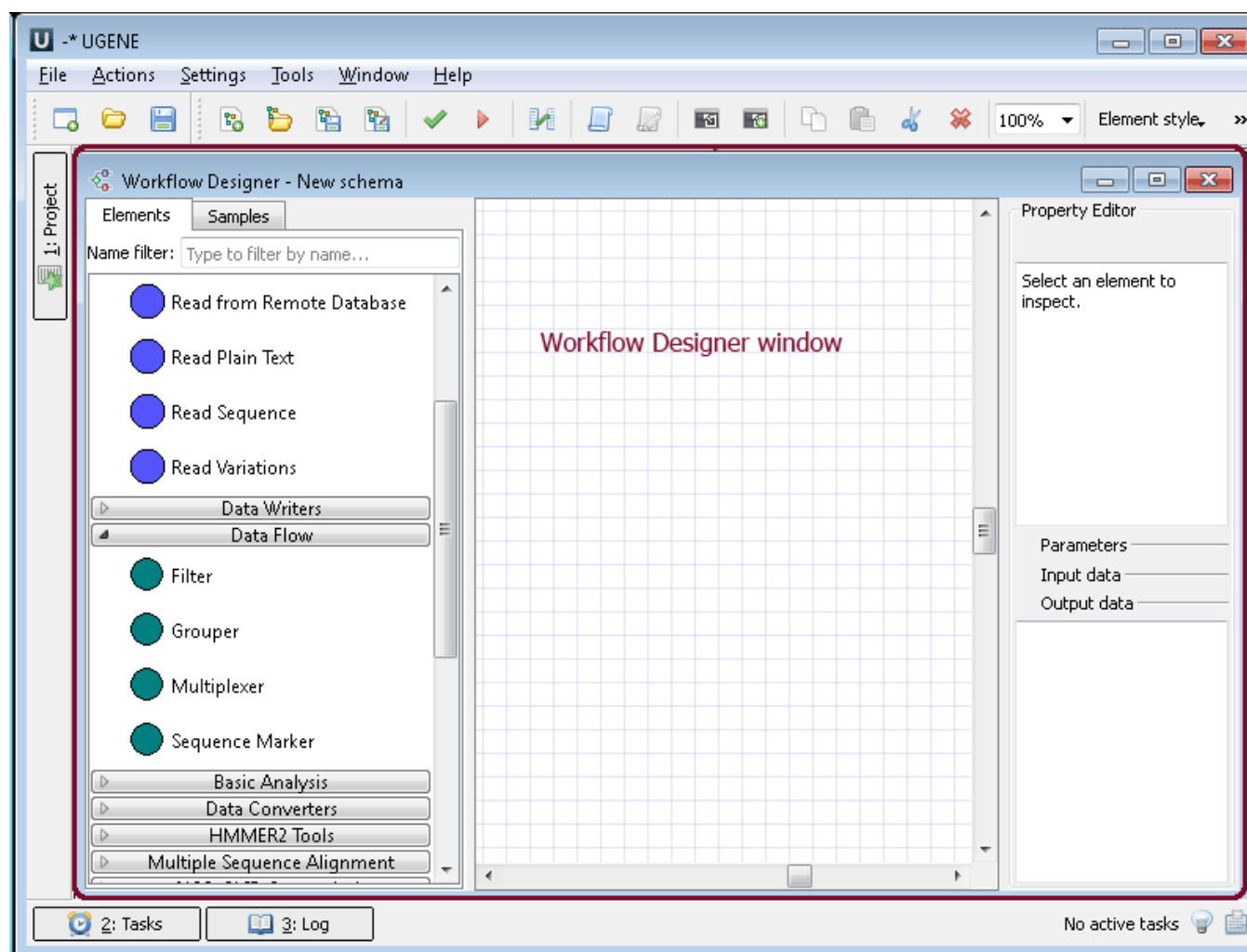


# Workflow Designer: pipelines and repeatable experiments

**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:

U -\* UGENE

File Actions Settings Tools Window Help

Run

100% Element style >>

Workflow Designer - New schema

Elements Samples

Name filter: Type to filter by na...

Data Readers

Data Writers

Data Flow

Basic Analysis

Amino Translation

Annotate with DAS

Annotate with UQL

CD-Search

Collocation Search

Export PHRED Qual

Fetch Sequences by

Filter Annotations k

Find Pattern

Workflow

**Find Pattern**

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](#).

Sequence

**Read Sequence**

Reads sequence(s) from [murine.gb](#).

Pattern Annotations

**Write Sequence**

Save all sequences from [Read Sequence](#) to [pattern.gb](#).

Property Editor

Element name: Write Sequence

**Write Sequence** : Writes all supplied sequences to file(s) in selected format.

To configure the parameters of the element go to "Parameters" area below. **Parameters**

Parameters

| Name                 | Value      |
|----------------------|------------|
| Accumu...bjects      | True       |
| <b>Docum...ormat</b> | genban     |
| Split sequence       | 1          |
| Output file          | pattern.gb |
| Existing file        | Rename     |

Input data

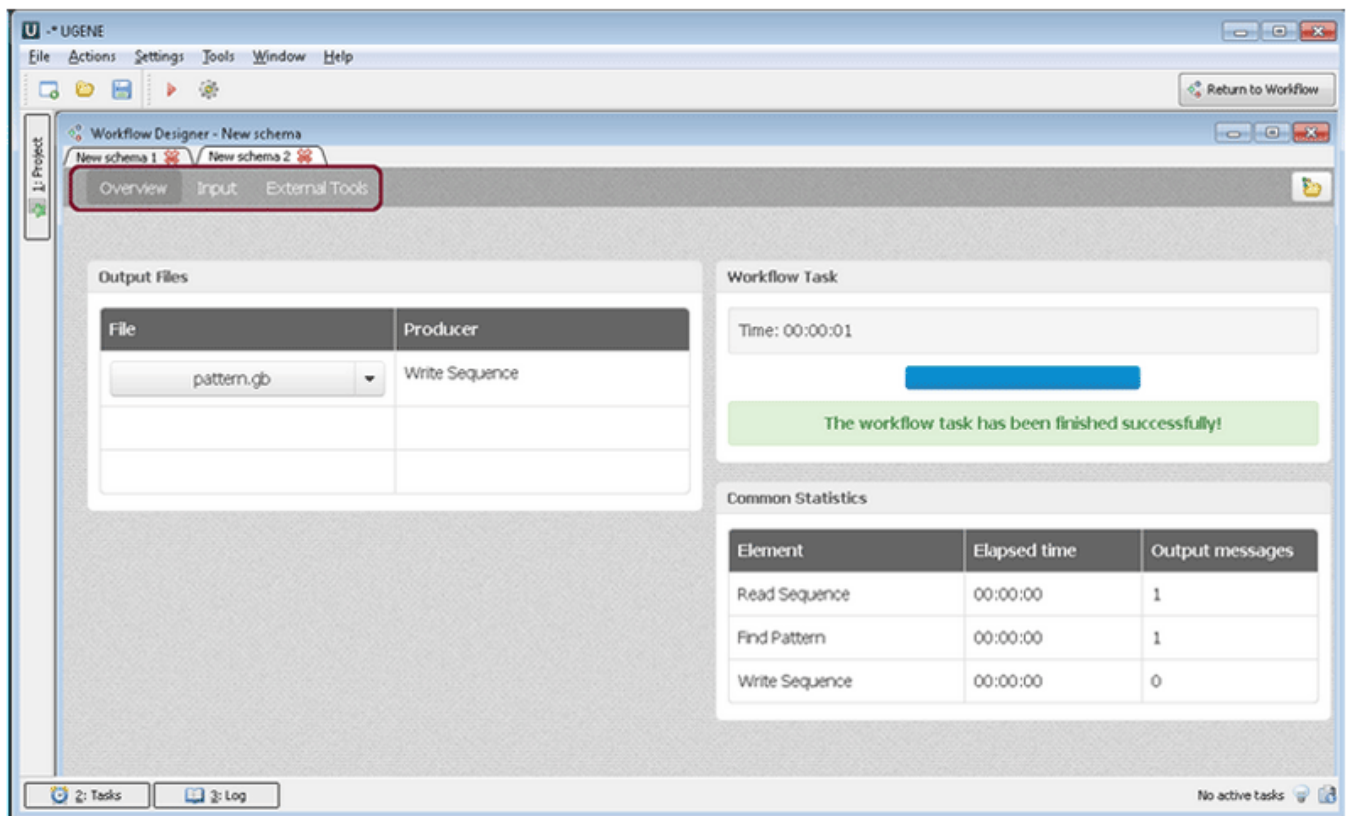
|                     |             |
|---------------------|-------------|
| Set of a...otations | <Lis...ues> |
| Sequence            | Sequ...nce) |
| Location            | <empty>     |

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

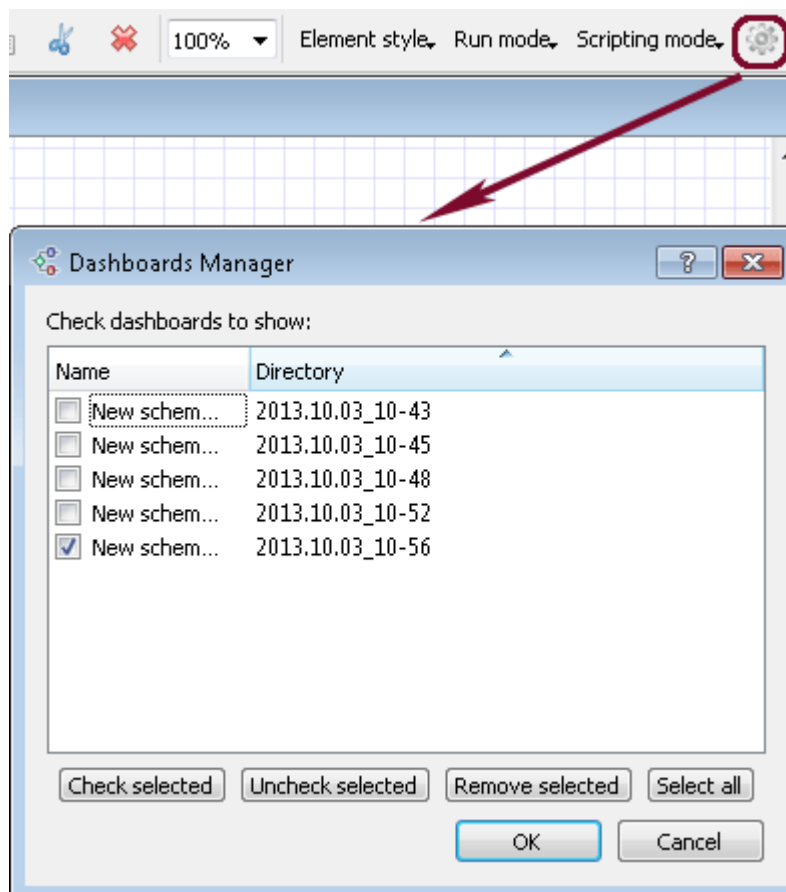
2: Tasks 3: Log

No active tasks

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](#).