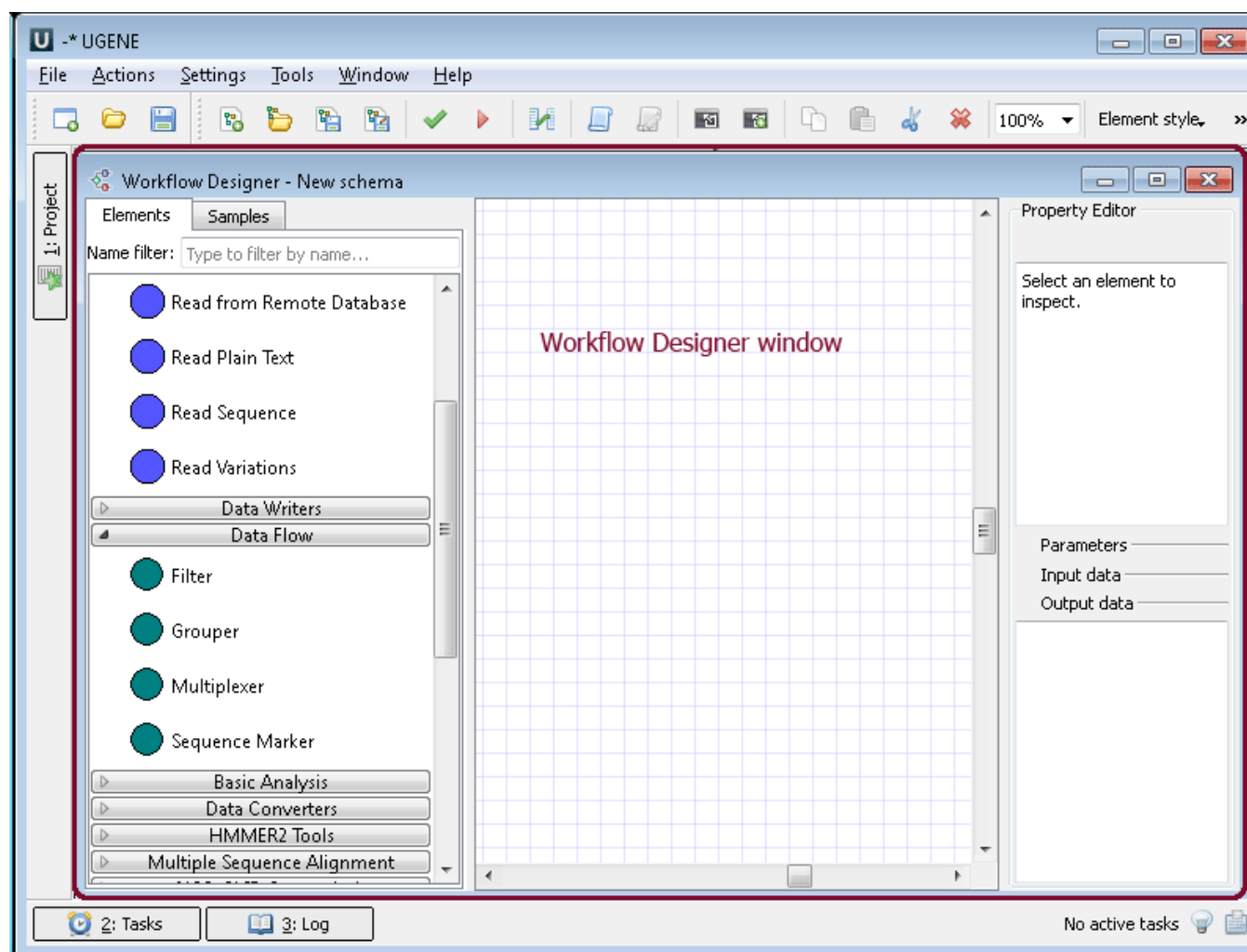


Workflow Designer: pipelines and repeatable experiments

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 by
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.

Read Sequence
Reads sequence(s) from murine.gb.

Write Sequence
Save all sequences from Read Sequence to pattern.gb.

Sequence

Pattern Annotations

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

Name	Value
Accumulate objects	True
Document format	genbank
Split sequence	1
Output file	pattern.gb
Existing file	Rename

Input data

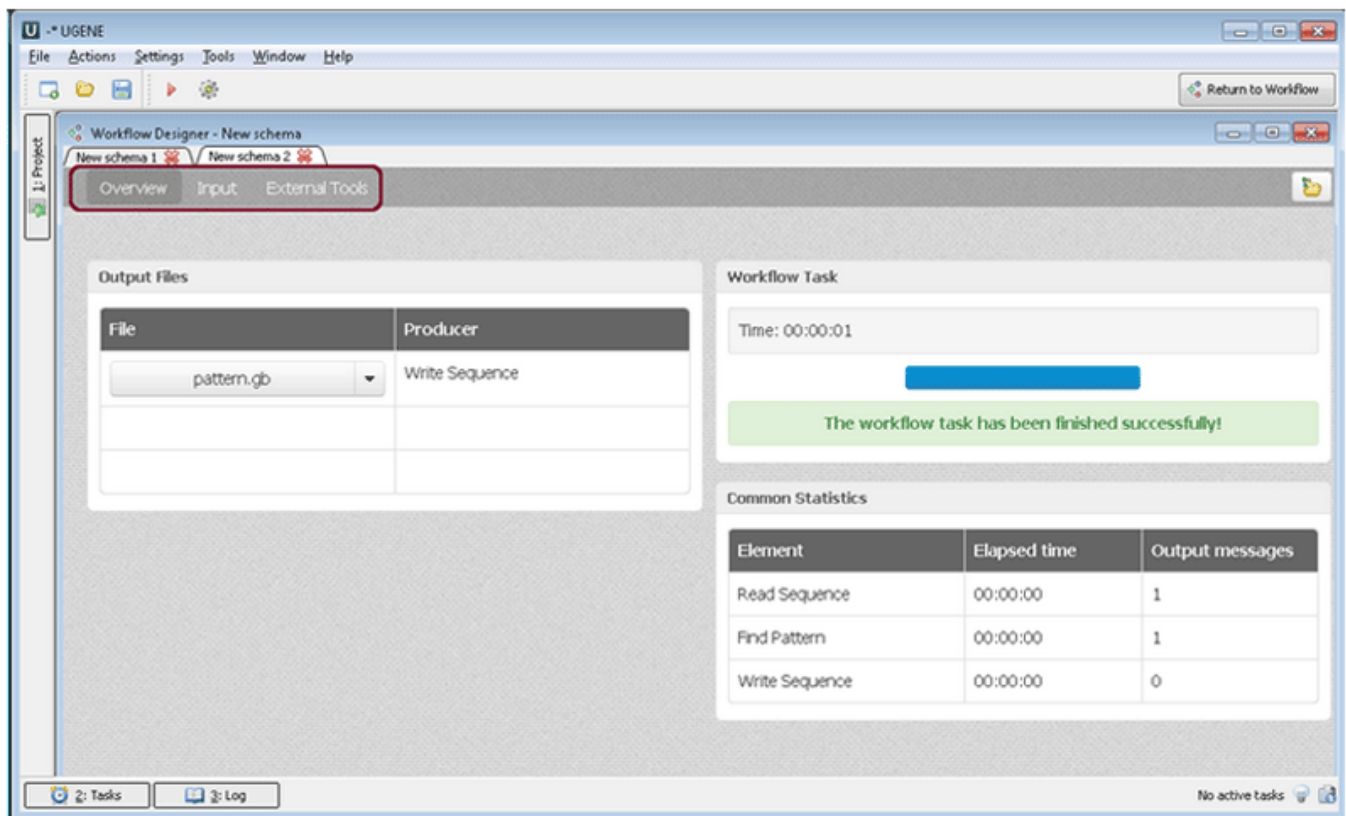
Set of annotations	<List of sequences>
Sequence	Sequence
Location	<empty>

Document format :
Document format of output file

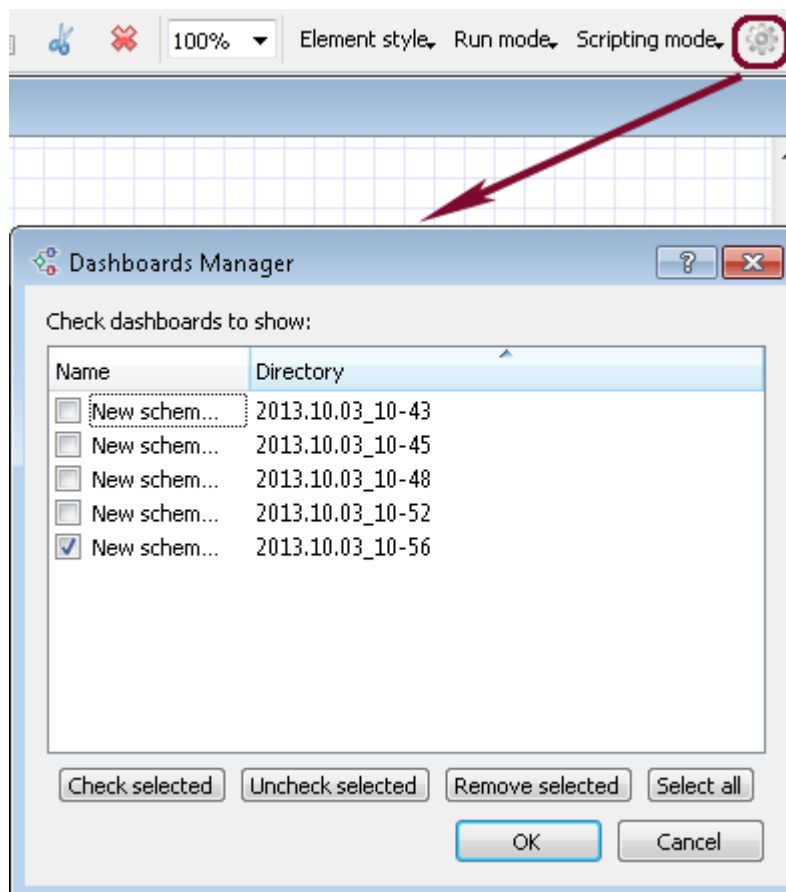
2: Tasks 3: Log

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](#).