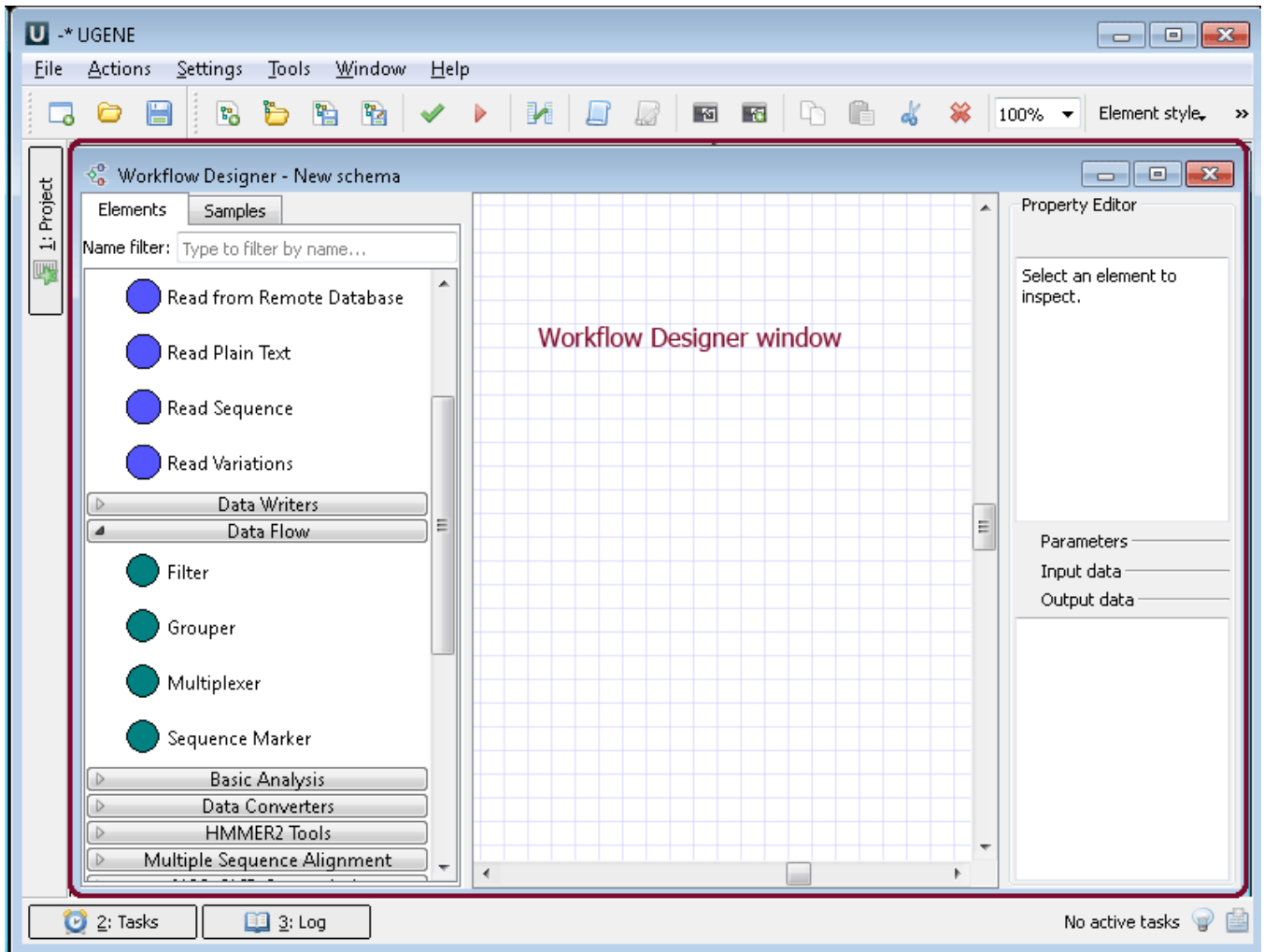


# Workflow Designer: pipelines and repeatable experiments

**Workflow Designer.** UGENE *Workflow Designer* is a central part of [UGENE](#) that allows a molecular biologist to create and run complex computational workflows even if he or she is not familiar with any programming language.

A workflow comprises reproducible, reusable and self-documented research routine, with a simple and unambiguous visual representation suitable for publications. A workflow can be run both locally and remotely, either using graphical interface or launched from the command line. Elements in workflow correspond algorithms integrated into [UGENE](#). Additionally you can create custom workflow elements using integrated scripting language, or by connecting arbitrary external command line utility.

To launch the Workflow Designer select the *Tools Workflow Designer* item in the UGENE main menu. The following window appears:



**Example 4:** You can find pattern in a sequence or in sequences and save it as annotations using the following workflow:

The screenshot displays the UGENE Workflow Designer interface. The main workspace shows a workflow diagram with three elements: 'Read Sequence', 'Find Pattern', and 'Write Sequence'. The 'Read Sequence' element is connected to 'Find Pattern', which is in turn connected to 'Write Sequence'. The 'Find Pattern' element's description includes a sample pattern: `TTCCGAGGGACACTAGGCTGACTC` and `CATC`. The 'Write Sequence' element's parameters are detailed in the Property Editor on the right.

**Workflow Diagram:**

```

graph TD
    ReadSequence[Read Sequence] -- Sequence --> FindPattern[Find Pattern]
    FindPattern -- Pattern Annotations --> WriteSequence[Write Sequence]
  
```

**Find Pattern Element Description:**

Searches regions in each sequence from [Read Sequence](#) similar to `TTCCGAGGGACACTAGGCTGACTC` `CATC` pattern(s). A substring must [match a pattern exactly](#). Searches in [both strands](#) of a sequence. Outputs the regions found annotated as [misc feature](#).

**Write Sequence Element Parameters:**

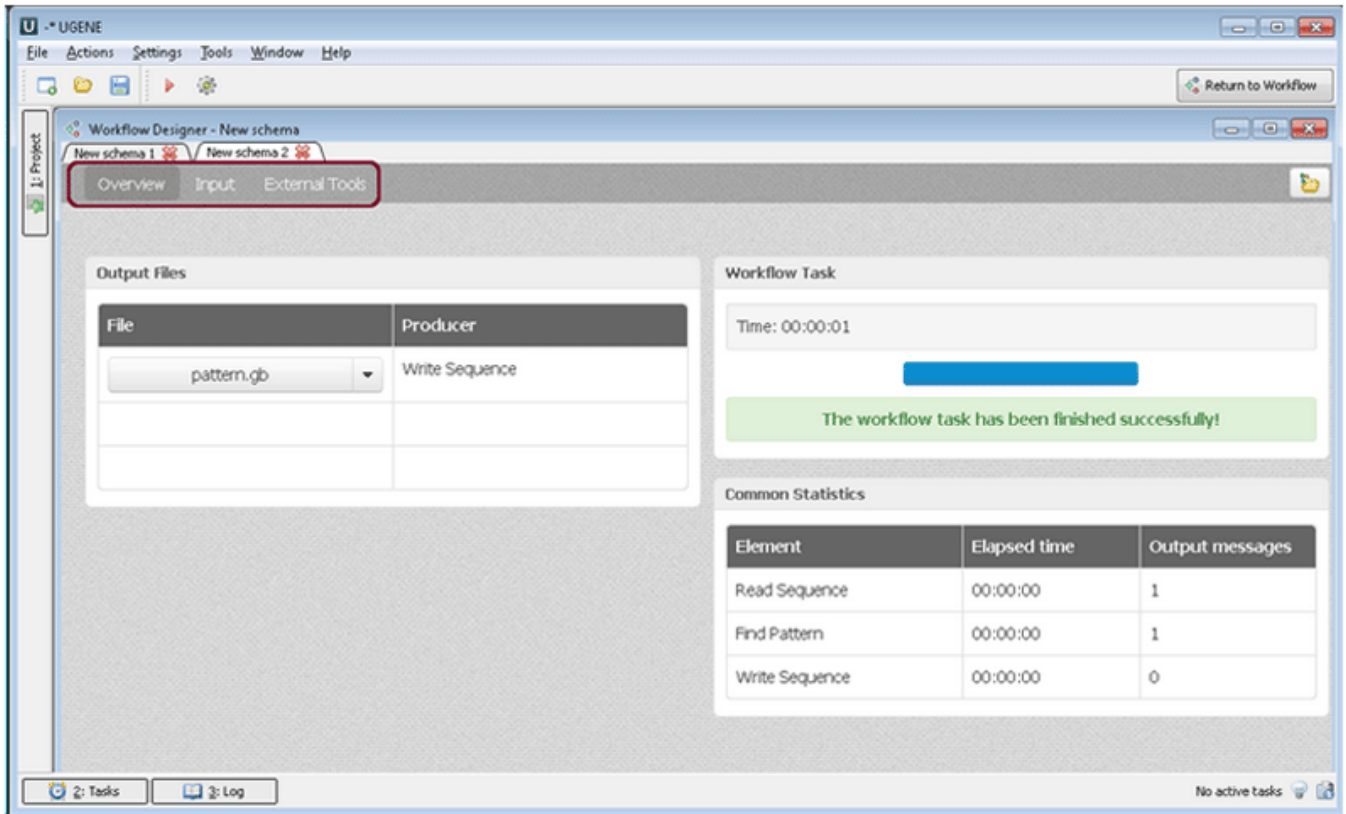
Name	Value
Accumu...bjects	True
Docum...ormat	genban
Split sequence	1
Output file	pattern.gb
Existing file	Rename

**Input data:**

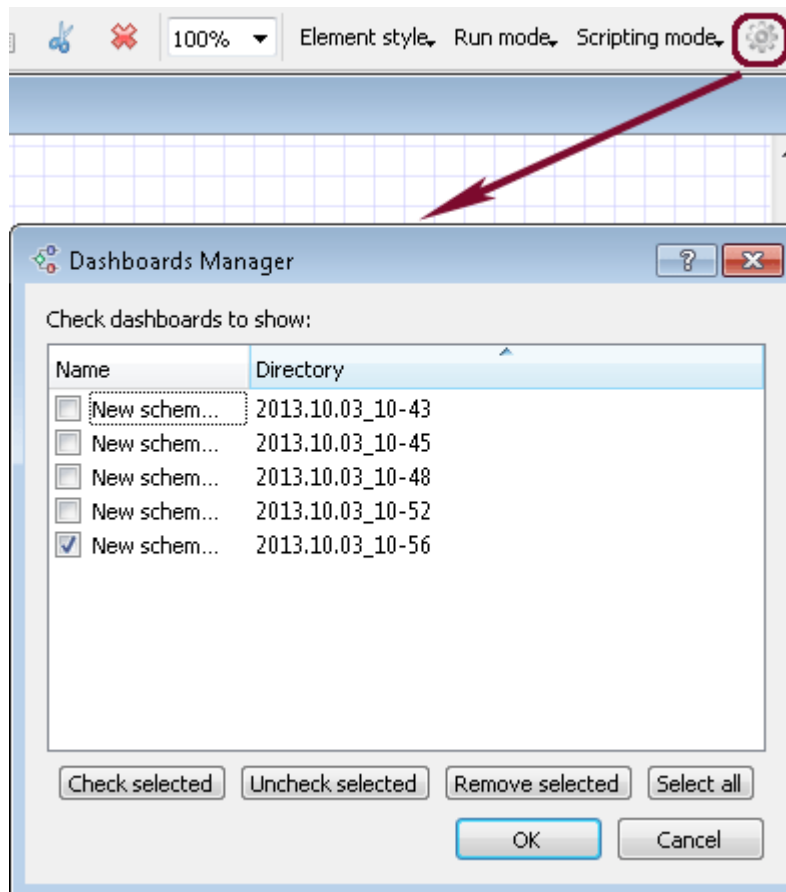
Set of a...otations	<Lis...ues>
Sequence	Sequ...nce)
Location	<empty>

**Document format:** Document format of output file

Create the workflow, choose parameters and click the *Run* button. If you want to search pattern in many sequences you can add these sequences into *Read Sequence* element. After the end of the running process a report appears. The report include all information about workflow.



All your workflows have been saved and you can navigation between it and use it with a help of the *Dashboards Manager*:



Note that workflows in UGENE are easy to read and share, can be reused multiple times and compiled into a separate standalone command line tools!

For more detailed information about Workflow Designer use the [Workflow Designer Documentation](#).