

UGENE

An Introduction 2022

Quick Start Guide

This document contains a quick introduction to UGENE. For more detailed information, you can find the UGENE User Manual and other special manuals in project website: <http://ugene.unipro.ru>.

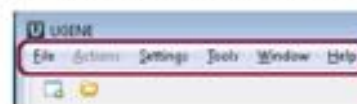
What is UGENE?

What you can do in UGENE?

- View, edit and annotate DNA, tRNA and protein sequences
- View, edit and align multiple sequence alignments
- View, align and assemble short reads
- 3D structures and surface algorithms
- Workflow Designer: pipelines and repeatable experiments

What you can do in UGENE?

When open UGENE for the first time, there is an empty UGENE window with the main menu bar on the top of the window:



Using these menus you can run many algorithms, configure different settings and get help:

Menu	Description
File	A set of project/file level operations. Example: create, open, etc. a project; open a document; access remote database to download a file.
Actions	Various actions associated with the active window. Example: export, remove, edit, analyze a sequence using different plugins (for the <i>Sequence View</i>), edit, align, change the consensus mode (for the <i>Alignment Editor</i>).
Settings	Application, plugins and tools settings.
Tools	Various tools, independent of an active window. This menu is extended by different plugins. Example: HMMER2 / HMMER3 tools, SITECON, Workflow Designer.
Window	A list of active windows and basic manipulations with the windows. Example: close all windows, tile windows, select next window.
Help	Application help and check for updates.

The menus can be dynamically populated with new actions added by plugins.

You can select and analyze different files such as sequences, multiple sequence alignments, short reads assemblies and etc. To open a file click on the **File**→**Open** or click on the **Open** icon and choose the file.



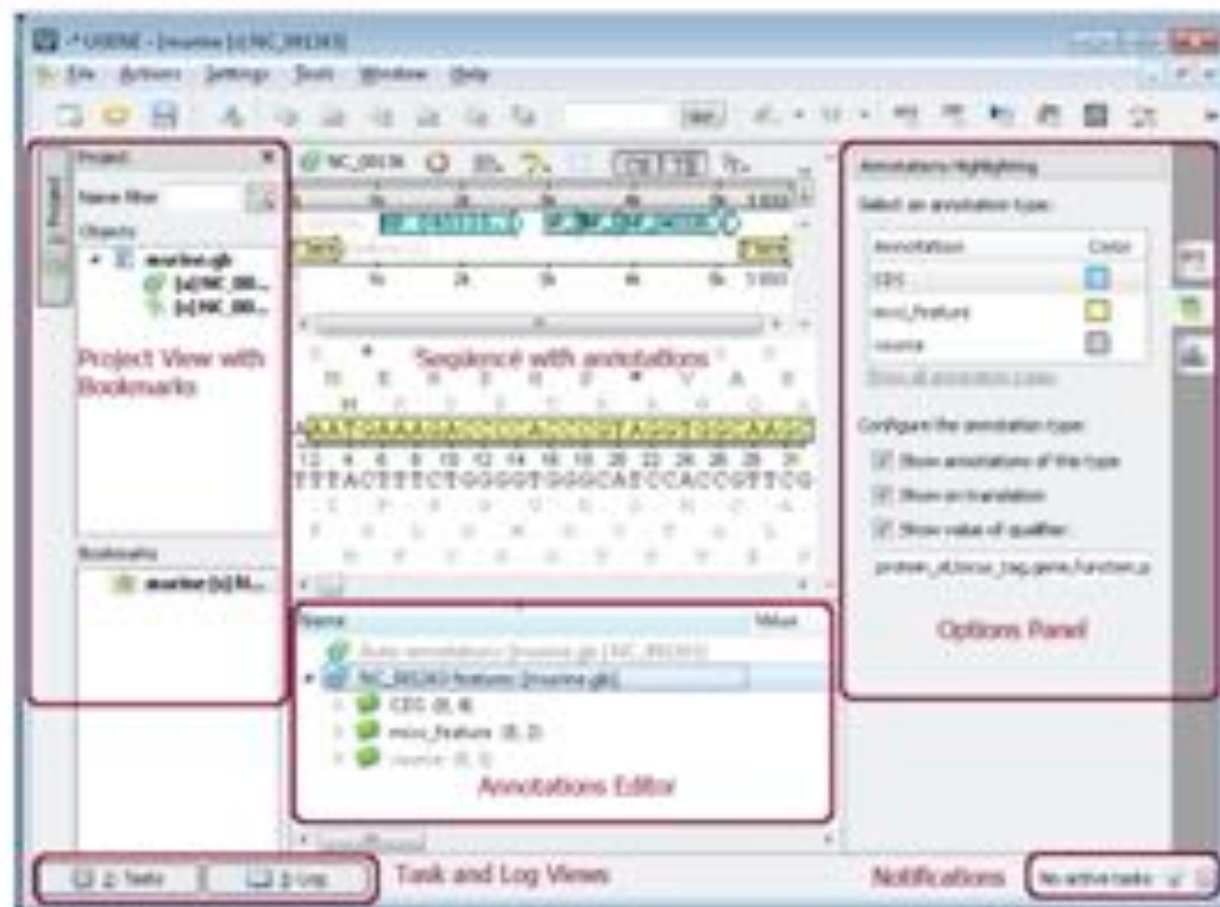
You can use UGENE sample files. There are the following sample data: ABIF, ACE, Assembly, CLUSTALW, EMBL, FASTA, FASTQ, Genbank, GFF, HMM, MAGE, MSF, Newick, PDB, Rasm, SCF, Stockholm, Swiss-Prot. These files are located in the main UGENE directory: `ugene\data\samples`.

- View, edit and annotate ChIP, RNA and protein sequences
- View, edit and align multiple sequence alignments
- View, align and assemble short reads
- 3D structures and surface algorithms
- Workflow Designer: pipelines and repeatable experiments

View, edit and annotate DNA, RNA and protein sequences

DNA, RNA or protein sequences (Sequence View). The *Sequence View* is one of the major object views in UGENE aimed to visualize and edit DNA, RNA or protein sequences along with their properties like annotations, chromatograms, 3D models, statistical data, etc. For each le

UGENE analyzes the file content and automatically opens the most appropriate view. To activate the Sequence View open any file with one sequence. For example you can use the `Eugene\data\samples\Genbank\Murine.gb` file provided with UGENE. After opening the UGENE the Sequence View window appears:



After that click the Search button. If the pattern there is or there are in the sequence it appears as new annotation(s):

U UGENE - [COI[m] COI]

File Actions Settings Tools Window Help

Project

Consensus

T A G T T T A T T A A T T C G A G C T G A A

1 2 4 6 8 10 12 14 16 18 20 22

Phaneroptera_falcata 1 T A A G A C T T C T A A T T C G A G C C G A A 24

Isophya_altaica_EF5 1 T A A G C T T A C T A A T T C G G G C C G A A 24

Bicolorana_bicolor_1 1 T T A G T T T A T T A A T T C G A G C T G A A 24

Roeselia_roeseli 1 T C A G T C T A T T A A T T C G A G C A G A A 24

Montana_montana 1 T C A G T T T A T T A A T T C G A G C T G A A 24

Mecoptera_japonica 1 T T A G T C T A C T A A T T C G A G C T G A A 24

Gampsocleis_sedaki 1 T C A G A T T A T T A A T T C G A G C T G A A 24

Deracantha_deracar 1 T T A G A T T G C T A A T T C G A G C C G A A 24

Zychia_baranovi 1 T T A G A T T A T T A A T T C G G G C T G A A 24

Tettigonia_viridissima 1 T A A G T C T A T T A A T T C G A G C T G A A 24

Conocephalus_disco 1 T T A G C T T A T T A A T T C G T G C T G A A 24

Conocephalus_xp 1 T T A G C T T A T T A A T T C G A G C T G A A 24

Conocephalus_perce 1 T T A G C T T A T T A A T T C G A G C C G A A 24

Mecopoda_elongata 1 T A A G T C T T T T A A T T C G A G C T G A A 24

Mecopoda_elongata 1 T A A G T C T T T T A A T T C G A G C T G A A 24

Mecopoda_xp_Mal 1 T A A G T C T T T T A A T T C G A G C T G A A 24

Podisma_sapporensis 1 T A A G A A T A A T T A T T C G A A C A G A A 24

Metrodes_pupus_EF1 1 T A A G C C T T T T A A T T C G T T C A G A A 24

Alignment Editor

Options Panel

General

Reference sequence

Select and add

Alignment info

Length: 604

Sequence number: 18

Consensus mode

Consensus type: Default

Threshold: 100%

Find: Ln 1 / 18 Col 1 / 604 Pos 1 / 601

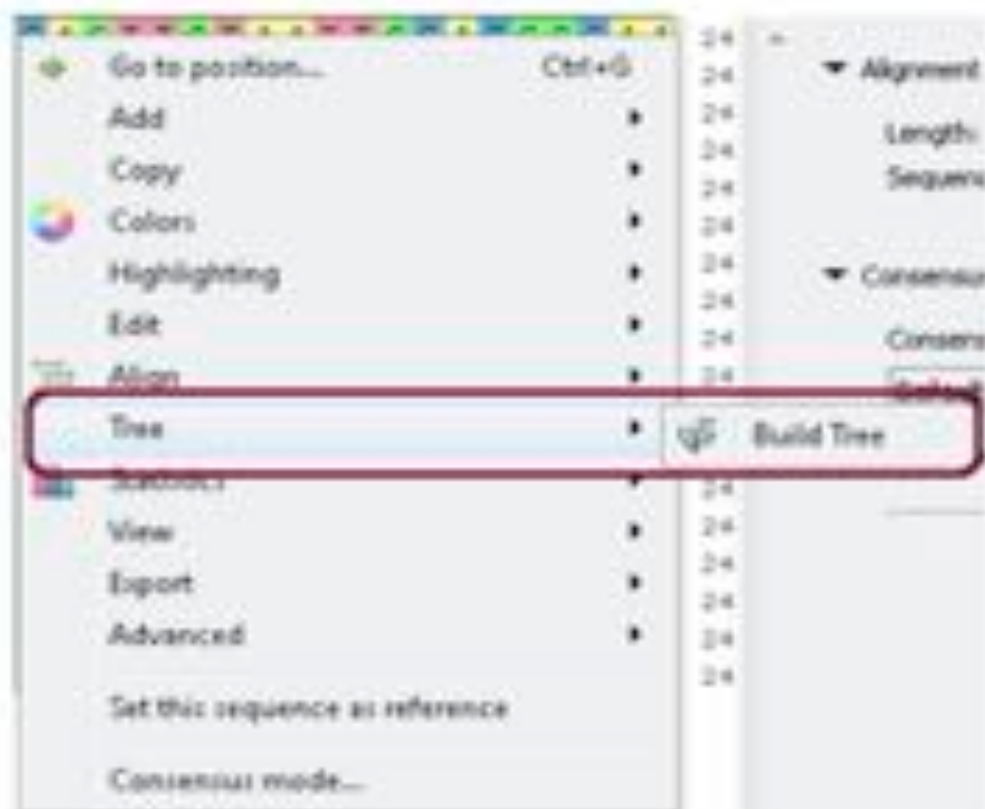
Tasks Log

No active tasks

a. From the toolbar, Click to the tree icon:

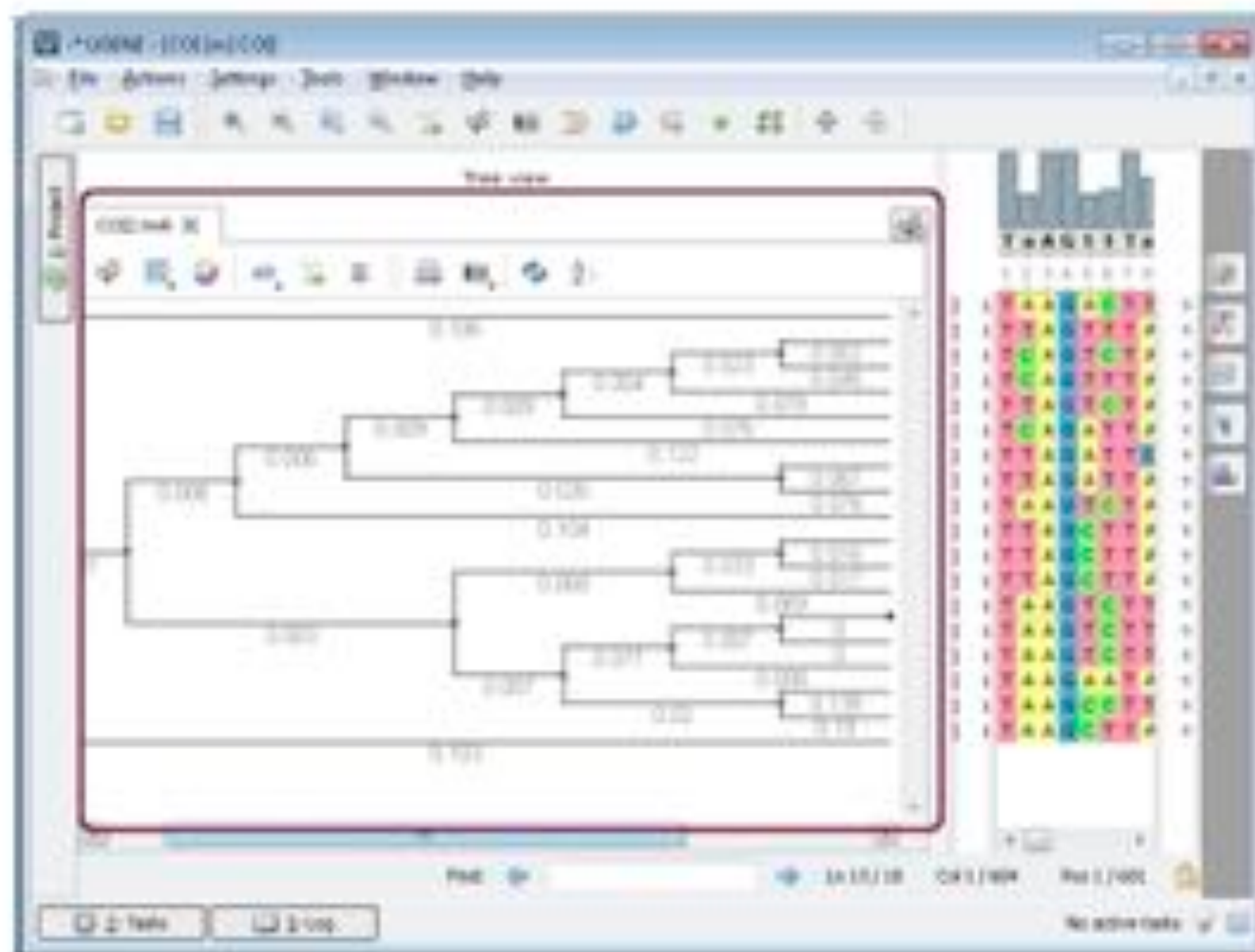


b. From the context menu:

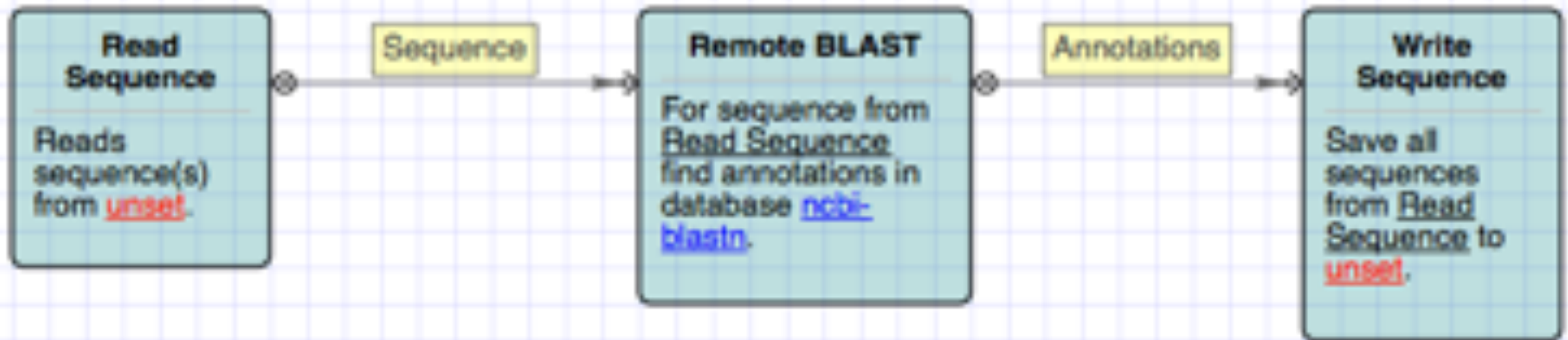


c. From the Options Panel:

After calculation the tree appears in the MSA Editor in a separate window:



Sequence search



BLAST

Remote BLASTing Wizard

Remote Nucleotide BLAST

Remote BLAST Parameters

Database	Nucleotide collection - nr
Expected value	10.000000
Results limit	10
Megablast	True

Additional
Show additional parameters

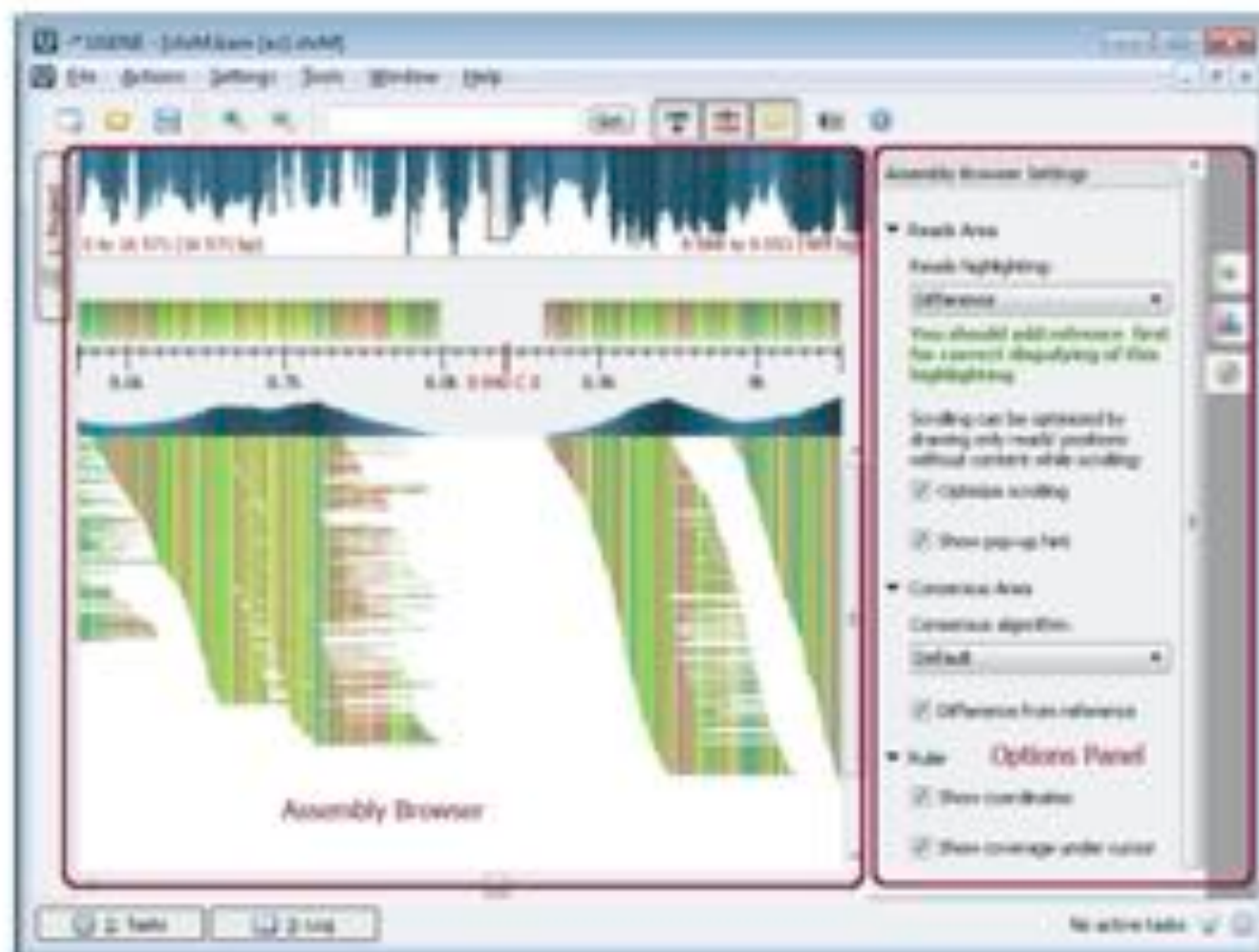
U GENE

Defaults < Back Next > Cancel Help

The screenshot displays the Galaxy web interface for a bioinformatics analysis. On the left, the 'Project' panel shows a list of datasets and tools, with 'NC_004718 sequence' selected. The main workspace shows a genomic track for 'NC_004718 sequence' with annotations for 'orf1ab' and 'mat_peptide'. Below the track, a table lists the 'mat_peptide' entries with their coordinates and values. The 'Tasks' panel at the bottom shows the workflow progress, including 'HMM search' and 'Read HMM profile' tasks, all of which are completed.

Name	Value
mat_peptide	10905..11772
mat_peptide	11773..12021
mat_peptide	12022..12615
mat_peptide	12616..12954
mat_peptide	12955..13373
db_xref	GI:25837503
evidence	not_experimental
gene	orf1ab
locus_tag	can1

Task name	Task state description	Task progress	Actions
HMM search: file ResultsHmms.hmm	Finished	100%	
Read HMM profile: ResultsHmms.hmm	Finished	100%	
HMM search with "	Finished	100%	



Using the Assembly Browser you can: browsing and zooming assembly, getting information about reads, short reads visualization, associating reference sequence, consensus sequence, exporting.

Example 3: Highlighting the strand of reads. You can do this using the context menu or the Options Panel.

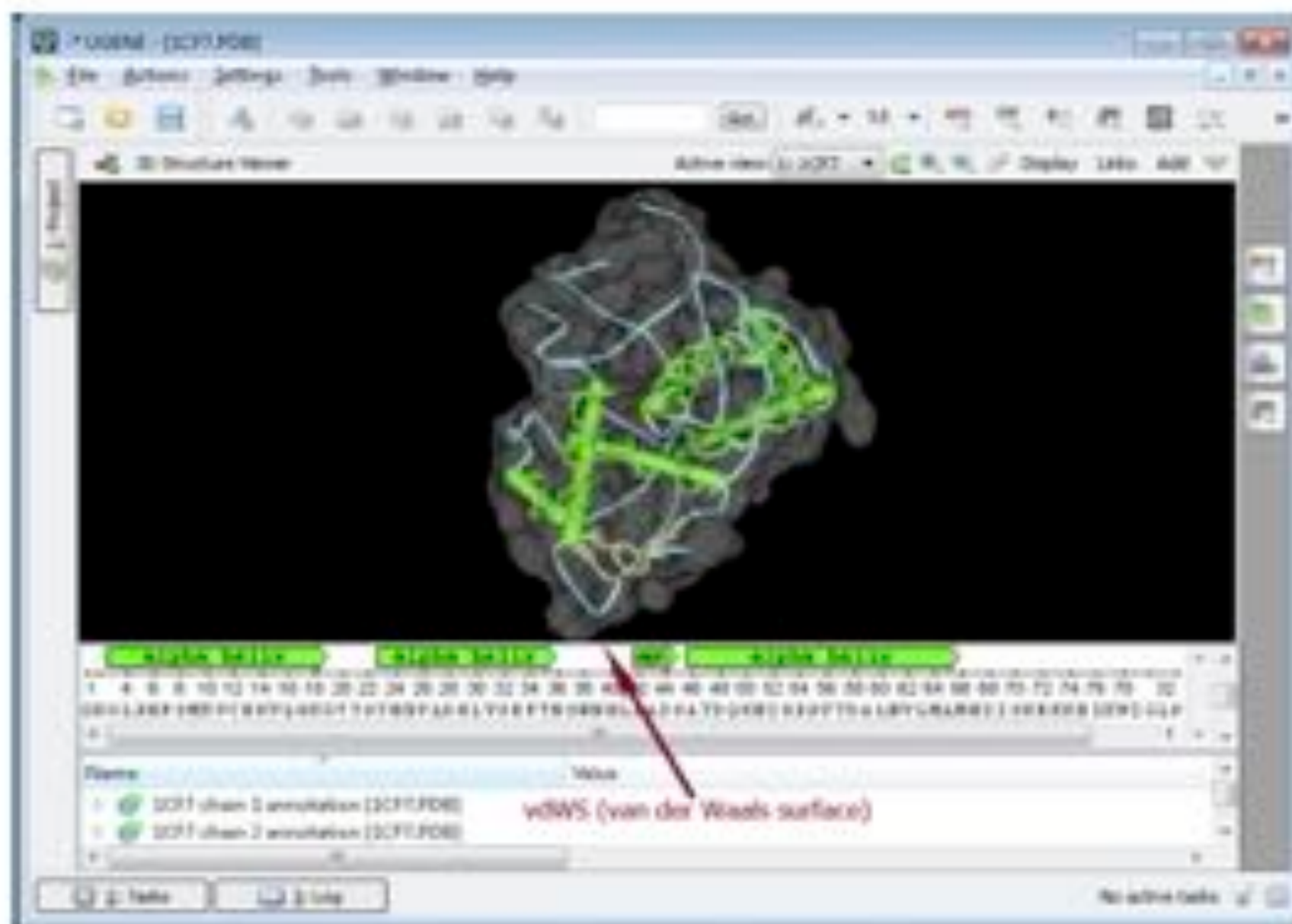


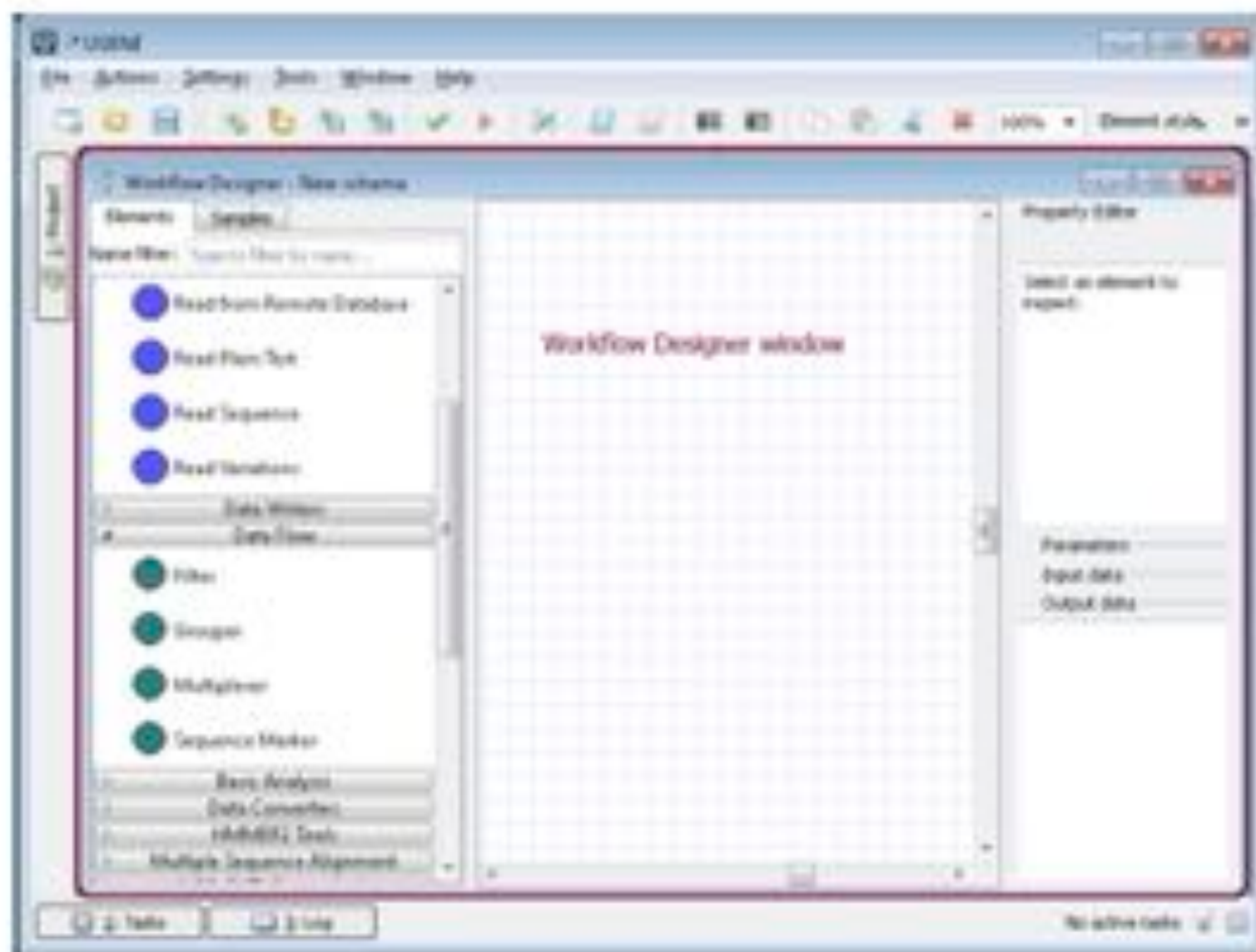
3D structures and surface algorithms

3D structures (3D Structure Viewer). The 3D Structure Viewer is intended for visualization of 3D structures of biological molecules. Using the 3D Structure Viewer you can work with data from the Protein Data Bank (PDB) - a repository for the 3D structural data of large biological molecules, such as proteins and nucleic acids, maintained by the Worldwide Protein Data Bank (wwPDB). You can work as well with data from the NCBI Molecular Modeling DataBase (MMDb), also known as "Entrez Structure", a database of experimentally determined structures obtained from the RCSB Protein Data Bank.

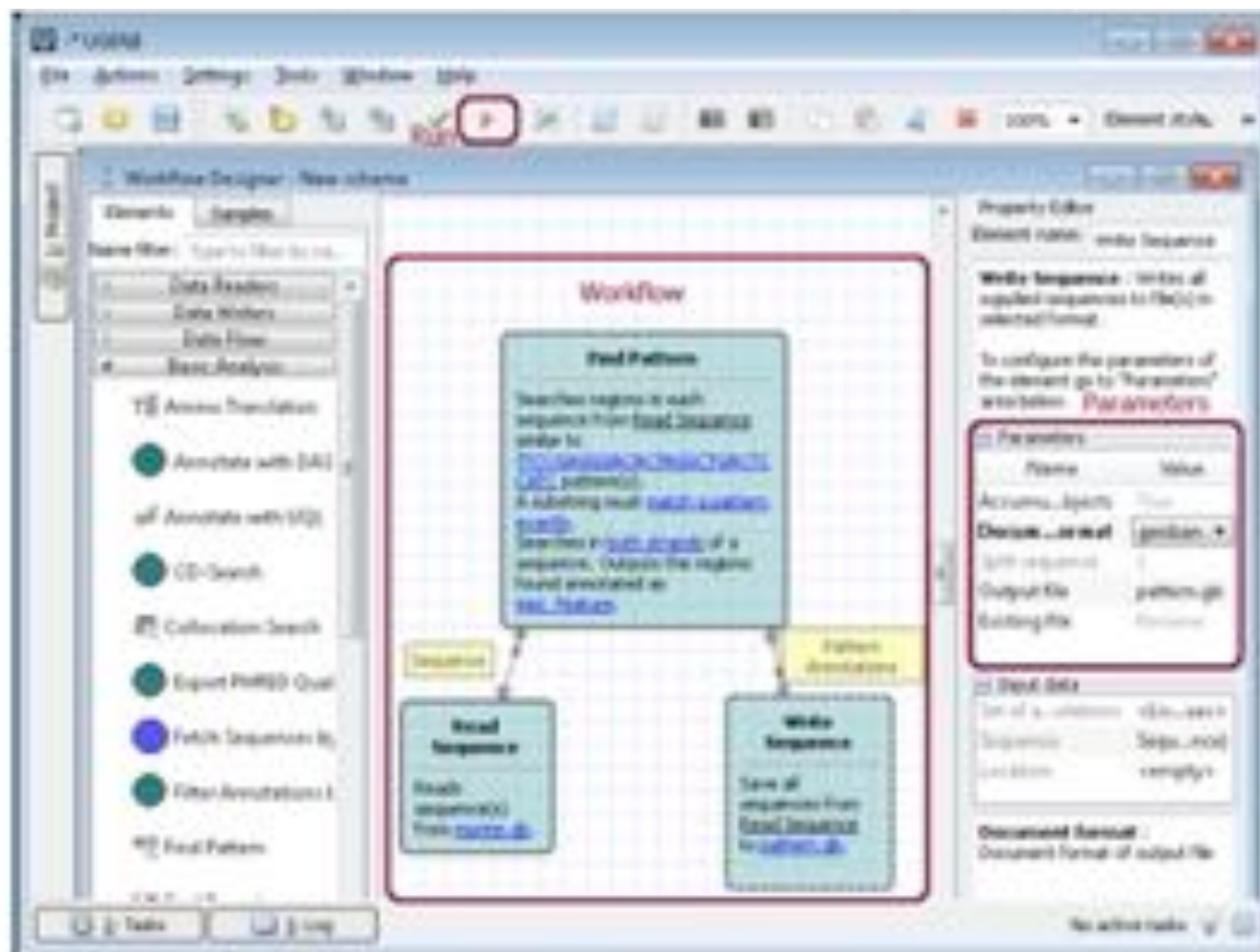
The 3D Structure Viewer is opened automatically when you open a PDB or MMDb file. For example, open *Supernote\data\samples\PDB\1CF7.PDB*. The 3D Structure Viewer adds a view to the upper part of the *Sequence View*.



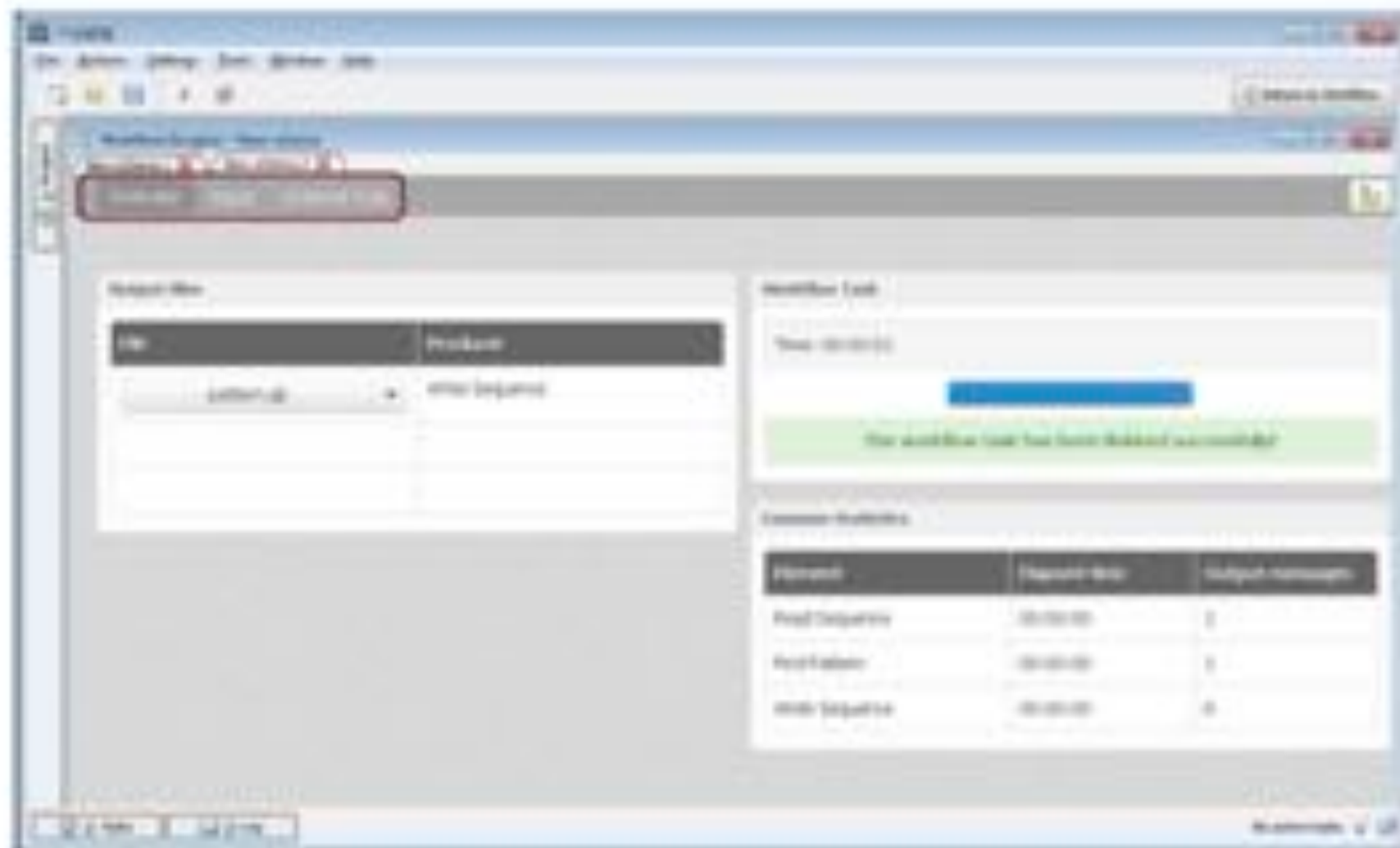




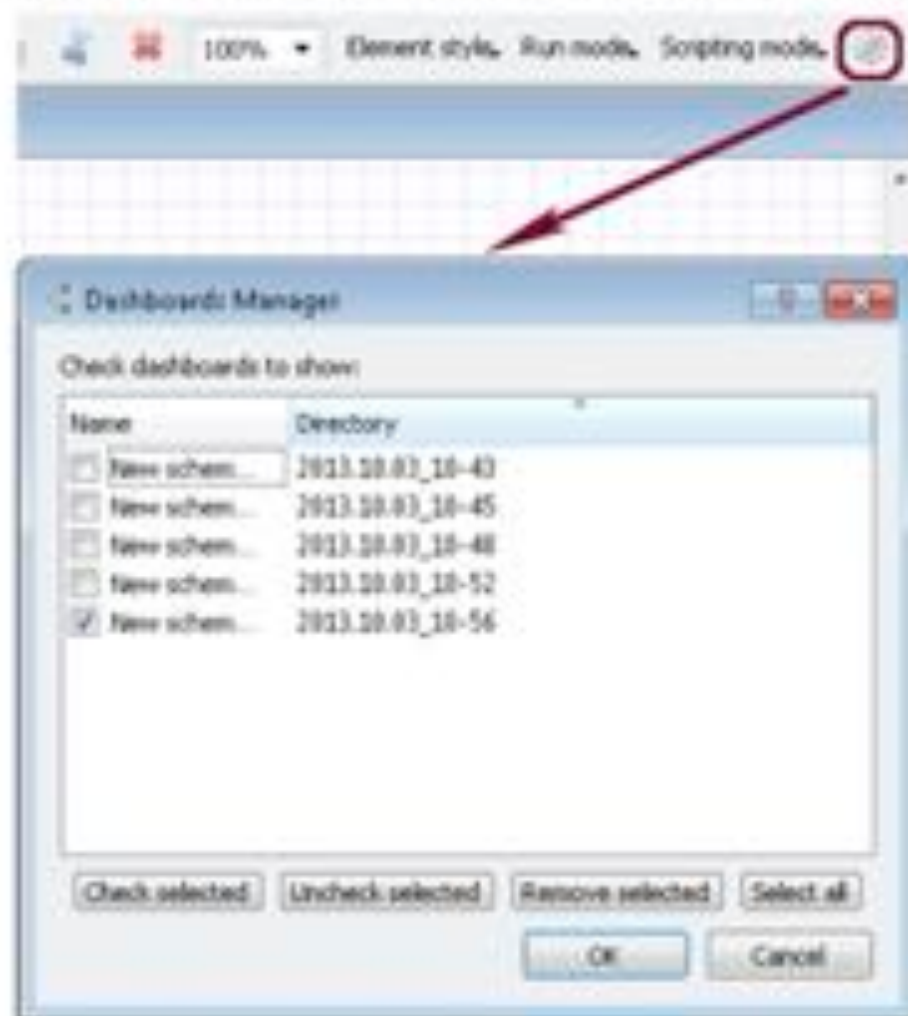
Example 4. You can find pattern in a sequence or in sequences and save it as annotations using the following workflow:



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 tool!

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

Tutorials:

- <https://www.youtube.com/watch?v=2pZszPGKnT8>
- <http://bioinformatics.hgen.slu.se/SLUBIO2018/SLUBIO2018/UGENE.html>