





**MBC**  
(1998-)



**ATC EMBL**  
(2010-)



**DUKE-NUS**  
(2016-)

# Single-Cell Omics

EMBO PRACTICAL COURSE



## LOCATION & DATES

EMBL Heidelberg, Germany  
12 - 18 May 2019

## DEADLINES

Application closed



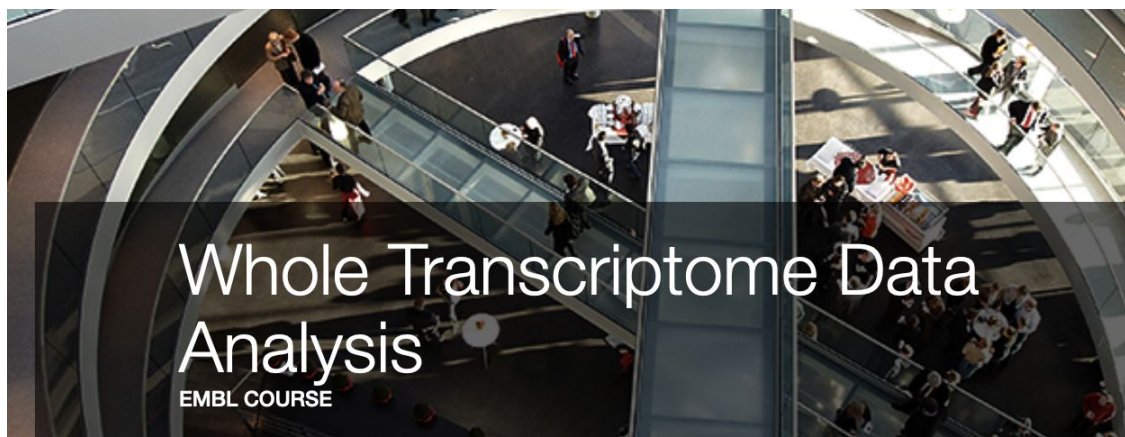
**EMBO**  
*Practical Course*



**EMBO**  
**Practical Course**

**Date:** 13 - 18 Nov 2022

**Location:** EMBL Heidelberg



# Whole Transcriptome Data Analysis

EMBL COURSE

## LOCATION & DATES

EMBL Heidelberg, Germany  
30 Sep - 4 Oct 2019

## DEADLINES

Application closed

**Date:** 29 May - 3 Jun 2022

**Location:** EMBL Heidelberg

# Infrastructure since 2020

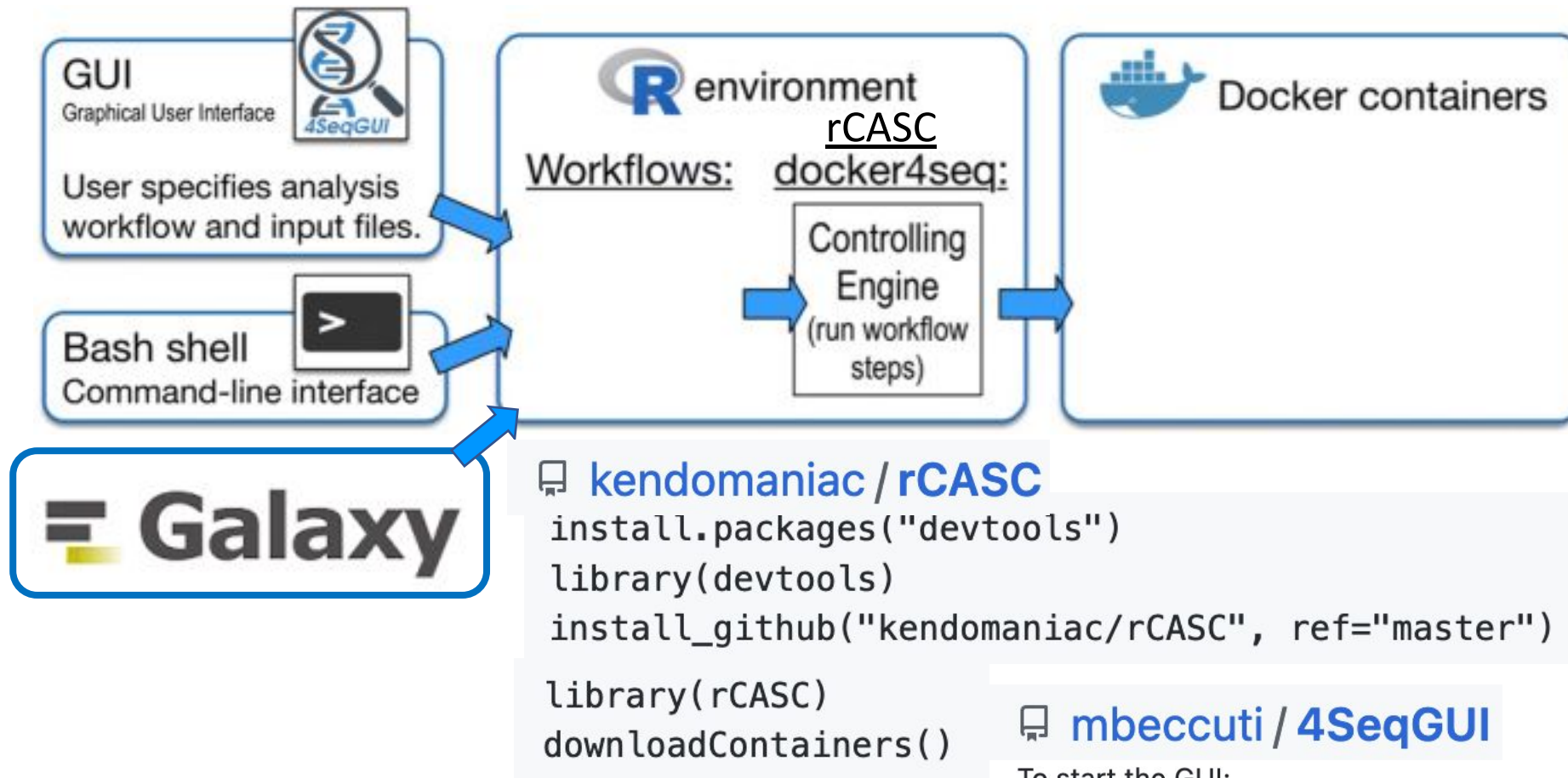
- Italy: students (15) use their computer as terminals and run their analyses on miniPC (32 GB RAM 1Tb SSD, 6 cores, linux)
- Germany: computer room with 30 workstations (32 Gb RAM, 512Gb SSD, 12 cores, linux)
- Singapore: students (15-20) use their computer as terminals and run their analyses on a local server (512 Gb RAM 128 cores, linux)

# Infrastructure from 2022

- Italy: students will use their computer as terminals and run their analyses on a cloud computing infrastructure (linux).
- Germany: students will use their computer as terminals and run their analyses on a cloud computing infrastructure (linux).
- Singapore: students will use their computer as terminals and run their analyses on a local server (linux).

# Course characteristics

- Devoted to life scientists without any previous knowledge in scripting/programming and data analysis.
- Five days theory & hands-on covering RNAseq and scRNAseq.
  - Each day starts with “R pils” and ends with “R exercises”
  - Course starts using only a GUI and ends using only R scripts
- Topics:
  - Lecture on RNAseq and scRNAseq (experimental design and technical critical points) (T)
  - Lecture on reproducibility in bioinformatics (T)
  - Data QC (RNAseq/scRNAseq) (T&P)
  - Data reduction (RNAseq/scRNAseq) (T&P)
  - Differential expression (RNAseq) (T&P)
  - Clustering (scRNAseq) (T&P)
  - Cluster-specific markers detection (scRNAseq) (T&P)
  - Biological features characterization (RNAseq/scRNAseq) (T&P)
  - Revision exercises



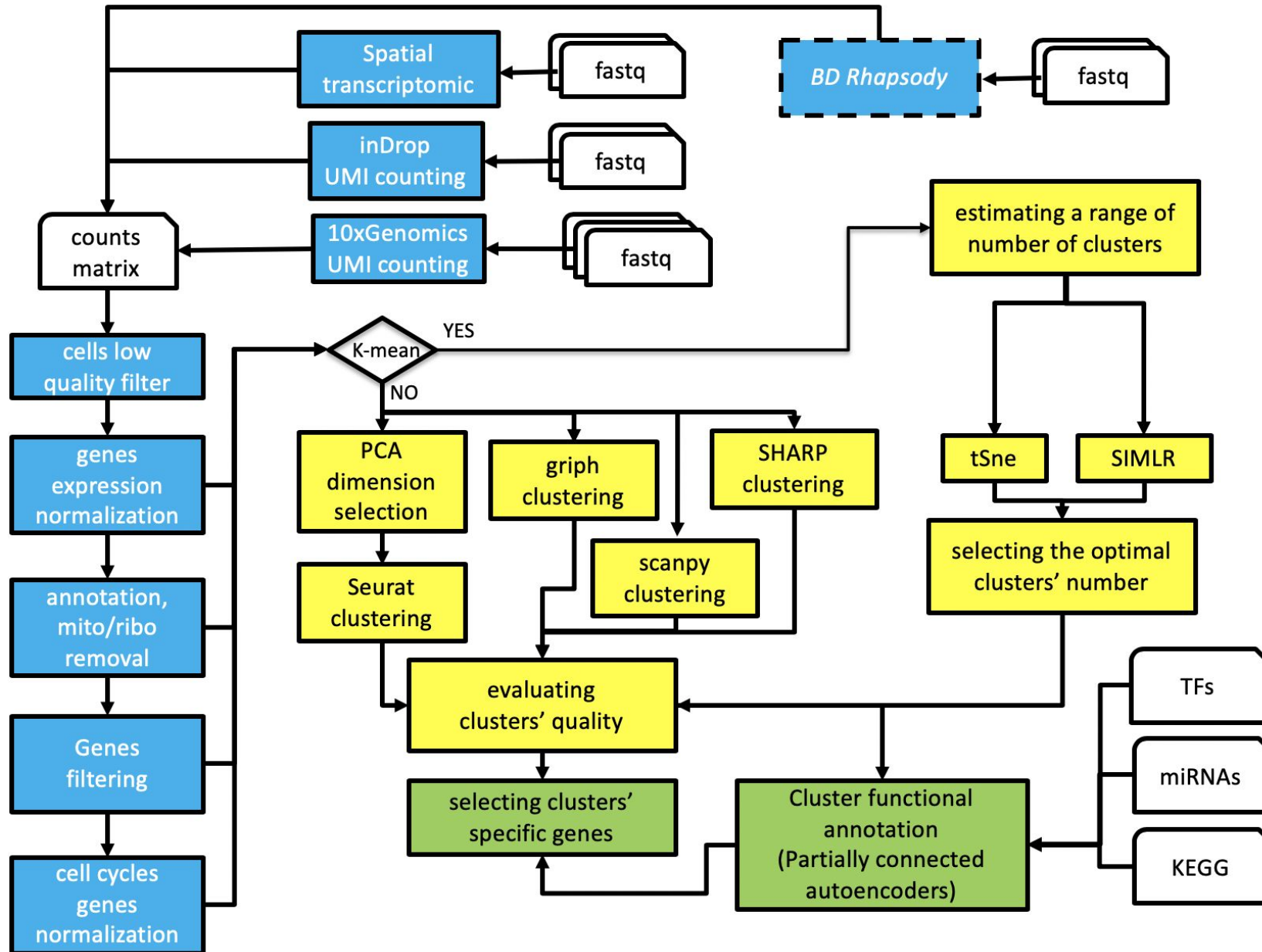
To start the GUI:

1. open a terminal;
2. go to 4SeqGUI folder;
3. execute the GUI with the bash script "4SeqGUI.sh"

Tangaro et al. BMC Bioinformatics. 2021 Nov 8;22(Suppl 15):544  
 Alessandri et al. Int. J. Mol. Sci. 2021, 22(23), 12755  
 Alessandri et al. NPJ Syst Biol Appl. 2021 Jan 5;7(1):1  
 Alessandri et al. Gigascience. 2019 Sep 1;8(9):giz105  
 Kulkarni et al. BMC Bioinformatics. 2018 Oct 15;19(Suppl 10):349  
 Beccuti et al. Bioinformatics. 2018 Mar 1;34(5):871-872  
 Sanges et al. Bioinformatics. 2007 Dec 15;23(24):3406-8



Alessandri et al. GigaScience 2019





command.R x

Source on Save

Run

Source

```

1 library(rCASC)
2 scratch = "/Users/raffaelecalogero/IDrive-Sync/bertotti/paneth_only/scratch"
3 genelist = "/Users/raffaelecalogero/IDrive-Sync/bertotti/paneth_only/geneList.csv"
4
5 wrapperMixModelsUmap(group="docker", scratch.folder=scratch, file=paste(getwd(), "/log2cpm.csv",
6                               separator=",", seed=111, epochs=1000, k=2, finalName="crc322ctx", geneList=genelist)
7

```

7:1

(Top Level)

R Script

Console

Terminal x

Jobs x

R 4.1.0 · ~/Documents/data/rCASC/

R version 4.1.0 (2021-05-18) -- "Camp Pontanezen"  
 Copyright (C) 2021 The R Foundation for Statistical Computing  
 Platform: x86\_64-apple-darwin17.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.  
 You are welcome to redistribute it under certain conditions.  
 Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.  
 Type 'contributors()' for more information and  
 'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or  
 'help.start()' for an HTML browser interface to help.  
 Type 'q()' to quit R.

&gt;

Environment

History

Connec

```

To Source
separator= , , seed=111, epochs=100...
getwd()
library(rCASC)
scratch = "/Users/raffaelecaloger...
genelist = "/Users/raffaelecaloge...
wrapperMixModelsUmap(group="docke...
separator=",", seed=111, epochs=100...
setwd("~/IDrive-Sync/bertotti/pan...
getwd()

```

Files

Plots

Packages

Help

New Folder Delete Rename

e &gt; Documents &gt; data &gt; rCASC

	Name
<input type="checkbox"/>	.Rhistory
<input type="checkbox"/>	CASC.Rproj
<input type="checkbox"/>	DESCRIPTION
<input type="checkbox"/>	docs
<input type="checkbox"/>	fig1.png
<input type="checkbox"/>	inst
<input type="checkbox"/>	LICENSE
<input type="checkbox"/>	man
<input type="checkbox"/>	NAMESPACE
<input type="checkbox"/>	R
<input type="checkbox"/>	rCASC.Rproj
<input type="checkbox"/>	README.md
<input type="checkbox"/>	vignettes

s table

at

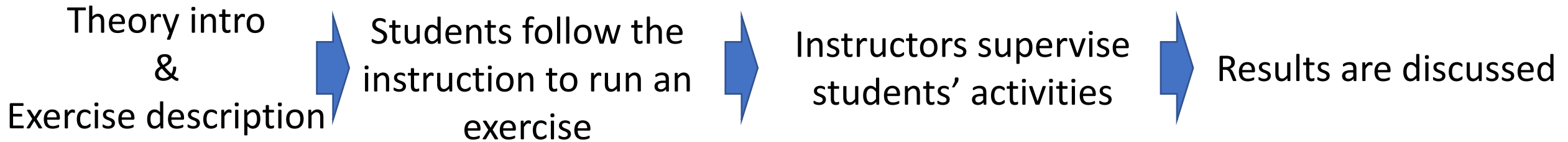
R

e

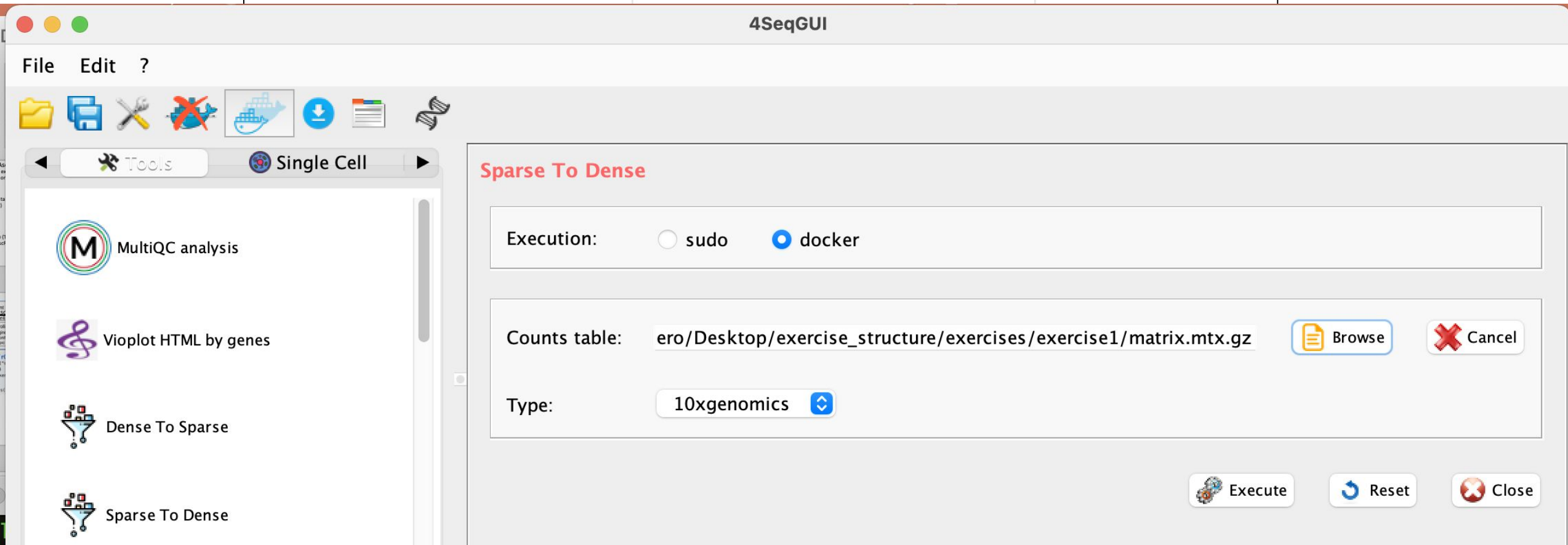
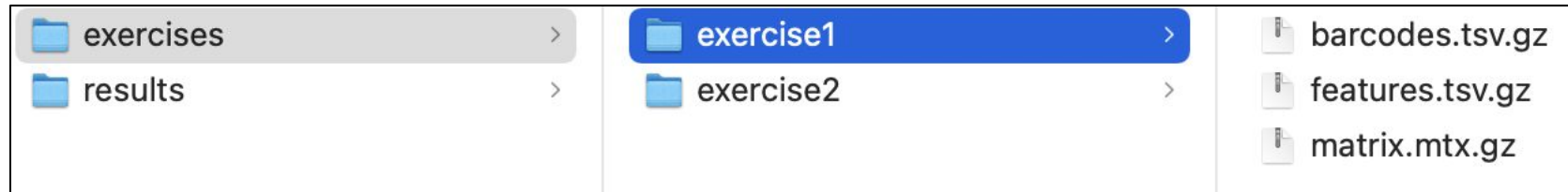
met

# Course exercises as a real experiment

- The course exercises are build following the working path of a real experiment.
- Each section of the course is organized in the following way:



# Course as a cooking show





[raffaele.calogero@unito.it](mailto:raffaele.calogero@unito.it)