usegalaxy.no tools and workflows

Given by who

ELIXIR Norway, Norwegian e-infrastructure for Life Sciences and usegalaxy.no

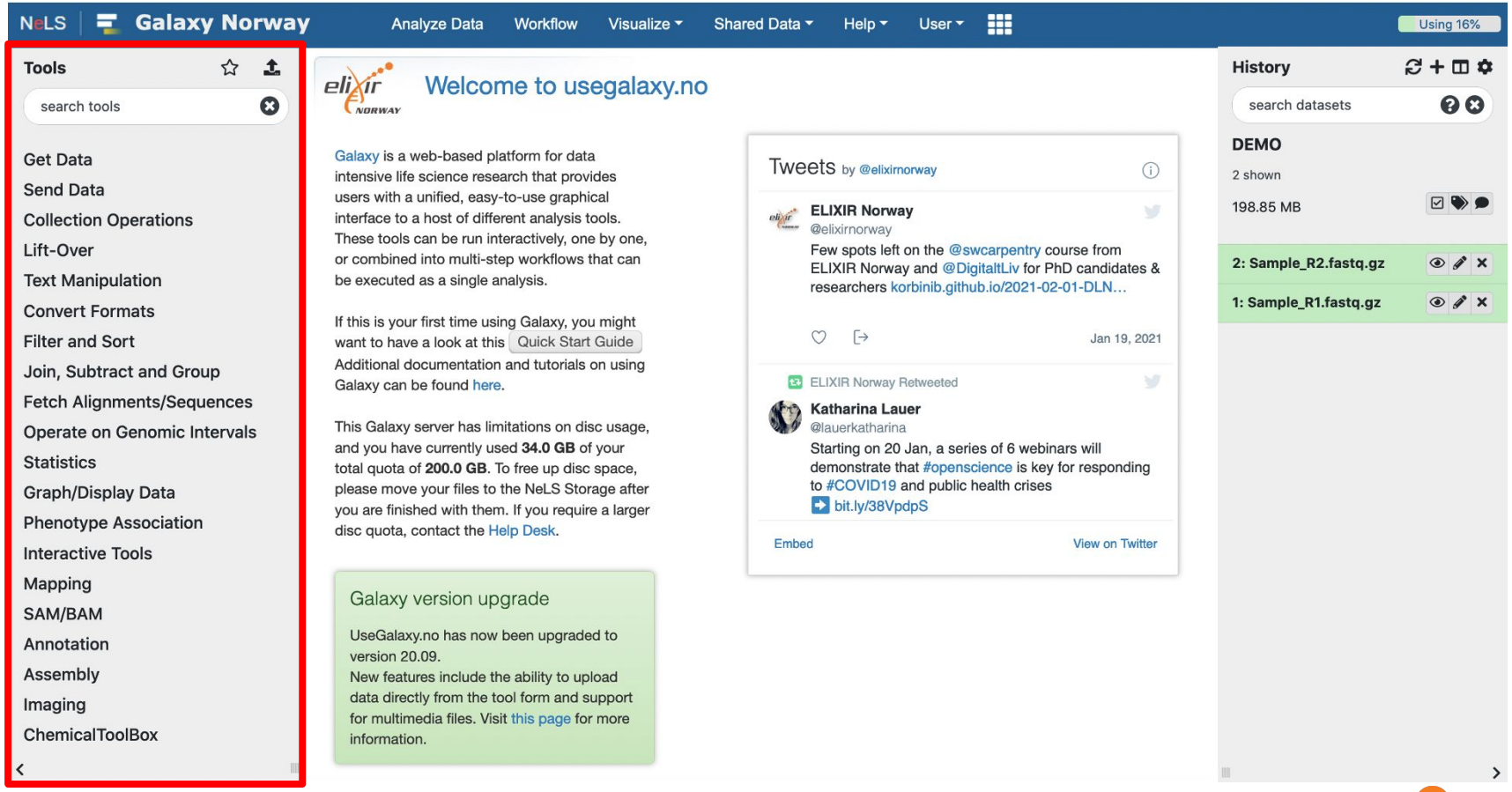
Galaxy tools

Tools are available from the Tool menu

Organised under sub-menus

Possible to browse and search by name

You can make your own list of favourite tools

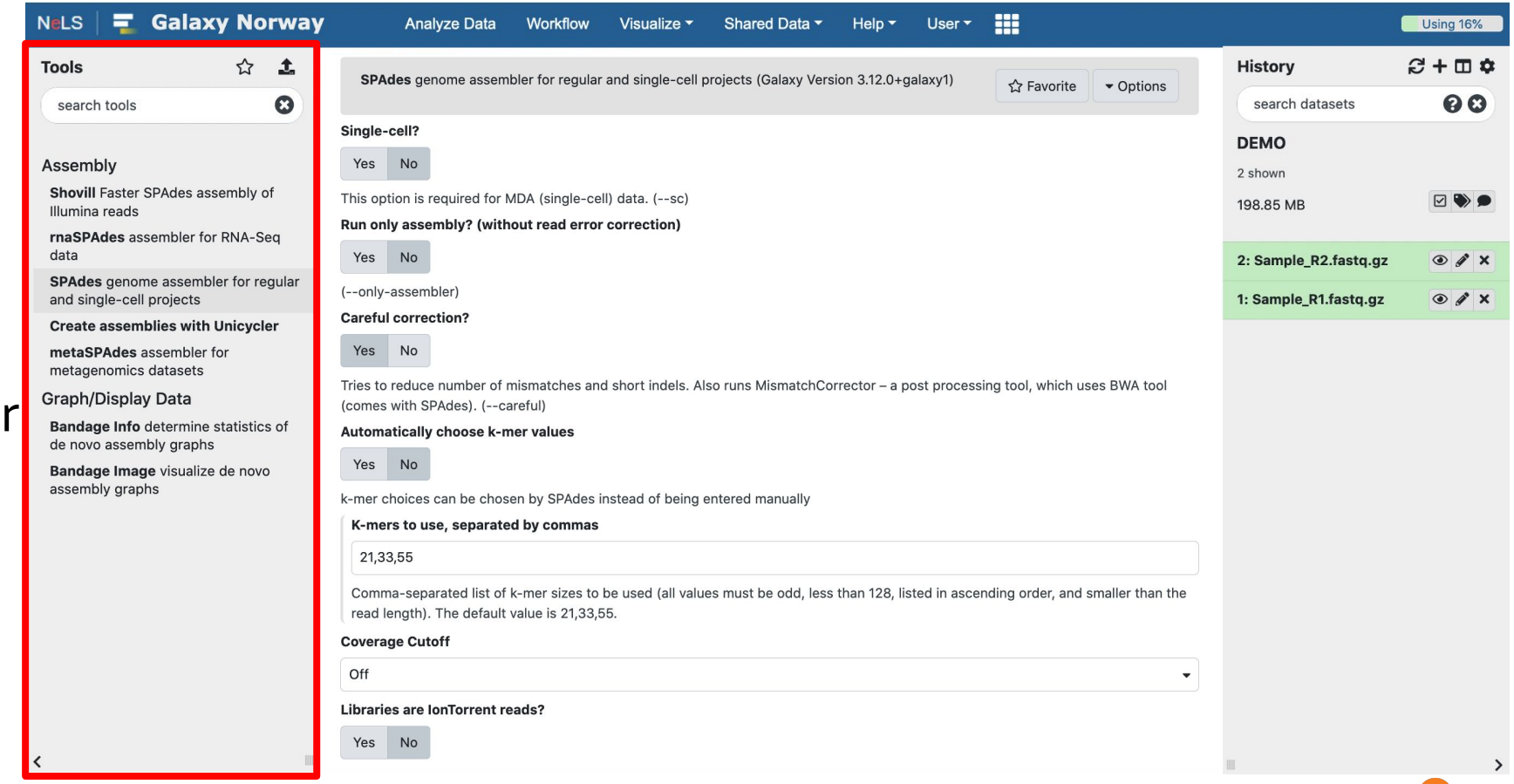


Galaxy tools = command line tools

Command line tools are wrapped into Galaxy so they become accessible with a GUI

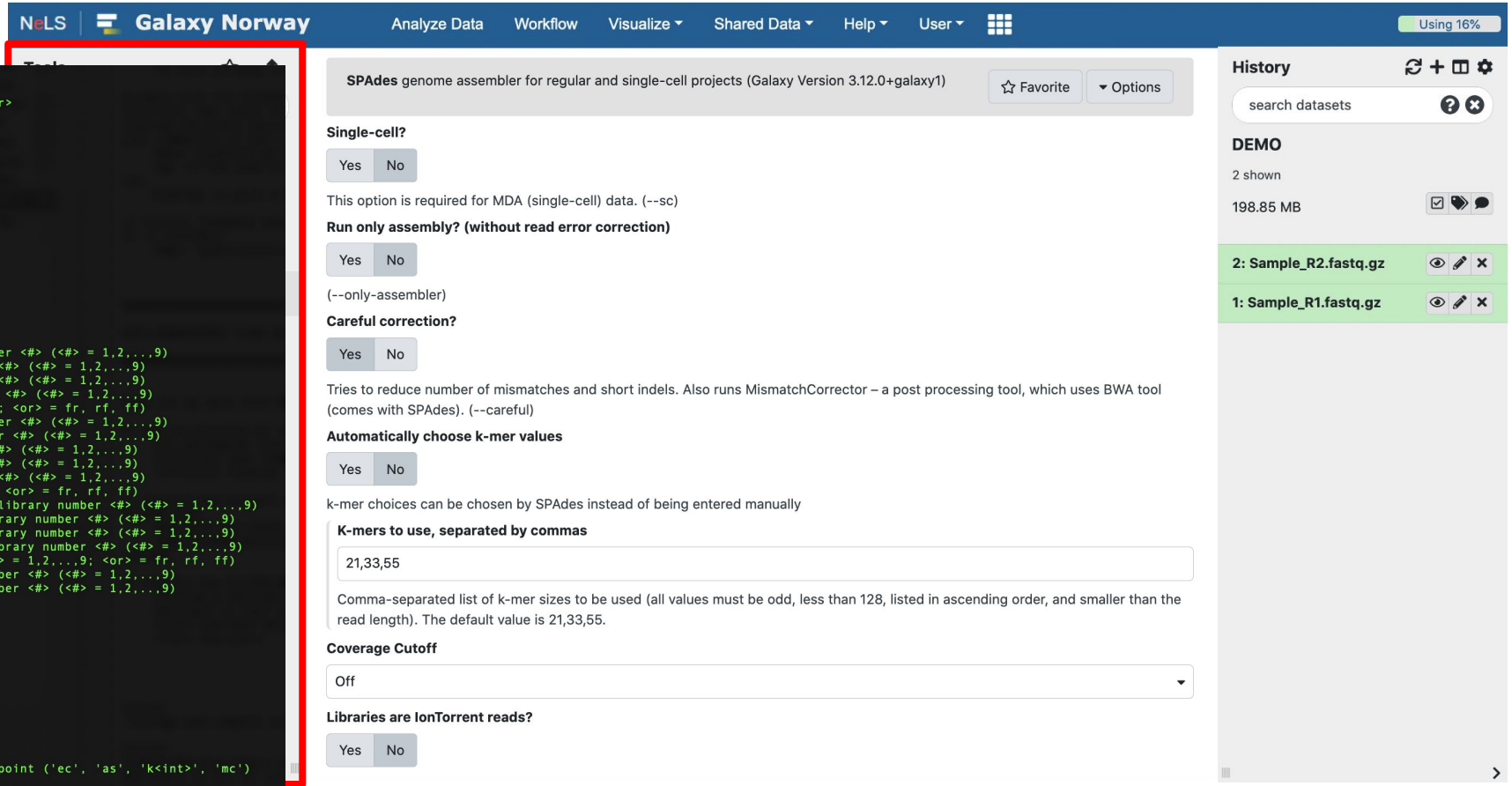
Some Galaxy tools may have reduced the number of optional parameter settings for the tool

Example here is the assembly tool called SPAdes



Command line vs Galaxy

```
SPAdes genome assembler v3.11.1

Usage: /Users/service/tools/SPAdes-3.11.1-Darwin/bin/spades.py [options] -o <output_dir>

Basic options:
-o      <output_dir>    directory to store all the resulting files (required)
--sc                    this flag is required for MDA (single-cell) data
--meta                  this flag is required for metagenomic sample data
--rna                   this flag is required for RNA-Seq data
--plasmid               runs plasmidSPAdes pipeline for plasmid detection
--iontorrent            this flag is required for IonTorrent data
--test                  runs SPAdes on toy dataset
-h/--help               prints this usage message
-v/--version            prints version

Input data:
--12    <filename>      file with interlaced forward and reverse paired-end reads
-1      <filename>      file with forward paired-end reads
-2      <filename>      file with reverse paired-end reads
-s      <filename>      file with unpaired reads
--pe<#>-12      <filename>      file with interlaced reads for paired-end library number <#> (<#> = 1,2,..,9)
--pe<#>-1       <filename>      file with forward reads for paired-end library number <#> (<#> = 1,2,..,9)
--pe<#>-2       <filename>      file with reverse reads for paired-end library number <#> (<#> = 1,2,..,9)
--pe<#>-s       <filename>      file with unpaired reads for paired-end library number <#> (<#> = 1,2,..,9)
--pe<#>-<or>    orientation of reads for paired-end library number <#> (<#> = 1,2,..,9; <or> = fr, rf, ff)
--s<#>          <filename>      file with unpaired reads for single reads library number <#> (<#> = 1,2,..,9)
--mp<#>-12      <filename>      file with interlaced reads for mate-pair library number <#> (<#> = 1,2,..,9)
--mp<#>-1       <filename>      file with forward reads for mate-pair library number <#> (<#> = 1,2,..,9)
--mp<#>-2       <filename>      file with reverse reads for mate-pair library number <#> (<#> = 1,2,..,9)
--mp<#>-s       <filename>      file with unpaired reads for mate-pair library number <#> (<#> = 1,2,..,9)
--mp<#>-<or>    orientation of reads for mate-pair library number <#> (<#> = 1,2,..,9; <or> = fr, rf, ff)
--hqmp<#>-12    <filename>      file with interlaced reads for high-quality mate-pair library number <#> (<#> = 1,2,..,9)
--hqmp<#>-1     <filename>      file with forward reads for high-quality mate-pair library number <#> (<#> = 1,2,..,9)
--hqmp<#>-2     <filename>      file with reverse reads for high-quality mate-pair library number <#> (<#> = 1,2,..,9)
--hqmp<#>-s     <filename>      file with unpaired reads for high-quality mate-pair library number <#> (<#> = 1,2,..,9)
--hqmp<#>-<or>  orientation of reads for high-quality mate-pair library number <#> (<#> = 1,2,..,9; <or> = fr, rf, ff)
--nxmate<#>-1   <filename>      file with forward reads for Lucigen NxMate library number <#> (<#> = 1,2,..,9)
--nxmate<#>-2   <filename>      file with reverse reads for Lucigen NxMate library number <#> (<#> = 1,2,..,9)
--sanger        <filename>      file with Sanger reads
--pacbio        <filename>      file with PacBio reads
--nanopore      <filename>      file with Nanopore reads
--tslr  <filename>      file with TSLR-contigs
--trusted-contigs       <filename>      file with trusted contigs
--untrusted-contigs     <filename>      file with untrusted contigs

Pipeline options:
--only-error-correction runs only read error correction (without assembling)
--only-assembler        runs only assembling (without read error correction)
--careful               tries to reduce number of mismatches and short indels
--continue              continue run from the last available check-point
--restart-from  <cp>    restart run with updated options and from the specified check-point ('ec', 'as', 'k<int>', 'mc')
--disable-gzip-output   forces error correction not to compress the corrected reads
--disable-rr            disables repeat resolution stage of assembling

Advanced options:
--dataset       <filename>      file with dataset description in YAML format
-t/--threads    <int>           number of threads
                                [default: 16]
-m/--memory     <int>           RAM limit for SPAdes in Gb (terminates if exceeded)
                                [default: 250]
--tmp-dir       <dirname>       directory for temporary files
                                [default: <output_dir>/tmp]
-k              <int,int,...>   comma-separated list of k-mer sizes (must be odd and
```



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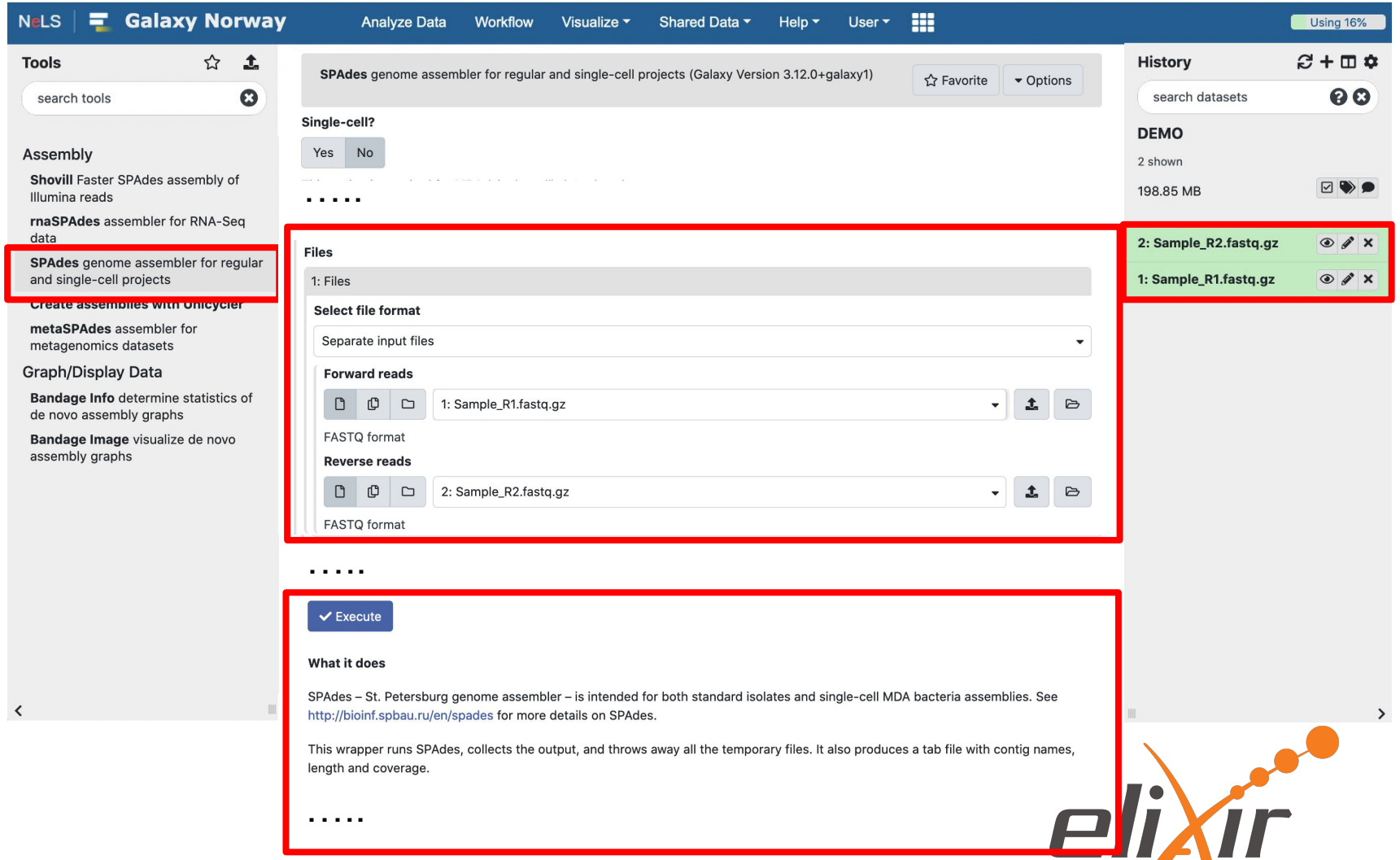
Running tools in Galaxy

Example running the tool SPAdes

Choose parameter settings

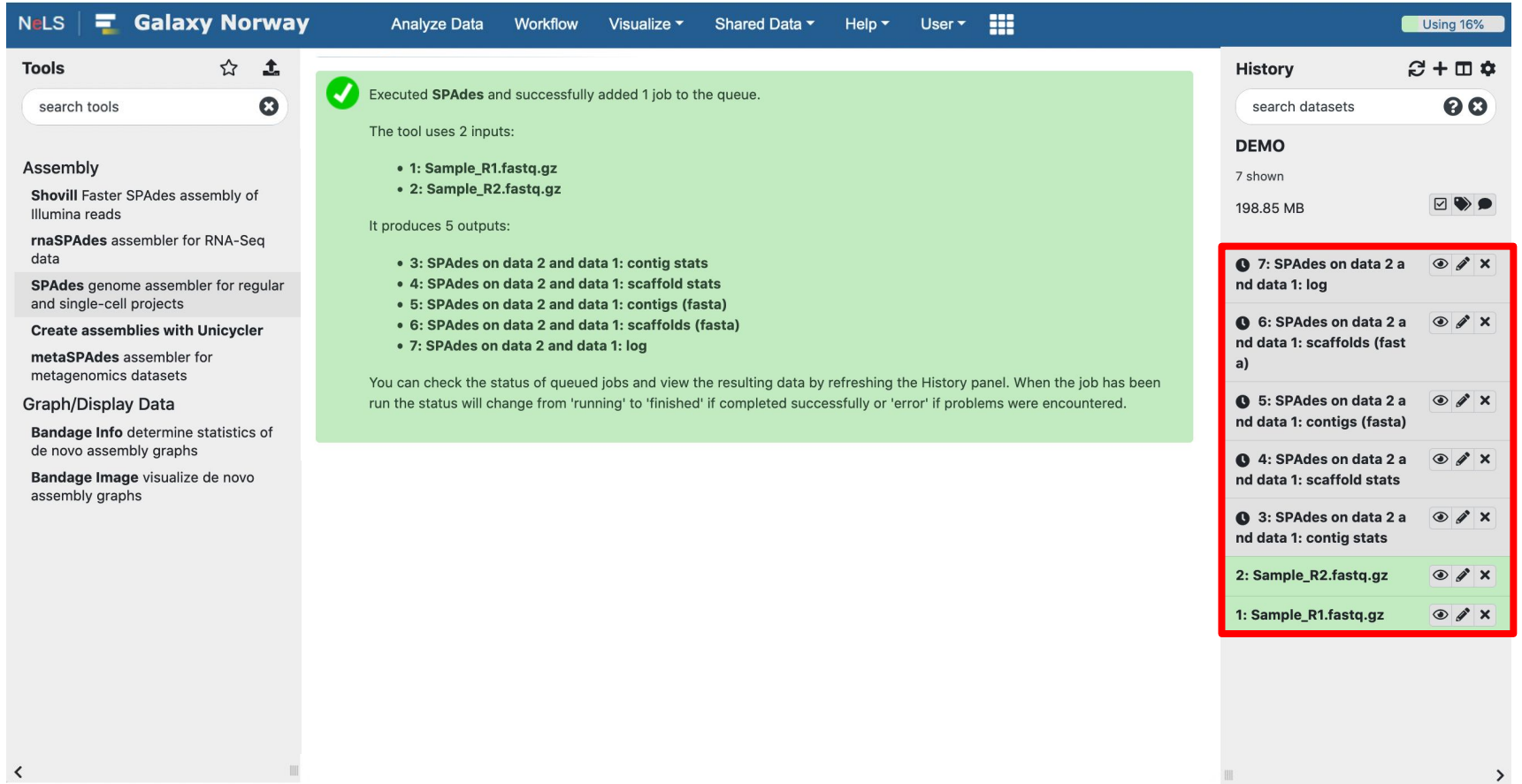
Select input files

Most tools comes with a detailed description of usage



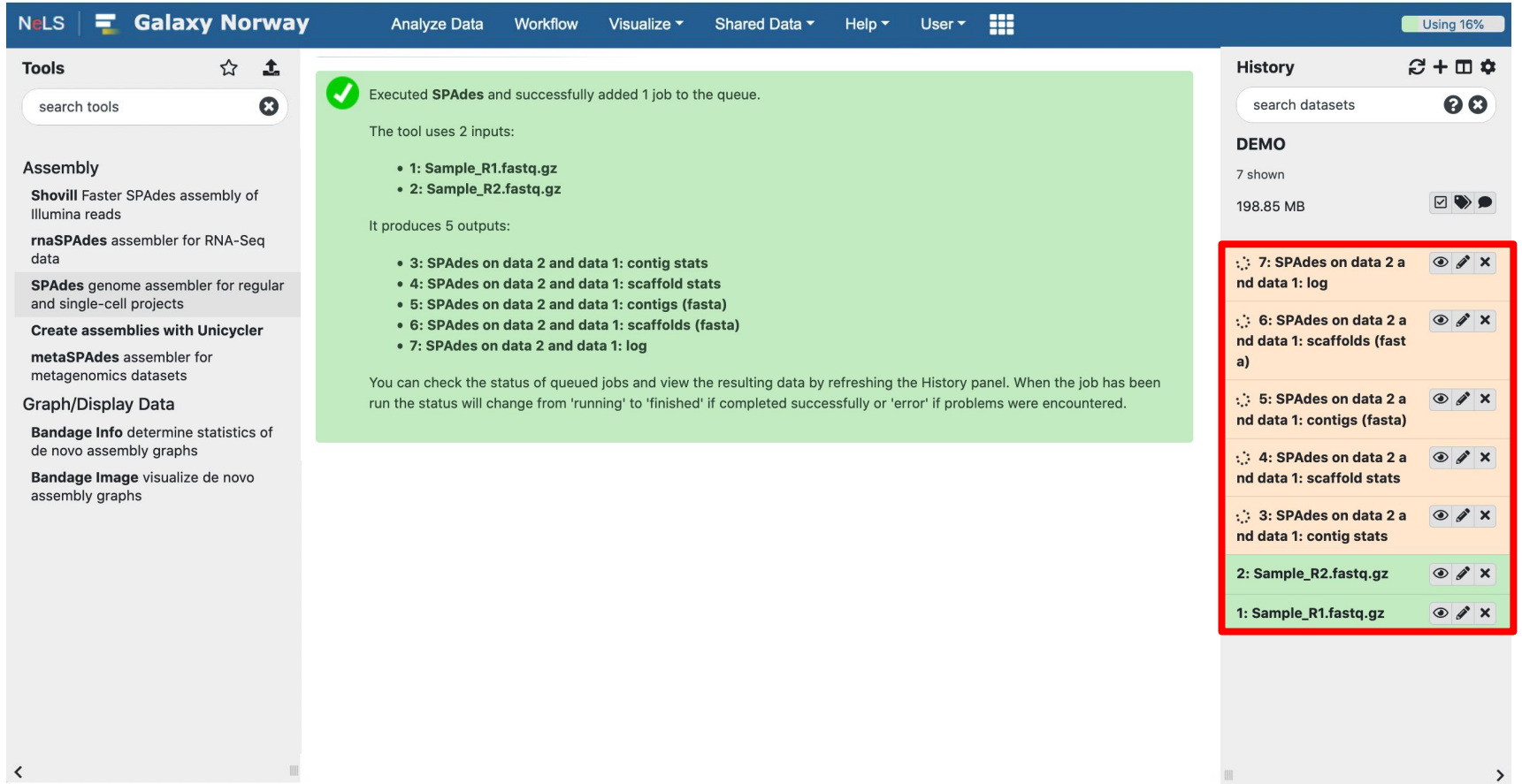
Running tools in Galaxy

The result files are first displayed in grey boxes. This means the job is pending.



Running tools in Galaxy

When the job is running, the files turns yellow



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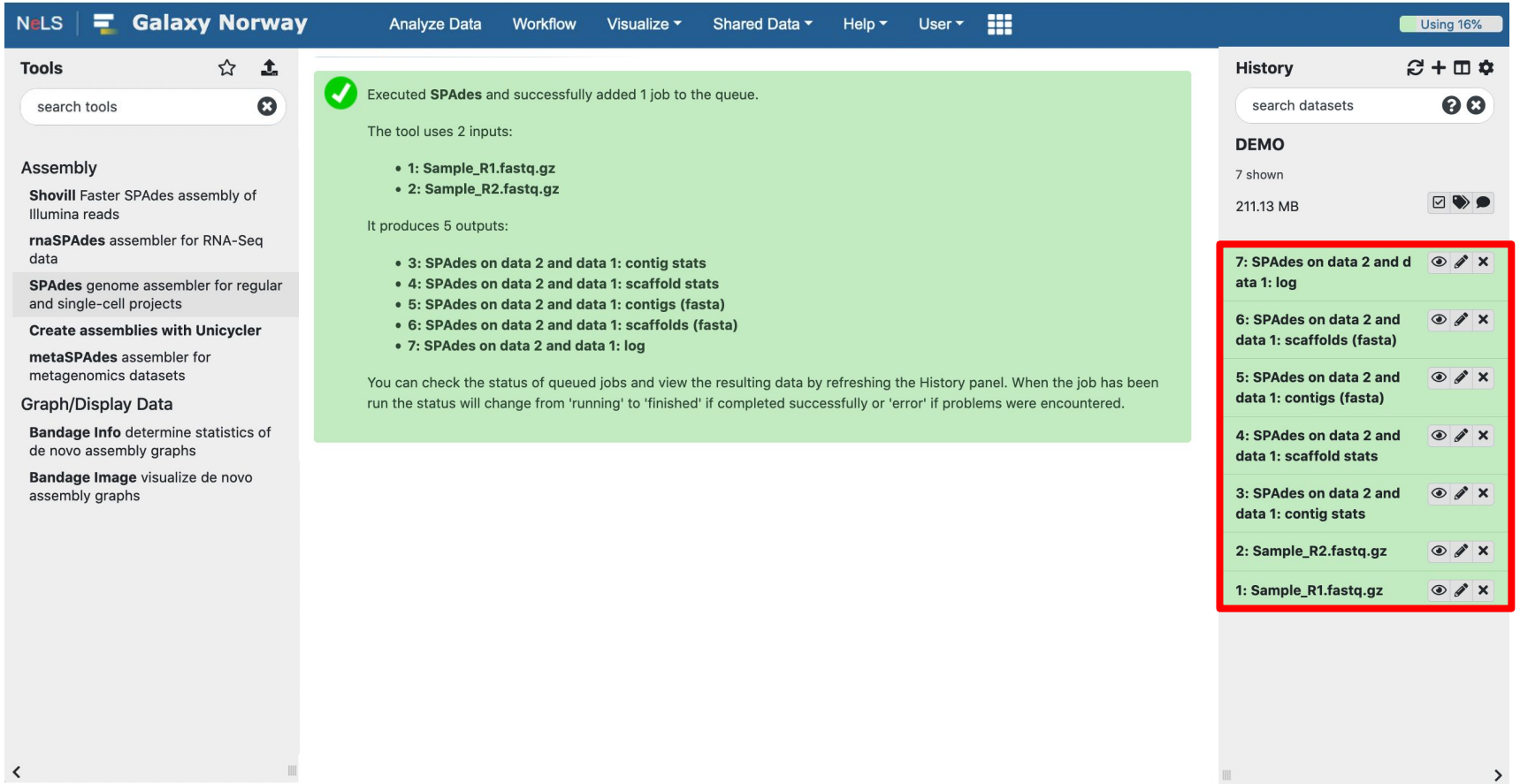
Running tools in Galaxy

When the job finish successfully, the files turn green



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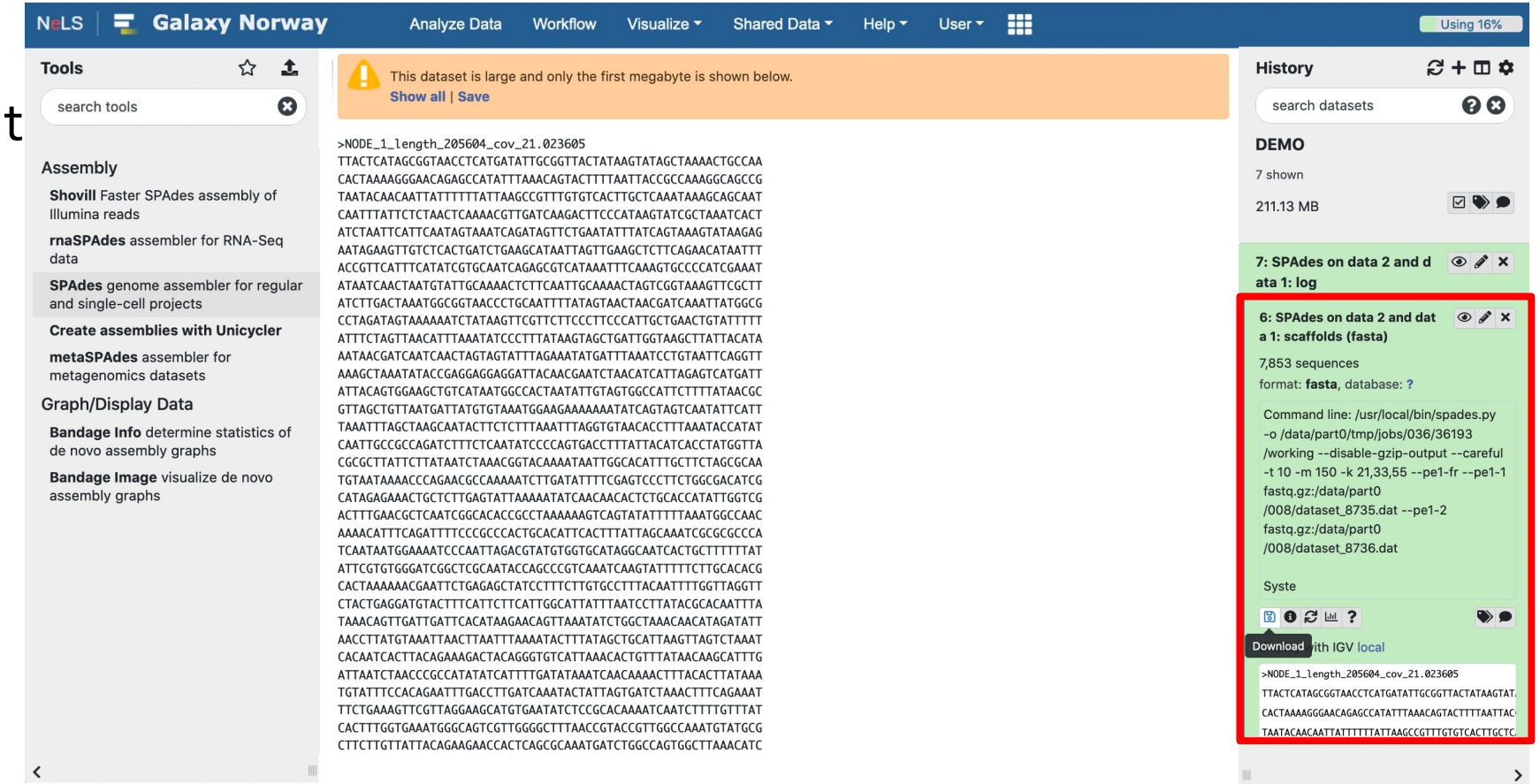
Tool output

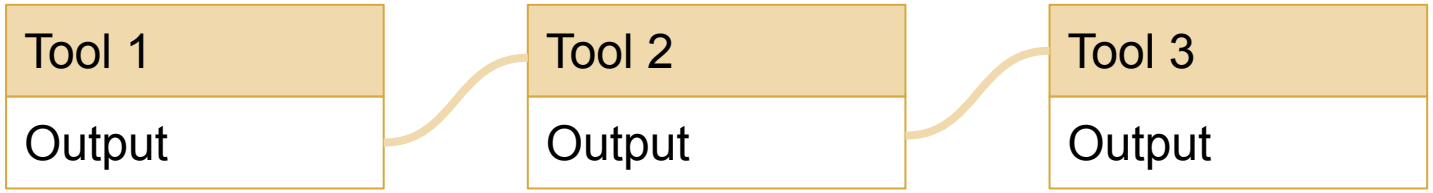
It is possible to preview the output (result), view it in the main window or download the dataset

You can also copy the dataset over to another history



Galaxy workflows

A workflow in Galaxy is basically a string of tools, where the output from one tool becomes the input for the next

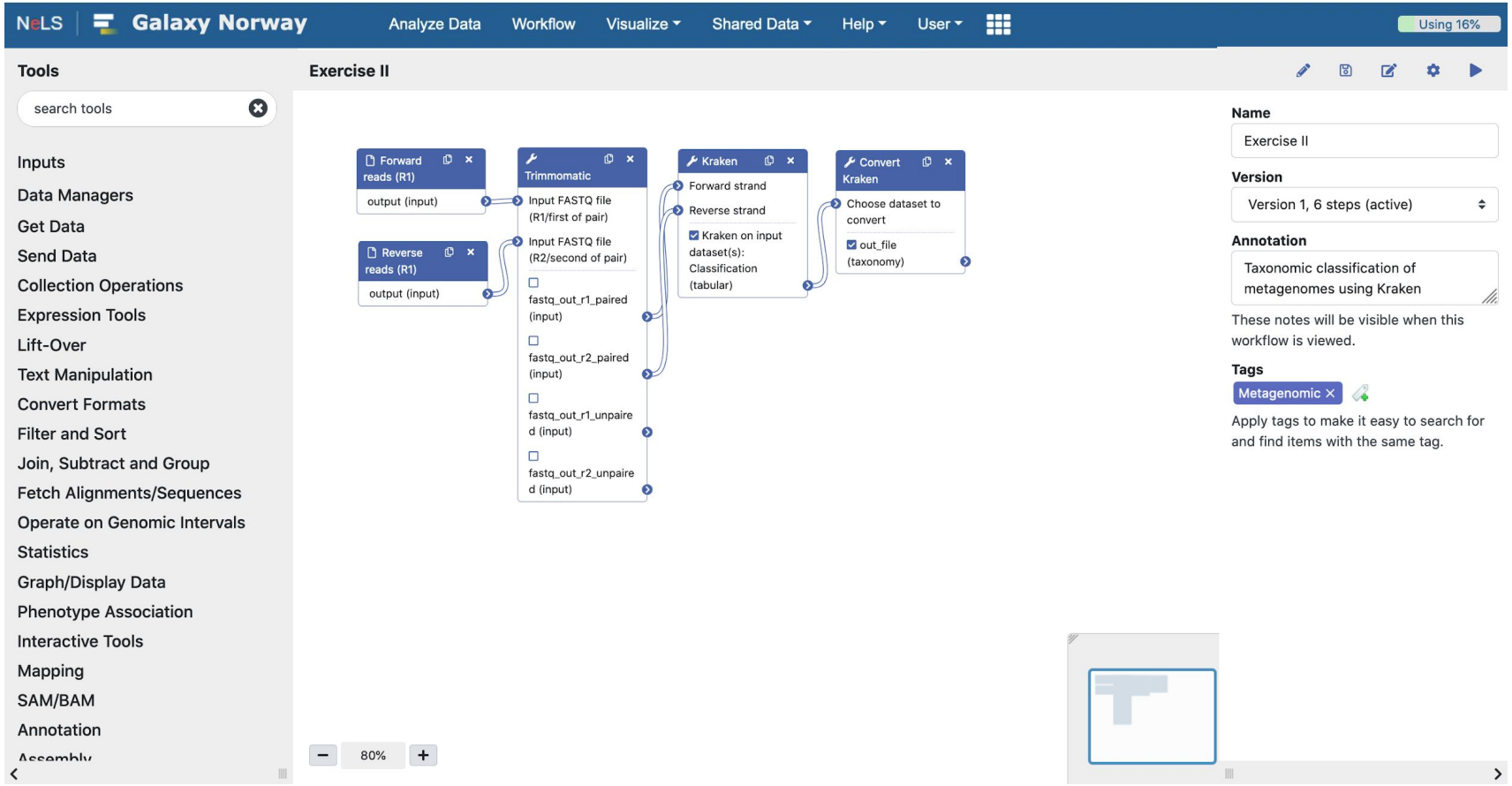


Galaxy workflows

The “nodules” indicate which output file from one acts as input for the next tool

Each workflow has a name and version

Additional text that describe the workflow and tags can be added

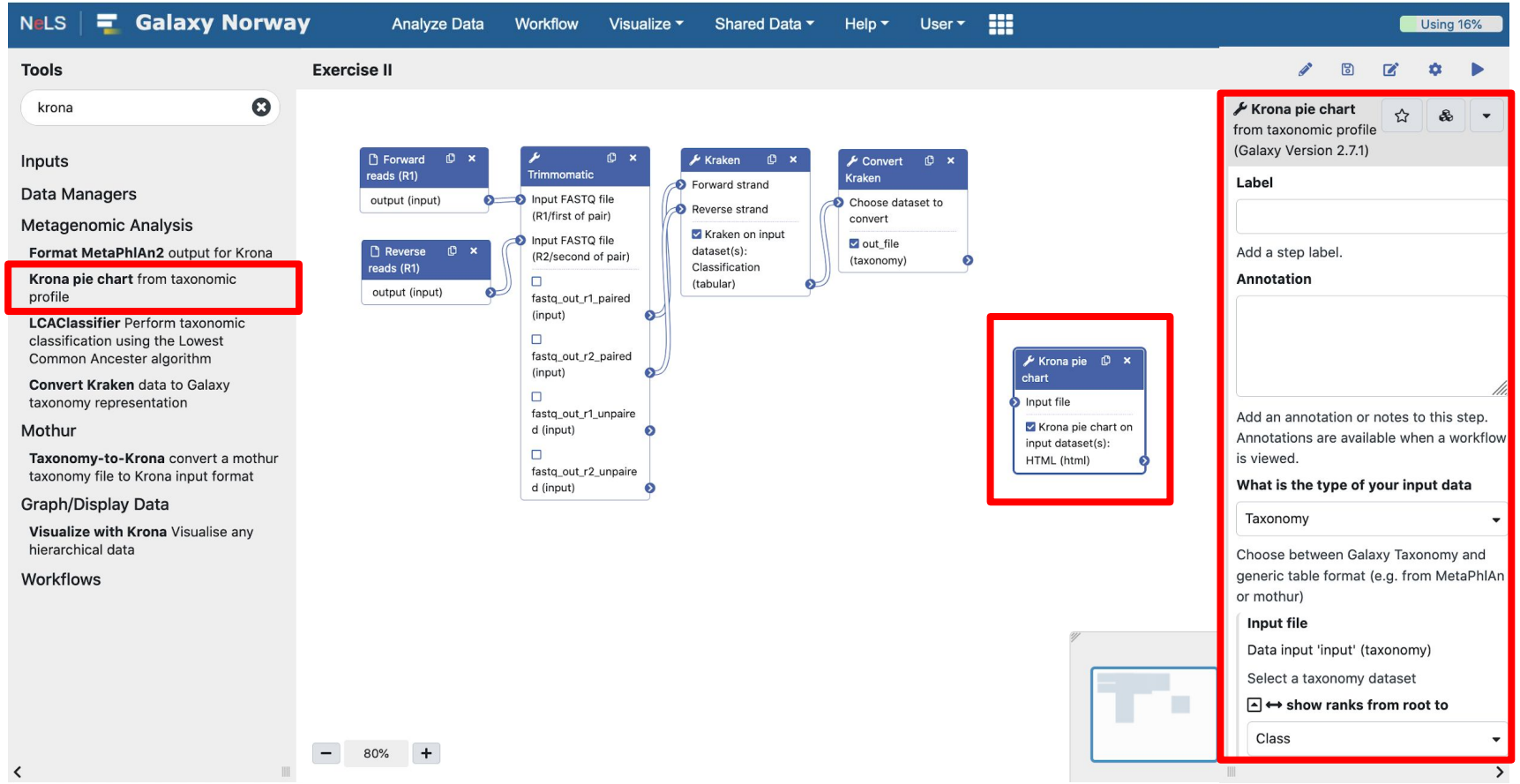


Galaxy workflows

New tools can be added by clicking on the tool in the Tool menu

The tool will appear in the workflow editor

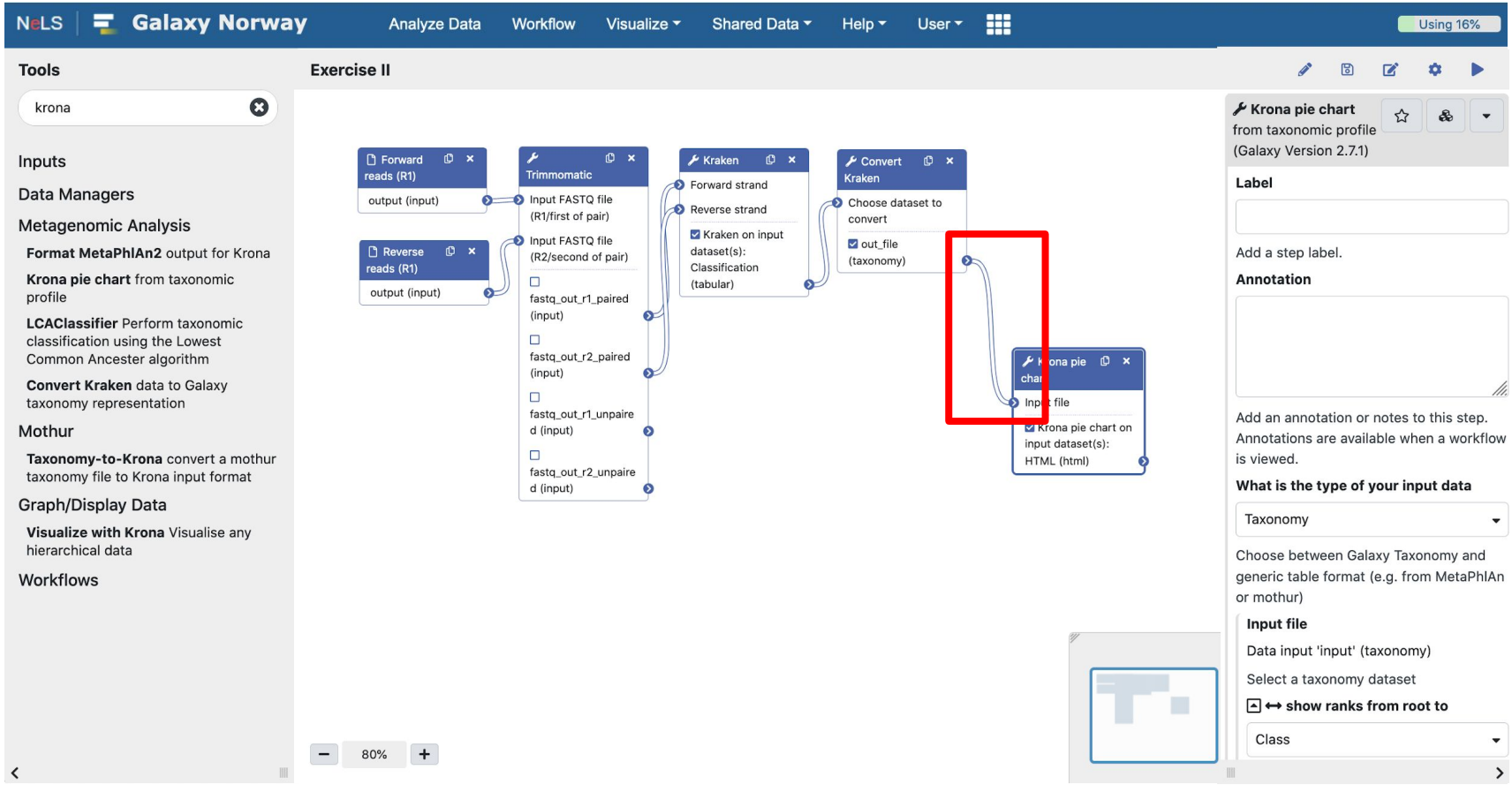
Tool parameter settings can be pre-set or made up to the user to set when running the workflow



Galaxy workflows

The output from another tools can be connected as an input for the new tool

Remember to save the modified workflow

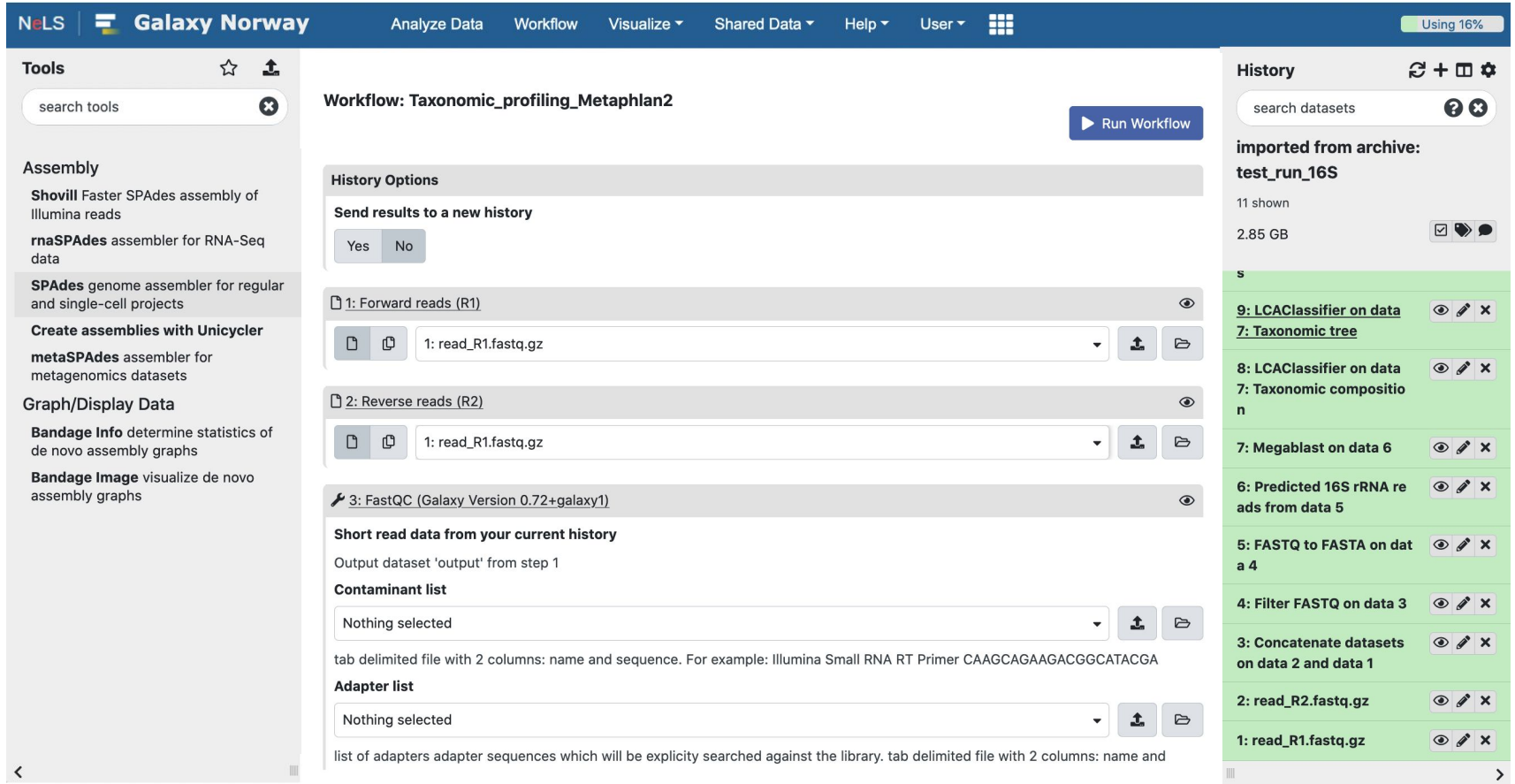


Galaxy – Running workflows

Select input files

Tools in the workflow will run successively

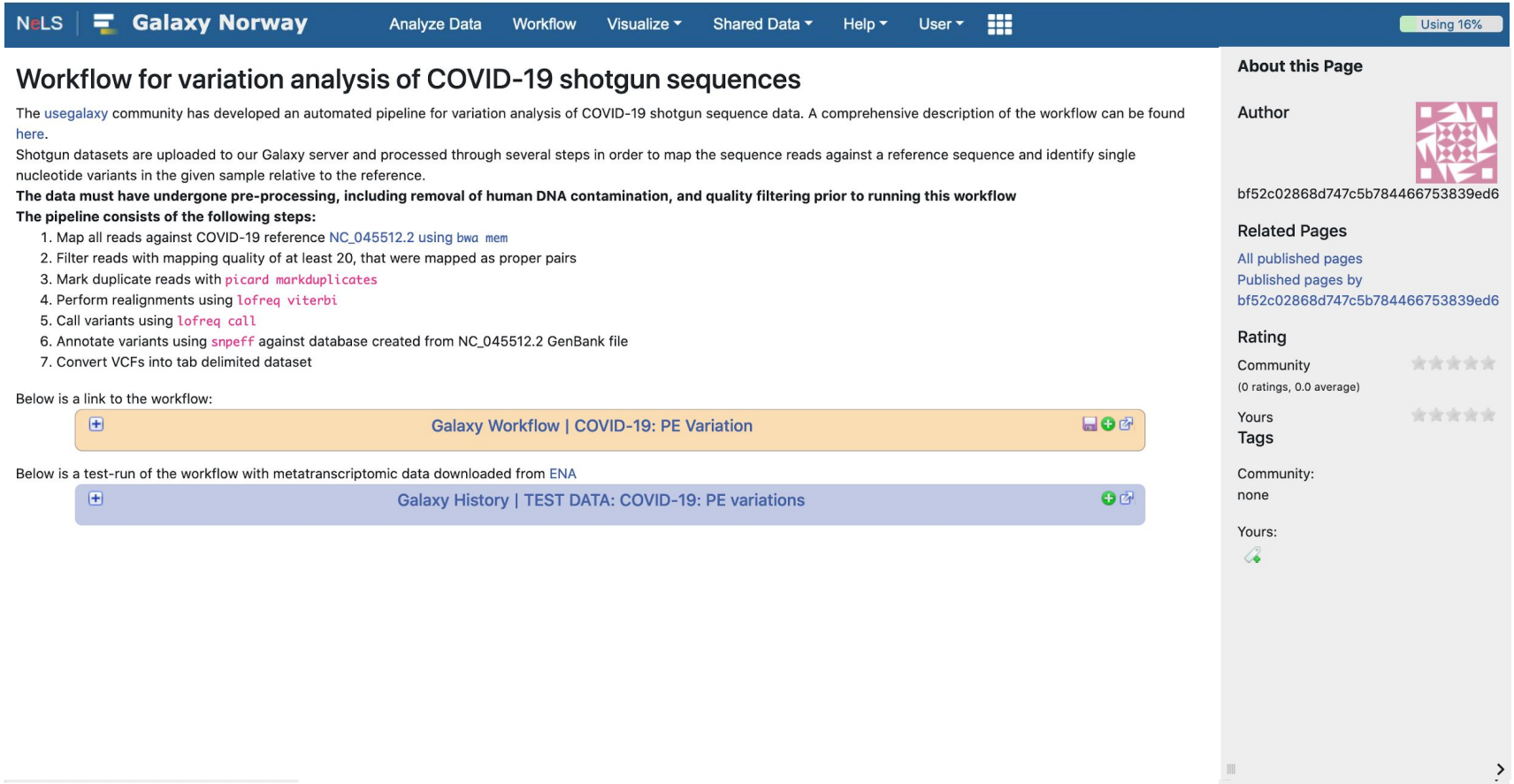
You can view and download the result files



Workflow documentation in Usegalaxy.no

Each NeLS supported workflow is documented with instructions how to use it

Also test data sets available for each workflow

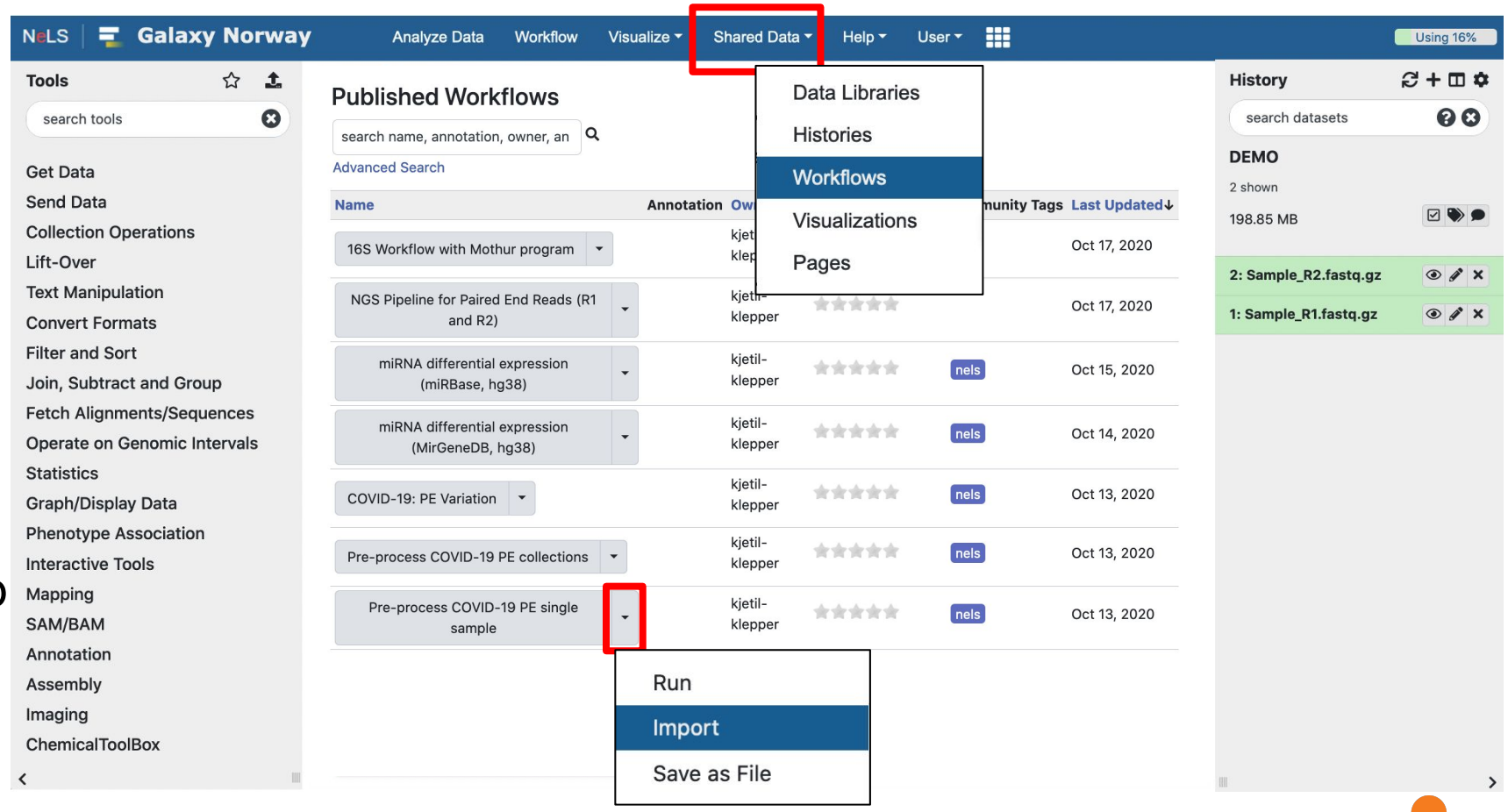


Shared workflows in usegalaxy.no

List of all workflows that are shared with all usegalaxy.no users

You can import shared data to you user

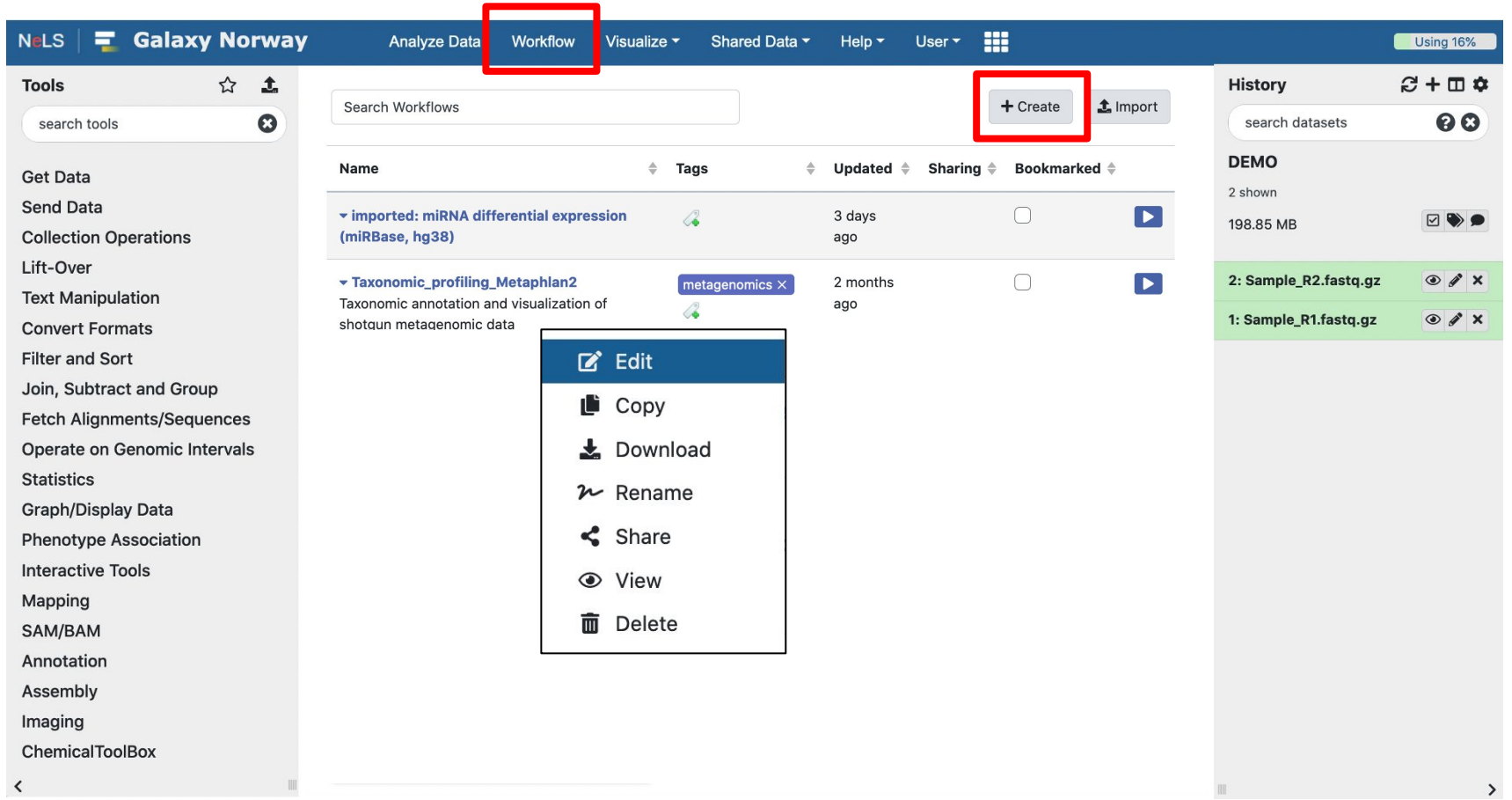
By selecting any workflow you can run data analysis, import into your user or save it on another computer



Your imported and self made workflows

You can also create new workflows here

For beginners a good tip is to import an existing workflow, and modify it to meet your needs. The workflow will only be changed in your version



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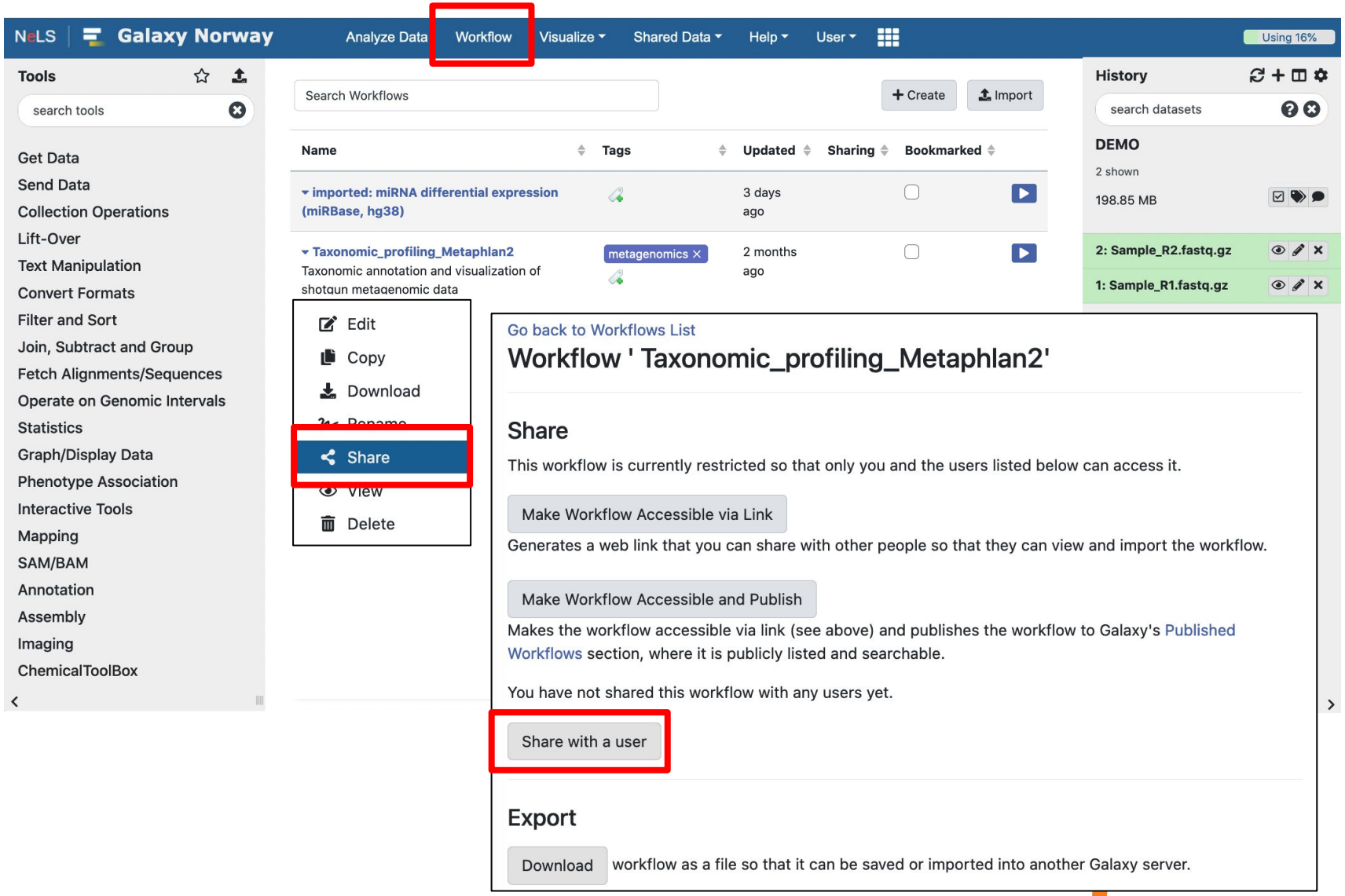
Sharing your workflows in usegalaxy.no

Self made or modified workflows can be shared with other usegalaxy.no users or made accessible via a link

You can also download a workflow and import it in another Galaxy



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