UGENE Workflow Designer.

Flexible control and extension of pipelines with scripts

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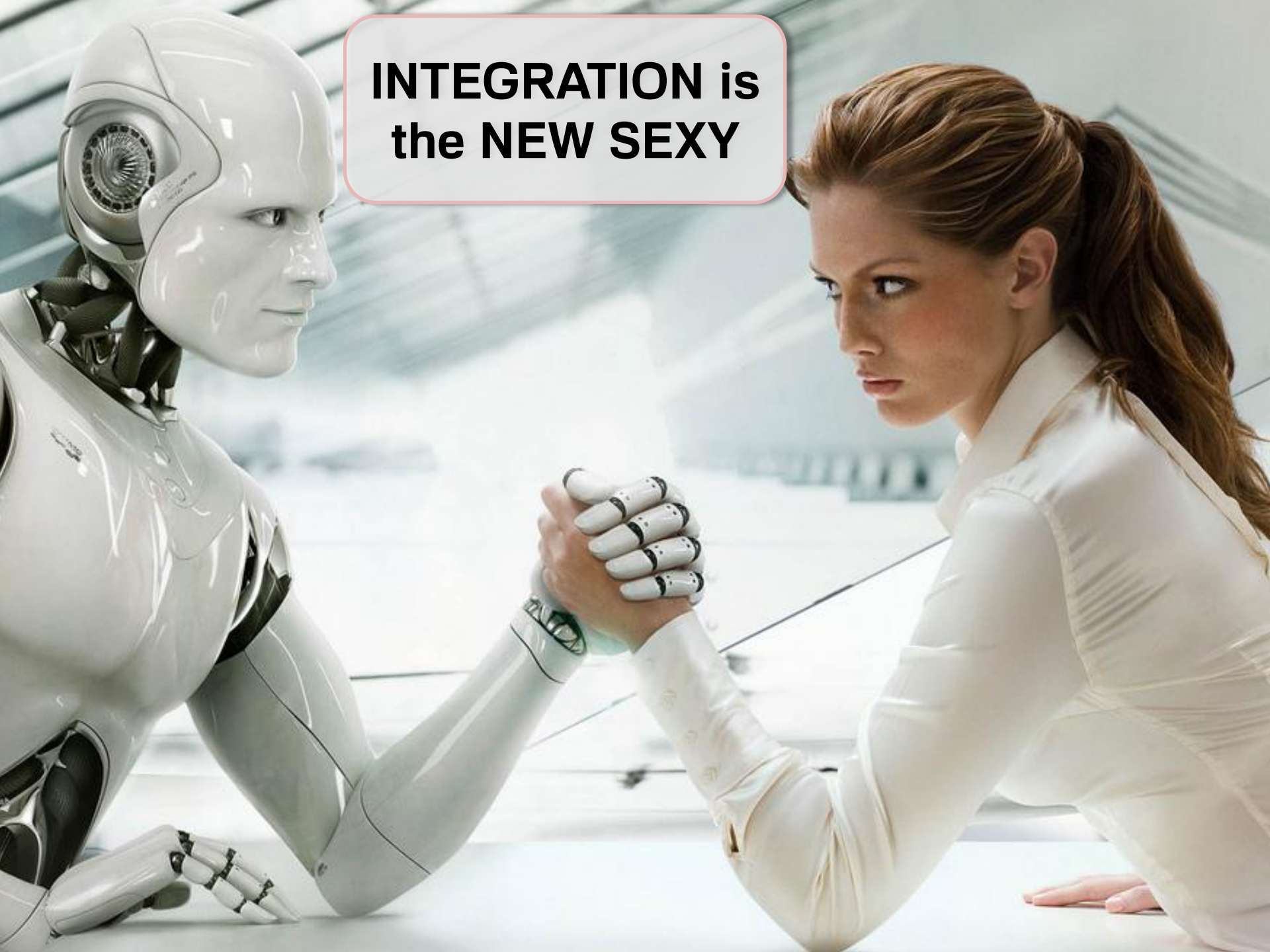
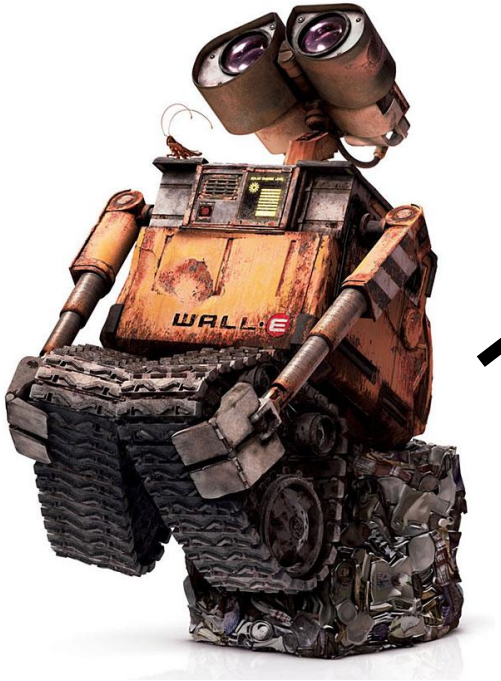

INTEGRATION is
the NEW SEXY

Software development in Bioinformatics

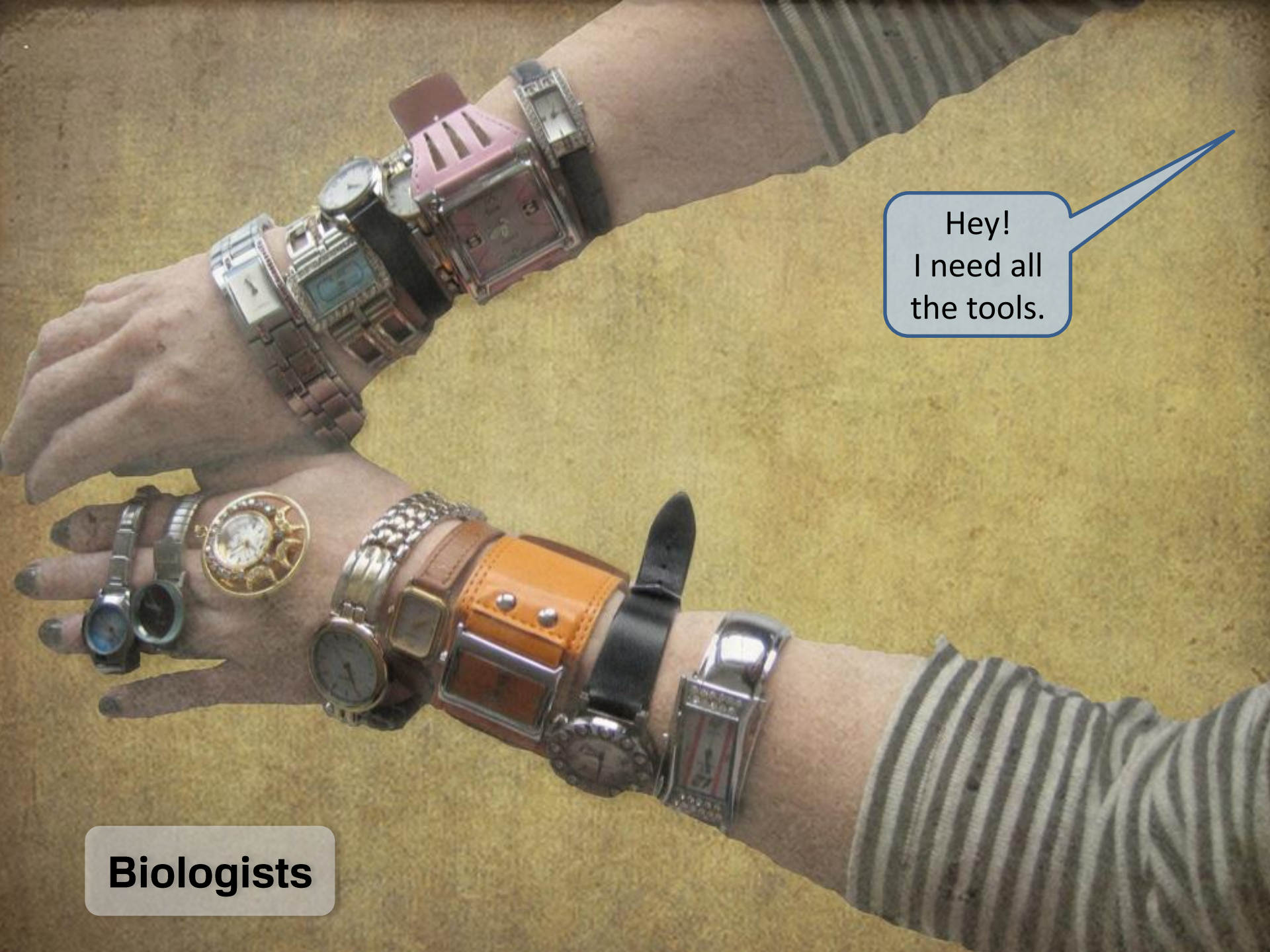
Yeah! I've come up with a new tool



Web Images Maps More

About 68,700 results (0.27 seconds)

Ooh… It's already there

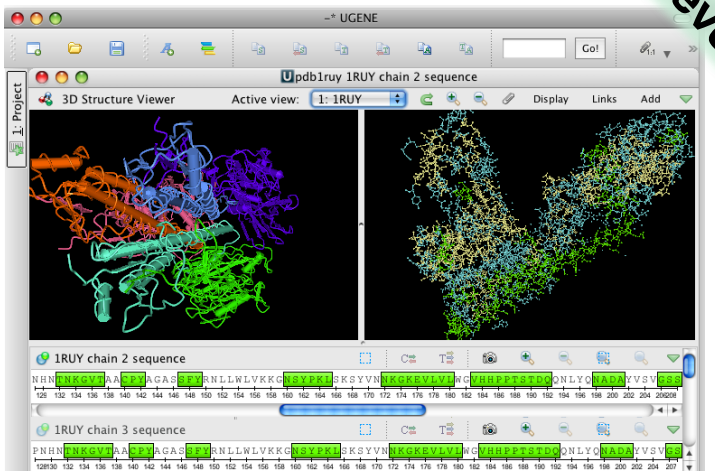

Hey!
I need all
the tools.
Biologists

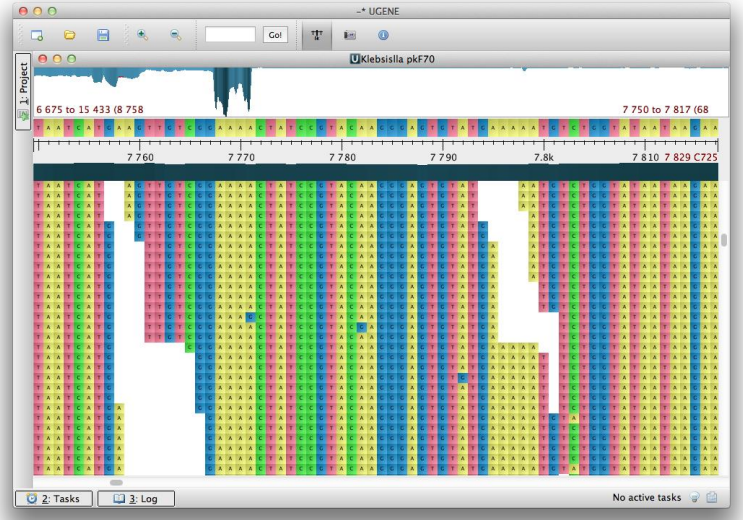
UGENE

Open-source

>5 years of development

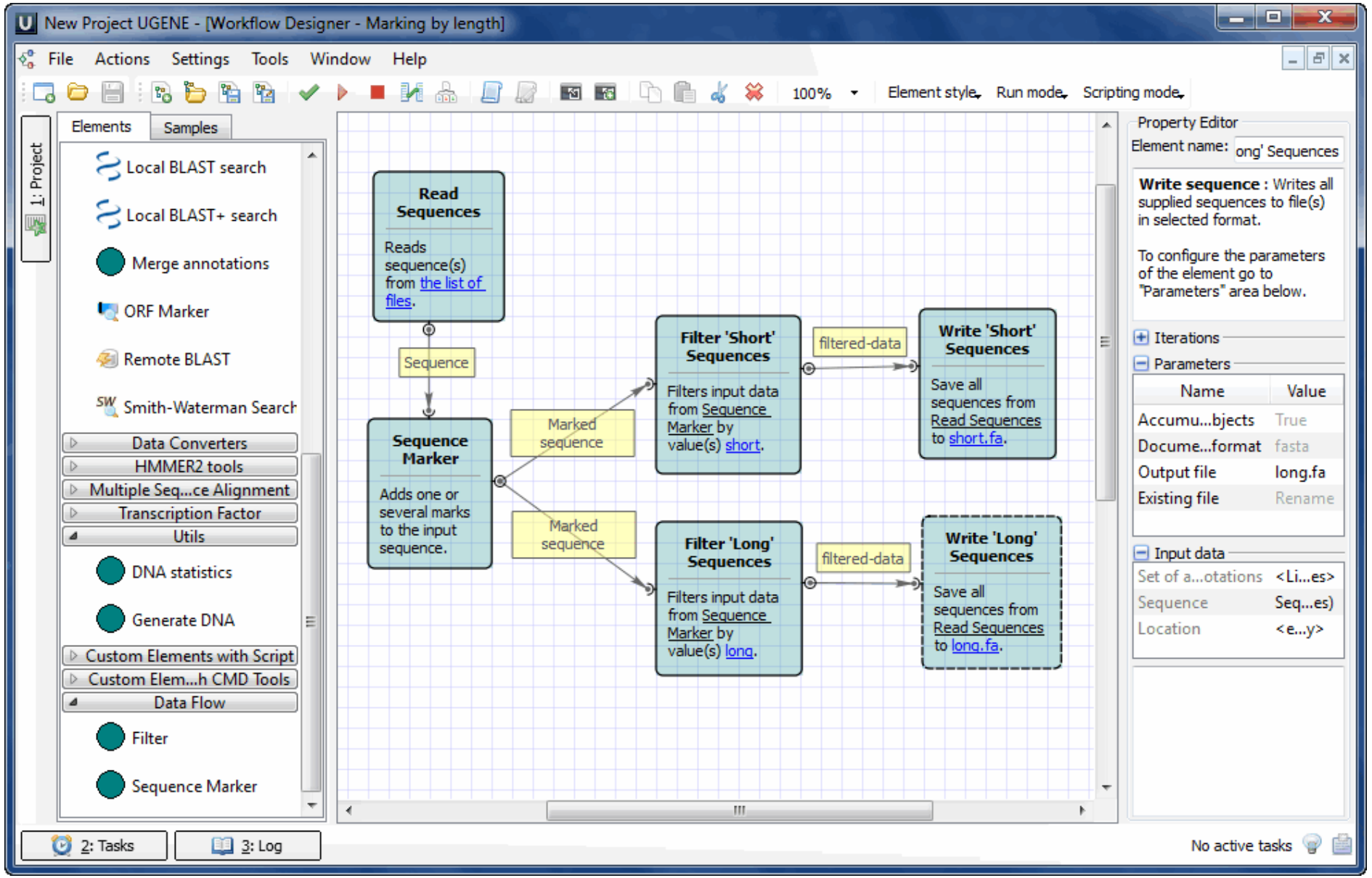
- Multiple Alignment: MUSCLE, Kalign, Clustal, Mafft, T-Coffee
- Ultra fast repeat finder





- HMMER, ORF Finder, Restriction sites
- Remote databases queries (BLAST, CDD, DAS, etc.)
- Phylogenetic trees
- TFBSs
- >20 data formats

UGENE Workflow Designer



UGENE Workflow Designer Features

On **local** machine

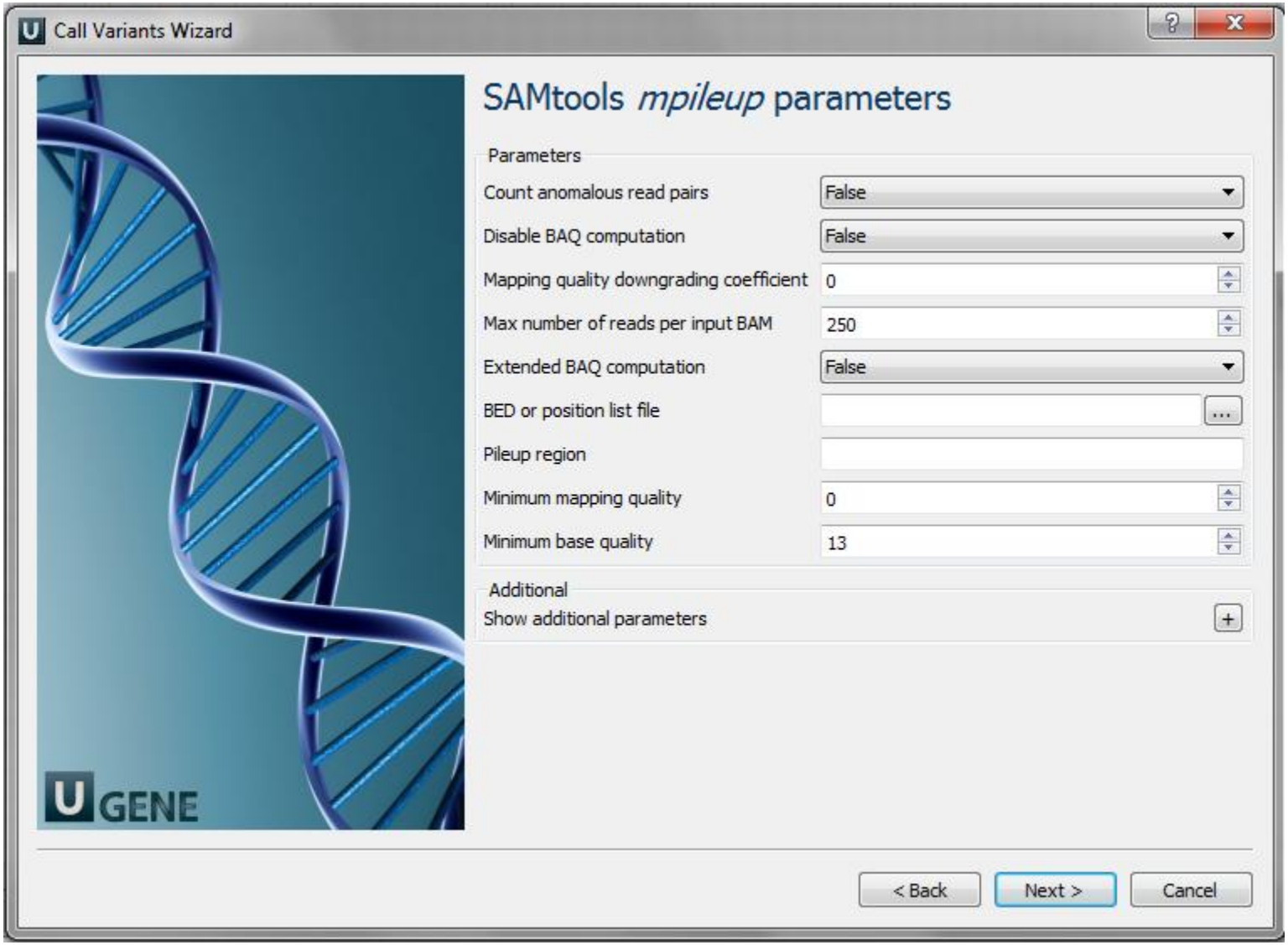
Share files with schemes

Imports data to internal DB

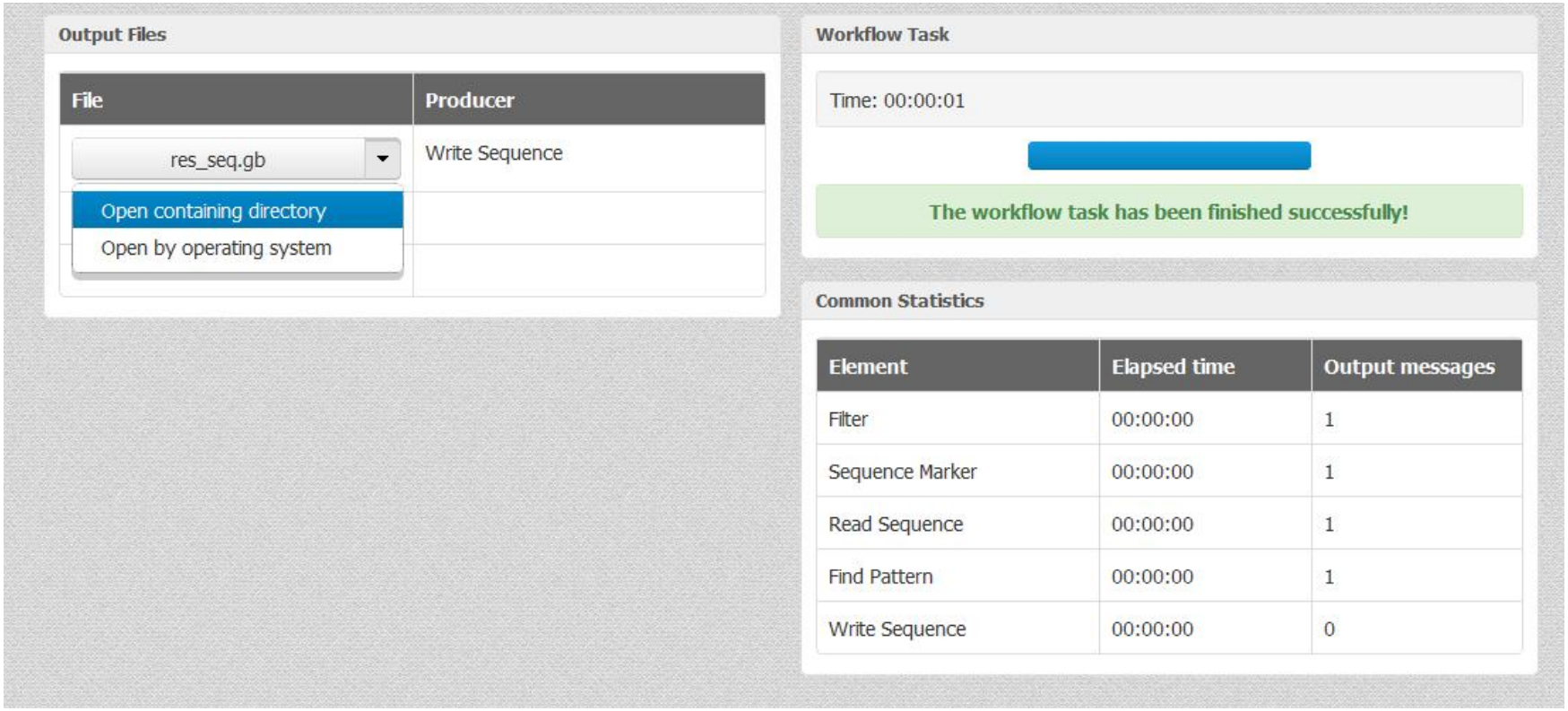
Or passes file URLs

Extension with external instruments

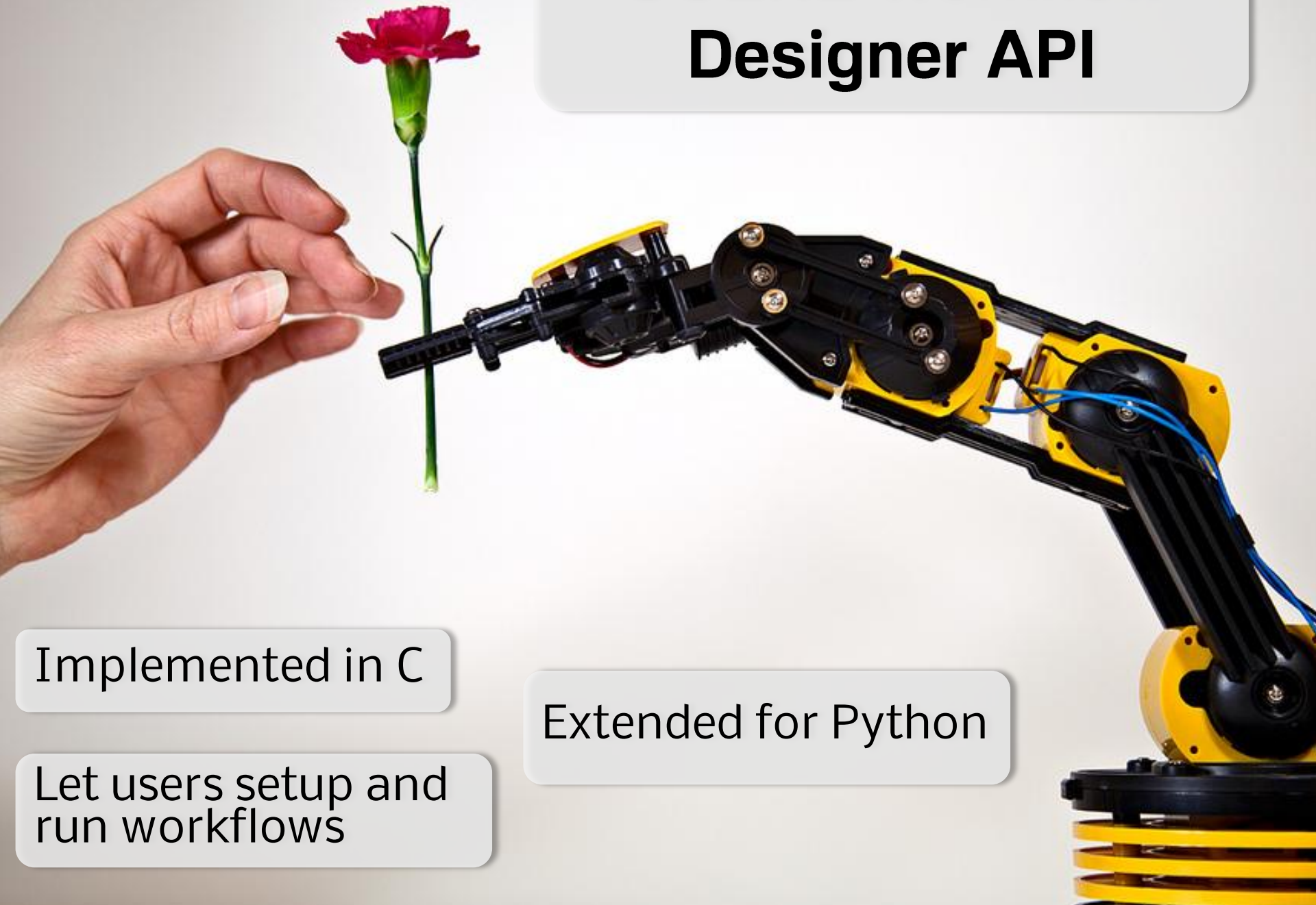
Wizards to setup the parameters



Dashboard for results and statistics



UGENE Workflow Designer API



Implemented in C

Extended for Python

Let users setup and run workflows

Running Single Algorithm Scheme

File inputs

```
import u2py
u2py.initContext( './' )

inputFile = '../../data/samples/FASTA/chrUn_gl000231.fa'
outputFile = '../../data/samples/FASTA/ann.gb‘

u2py.Scheme.launchSas( 'repeats-search', inputFile, outputFile )

u2py.releaseContext( )
```

BioPython Objects

Object inputs

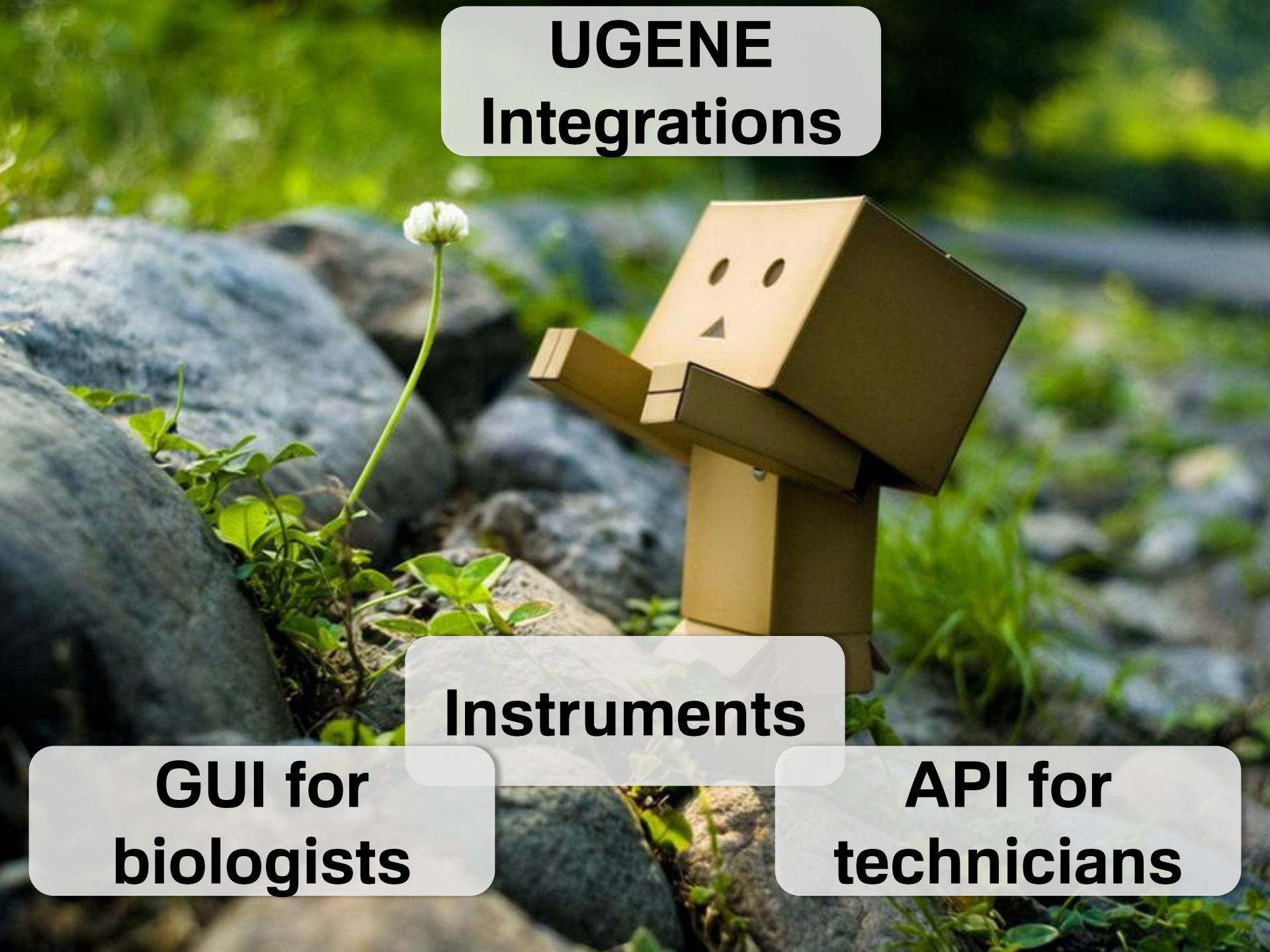
```
from Bio.Align import MultipleSeqAlignment
from Bio import AlignIO
import u2py
u2py.initContext( './' )

#read an alignment
inputAlignments = []
inputFile = open( '../../data/samples/CLUSTALW/COI_copy1.sto', 'rU' )
inputAlignments.append( AlignIO.read( inputFile, 'stockholm' ) )
inputFile.close( )

#create a scheme
scheme = u2py.Scheme( 'muscle', inputAlignments )
scheme.setElementAttribute( 'Write Alignment', 'document-format', 'stockholm' )

#run the scheme
outputAlignments = scheme.launch( )

scheme.cleanUp( )
u2py.releaseContext( )
```


UGENE
Integrations
Instruments
GUI for
biologists
API for
technicians

Thank you!

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