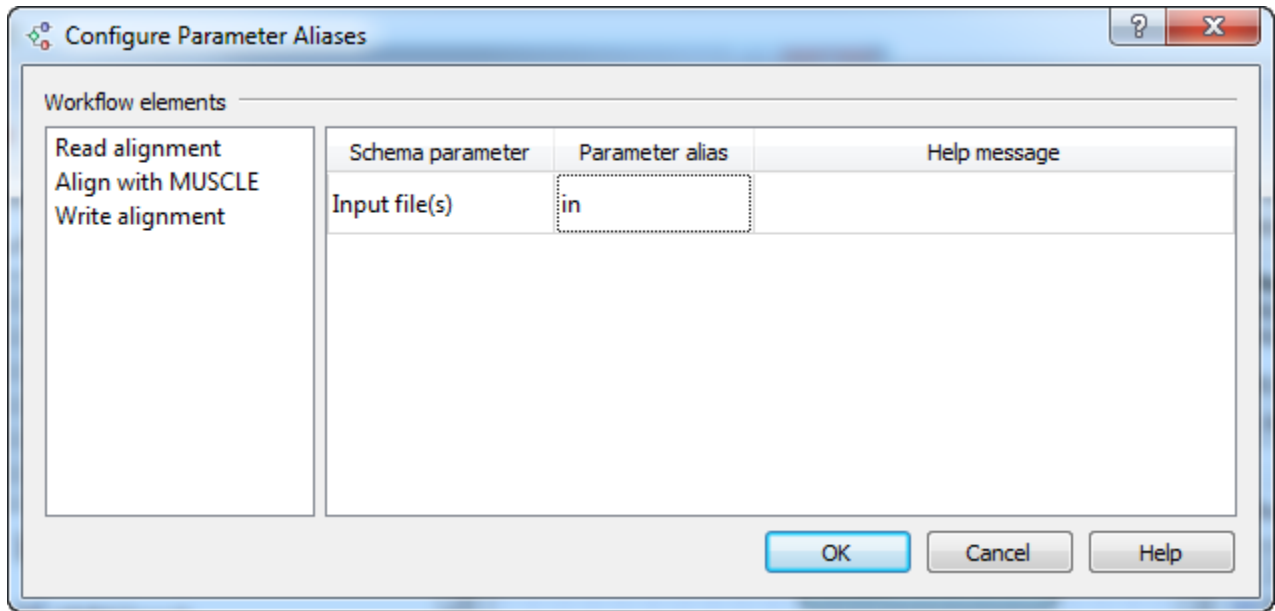
- Create the workflow in the Workflow Designer. For example on the image below the *Align sequences with MUSCLE* sample workflow is used:



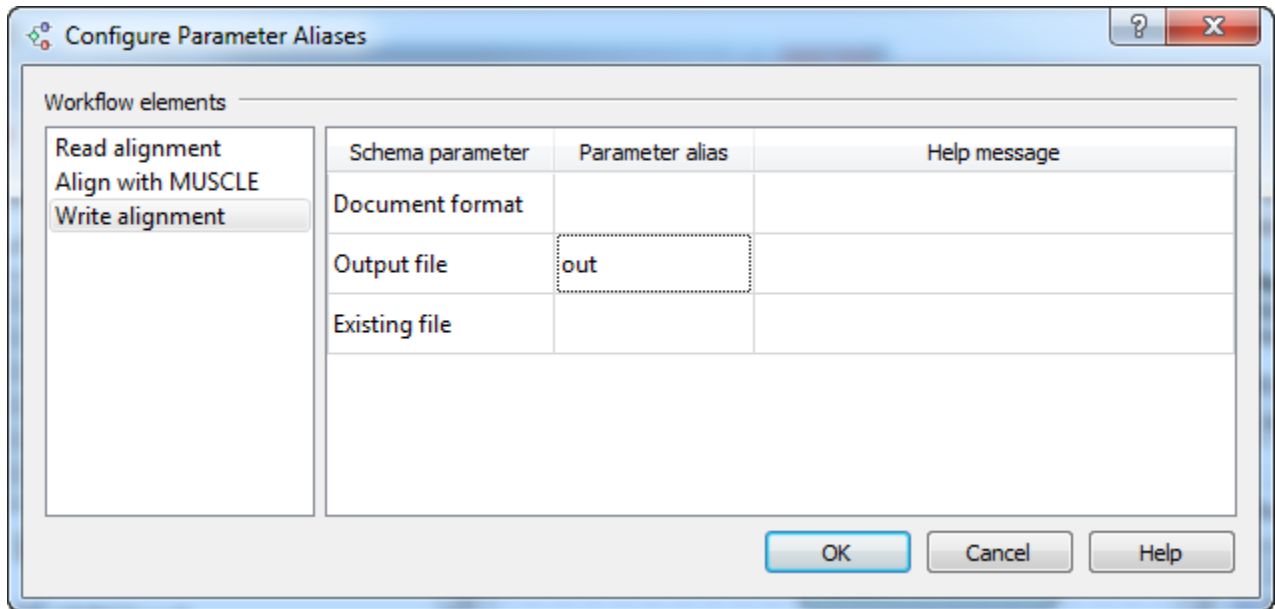
- Now you should configure aliases for those parameters and ports and slots that you are going to use from the command line. To do it select the *Actions > Set parameter aliases...* item in the main menu or the *Set parameter aliases* toolbar button. The following dialog appears:



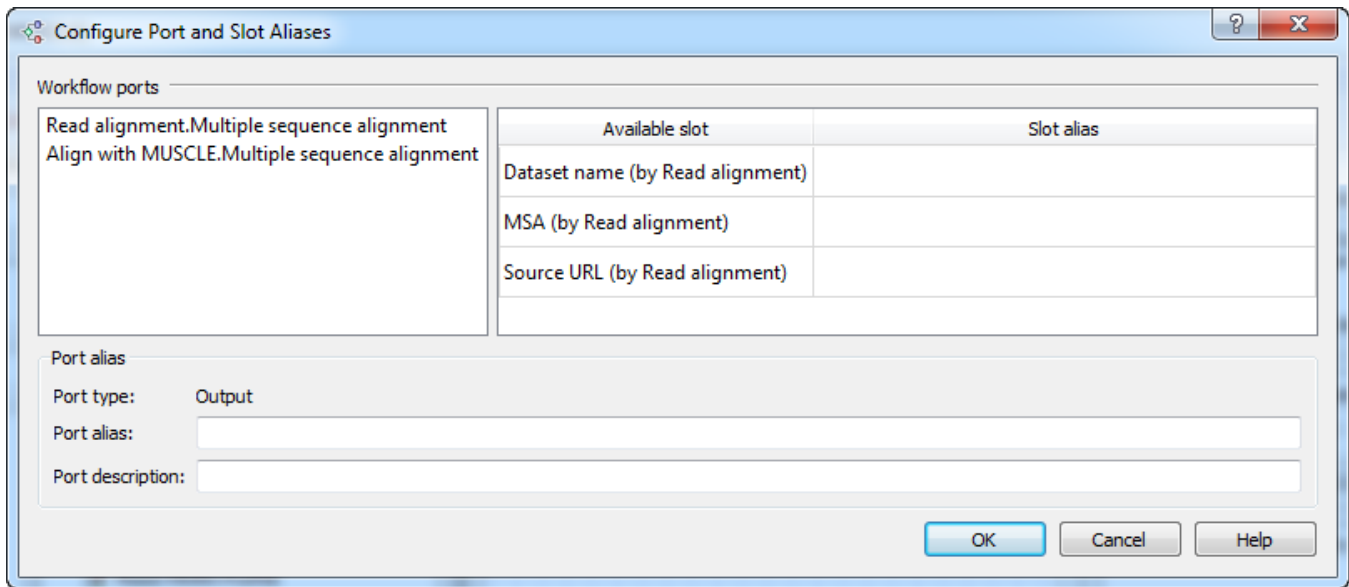
It contains the list of objects that corresponds to the *elements* of the workflow. For each object the list of parameters is available for which you can assign command line aliases. For example, assign alias **in** to parameter *Input file* (of the *Read alignment* element):



And alias **out** to parameter *Output file* (of the *Write Stockholm* element).



To select ports and slots aliases use the following dialog by the *Actions->Configure port and slot aliases* main menu item:



Press the *Ok* button to save aliases and close the dialog. When you create aliases you can import workflow to element by the *Actions->Import workflow to element* main menu item.

- *Save the workflow* to a file: if you follow the example, choose the *Actions & Save workflow as...* item in the main menu, browse for the file location and enter **mySchema** as the workflow name. This name will be used to launch the workflow from the command line.
- Launch the workflow from the command line:

```
[path_to_ugene\]ugene --task={schema_name} [--{parameter1}={value1} [--{parameter2}={value2} ...]]
```

The run information will be saved into the text file. By default it is the working directory.

For example on Windows the command can look as follows:

```
ugene --task=C:\mySchema --in=C:\COI.aln --out=C:\COI.sto
```



In this example the path to the directory with the UGENE executable is added to the system PATH variable.