

2020 生物醫學大數據淘金工作坊 Part 3

Web portal for Single cell RNA-seq



Presenter:

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2020.04

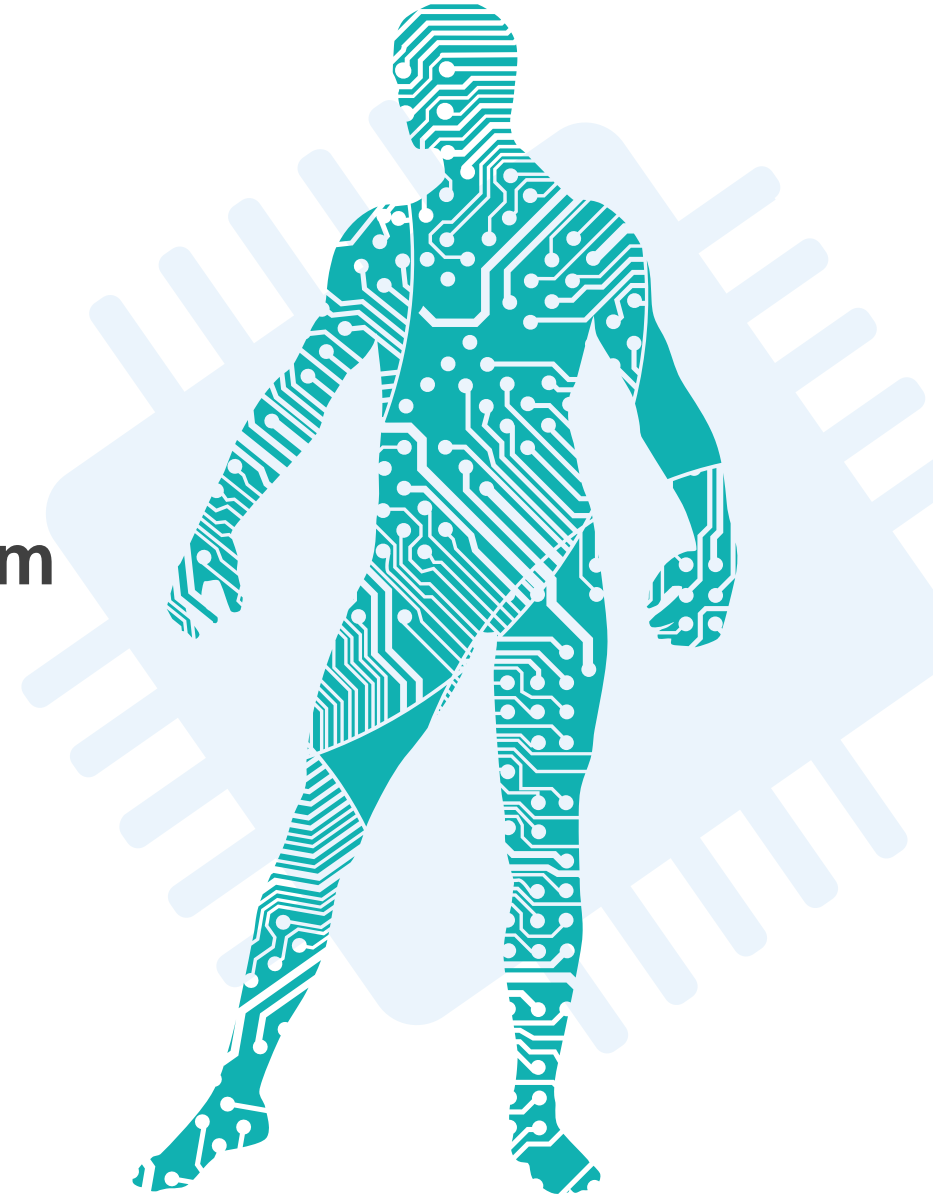
Outline

01 Introduction

single-cell RNA sequencing

02 Galaxy-based pre-processing system

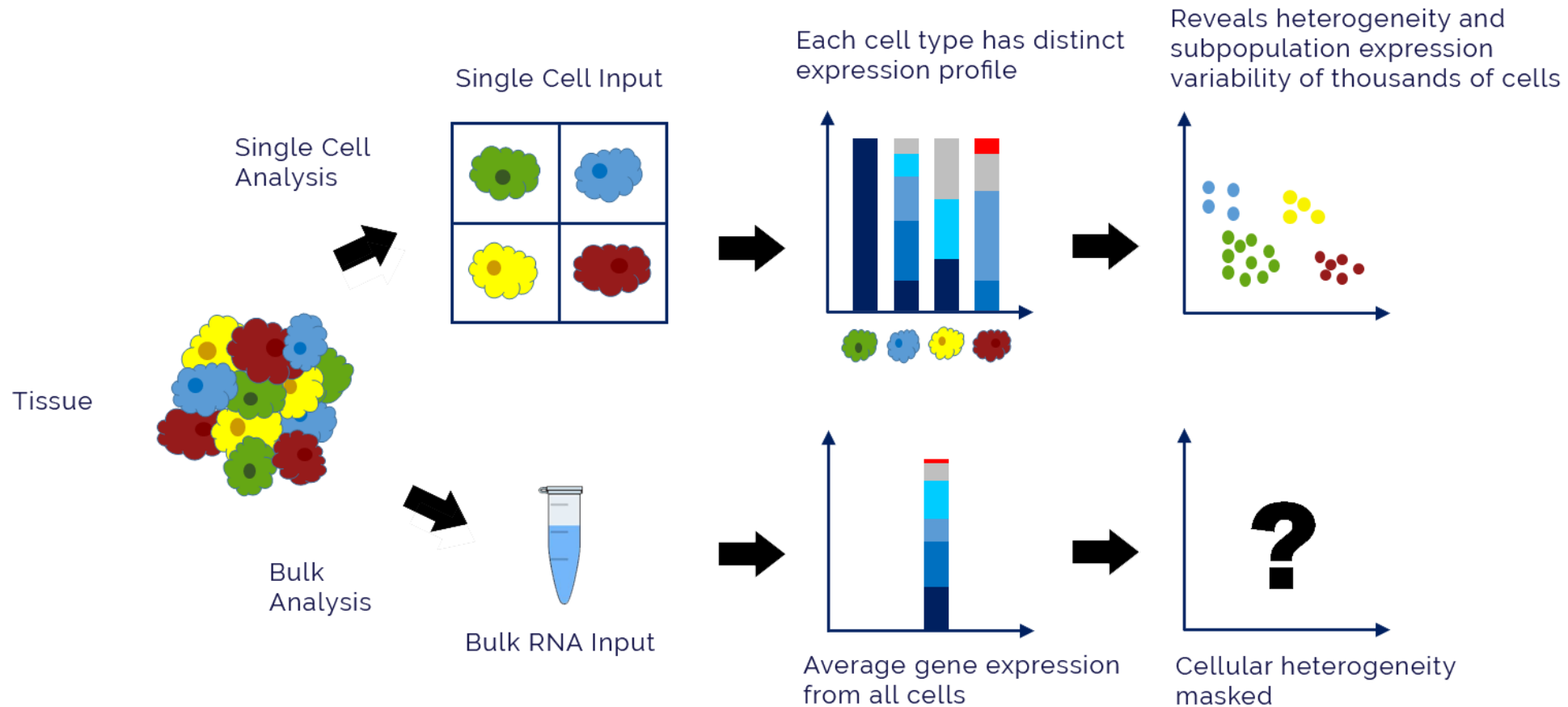
03 Seashell: web portal for single cell RNA-seq analysis and visualization



Introduction

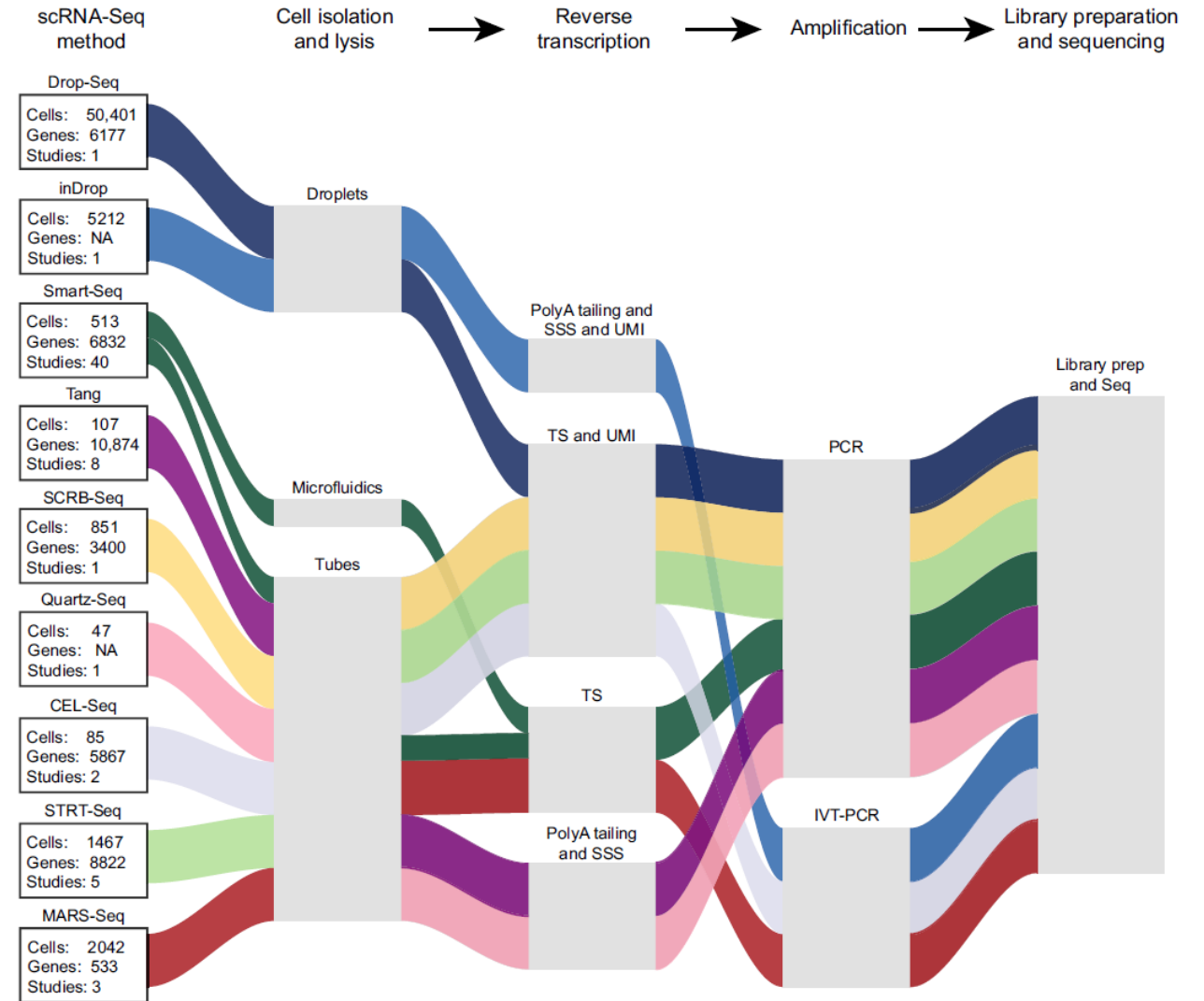
➤ Single-cell RNA sequencing (scRNA-seq)

scRNA-seq technologies have combined effective single-cell isolation strategies with highly sensitive molecule detection approaches, showing promise in unravelling the heterogeneity of complex tissues or organs.



Single-cell RNA sequencing

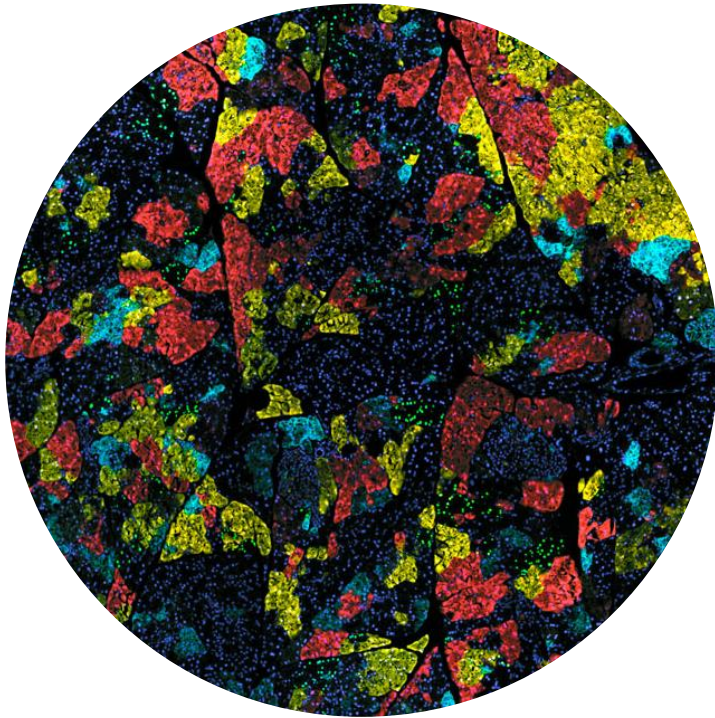
➤ A variety of scRNA-seq protocols



Single-cell RNA sequencing

➤ A growing number of application

Heterogeneity of cancer cells



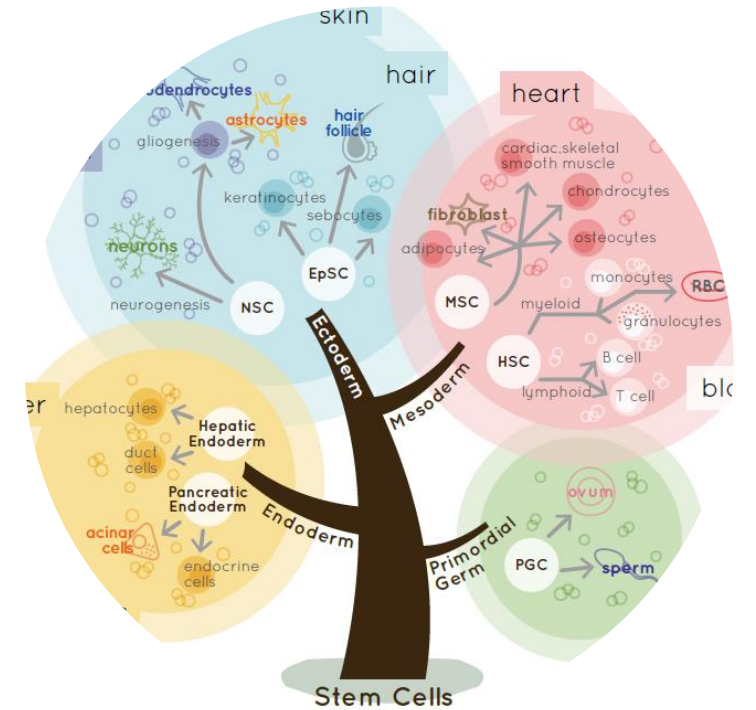
<https://www.rna-seqblog.com/new-single-cell-rna-sequencing-methods-could-lead-to-better-regenerative-therapies/>

Diversity of T cell receptor



Vallejo, Abbe N. "Immune remodeling: lessons from repertoire alterations during chronological aging and in immune-mediated disease." *Trends in molecular medicine* 13.3 (2007): 94-102.

Differentiation of stem cells

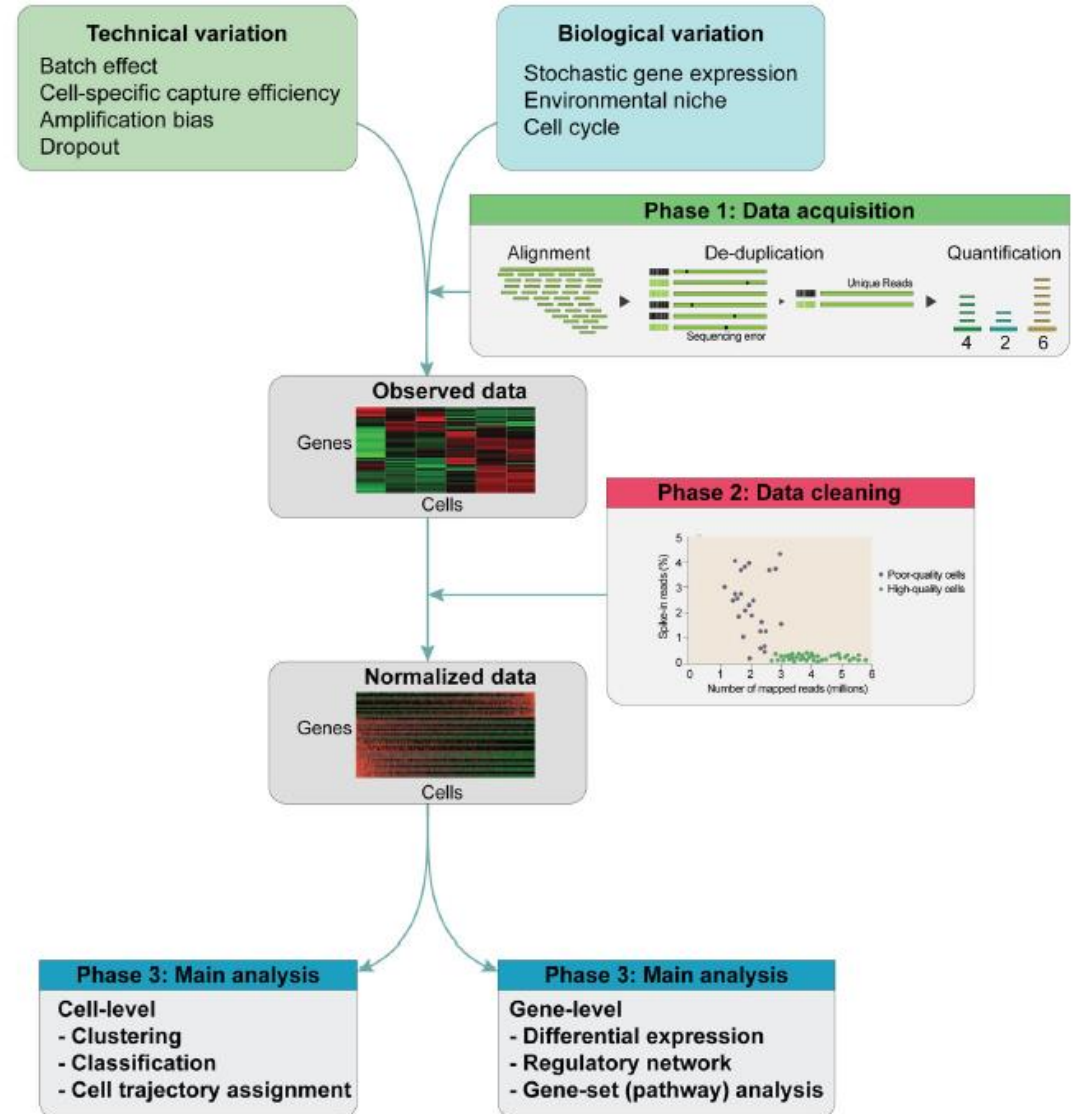


<https://www.bio-connect.nl/stem-cell-and-the-regenerative-medicine-ready-for-the-patients/cnt/page/5050>

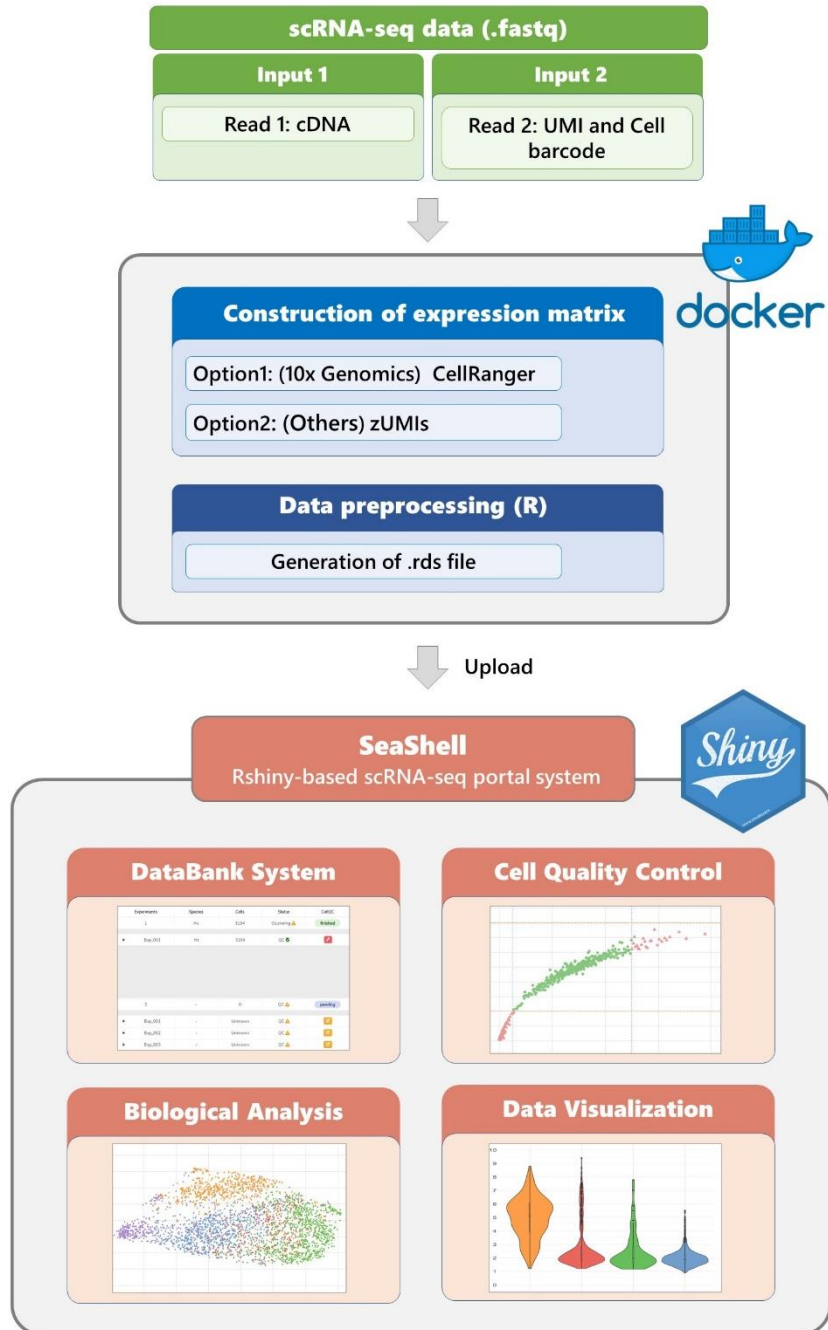
Single-cell RNA sequencing

➤ Increasing difficulties of processing sequencing data

- Serious batch effect
- Demanding computing power
- etc



Workflow of analysis



The portal system can be divided into two parts:



Galaxy-based docker image for data preprocessing




Users can run this docker image by a Galaxy-based GUI, and then easily obtain expression matrices for further analysis.



RShiny-based web portal system

The web-portal system was well-developed by R language, JavaScript D3 library, and other visualization tools, allowing researchers to automatically perform a user-friendly and up-to-date scRNA-seq analysis pipeline on scRNA-seq experiments. The analysis pipeline contains: cell quality control, normalization, cluster analysis, differentially expressed genes analysis, marker identification, gene ontology analysis, and other popular tools.

* Now only available for 10x drop-seq raw data



Galaxy-based pre-processing system



1. Start the galaxy web server

01

Download docker image and Create a directory first for data acquisition

```
$ docker pull lsbnb/galaxy_sc  
$ mkdir YOUR_DIR
```

02

Run the docker

```
# port can be changed  
# "YOUR_DIR" will be the directory shared with docker container  
$ docker run -d -t -i -p 8081:80 -v \  
(`pwd`)/YOUR_DIR/./root/galaxy/database/ftp/rnaanalysis@galaxy.org/ \  
lsbnb/galaxy_sc /bin/bash
```

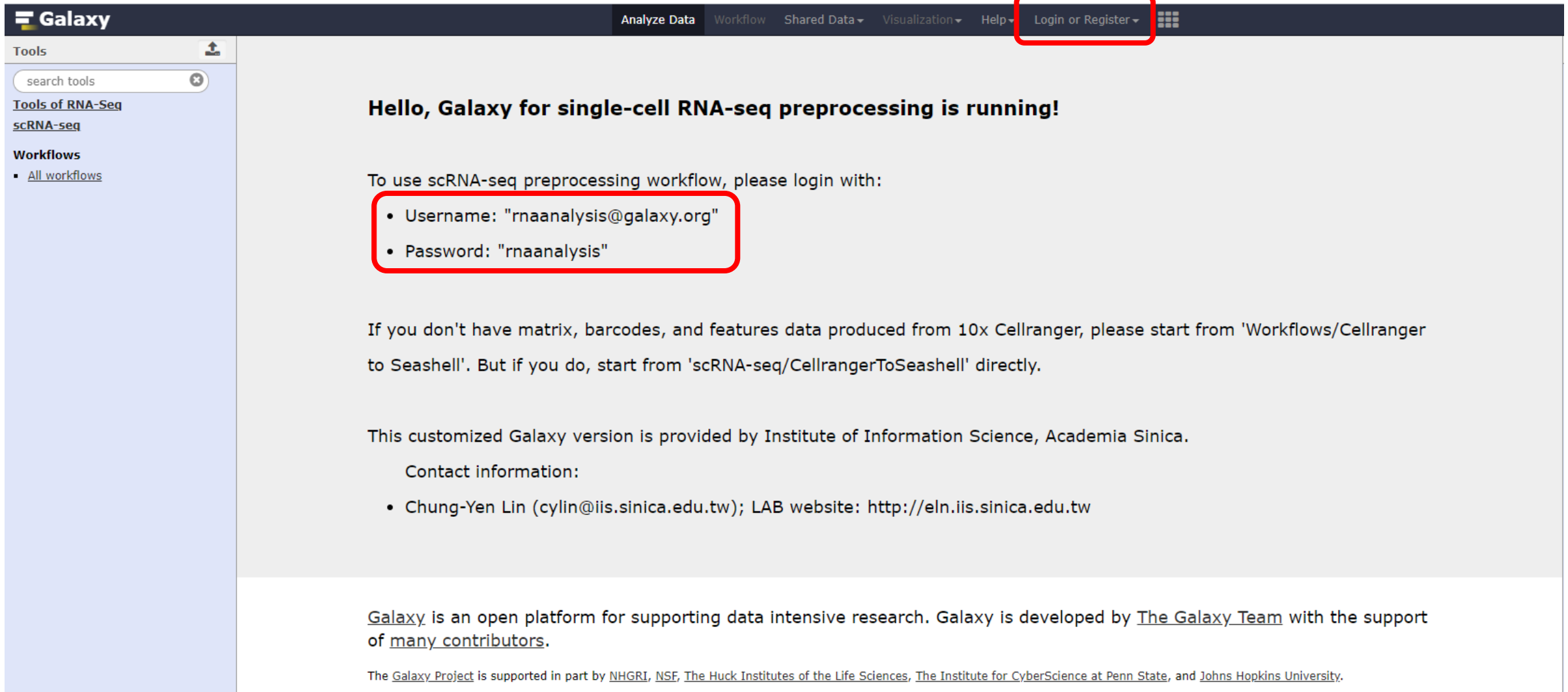
03

Access to the galaxy web server

http://[Your IP]:8081 will be the access to galaxy web server

1. Start the galaxy web server

Login



The screenshot shows the Galaxy web server interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'Login or Register'. The 'Login or Register' link is highlighted with a red box. The main content area displays a message: 'Hello, Galaxy for single-cell RNA-seq preprocessing is running!'. Below this, it asks the user to login with the following credentials: Username: 'rnaanalysis@galaxy.org' and Password: 'rnaanalysis'. These credentials are also highlighted with a red box. The interface includes a left sidebar with 'Tools' and 'Workflows' sections, and a footer with information about the Galaxy project and its supporters.

Galaxy

Analyze Data Workflow Shared Data Visualization Help Login or Register

Tools

search tools

Tools of RNA-Seq
scRNA-seq

Workflows
All workflows

Hello, Galaxy for single-cell RNA-seq preprocessing is running!

To use scRNA-seq preprocessing workflow, please login with:

- Username: "rnaanalysis@galaxy.org"
- Password: "rnaanalysis"

If you don't have matrix, barcodes, and features data produced from 10x Cellranger, please start from 'Workflows/Cellranger to Seashell'. But if you do, start from 'scRNA-seq/CellrangerToSeashell' directly.

This customized Galaxy version is provided by Institute of Information Science, Academia Sinica.

Contact information:

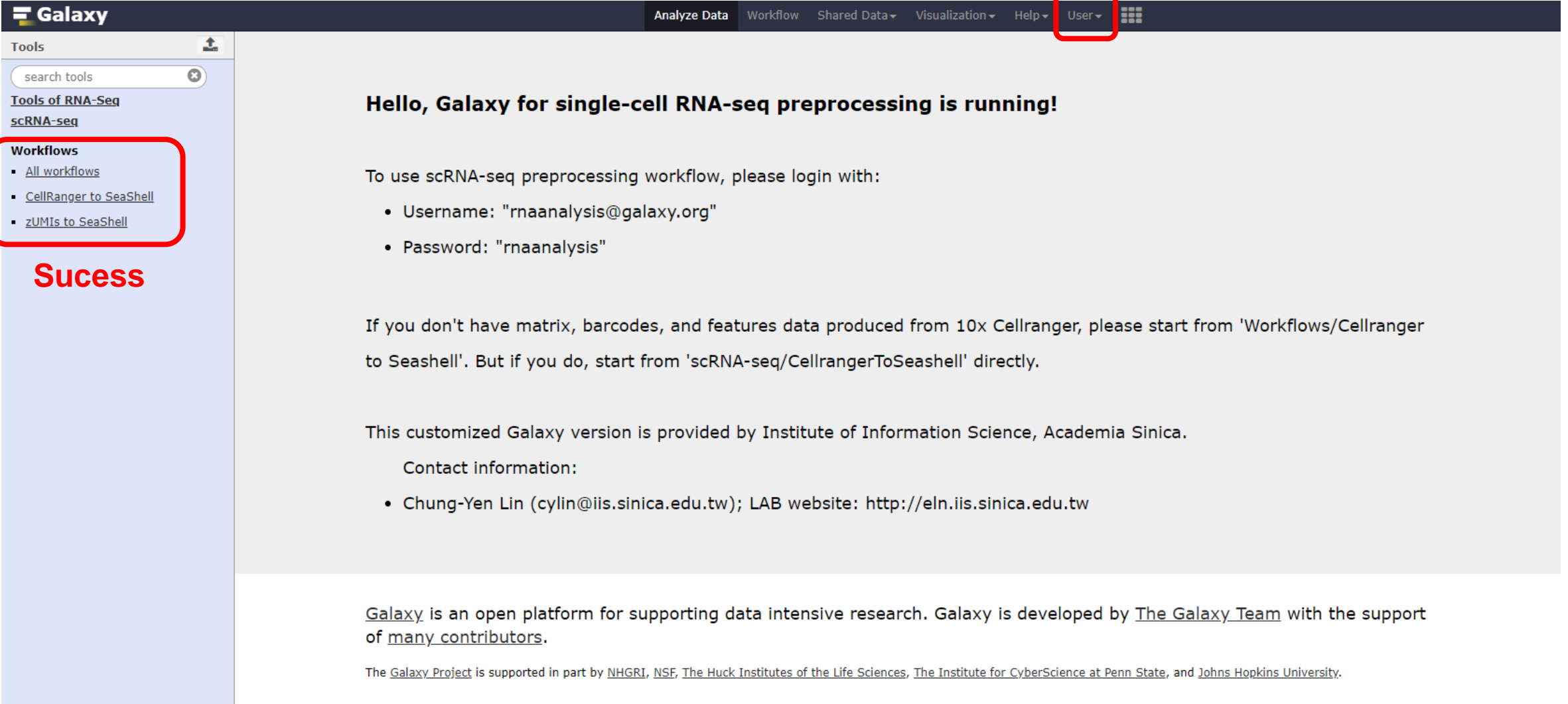
- Chung-Yen Lin (cylin@iis.sinica.edu.tw); LAB website: <http://eln.iis.sinica.edu.tw>

Galaxy is an open platform for supporting data intensive research. Galaxy is developed by The Galaxy Team with the support of many contributors.

The Galaxy Project is supported in part by NHGRI, NSF, The Huck Institutes of the Life Sciences, The Institute for CyberScience at Penn State, and Johns Hopkins University.

1. Start the galaxy web server

- If successfully login



The screenshot shows the Galaxy web server interface. The top navigation bar includes 'Galaxy', 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User' (highlighted with a red box). The left sidebar contains 'Tools' (with a search bar), 'Tools of RNA-Seq', 'scRNA-seq', and 'Workflows' (highlighted with a red box). The 'Workflows' section lists 'All workflows', 'CellRanger to SeaShell', and 'zUMIs to SeaShell'. Below the sidebar, the word 'Success' is displayed in red. The main content area features a large heading: 'Hello, Galaxy for single-cell RNA-seq preprocessing is running!'. Below this, it instructs users to login with the following details:

- Username: "rnaanalysis@galaxy.org"
- Password: "rnaanalysis"

Additional instructions state: 'If you don't have matrix, barcodes, and features data produced from 10x Cellranger, please start from 'Workflows/Cellranger to Seashell'. But if you do, start from 'scRNA-seq/CellrangerToSeashell' directly.'

At the bottom, it notes: 'This customized Galaxy version is provided by Institute of Information Science, Academia Sinica. Contact information: Chung-Yen Lin (cylin@iis.sinica.edu.tw); LAB website: http://eln.iis.sinica.edu.tw'

Footer text: 'Galaxy is an open platform for supporting data intensive research. Galaxy is developed by [The Galaxy Team](#) with the support of [many contributors](#). The [Galaxy Project](#) is supported in part by [NHGRI](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).'

2. Download your reference genome

The screenshot displays the Galaxy web interface. At the top, the 'Galaxy' logo is on the left, and navigation tabs for 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User' are on the right. The left sidebar contains a 'Tools' section with a search bar and a list of tools under 'Tools of RNA-Seq' and 'scRNA-seq'. The 'DownloadRef' tool is highlighted with a red box, and a red arrow points to it with the text 'Click here'. The main panel shows the 'DownloadRef' tool configuration. The title is 'DownloadRef : Download reference files from server (Galaxy Version 1.0.1)'. Below the title is a 'Reference' dropdown menu with 'CellRanger Human(hg38)' selected, highlighted by a red box. A red arrow points to this dropdown with the text 'Choose reference genome'. Below the dropdown is a blue 'Execute' button. The description of the tool is 'Download reference files from server.'

Galaxy

Analyze Data Workflow Shared Data Visualization Help User

Tools

search tools

Tools of RNA-Seq

scRNA-seq

Upload File from your computer

DownloadRef : Download reference files from server

CellRanger : CellRanger

zUMIs : zUMIs

CellrangerToSeashell : Use cellranger output files to Seashell file

zUMIsToSeashell : Use zUMIs output files to Seashell file

Workflows

- All workflows
- CellRanger to SeaShell
- zUMIs to SeaShell

DownloadRef : Download reference files from server (Galaxy Version 1.0.1) Options

Reference

CellRanger Human(hg38)

Execute

Choose reference genome

Download reference files from server.

2. Download your reference genome

The screenshot displays the Galaxy web interface. At the top, a dark navigation bar contains the text 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User', along with a grid icon and the text 'Using 698.8 MB'. Below this, the 'DownloadRef : Download reference files from server (Galaxy Version 1.0.1)' tool is visible. It features a dropdown menu labeled 'Referece' with 'CellRanger Human(hg38)' selected, and an 'Execute' button. Below the tool, the text 'Download reference files from server.' is present. On the right side, the 'History' panel shows a search bar and a list of jobs. The job '34: Download CellRanger Human Reference' is highlighted with a red box, indicating it is the current job being executed.

Downloading

3. Prepare your sequencing data

01

Create “cellranger_input” and “YOUR_SAMPLE” folder in the directory shared with docker

```
# ./YOUR_DIR/cellranger_input/YOUR_SAMPLE/
```

02

Put your fastq files in “cellranger_input”

```
# ./YOUR_DIR/cellranger_input/YOUR_SAMPLE /[Sample Name]_S1_L00[Lane Number]_R1_001.fastq.gz  
# ./YOUR_DIR/cellranger_input/YOUR_SAMPLE /[Sample Name]_S1_L00[Lane Number]_R2_001.fastq.gz  
# ./YOUR_DIR/cellranger_input/YOUR_SAMPLE /[Sample Name]_S1_L00[Lane Number]_I1_001.fastq.gz  
# If you don't know how to name your fastq files, please refer to 10x Genomics:  
# https://support.10xgenomics.com/single-cell-gene-expression/software/pipelines/latest/using/fastq-input
```

03

Enter name of “YOUR_SAMPLE” and other parameters to galaxy workflow

3. Prepare your sequencing data

Click here [CellRanger to SeaShell](#)

“YOUR_SAMPLE”

Selecce correct reference genome

Custom name


Enter a number more than the number of cells you expect


Custom name

Run workflow

4. Run the galaxy pipeline

Run

Tools 

search tools 


Tools of RNA-Seq

scRNA-seq

Workflows

- All workflows
- CellRanger to SeaShell
- zUMIs to SeaShell

Workflow: CellRanger to SeaShell

 Run workflow

History Options

Send results to a new history

Yes No

1: CellRanger (Galaxy Version 1.0.1)

Input folder name (Please make this folder into `./YOUR_DIR/cellranger_input/` and put your files into there)

Reference

hg38

Expect cells

3000

Output Name

2: CellrangerToSeashell (Galaxy Version 1.0.1)

matrix.mtx.gz

Output dataset 'matrix.mtx.gz' from step 1

barcodes.tsv.gz

Output dataset 'barcodes.tsv.gz' from step 1

features.tsv.gz

Output dataset 'features.tsv.gz' from step 1

Expect cell numbers

20000

Output Name

4. Run the galaxy pipeline

Galaxy

Analyze Data Workflow Shared Data Visualization Help User Using 698.8 MB

Tools

search tools

Tools of RNA-Seq

scRNA-seq

Workflows

- All workflows
- CellRanger to SeaShell
- zUMIs to SeaShell

Successfully invoked workflow **CellRanger to SeaShell**.
You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

search datasets

My history
5 shown, 47 deleted
623.65 MB

- 52: test3 Cellranger ToSeashell
- 51: test2 cellranger features
- 50: test2 cellranger barcodes
- 49: test2 cellranger matrix
- 48: Downloading Cellranger Human Reference

Running
It may takes for a long time

下載 (5)


下載 (4)

全部顯示

下午 03:52
2020/4/23

5. Download the .rds file

Download



History

search datasets

My history
5 shown, 47 [deleted](#)
639.14 MB

52: test3 CellrangerTo Seashell
data
格式: data, 数据库: ?

51: test2 cellranger features

50: test2 cellranger barcodes

49: test2 cellranger matrix

48: Download CellRanger Human Reference

The screenshot shows a 'History' window with a search bar and a list of datasets. The dataset '52: test3 CellrangerTo Seashell' is highlighted in green. A red box highlights the 'Download' icon (a floppy disk) in the action bar for this dataset. Other icons in the action bar include a refresh icon, a question mark, and a share icon.

From pre-processed 10x data

01

Put (1) matrix.mtx.gz (2) barcodes.tsv.gz (3) features.tsv.gz in "YOUR_DIR"

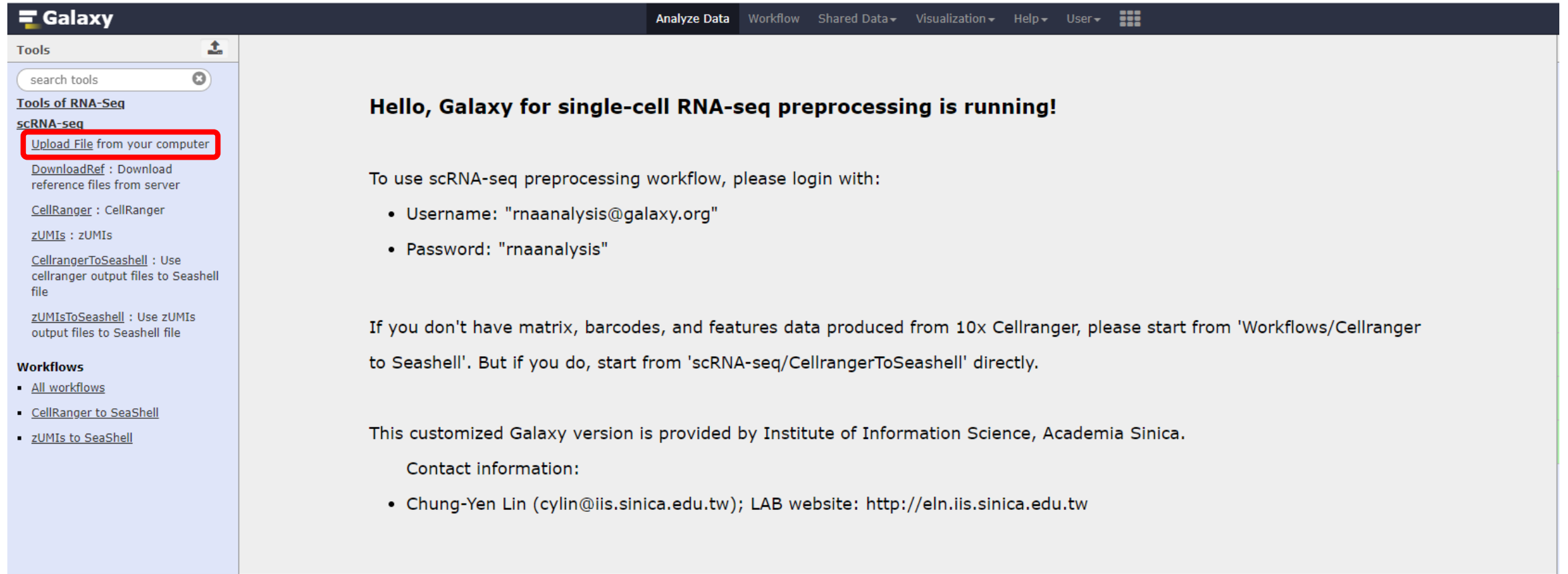
02

Upload these files to galaxy server by ftp

03

Run galaxy workflow "scRNA-seq/CellrangerToSeashell"

Upload files to galaxy server by ftp



The screenshot shows the Galaxy web interface. The top navigation bar includes 'Galaxy' and menu items: 'Analyze Data', 'Workflow', 'Shared Data', 'Visualization', 'Help', and 'User'. The left sidebar is titled 'Tools' and contains a search bar and a list of tools under 'Tools of RNA-Seq'. The 'scRNA-seq' section is expanded, and the 'Upload File from your computer' option is highlighted with a red box. The main content area displays a message: 'Hello, Galaxy for single-cell RNA-seq preprocessing is running!' followed by login instructions for 'rnaanalysis@galaxy.org' with username 'rnaanalysis@galaxy.org' and password 'rnaanalysis'. It also provides instructions on where to start based on whether the user has matrix, barcodes, and features data from 10x Cellranger. At the bottom, it mentions the customized Galaxy version is provided by the Institute of Information Science, Academia Sinica, and provides contact information for Chung-Yen Lin.

Galaxy

Analyze Data Workflow Shared Data Visualization Help User

Tools

search tools

Tools of RNA-Seq

scRNA-seq

Upload File from your computer

[DownloadRef](#) : Download reference files from server

[CellRanger](#) : CellRanger

[zUMIs](#) : zUMIs

[CellrangerToSeashell](#) : Use cellranger output files to Seashell file

[zUMIsToSeashell](#) : Use zUMIs output files to Seashell file

Workflows

- All workflows
- CellRanger to SeaShell
- zUMIs to SeaShell

Hello, Galaxy for single-cell RNA-seq preprocessing is running!

To use scRNA-seq preprocessing workflow, please login with:

- Username: "rnaanalysis@galaxy.org"
- Password: "rnaanalysis"

If you don't have matrix, barcodes, and features data produced from 10x Cellranger, please start from 'Workflows/Cellranger to Seashell'. But if you do, start from 'scRNA-seq/CellrangerToSeashell' directly.

This customized Galaxy version is provided by Institute of Information Science, Academia Sinica.

Contact information:

- Chung-Yen Lin (cylin@iis.sinica.edu.tw); LAB website: <http://eln.iis.sinica.edu.tw>

Upload files to galaxy server by ftp

The screenshot shows the Galaxy web interface with a modal dialog titled "Download from web or upload from disk". The dialog has three tabs: "Regular", "Composite", and "Collection". A sub-dialog titled "FTP files" is open, showing a list of files available for upload. The sub-dialog includes a search bar, a "Type (select)" dropdown, and a list of files with checkboxes, names, and sizes. The "Choose FTP file" button is highlighted with a red box.

FTP files

and password).

Available files: 46 files 78.5 GB

<input type="checkbox"/>	Name	Size
<input type="checkbox"/>	cellranger_input/small_test/hgmm_100_S1_L001_R1_001.fastq.gz	19.1
<input type="checkbox"/>	cellranger_input/small_test/hgmm_100_S1_L001_R2_001.fastq.gz	69.4
<input type="checkbox"/>	filtered_feature_bc_matrix/barcodes.tsv.gz	529 B
<input type="checkbox"/>	filtered_feature_bc_matrix/features.tsv.gz	297.0
<input type="checkbox"/>	filtered_feature_bc_matrix/matrix.mtx.gz	416.0

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

Upload files to galaxy server by ftp

The screenshot shows the Galaxy web interface with a modal dialog box for uploading files. The dialog box is titled "Download from web or upload from disk" and has tabs for "Regular", "Composite", and "Collection". It displays a table of files being uploaded:

Name	Size	Type	Genome	Settings	Status
filtered_feature_bc_matrix/barcodes.tsv.gz	529 b	Auto-det...	----- Additional S...	⚙️	100% ✓
filtered_feature_bc_matrix/features.tsv.gz	297.6 KB	Auto-det...	----- Additional S...	⚙️	100% ✓
filtered_feature_bc_matrix/matrix.mtx.gz	416.6 KB	Auto-det...	----- Additional S...	⚙️	100% ✓

Below the table, there are dropdown menus for "Type (set all):" (set to "Auto-detect") and "Genome (set all):" (set to "----- Additional Species..."). At the bottom of the dialog, there are buttons for "Choose local file", "Choose FTP file", "Paste/Fetch data", "Pause", "Reset", "Start", and "Close". The "Start" button is highlighted with a red box and the word "Click" next to it.

Run galaxy workflow



Tools



search tools

Tools of RNA-Seq

scrNA-seq

[Upload File](#) from your computer

[DownloadRef](#) : Download reference files from server

[CellRanger](#) : CellRanger

[zUMIs](#) : zUMIs

[CellrangerToSeashell](#) : Use cellranger output files to Seashell file

[zUMIsToSeashell](#) : Use zUMIs output files to Seashell file

Workflows

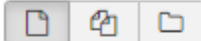
- [All workflows](#)
- [CellRanger to SeaShell](#)
- [zUMIs to SeaShell](#)

CellrangerToSeashell : Use cellranger output files to Seashell file (Galaxy Version 1.0.1)

Options

matrix.mtx.gz

Choose correct file



55: matrix.mtx

barcodes.tsv.gz



54: features.tsv

features.tsv.gz



53: barcodes.tsv

Expect cell numbers

20000

Output Name

test

Execute

Use cellranger output files to Seashell file.



Seashell

Authentication

Please authenticate

Username:

Password:

Login

Homepage

SeaShell

Home

Databank

Visualization

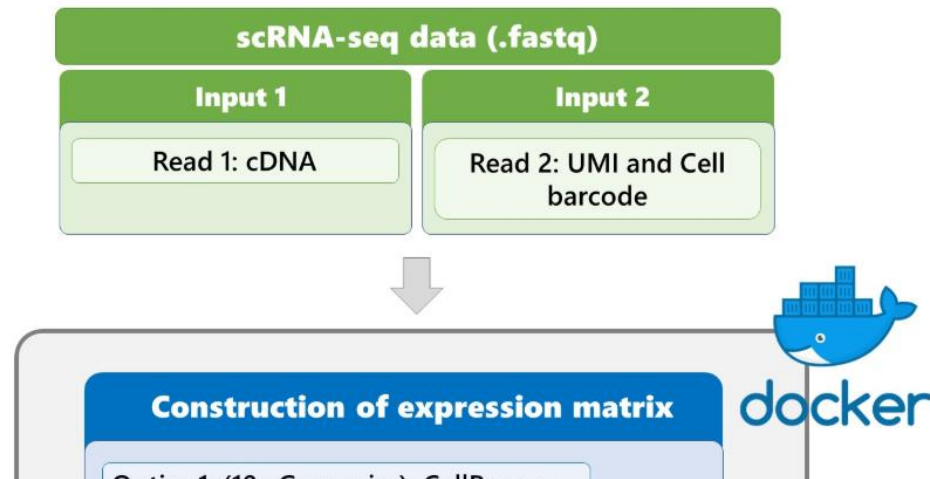
Help

Welcome to SeaShell !

Our web service provides an user-friendly interface to process and manage your single-cell data.

START

Click " START"



Workflow

01

Upload rds file to SeaShell

02

Cell QC, Normalization, and Clustering

03

Visualization and Gene analysis

Databank

➤ Create new project

SeaShell [Home](#) [Databank](#) [Visualization](#) [Help](#)









Databank

The management system of single-cell experiments can be used to pre-process raw sequencing files and link to other data analysis module.

 New Project

Create new project

Edit mode

Single-cell experiments		Projects	Experiments	Species	Cells	Status	CellQC	Record	Brief	Normalization	Clustering
○	▼	PBMC	1	-	0	QC ⚠	pending	-			
			▶ 5K	-	Unknown	QC ⚠		-			
○	▶	small_test	2	-	0	QC ⚠	pending	-			

Databank

➤ Create new project

Upload **All single-cell experiments** (rds files) to one project. (For example: Control and Drug experiments)



Name

Please enter your project name

APPLY



test

Please upload **ALL** your single-cell experiment

It is not allowed to add or remove a single experimnt individually later.

OK

CANCEL

Databank

➤ Create new project

Upload **All single-cell experiments** (rds files) to one project. (For example: Control and Drug experiments)

Databank

The management system of single-cell experiments can be used to pre-process raw sequencing files and link to other data analysis module.

Add or Remove a row

Project test	Experiment 1 Control	Pre-processed data Browse... test1.rds Upload complete
	Experiment 2 Drug	Pre-processed data Browse... test1.rds Upload complete



Upload all files

 New Project

Databank

➤ Create new project

Upload **All single-cell experiments** (rds files) to one project. (For example: Control and Drug experiments)

Databank

The management system of single-cell experiments can be used to pre-process raw sequencing files and link to other data analysis module.

+ New Project

Edit mode

Single-cell experiments		Projects	Experiments	Species	Cells	Status	CellQC	Record	Brief	Normalization	Clustering
<input type="radio"/>	▶	PBMC	1	-	0	QC ⚠	pending	-	<input checked="" type="checkbox"/>	<input type="lock"/>	<input type="lock"/>
<input type="radio"/>	▶	small_test	2	-	0	QC ⚠	pending	-	<input checked="" type="checkbox"/>	<input type="lock"/>	<input type="lock"/>
<input type="radio"/>	▼	test	2	-	0	QC ⚠	pending	-	<input checked="" type="checkbox"/>	<input type="lock"/>	<input type="lock"/>
			▶	Control	-	Unknown	QC ⚠		<input checked="" type="checkbox"/>		
			▶	Drug	-	Unknown	QC ⚠		<input checked="" type="checkbox"/>		

Hint

Click to perform cell QC respectively

Cell QC

Real time
qualified cell
numbers

Quality Control

Cell quality control will be performed on your single-cell experiment

test

Projects



Control

Experiment



20%

Progress



41

Qualified cell numbers

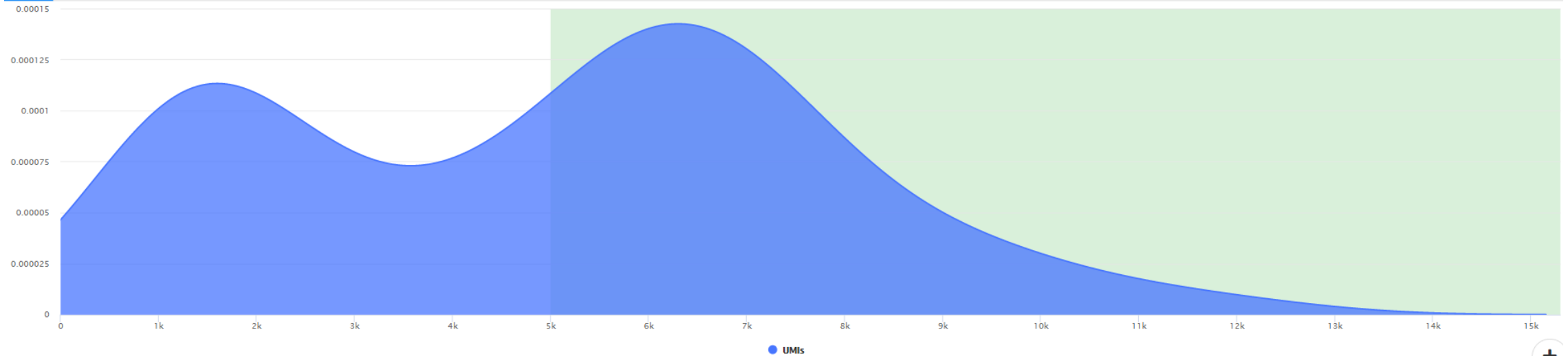


Step1. Select cell population based on total UMI counts

Set threshold



UMIs Genes Scatter2D Outliers



Cell QC

Quality Control

Cell quality control will be performed on your single-cell experiment

test

Projects



Control

Experiment



50%

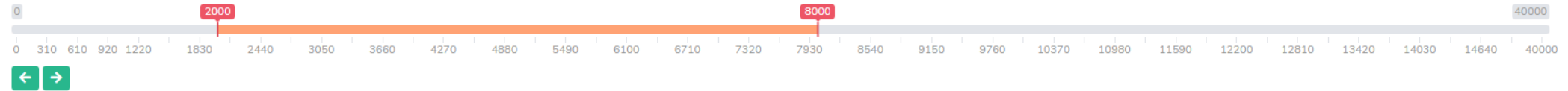
Progress



33

Qualified cell numbers

Step2. Select cell population based on total GENE numbers



UMIs Genes Scatter2D Outliers



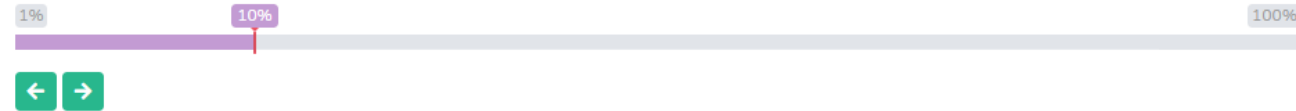
Cell QC

➤ Check by 2D scatter plot

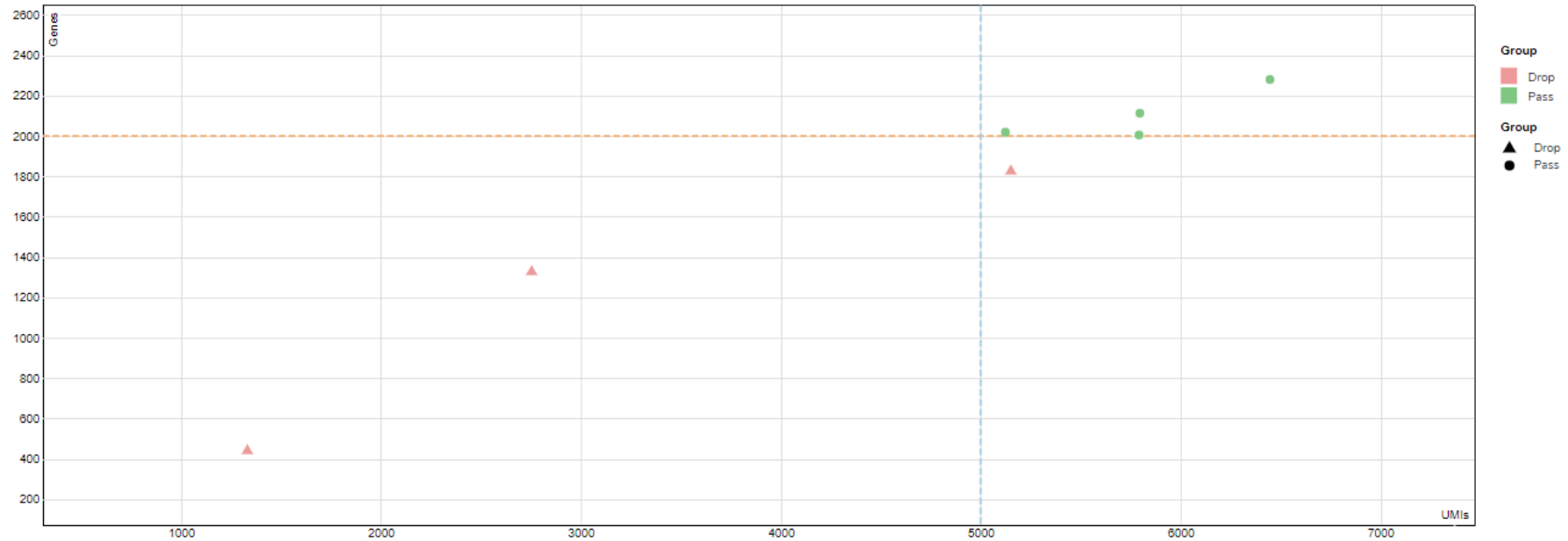
Step3. Check selected cell population

Main population are defined by UMI counts AND gene numbers

Number of observations



UMIs Genes Scatter2D Outliers



Cell QC

➤ Secondary cell QC

Step4. Define outliers by statistical distribution

Outliers are defined as cells certain median absolute deviation (MAD) away from the median in the following distribution.

UMI




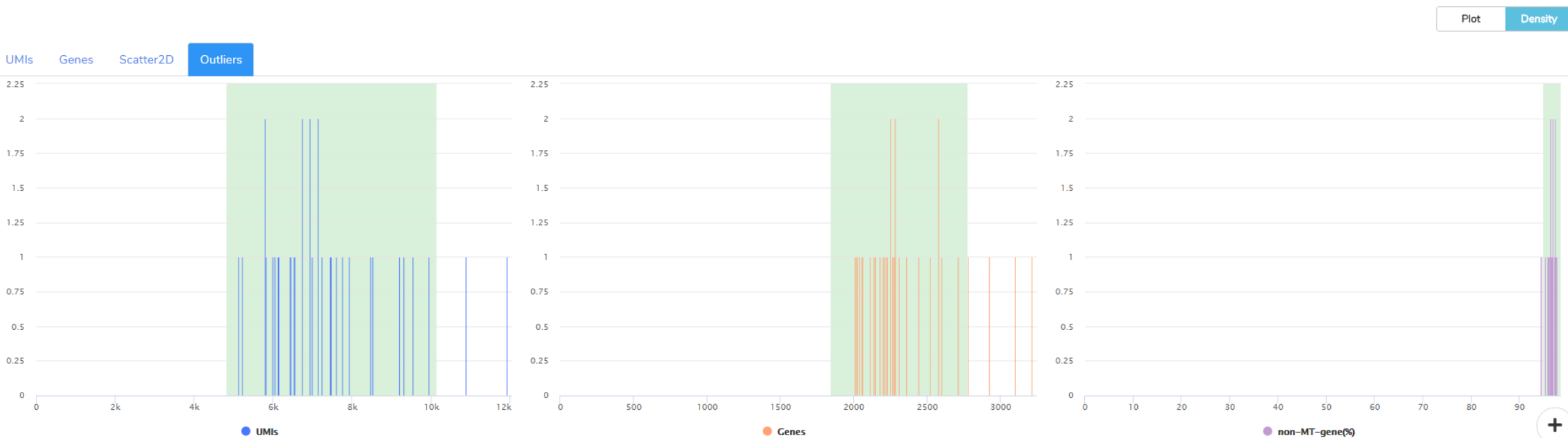
GeneNumber



non-MT-gene(%)



←  Save QC result



Cell QC

Databank

The management system of single-cell experiments can be used to pre-process raw sequencing files and link to other data analysis module.

[+ New Project](#)

Edit mode

Single-cell experiments

		Projects	Experiments	Species	Cells	Status	CellQC	Record	Brief	Normalization	Clustering
○	▶	PBMC	1	-	0	QC ⚠	pending	-	✍	🔒	🔒
○	▶	small_test	2	-	0	QC ⚠	pending	-	✍	🔒	🔒
○	▼	test	2	Hs	54	Normalization ⚠	finished	-	✍	📄	🔒
	▶	Control		Hs	27	QC ✅	🔧	📄	✍		
	▶	Drug		Hs	27	QC ✅	🔧	📄	✍		

Perform normalization

Success and new tips

Normalization

Normalization

Normalization will be performed for all cells in the project to remove unwanted technical bias.

Method

scran

Min average counts per gene

Default

Number of HVGs for RLE plot

Default

test

Project



54

Qualified cell numbers



Start

Click "Start" directly

Normalization

Normalization

Normalization will be performed for all cells in the project to remove unwanted technical bias.

Method

scran

Min average counts per gene

Default

Number of HVGs for RLE plot

Default

SAVE

CANCEL

test

Project



54

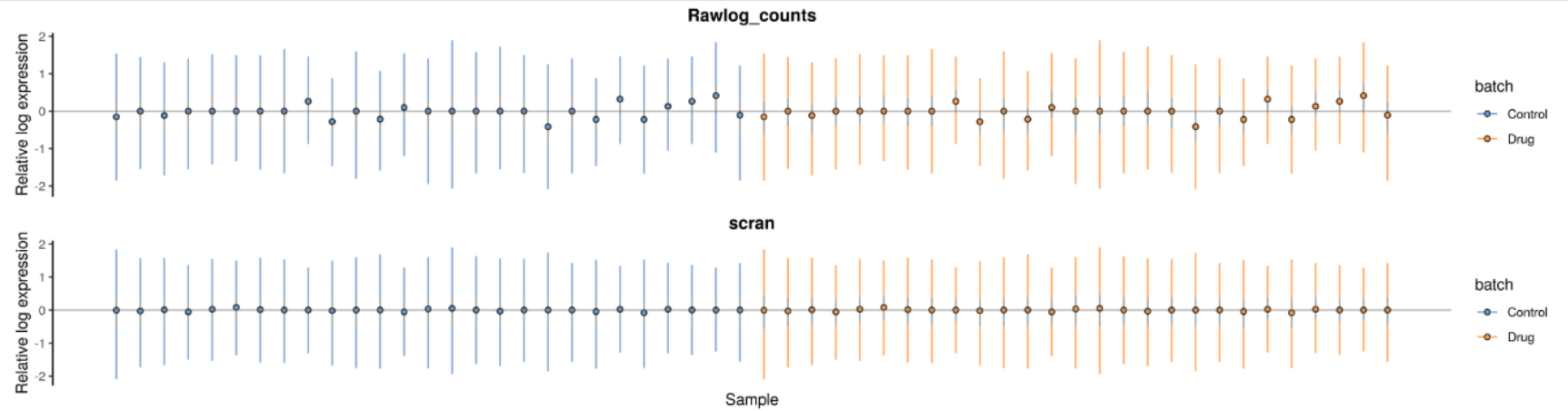
Qualified cell numbers

RLE plot

RLEplot

Size Factors

Min.	0.723
1st Qu.	0.8867
Median	0.9796
Mean	1
3rd Qu.	1.0877
Max.	1.373



Clustering

PBMC

Project

Cluster analysis

Clustering will be performed to uncover hidden subpopulations of cells.

Dimensionality Reduction

UMAP

Number of highly variable genes used

500

UMAP or tSNE

Clustering method

SC3

Number of clusters

3

DEG test method

MAST

MAST or wilcox

Cell-type classification

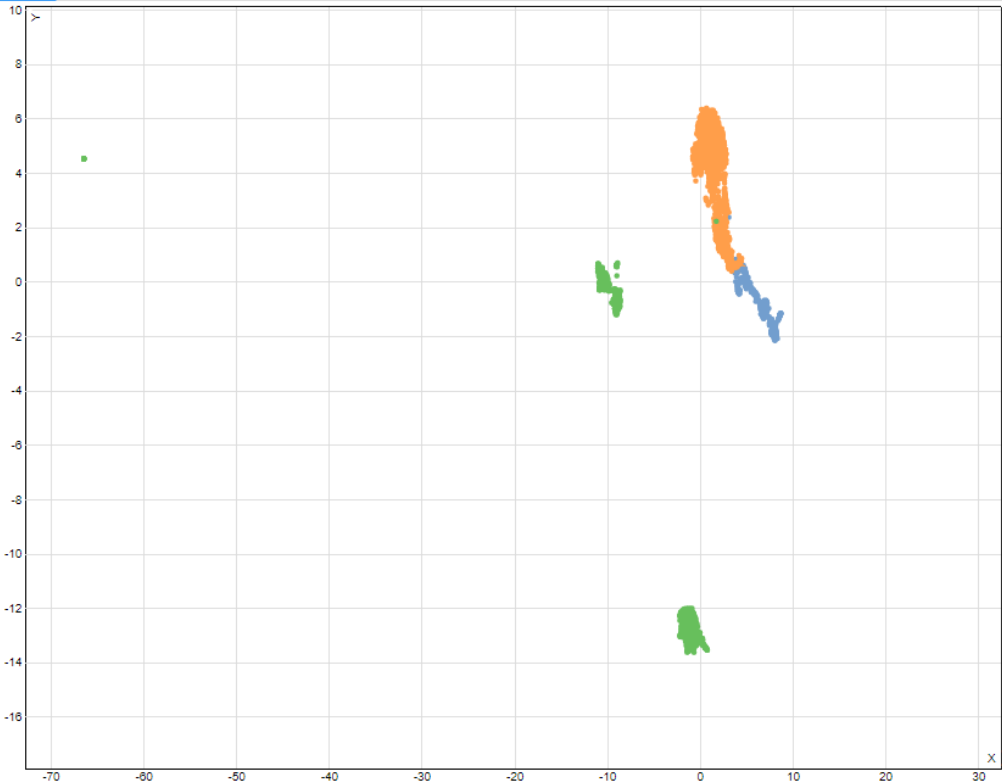
None

Start

Clustering

DEG preview

Cluster analysis



Cluster
1
2
3

1

Positive only

Rank	Gene	Adjusted P-value	Fold change(log)	Type
1	IL7R	0.00e+00	1.83e+00	Positive
2	TRAC	0.00e+00	1.40e+00	Positive
3	LDHB	0.00e+00	1.34e+00	Positive
4	TCF7	0.00e+00	1.19e+00	Positive
5	CD3E	0.00e+00	1.11e+00	Positive
6	NOSIP	0.00e+00	9.63e-01	Positive
7	LEF1	0.00e+00	9.36e-01	Positive
8	TRABD2A	0.00e+00	9.23e-01	Positive
9	CD3G	0.00e+00	9.09e-01	Positive
10	CD3D	0.00e+00	8.80e-01	Positive
11	SARAF	0.00e+00	8.67e-01	Positive
12	LTB	0.00e+00	8.61e-01	Positive
13	MAL	0.00e+00	8.60e-01	Positive
14	RCAN3	0.00e+00	8.52e-01	Positive
15	RPS12	0.00e+00	8.46e-01	Positive

1-15 of 911 rows

Previous 1 2 3 4 5 ... 61



Visualization

Visualization

A plenty of visualization tools can be perform on well-processed project.

PBMC

Vis

Select processed projects

-
Project



-
Clusters



Loading your project: PBMC...

It takes about 0.5~1 mins depending on cell numbers

Visualization

Visualization

A plenty of visualization tools can be perform on well-processed project.

PBMC

Project



3

Clusters



3,456

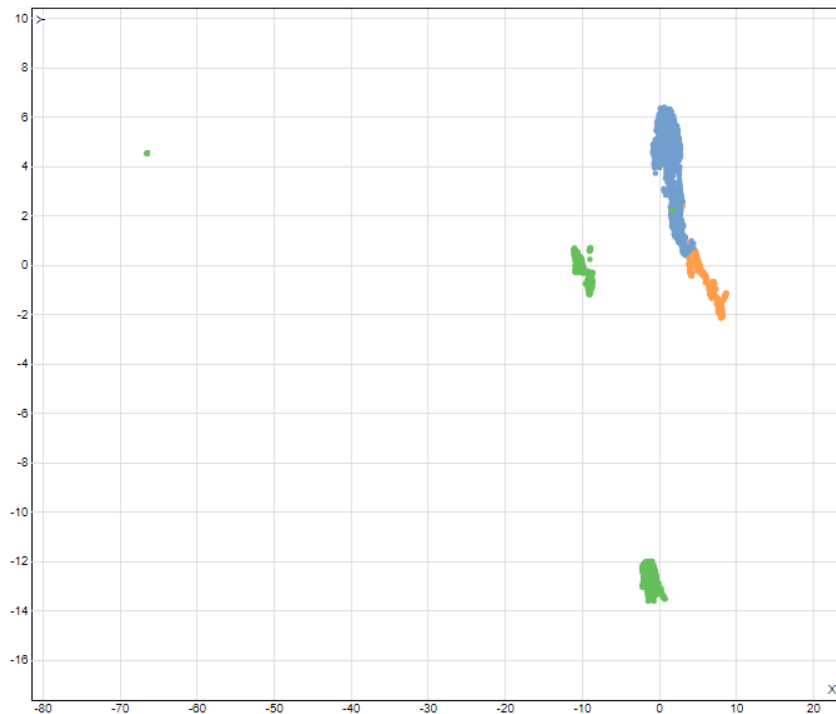
Qualified cell numbers



PBMC

Vis

Rename your cluster by DEGs



Cluster
■ T cell
■ 2
■ 3



DEGselector

Expression plot

Violin plot

GO analysis

Rank	Gene	Adjusted P-value	Fold change(log)	Type
1	IL7R	0.00e+00	1.83e+00	Positive
2	TRAC	0.00e+00	1.40e+00	Positive
3	LDHB	0.00e+00	1.34e+00	Positive
4	TCF7	0.00e+00	1.19e+00	Positive
5	CD3E	0.00e+00	1.11e+00	Positive
6	NOSIP	0.00e+00	9.63e-01	Positive
7	LEF1	0.00e+00	9.36e-01	Positive
8	TRABD2A	0.00e+00	9.23e-01	Positive
9	CD3G	0.00e+00	9.09e-01	Positive
10	CD3D	0.00e+00	8.14e-01	Positive

DEG filter

01-Cluster

T cell

Rename cluster

02-FoldChange

1.5

03-adjPvalue

0.1

04-Type

Positive only

Send to GO

Use these DEGs for GO analysis

1-10 of 462 rows

Previous 1 2 3 4 5 ... 47 Next



Visualization

Visualization

A plenty of visualization tools can be perform on well-processed project.

PBMC

Project



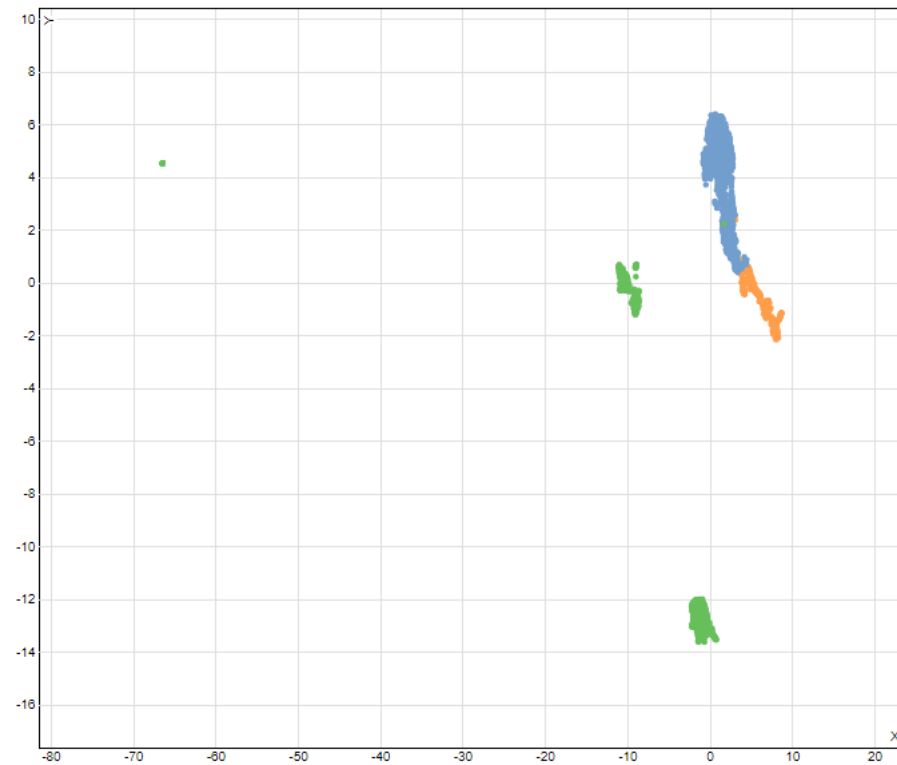
3

Clusters



PBMC

Vis Save

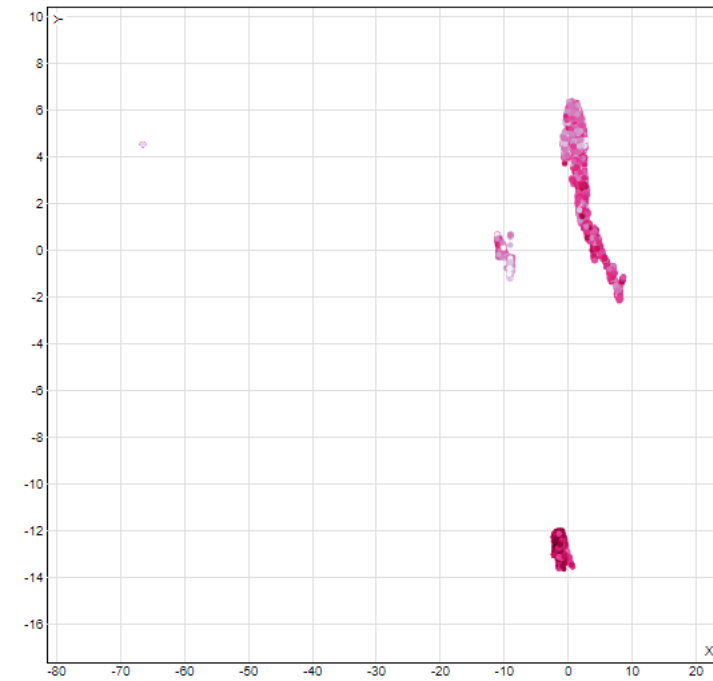


DEGselector

Expression plot

Violin plot

GO analysis



Visualization

Visualization

A plenty of visualization tools can be perform on well-processed project.

PBMC

Project



3

Clusters

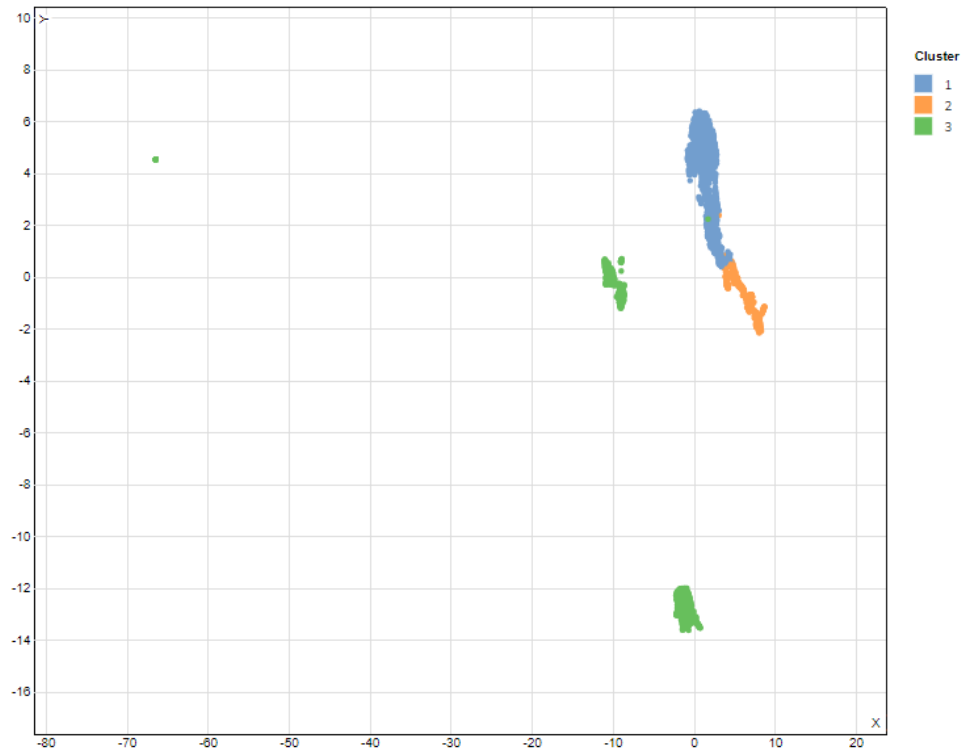


3,45

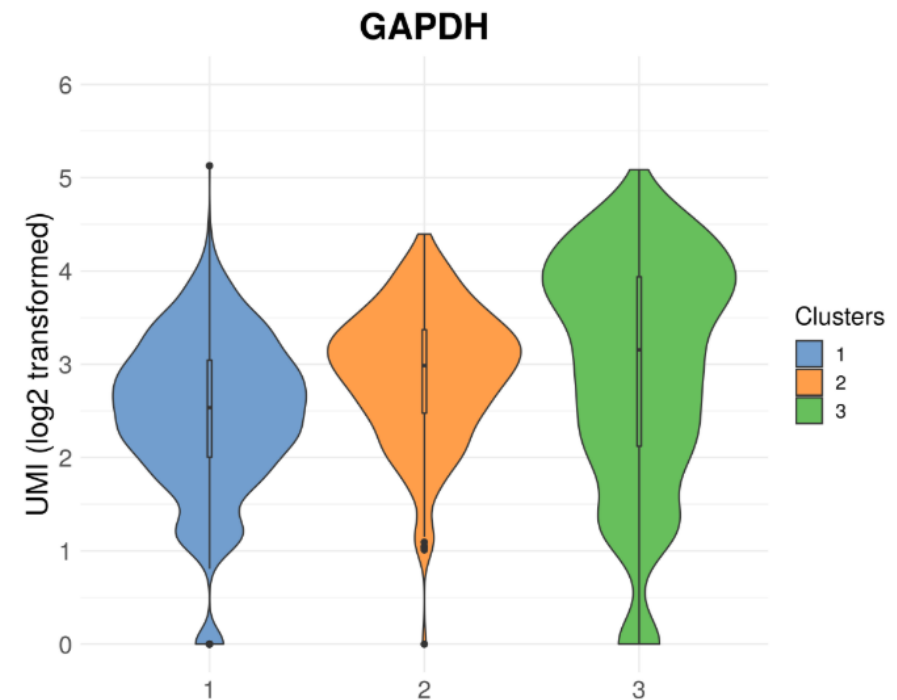
Qualified c

PBMC

Vis Save



DEGselector Expression plot Violin plot GO analysis



Visualization

Visualization

A plenty of visualization tools can be perform on well-processed project.

PBMC

Project



3

Clusters

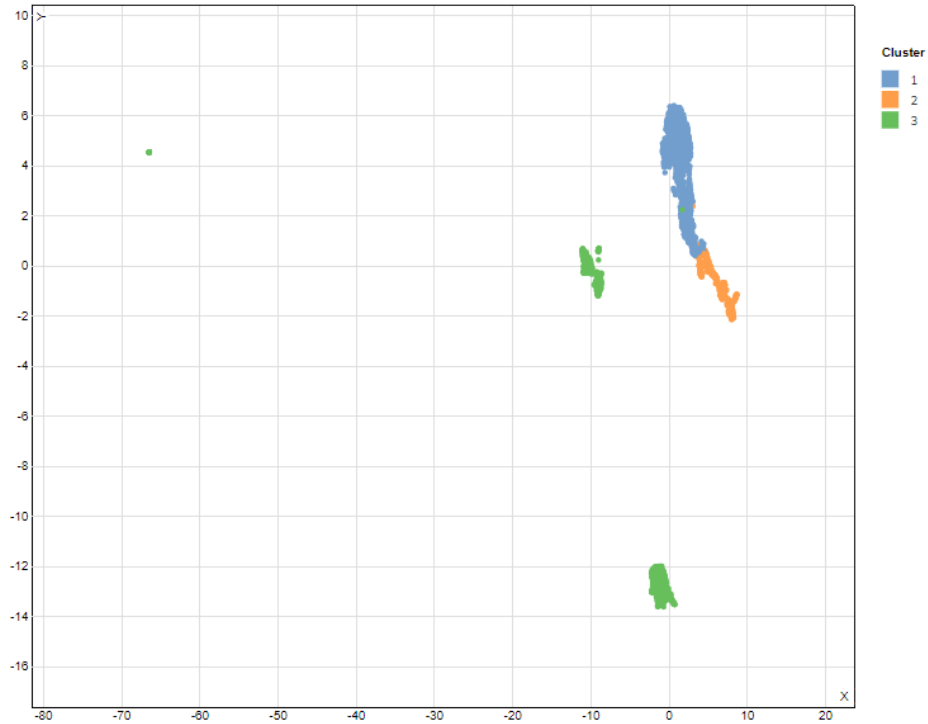


3,456

Qualified cell numbers

PBMC

Vis Save

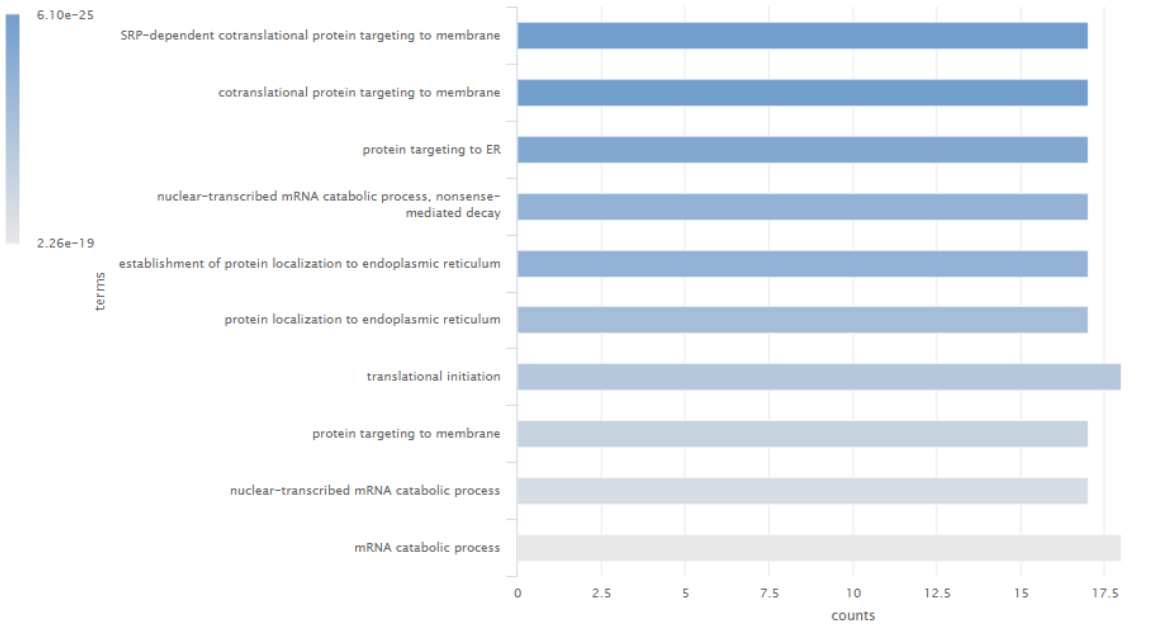


DEGselector

Expression plot

Violin plot

GO analysis



Contact



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